Breeding Groundnut for Drought Tolerance

By

Seltene Abady Tesfamariam

BSc Plant Sciences and MSc Plant Breeding (Haramaya University, Ethiopia)

A thesis submitted in fulfilment of the requirements for the degree of Doctor of Philosophy (PhD) in Plant Breeding

African Center for Crop Improvement

School of Agricultural, Earth and Environmental Sciences

College of Agriculture, Engineering and Science

University of KwaZulu-Natal

Republic of South Africa

January 2021

Thesis abstract

Groundnut (*Arachis hypogaea* L.) is one of the world's most important grain legumes for its quality edible oil and higher protein content. It is the major cash crop in the semiarid tropics where production is mainly under rain-fed condition. Recurrent drought is the major cause of low yields of groundnut in sub-Saharan Africa (SSA). Farmers in SSA grow unimproved groundnut varieties which are vulnerable to drought stress and insect pests and disease attack. Therefore, there is need to develop drought tolerant, locally adapted and high yielding groundnut varieties for sustainable production of the crop. Breeding groundnut for drought tolerance requires inexpensive, reproducible and high throughput screening systems. Understanding the agro-morphological, physiological and molecular bases of drought tolerance aid in the development and release of new varieties with drought tolerance. Therefore, the objectives of this study were: (1) to assess farmers' perceived production constraints, variety choice, and preferred traits of groundnut in eastern Ethiopia to guide future groundnut variety development and release, (2) to determine drought tolerance, kernel and fodder yield and quality amongst diverse groundnut genotypes for direct production or breeding, (3) to assess the genetic diversity and population structure among 100 groundnut genotypes using agronomic traits and high density single nucleotide polymorphism (SNP) markers, (4) to determine the combining ability effects of eight selected drought tolerant groundnut parental lines and their F_2 families under drought-stressed (DS) and non-stressed (NS) conditions to select best performing parents and families for drought tolerance breeding.

In the baseline work, participatory rural appraisal studies were conducted in two major groundnut-producing districts (Babile and Fedis) in eastern Ethiopia. The following data were collected involving 150 participant farmers: demographic descriptors, groundnut farming system, farmers' knowledge about improved groundnut varieties, constraints to groundnut production, market access, and varietal trait preference. Chi-square and t-test analyses were conducted to determine statistical significance among the parameters across districts. Participant farmers identified drought stress (reported by 90% of respondents), poor soil fertility (88%), poor seed supply systems (67%), pre-harvest diseases (root rot and leaf spot) (59.5%), low yielding varieties (52.5%), low access to extension services (41.5%), low access to credit (21.5%) and limited availability of improved varieties (18.5%) as the major groundnut production constraints. The study identified the following farmer-preferred traits: high shelled yield (reported by 27.67% of respondents), early maturity (16.84%), and tolerance to drought stress (13.67%), market value (11.17%), good grain quality (10%), adaptability to local growing conditions (5.8%), and resistance to diseases (5.17%). Therefore, the aforementioned production constraints and farmer-preferred traits are key drivers that need to be integrated into groundnut breeding and variety release programs in eastern Ethiopia.

In the second study, 100 groundnut genotypes were evaluated at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)/India during 2018/19 and 2019/20 under drought-stressed (DS) and non-stressed (NS) conditions using a 10 x 10 alpha lattice design with two replications. Seed and haulm samples collected at physiological maturity from DS and NS experiments to estimate Kernel and haulm quality parameters using near infrared spectroscopy (NIRS). Data were collected on kernel yield (KY), oil content (OC), oil yield (OY), protein content (PC), palmitic acid content (PAC), stearic acid content (SAC), oleic acid content (OAC) and linoleic acid content (LAC), haulm yield (HY) and fodder quality parameters such as the contents of dry matter (DM), ash, nitrogen (NC), neutral detergent fiber (NDFDM), acid detergent fiber (ADFDM), acid detergent lignin (ADLDM), *in vitro* digestibility (IVOMD) and metabolizable energy (ME). Data were subjected to parametric and non-parametric statistical analyses. Combined analysis of variance revealed significant ($P< 0.05$) genotype differences for all assessed traits. Genotype × water regime interaction effects were significant for KY, OC, ash content, NC, NDFDM and ADLDM. Kernel yield positively and significantly ($P<0.05$) correlated with oil yield ($r = 0.99$), LAC ($r = 0.13$), ash ($r = 0.32$), NDFDM ($r = 0.54$) under DS condition. Haulm yield was positively and significantly ($P<0.05$) correlated with OC ($r = 0.24$), NDFDM ($r = 0.19$), ADFDM ($r = 0.18$) and ADLDM ($r = 0.17$) under DS condition. Cluster analysis grouped the test genotypes into 12 distinct genetic groups. The study identified genotypes, ICGV 10178, ICGV 01260, ICGV 06175 and ICGV 10379 with high kernel and haulm yields, and CGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063, with high oleic acid content. Furthermore, genotypes, ICGV 7222, ICGV 10143, ICGV 6040, ICGV 03042, ICGV 06175, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, were selected with relatively better drought tolerance. The selected genotypes are recommended for further breeding and variety release under drought stress environments.

In the third study, 99 of the test genotypes were profiled with 16, 363 SNP markers. The following phenotypic data collected during the second study were used for complementing the SNP data: days to 50% flowering (DF), SPAD chlorophyll meter reading (SCMR), Plant height (PH), number of primary branches (PB), specific leaf area (SLA), leaf relative water content (LRWC), total biomass (TBM), pod yield (PY), harvest index (HI), hundred seed weight (HSW), shelling percentage (SHP) and kernel yield per plant (KY) and days to maturity (DM). Analysis of variance, Pearson's correlation coefficient, principal component and stress tolerance index were calculated. Pod yield per plant (PY), seed yield per plant (SY) and harvest index (HI) were significantly ($p < 0.05$) affected by genotype × environment interaction effects. Genotypes, ICGV 07222, ICGV 06040, ICGV 01260, ICGV 15083, ICGV 10143, ICGV 03042, ICGV 06039, ICGV 14001, ICGV 11380 and ICGV 13200, exhibited higher pod yield under both drought-stressed and non-stressed conditions. Pod yield exhibited significant ($p \leq 0.05$) correlation with SY, HI and total biomass (TBM) under both test conditions. Based on the principal component analysis, PY, SY,

HSW, SHP and HI contributed maximum variability for yield under the two water regimes. Hence, selection of these traits could be successful for screening of groundnut genotypes under drought-stressed and non-stressed conditions. Model-based population structure analysis grouped the studied genotypes into three sub-populations, whilst cluster analysis resolved the collections into five clusters based on pedigree, selection history, and market type. Cluster III and Cluster V consisted of the Spanish bunch types, late leaf spot (*Phaeoisariopsis personata)* and rust (*Puccinia arachidis*) resistant, and drought-tolerant genotypes. Analysis of molecular variance revealed that 98% of the total genetic variation was attributed to among individuals, while 2% of the total variance was due to variation among the subspecies. The genetic distance between the Spanish bunch and Virginia bunch types ranged from 0.11 to 0.52. Genotypes, ICGV 13189, ICGV 95111, ICGV 14421, and ICGV 171007, were selected for further breeding based on their wide genetic divergence. Data presented in this study will guide groundnut cultivar development emphasizing economic traits and adaptation to water-limited agro-ecologies including in Ethiopia.

The fourth study examined the combining ability effects of eight selected drought tolerant groundnut parental lines and their F_2 populations under drought-stressed (DS) and non-stressed (NS) conditions under glasshouse and field conditions at ICRISAT in 2020 rainy season. Data were collected on days to 50% flowering (DF), number of primary branches (PB), plant height (PH) (cm), SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) (cm^2/g), pod yield (PY) (g $plant^{-1}$), shelling percentage (SHP) (%), kernel yield (KY) (g $plant^{-1}$), total biomass (TBM) (g $plant^{-1}$) and harvest index (HI) (%). ICGV 10178 was the best combiner genotype to increase SCMR, PY, SHP, KY, TBM and HI and, reduce SLA. The general combining ability (GCA) effects of parents were significant ($P<0.05$) for all assessed traits under all testing conditions except for PB under DS and NS conditions in the glasshouse. The specific combining ability (SCA) effects of progenies were significant ($P<0.05$) for all assessed traits except for PH across all testing environments and PB under field condition. Genotype ICGV 10178 was the best general combiner with positive contribution to SCMR, PY, SHP, KY, TBM and HI and reduced SLA. Crosses, ICGV 10178 X ICGV 11369, ICGV 10373 x ICGV 15083, ICGV 98412 x ICGV 15094 and ICGV 10178 X ICGV 98412, were the best specific combiners for enhanced pod yield and drought tolerance. Higher GCA: SCA rations were recoded for PY, KY and TBM across all the testing environments suggesting the predominant role of additive genes conditioning the inheritance of these traits. Therefore, the above new families are recommended for genetic advancement through single seed descent selection method to develop improved pure line groundnut varieties with high pod yield and drought tolerance.

Declaration

I, Seltene Abady Tesfamariam, declare that:

1. The research reported in this thesis, except where otherwise indicated, and is my original research.
2. This thesis has not been submitted for any degree or examination at any other University.
3. This thesis does not contain other persons' data, pictures, graphs or other Information, unless specifically acknowledged as being sourced from other persons.
4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

a. Their words have been re-written but the general information attributed to them has been referenced.

b. Where their exact words have been used, then their writing has been placed in italics and inside quotation marks, and referenced.

5. This thesis does not contain text, graphics or tables copied and pasted from the Internet, unless specifically acknowledged, and the source being detailed in the thesis and in the reference sections.

Signed 

.....

Seltene Abady Tesfamariam

As the candidate's supervisors, we agree to the submission of this thesis:

.....

Prof. Shimelis Hussein (Supervisor)

.....

Dr. P. Janila (Co-Supervisor)

Acknowledgments

I would like to express my heartfelt and sincere gratitude to my supervisor, Prof. Hussein Shimelis, Chair of Crop Science and Deputy Director for the African Center for Crop Improvement (ACCI) at the University of KwaZulu-Natal (UKZN) in South Africa, for his consistent guidance and invaluable suggestions and comments throughout the thesis work.

I would like to express my sincere gratitude to my co-supervisor, Dr. P. Janila, Principal Scientist, Groundnut Breeding, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)/India for providing me an opportunity to conduct my research at ICRISAT and for her consistent support throughout the study.

I am grateful to the following individuals and institutions who contributed to the success of the research:

- The Consultative Groups on International Agricultural Research's (CGIAR) Research Program on Grain Legume and Dry Land Cereals (CRP-GLDC) are sincerely acknowledged for providing the research fund through the Organization of the Petroleum Exporting Countries (OPEC) Fund for International Development (OFID) in Groundnut Breeding Program at ICRISAT/India.
- The groundnut Breeding Program of ICRISAT/India is sincerely acknowledged for providing excellent research facilities and the germplasm used in the study.
- UKZN is sincerely thanked for the opportunity to peruse my PhD studies in Plant Breeding.
- The International Livestock Research Institute (ILRI) based at ICRISAT/India is acknowledged for the assistance in the analysis of groundnut haulms for fodder quality and digestibility.
- Crop physiology department based at ICRISAT/India is sincerely recognized for providing research facilities for measuring physiological parameters.
- The Ethiopian Institute of Agricultural Research is acknowledged for financial support through the National Groundnut Research Program.
- The International foundation for Science (IFS) is sincerely acknowledged for providing research fund through the grant number I-3-C-6245-1.
- Haramaya University, is acknowledged for granting me study leave and the overall research support.

- Dr. Abdi Mohammed, Mr. Desalegn Yadata, Mis Eftihom Negera, Mis Azeb Tegenu, Mr. Abiyot, Mr. Nebiyu and Mr. Kaba Kebede of Haramaya University are sincerely appreciated for their technical support during the study.
- Dr. Sunil Chaudhari, Dr. Dnyaneshwar Deshmukh, Mr. Surendra S. Manohar, Mr. Ankush Wankhade, Dr. Shasidhar Yaduru, Mr. V. Papaiah, Mr. B. Abhishak, Mr. K. Ranjith and Mrs B. Aparena of ICRISAT/India Groundnut Breeding Program are sincerely thanked for their technical support during my research trials at ICRISAT/India.
- Ms. R. Rebecca and Mr. K. Pratap from ICRISAT's Learning System Unit are thanked for their support throughout the study.
- Mrs Rowelda Donnelly and Lyndre Joan Anderson of UKZN's ACCI are sincerely acknowledged for administrative support throughout the study.
- Dr. Jacob Mashillo and Dr. Admire Shayanowako from the University of KwaZulu-Natal are sincerely thanked for their support and guidance during the write up of some of the chapters.
- My family, including Etabez, Abenezer, Abady, Tsega Tewelde, Zemicael Wahsom, Genet Abady, Embeba Abady, Hana Abady, Yared Abady, Roza Abady and Lula Abady are sincerely thanked for their appreciation and encouragement.
- Praise to God who has made everything happen.

Dedication

This thesis is dedicated to my beloved wife Etabez Abebe and my son Abenezer Seltene.

Publications emanating from this thesis

Chapter-1

Seltene Abady, Hussein Shimelis, Pasupuleti Janila and Jacob Mashilo (2019). Groundnut improvement in sub-Saharan Africa: A review, Acta Agriculturae Scandinavica, Section B -Soil & Plant Science**,** 69 (6): 528–545, Doi: https://doi.org/10.1080/09064710.2019.1601252

Chapter-2

Seltene Abady, Hussein Shimelis and Pasupuleti Janila (2019). Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding. Journal of Crop Improvement, 33 (4): 505–521, Doi: https://doi.org/10.1080/15427528.2019.1625836

Chapter-3

Seltene Abady, Hussein Shimelis, Pasupuleti Janila, Jacob Mashilo, Sunil Chaudhari and Surendra S. Manohar (2021). Assessment of the genetic diversity of groundnut (Arachis hypogaea L.) genotypes for kernel yield, and oil and fodder quantity and quality under drought conditions. Crop Science. 2021: 1-18, Doi: https://doi.org/10.1002/csc2.20483

Contents

Thesis introduction

Background

Groundnut or peanut (*Arachis hypogaea* L., 2n = 4x = 40, AABB) is one of the world's most important grain legume crops. It is predominantly self-pollinating crop and evolved from a hybridization between two diploid species, *A*. *duranensis* (A genome donor), and *A*. *ipaensis* (B genome) followed by a spontaneous chromosomal duplication (do Nascimento et al. 2018). It is a major commodity crop grown in the semi-arid tropics where it is mainly cultivated under rainfed condition. Groundnut has wide adaptation and grows under varied soil and climatic conditions spanning between 40° N and S latitudes (Acur et al. 2020). Globally, groundnut is cultivated on 29.59 million ha, with an annual total production of 48.75 million tons (FAOSTAT 2018). The leading groundnut producing countries in the world are India (15.98%), China (15.20%), Nigeria (13.09%), Sudan (10.57%) and Senegal (3.75%) (FAOSTAT 2020).

Groundnut grains are a rich source of high-quality edible oil varying from 45-56%, easily digestible protein of 12-36% and carbohydrates of 10-20% (Yol et al. 2017; Sarvamangala et al. 2011). Also the grains are a rich source of vitamins such as A, D, E and K and minerals, including calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium (Jithender et al. 2019; Nigam, 2014). Groundnut haulms is an excellent source of fodder for livestock (Samireddypalle et al. 2017). Groundnut improves the soil nitrogen content through nitrogen fixation that makes it an important component for crop rotation (Ajeigbe et al. 2014). Therefore, the multiple uses of groundnut make it an excellent food and cash crop for domestic, regional and international markets.

Drought stress is one of the leading constraints to groundnut production globally. Drought stress associated with seasonal fluctuation of rainfall and as part of climate change, is currently the leading threat to the world's food production and supply (Mohammed et al. 2018; Budak *et al*, 2013). In sub-Saharan Africa (SSA), more than 80% of the smallholder farmers are engaged in rain-fed crop production systems where rainfall is low and erratic (Muzari *et al.,* 2012). Rainfall variability is likely to increase in SSA over the coming decade, impacting on food security (Ngcamu and Chari 2020; OECD/FAO. 2016). For example, Mekonnen et al. (2017) reported considerable rainfall variability in Ethiopia which has been significantly affecting rainfed agriculture. In Eastern Ethiopia, where groundnut is a major crop, drought stress occurring during flowering stage is a key abiotic constraint (Abady et al. 2019).

Groundnut production and constraints in Ethiopia

Groundnut is widely grown in the warm lowland areas of Ethiopia. The major groundnut producer regions in Ethiopia are Oromia (contributing to 59.2% of the total national production), Benshangul-Gumuz (24.83%), Amhara (7.43%), and Harari (3.29%) (CSA, 2018). The total land coverage and national mean yield of groundnut in Ethiopia are estimated to be 80, 842 ha and 1.76 tons/ha, respectively (CSA, 2018). Babile, Fedis and Gursum situated in eastern Ethiopia are the leading districts in groundnut production in the country. In Ethiopia, groundnut is commonly produced for food, cash income and animal feed (EIAR, 2017).

Twenty improved groundnut varieties were released in Ethiopia along with their improved cultural practices. In the past groundnut research focused on germplasm evaluation using introductions from India, Mali and Malawi. During the last 33 years, marked progress had been made in groundnut genetic improvement for yield (Hagos *et al.*, 2012). Yusuf *et al*., (2017a) reported significant increase in grain yield, 100 seed weight, and harvest index attributable to genetic gain in groundnut improvement in Ethiopia. The national mean yield is 1.796 tons/ha, and the total area under groundnut production is 80,841.57 ha (CSA 2018).

Groundnut productivity in Ethiopia is low compared to the potential yield reaching up to 2.4 t/ha elsewhere. The low yield level is attributed to several biotic, abiotic and socio-economic factors. Drought stress, poor soil fertility, lack of access to improved seed, lack of improved varieties and diseases are the most important groundnut constraints in the country (Abady et al. 2019; Chala *et al*. 2014). Further, there is a lack of modern production and post-harvest technologies. The main focus in groundnut research and development in Ethiopia includes developing modern varieties that are high yielding, adapted to the growing environments, and resilient to multiple stresses such as drought stress, new insect pests and diseases (EIAR 2017).

Over the past decades extreme variability was witnessed in the amount of rainfall received and its distribution globally including in Ethiopia. Production of sustainable and reliable food supply is challenged by temporal and spatial variation in total rainfall and its distribution (Mohammed et al. 2018). This has negatively affected groundnut production which is largely practiced in arid and semi-arid regions of the country. In these areas moisture stress occurs during the main cropping season leading to significant yield loss or crop failure affecting the livelihoods of millions of smallholder farmers.

Rationale of the research

Drought stress is one of the major production constraints in the major groundnut production areas in Ethiopia. Breeding for drought tolerant and early maturing groundnuts is considered to be the most economic and sustainable means to cope with the drought problem (Desmae et al. 2017). A limited number of introduced groundnut varieties were released for cultivation in Ethiopia. However, these varieties are late maturing and low yielding, and were not bred for drought tolerance (Ministry of Agriculture 2019). In addition, there is a need to develop and deploy dual-purpose groundnut cultivars with high kernel and haulm yields and associated quality parameters with drought tolerance for production in mixed crop-livestock farming systems. In the past there was no dedicated groundnut breeding program that aimed at breeding genotypes with high kernel and haulm yields with quality attributes under drought stress environments. There is limited study on the genetic diversity in general and drought tolerance and earliness of groundnut genotypes in particular in Ethiopia using diverse genetic pools. Therefore, the groundnut improvement in Ethiopia should begin on screening of genetically diverse drought tolerant and early maturing groundnut genotypes to select elite lines for genetic improvement and variety release. Recently, Yusuf et al. (2017b) studied the genetic diversity in using local groundnut germplasm in Ethiopia using agro-morphological markers and the result revealed that there was a small range of genetic diversity among the tested genotypes. This requires broadening the genetic basis of the crop for breeding.

Understanding the magnitude of genetic variation and genetic interrelationship among candidate genotypes using agro-morphological traits and molecular analysis is crucial for parental choice for effective breeding. This will allow for broadening the genetic basis of breeding populations in plant breeding programs. Breeding groundnut for drought tolerance requires inexpensive, reproducible and high throughput screening systems. Up-to-date and well-described production constraints and prioritized traits of groundnut are key drivers for developing new cultivars. Participatory rural appraisal is one of the most effective tools in capturing farmers' perceptions regarding their production constraints, variety choice and trait preferences. This should enable release of high-performing cultivars possessing suitable product profiles relevant to farmers and their value chains and will enhance the adoption rate of improved groundnut cultivars in the region.

Aim

The aim of the study was to develop farmer preferred, drought tolerant, dual-purpose and high yielding groundnut genotypes in Ethiopia

Research objectives

1. To assess farmers' perceived production constraints, variety choice, and preferred traits of groundnut in eastern Ethiopia to guide future groundnut variety development and release.
2. To determine drought tolerance, kernel and fodder yield and quality amongst diverse groundnut genotypes for direct production or breeding.
3. To assess the genetic diversity and population structure among 100 groundnut genotypes using agronomic traits and high density single nucleotide polymorphism (SNP) markers.
4. To determine the combining ability effects of eight selected drought tolerant groundnut parental lines and their F_2 families under drought-stressed (DS) and non-stressed (NS) conditions to select best performing parents and families for drought tolerance breeding.

Research hypothesis

I. Farmer's perception and their indigenous knowledge on drought copping mechanism have great implication for breeding groundnut varieties with better performance.
II. There are high heritability and positively correlated drought tolerant traits that can be used for effective selection in drought tolerant variety development.
III. There is valuable genetic diversity in the test groundnut genotypes for breeding for drought tolerance and earliness.
IV. The selected groundnut parents and crosses exhibit good combining ability for drought tolerance, yield and yield-related traits under drought stressed and non-stressed conditions for genetic advancement.

Outline of the thesis

This thesis consists of five different chapters in accordance with the number of objectives (see Table 1). Chapter 1 is written as a separate review paper, while chapters 2 to 5 are written as discrete research papers, each following the format of a stand-alone research paper (whether or not the chapter has already been published) followed by a general overview and implications of findings from the study. There are some overlaps and unavoidable repetitions of references and some introductory information between chapters. Chapter 1 was published in Acta Agriculturae Scandinavica, Section B -Soil & Plant Science doi: 10.1080/09064710.2019.1601252. Chapter 2 was published in Journal of Crop Improvement doi: 10.1080/15427528.2019.1625836 Chapter 3 was published in Crop Science. 2021; 1–18. https://doi.org/10.1002/csc2.20483.

Table 1. Thesis structure

Chapter	Title
-	Thesis introduction
1	Groundnut improvement in sub-Saharan Africa- A review
2	Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding
3	Assessment of the genetic diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield, oil and haulm quantity and quality under moisture stress conditions
4	Assessment of the genetic diversity and population structure of groundnut germplasm collections using phenotypic traits and SNP markers: implications for drought tolerance breeding
5	Combining ability analysis of groundnut (*Arachis hypogaea* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions
-	General overview and implications of the study

References

Abady, S., H. Shimelis and P. Janila. 2019. Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding. Journal of Crop Improvement, 33 (4): 505–521, Doi: https://doi.org/10.1080/15427528.2019.1625836

Acur, A., R.S. Arias, S. Odongo, S. Tuhaise, J. Ssekandi, J. Adriko, D. Muhanguzi, S. Buah and A. Kiggundu. 2020. Genetic diversity of aflatoxin-producing *Aspergillus flavus* isolated from selected groundnut growing agro-ecological zones of Uganda. BMC Microbiology 20: 252, Doi: https://doi.org/10.1186/s12866-020-01924-2

Ajeigbe, H.A., F. Waliyar, C.A. Echekwu, K. Ayuba, B.N. Motagi, D. Eniayeju and A. Inuwa. 2014. A farmer's guide to groundnut production in Nigeria. Patancheru 502 324, Telangana, India: International Crops Research Institute for the Semi-Arid Tropics. Pp. 36

Chala, A., B. Abate, M. Taye, A. Mohammed, T. Alemu and H. Skinnes. 2014. Opportunities and constraints of groundnut production in selected drylands of Ethiopia. DCG Report No.74. Drylands Coordination Group

Budak H., M. Kantar and K.Y. Kurtoglu. 2013. Drought tolerance in modern and wild wheat. The Scientific World Journal 10: 548246, Doi: https://doi.org/10.1155/2013/548246

Central Statistical Agency (CSA). 2018. Agricultural sample survey 2017/18: Report on area and production of major crops (private peasant holdings, main season), Vol.1. CSA, Addis Ababa

Desmae, H., P. Janila, M.K. Okori, B.N. Pandey, E. Motagi, O. Monyo, D. Mponda, D. Okello, C. Sako, C. Echeckwu, R. Oteng-Frimpong, A. Miningou, C. Ojiewo and R.K. Varshney. 2017. Genetics, genomics and breeding of groundnut (*Arachis hypogaea* L.). Plant Breeding 138:425–444, Doi: https://doi.org/10.1111/pbr.12645

do Nascimento, E.F.M.B., B.V. dos Santos, L.O.C. Marques, P.M. Guimarães, A.C.M. Brasileiro, S.C.M. Leal-Bertioli, D.J. Bertioli and A.C.G. Araujo. 2018 The genome structure of Arachis hypogaea (Linnaeus, 1753) and an induced Arachis allotetraploid revealed by molecular cytogenetics. Comparative Cytogenetics 12:111–140, Doi: https://doi.org/10.3897/CompCytogen.v12i1.20334

Ethiopian Institute of Agricultural Research (EIAR). 2017. Oil Seeds Research Strategy (2016-2030). http://www.eiar.gov.et

FAOSTAT. 2018. "Food and Agriculture Organization of the United Nations Database of Agricultural Production." FAO Statistical Databases, Accessed 25 December 2020. http://www.fao.org/faostat/

FAOSTAT. 2020. Food and Agriculture Organization of the United Nations Database of agricultural production. FAO Statistical Databases. Available at *http*: www.fao.org/faostat/ (accessed 14 January 2020)

Hagos, F., H. Zeleke and B. Woyossa. 2012. Genetic gain in yield and yield related traits of groundnut (*Arachis hypogea* L.) in Central Rift Valley of Ethiopia. East African Journal of Sciences 6: 125-13

Jithender, B., K. Upendar, C. Nickhil and P.J. Rathod. 2019. Nutritional and anti-nutritional factors present in oil seeds: An overview. International Journal of Chemical Studies. 7: 1159-1165

Mekonnen A.D., P.R. David and B. Woldeamlak. 2017. Teleconnections between Ethiopian rainfall variability and globalSSTs: observations and methods for model evaluation. Meteorology and Atmospheric Physics 129:173–186, Doi: https://doi.org/10.1007/s00703-016-0466-9

Ministry of Agriculture. 2019. "Crop Variety Register Issue No. 22. Plant Variety Release." Protection and Seed Quality Control Directorate. MoANRs, Addis Ababa, Ethiopia

Mohammed, Y., F. Yimer, M. Tadesse and K. Tesfaye, 2018. Variability and trends of rainfall extreme events in north east highlands of Ethiopia. International Journal of Hydrology 2: 594-605, Doi: https://doi.org/10.15406/ijh.2018.02.00131

Muzari, W., W. Gatsi and S. Muvhunzi. 2012. The Impacts of technology adoption on smallholder agricultural productivity in Sub-Saharan Africa: A Review. Journal of Sustainable Development 5: 69-77

Ngcamu, B.S. and F. Chari. 2020. Drought influences on food insecurity in Africa: A Systematic literature review. International Journal of Environmental Research and Public Health 2020:1-17, Doi: https://doi.org/10.3390/ijerph17165897

Nigam, S.N. 2014. Groundnut at a glance. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, A.P. 502 324, India. Pp 121

OECD/FAO. 2016. "Agriculture in Sub-Saharan Africa: Prospects and challenges for the next decade", inOECD-FAO Agricultural Outlook 2016-2025, OECD Publishing, Paris. DOI: http://dx.doi.org/10.1787/agr_outlook-2016-5-en

Samireddypalle A., O. Boukar, E. Grings, C.A. Fatokun, P. Kodukula, R. Devulapalli, I. Okike and M. Blümmel. 2017. Cowpea and groundnut haulms fodder trading and its lessons for multidimensional cowpea improvement for mixed crop livestock systems in West Africa. Frontiers in Plant Science 8:30, Doi: https://doi.org/10.3389/fpls.2017.00030

Sarvamangala, C., M.V.C. Gowda and R.K. Varshney. 2011. Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut (*Arachis hypogaea* L.). Field Crops Research 122: 49-59

Yol, E., R. Ustun, M. Golukcu and B. Uzun. 2017. Oil content, oil yield and fatty acid profile of groundnut germplasm in Mediterranean climates. Journal of the American Oil Chemists' Society 94:787: 804, Doi: https://doi.org/10.1007/s11746-017-2981-3

Yusuf, Z., H. Zeleke, W. Mohammed, S. Hussein and A. Hugo. 2017a. Genetic progress for yield, yield components and other agronomic characters of groundnut (*Arachis hypogea* L.) cultivars in eastern Ethiopia. International Journal of Plant Breeding and Crop Science 4: 237-242

Yusuf, Z., H. Zeleke, W. Mohammed, S. Hussein and A. Hugo. 2017b. Genetic divergence and association of traits among groundnut (*Arachis hypogaea* L.) genotypes in Ethiopia based on agromorphological markers. American Journal of Plant Biology 2: 8-18, Doi: https://doi.org/10.11648/j.ajpb.s.2017020501.12

Chapter 1

Groundnut improvement in sub-Saharan Africa: A review

Abstract

Groundnut (*Arachis hypogaea* L.) is a multi-purpose legume crop widely cultivated in sub-Saharan Africa (SSA). However, yield levels of the crop have remained relatively low in SSA owing to a range of biotic, abiotic and socio-economic constraints. A dedicated groundnut improvement program integrating new tools of and methodologies to breed varieties suitable for current and emerging agro-ecologies and market needs is essential for enhanced and sustainable groundnut production in SSA. The objective of this review was to highlight breeding progress, opportunities and challenges on groundnut improvement with regard to cultivar development and deployment in SSA in order to guide future improvement of the crop. The review analysed the role of new tools in breeding such as, high-throughput and automated phenotyping techniques, rapid generation advancement, single seed descent approach, marker-assisted selection, genomic selection, next-generation sequencing, genetic engineering and genome editing for accelerated breeding and cultivar development of groundnut.

Keywords: abiotic production constraints, aflatoxin content, groundnut breeding, genotyping, phenotyping

---

This chapter was published in Acta Agriculturae Scandinavica, Section B -Soil & Plant Science. Seltene Abady, Hussein Shimelis, Pasupuleti Janila and Jacob Mashilo (2019). Groundnut improvement in sub-Saharan Africa: A review 1-18. doi: 10.1080/09064710.2019.1601252

1.1. Introduction

Groundnut (*Arachis hypogaea* L., 2n = 4x = 40, AABB) is self-pollinating allotetraploid legume crop belonging to the *Fabaceae* family (Janila et al. 2016). Groundnut seeds are a rich source of oil (35-56%), protein (25-30%), carbohydrates (9.5-19.0%), minerals (P, Ca, Mg and K) and vitamins (E, K and B) (Gulluoglu et al. 2016). The crop has various industrial uses including products such as food, feed, paints, lubricants and insecticides (Variath and Janila 2017). Further, groundnut is an ideal crop in rotational systems to improve soil fertility due to its natural ability to fix atmospheric nitrogen (Jaiswa et al. 2017).

Groundnut yields in sub-Saharan Africa (SSA) are generally low (964 kg/ha) which is far less than potential yields of up to 3500 kg/ha reported elsewhere (African Institute of Corporate Citizenship 2016). The low yield levels of groundnut in SSA is attributed to various stresses such as abiotic (drought and low soil fertility) and biotic [pests such as aphids (*Aphis craccivora* Koch), leafminer (*Aproarema modicella* Deventer), thrips (*Thrips palmi* Karny, *Frankiniella schultzie* Trybom, *Scirtothrips dorsalis* Hood and *Caliothrips indicus) and* termites (Isoptera)], and diseases (i.e. groundnut rosette disease, leaf spot, rust). Further, farmers in the region cultivate unimproved varieties using poor agronomic practices and with limited access to extension and advisory services (Alemayehu et al. 2014; Debele and Ayalew 2015; Coulibaly et al. 2017; Desmae and Sones 2017; Mastewal et al. 2017). For example, in Senegal, water stress occurring during flowering and seed filling period reduced groundnut shelled yield by 33 and 50%, respectively (Faye et al. 2016). Groundnut rosette disease causes more severe yield losses than any of the groundnut viral diseases in the region (Okello et al. 2010). Early and late leaf spots caused 100% yield loss in Ghana (Gaikpa et al. 2015).

In SSA, efforts are being made to improve groundnut yield levels which aided in the release of few genetically superior and improved groundnut varieties (Desmae et al. 2017). Reports showed that introduced groundnut varieties had considerable resistance to both biotic and abiotic stresses (Debele and Ayalew 2015; Monyo and Varshney 2016; Coulibaly et al. 2017). In addition, groundnut varieties with some desirable quality attributes such as high oil content and larger seed size for confectionery purposes have also been recently popularized (Okello et al. 2010, Amare and Feysal 2012; Amare et al. 2017). Despite past successful efforts, there has been limited breeding progress in developing groundnut varieties combining desirable agronomic and quality attributes such as high fatty acid content in combination with high yield, short maturity, drought tolerance or resistance to foliar diseases which are the needs and preferences of farmers and groundnut value chains (Okello et al. 2010; Desmae et al. 2017). Therefore, it is an overriding

consideration to develop varieties with various quality attributes to boost productivity and quality of the crop in order to satisfy farmers' demands and value chains for food security and regional and local markets. An integrated groundnut improvement program incorporating conventional and molecular breeding tools may aid in accelerated groundnut cultivars development and deployment in SSA. Therefore, the objective of this review to highlight breeding progress, opportunities and challenges on groundnut improvement with regards to cultivar development and deployment in SSA in order to guide future improvement of the crop.

1.2. Status of groundnut production

Area under groundnut cultivation and total production showed marked increases during the period 1997 to 2016 in SSA (FAOSTAT 2016). For instance, Angola and Cameroon recorded rapid increase in both cultivated area and production between 1997 and 2016. Conversely, in Botswana and South Africa both cultivated area and production level declined between 1997 and 2016. Variable yield levels have also been observed for most SSA countries during the period 1997 to 2016. Angola recorded groundnut yield levels varying from 500 (during 1997) to 712 kg/ha (2016) which was a yield improvement of 30%. Cameroon recorded the lowest groundnut yield of 281 kg/ha in 1997 to the highest yield level of 1648 kg/ha in 2016, which was an increase of 83%. Contrastingly, South Africa and Mozambique showed a decline in groundnut yields between 1997 and 2016. Mozambique, Angola and Botswana recorded the lowest mean groundnut yields of 349, 442 and 491 kg/ha averaged across period 1997 to 2016, respectively. Ghana, Cameroon, Nigeria and South Africa have recorded the top yield levels > 1000 kg/ha across the same years. In general, increased groundnut production in SSA emanated from expansion of agricultural lands. Some reports (Monyo and Varshney 2016; Kebede et al. 2017) indicated that groundnut yields of 1,700 to 2,500 kg per/ha can be realized using elite/improved varieties in SSA yet farmers continue cultivating unimproved local varieties. Famer participatory variety selection is considered to be a useful tool to enhance access to improved seed and increased adoption rate of improved varieties in SSA (Ndjeunga 2010; Okello et al. 2010; Motagi et al. 2016; Monyo and Varshney 2016; Desmae et al. 2017).

1.3. Progress on groundnut variety development in SSA

In the last two decades, more than 100 improved and high yielding groundnut genotypes have been introduced, developed and released for cultivation in SSA (Desmae et al. 2017). Some of the released varieties are cultivated in several SSA countries (Table 1.1). For example, cultivar JL 24 is widely grown in Malawi, Mozambique and South Africa due to its considerable level of

drought tolerance and early maturity (Desmae and Sones 2017; Desmae et al. 2018). The reported yield levels of this variety in Malawi, Mali and Niger is 1500, 2000 and 2000 kg/ha, in that order (Minde et al. 2008**;** Ndjeunga 2010). Variety ICIAR 19 BT is cultivated in Nigeria and Niger due to its early maturity, high yield levels, high oil content and resistance to groundnut rosette disease. Aflatoxin contamination caused by the fungi *Aspergillus flavus* and *A. parasiticus* is an important biotic factor affecting groundnut product quality to sustainable groundnut production in SSA (Waliyar et al. 1994; Monyo et al. 2012; Guchi 2015; Njoroge et al. 2017) and is a potential threat to human and animal health globally (Waliyar et al. 2016). Further, aflatoxin contamination affects groundnut trade resulting financial losses estimated at about US$750 million per annum in SSA (Kamika and Takoy, 2011). Breeding for aflatoxin resistant groundnut genotypes is vital for human health and to enhance world trade (Waliyar et al. 2016). Some genetic resources developed by the International Crops Research Institute for Semi-Arid Tropics (ICRISAT) such as ICGV 87084, ICGV 87094, and ICGV 87110 are reportedly resistant to *A. flavus*. Furthermore, 12 groundnut accessions with resistance to aflatoxin were developed by the Agricultural Research Council in South Africa (Cilliers and Swanevelder 2003). Improved Spanish groundnut cultivars such as ICGV 91278, ICGV 91283, and ICGV 91284 were selected by ICRISAT showing considerable resistance for aflatoxin-producing fungus *(Upadhyaya* et al*. 2001b).* Groundnut accessions ICGs 13,603, 1415, 14,630, 3584, 5195, 6703 and 6888 were recommended for production for their low levels of aflatoxin content (<4 μg kg−1) which is far below the regulatory limits for EU (4 μg/kg), most developing countries (10 μg/kg), and the U.S.A. (20 μg/kg) (Magamba et al. 2017). Despite breeding progress, aflatoxin levels remain high in commercial groundnut products due to poor regulatory systems and other resource constraints. Effective post- and pre-harvest groundnut handling and processing are imperative to minimize aflatoxin contamination along the value chains of the crop (Magamba et al. 2017).

Table 1.1. Some of the major groundnut varieties cultivated in sub-Saharan Africa.

Name or code	Local names in different countries	Attributes	References
ICG 12991	Baka (Malawi) Serenut 4T (Uganda), Nametil (Mozambique) and Zambia	Early maturity, drought tolerance	Deom et al. 2006; Muitia 2011; Kanyika et al. 2015
JL 24	Sameké (Mali), Kakoma (Malawi), ICG 7827 (Mozambique), Luena (Zambia), JL24 (Congo), JL 24 (Sierra Leone), JL24 (South Africa)	Early maturity, drought tolerance, high oil content, high yield	Desmae and Sones 2017
ICIAR 19 BT	Samnut24 (Nigeria), ICIAR19BT (Niger)	Early maturity, high yield, high oil content, rosette disease resistance	Desmae et al. 2017
ICGV-98412	Oboshie (Ghana), Babile-1 (Ethiopia)	High yield, large seeded for confectionery	Kebede et al. 2017
Mwenje and Nyanda	-	Resistant to aphids, Hilda and grain moth	www.seedcogroup.com
ICGV-SM 90704	Serenut 2 (Uganda), Mamane (Mozambique)	High yield, medium maturity, rosette disease resistance	Kanyika et al. 2015
Harts	-	Tolerant to early and late leaf spot, high yielding	www.opot.co.za
ARC-Oleic2	-	High oleic acid content	www.opot.co.za
ARC-Opal1	-	Resistant to Botrytis stemrot	www.opot.co.za
ARC Sellie Plus	-	Low-oleic acid content, resistance to podworm	www.opot.co.za
Tufa	-	Drought tolerant, intermediate oleic-acid content	www.opot.co.za

1.4. Genetic resources for groundnut breeding

1.4.1. Gene banks

Groundnut genetic resources are currently maintained at various gene banks and research institutions and programs globally (Pandey et al. 2012; Desmae et al. 2017). The largest collection of groundnut accessions (~15,445) is held at ICRISAT gene bank in India (Pandey et al. 2012). Approximately 43% of groundnut collections at ICRISAT consists of landrace varieties, cultivars (7%), breeding lines (31%), and other genetic stocks (19%) (E.g. mutants and experimental germplasm) (Upadhyaya et al. 2002).

In SSA, most of the groundnut germplasm has been obtained from ICRISAT's regional gene banks such as Niamey located in Niger and from the USA (Okello et al. 2010; Monyo and Varshney 2016). Further, some SSA countries such as Malawi, Mali, Zimbabwe, Uganda and South Africa maintain groundnut genetic resources (Upadhyaya et al. 2001a; Okello et al. 2010) sourced from ICRISAT and USA. In most cases, the groundnut genetic resource held in various genebanks is available for research and breeding purposes subject to the signing of a material transfer agreement. For example, in South Africa, almost all groundnut genetic resources held by the Agricultural Research Council are available on request (Cilliers and Swanevelder 2003). Groundnut genetic resource held by ICRISAT are also available by interested scientists for scientific studies or breeding purposes (Upadhyaya et al. 2001b). However, it is worth noting that material transfer can sometimes become more stringent especially if the germplasm has patent rights (Okello et al. 2010). Groundnut genetic resources currently held at various gene banks are sources of useful genes for development of improved varieties with improved quality attributes and resistance to biotic and abiotic stress factors.

1.4.2. Synthetics and wild species to tap new alleles for groundnut breeding

The primary gene pool of the cultivated groundnut is very narrow for some important characteristics such as resistance to foliar diseases (e.g. late leaf spot and rust) and insect pests (e.g. thrips) (Kumari et al. 2014; Favero et al. 2015; Michelotto et al. 2017). Wild species may offer wide variability, particularly for biotic and abiotic stress breeding (Sharma et al. 2017). Utilization of wild groundnut germplasm in breeding programs has been restricted by reproductive barriers between wild and cultivated species. This presented technical difficulties in making large numbers of crosses due to ploidy differences between the two species (Kumari et al. 2014). Successful crosses between wild and cultivated species can be achieved through the development of synthetic groundnut (i.e. doubling of chromosome number of the hybrid which is developed from two diploid wild species) (Sharma et al. 2017). Several amphidiploid and

autotetraploid groundnuts have been developed using A- and B-genome accessions with high levels of resistance to multiple stresses (e.g. late leaf spot, stem rot and collar rot diseases) (Sharma et al. 2017). Wild species such as *A. batizocoi*, *A. gregoryi*, and *A. magna* can be used as female parents and many A-genome species can be used as male parents to introgress desirable genes into the cultivated groundnut (Favero et al. 2015). Amphidiploid and autotetraploid groundnut have been developed by ICRISAT (Table 1.2) which serve as useful genetic resource to transfer useful genes into the cultivated groundnut (Mallikarjuna et al. 2011; Michelotto et al. 2016). Leaf rust and late leaf spot resistance were successfully introgressed into the cultivated groundnut varieties (e.g. ICGV 91114, ICGS 76, ICGV 91278, JL 24, and DH 86) using two synthetic resistance sources, namely, ISATGR 278-18 and ISATGR 5B (Kumari et al. 2014). Resistance to thrips was introgressed into cultivated groundnut cultivars using amphidiploid species such as *A. batizocoi x A. kempff-mercadoi*, *A. gregoryi x A. stenosperma*, and *A. magna x A. cardenasii* (Michelotto et al., 2017). Introgression of the root-rot nematode resistance gene (Rma) into tetraploid groundnut from synthetic allotetraploid donor (TxAG6) has been widely practiced in modern cultivars (Nagy et al. 2010). Chromosome pairing, pollen and pod fertility analysis in hybrids between *A. hypogaea* and *A. amphidiploids* revealed that amphidiploids can be used as a genetic bridge for the transfer of genes from wild species to the cultivated groundnut (Singh 1986). Tetraploid (2n = 4x = 40) peanut (*Arachis hypogaea* L. subsp. *hypogaea* var. *hypogaea*) lines, GP-NC WS 16 and GP-NC WS 17 (SPT 06-07,) with resistance to multiple diseases including early leaf spot (ELS), *Cylindrocladium* black rot, *Sclerotinia* blight, and tomato spotted wilt were derived from interspecific hybridization from the diploid (2n = 2x = 20) wild species, *A. cardenasii* (Tallury et al. 2014). In general, the limited level of resistance for economically important traits such as resistance to leaf spot and rust in cultivated groundnut cultivars can be enhanced through the development of synthetic groundnut varieties. Recombination of cultivated and wild groundnut germplasm will likely improve agronomic, physiological and quality attributes resulting in development of superior genotypes with resistance to biotic and abiotic stress factors to boost production in SSA.

Table 1.2. List of synthetic tetraploid groundnuts developed at ICRISAT.

Sr. No.	Code	Origin	Species	Genome	References
1	ISATGR 1212	Synthetic amphidiploid	*A. duranenesis x A. ipaensis*	*AB*	Shilpa et al. 2013; Mallikarjuna et al. 2011
2	ISATGR 11A	Synthetic autotetraploid	*A. magna x A. valida*	*BB*	Shilpa et al. 2013; Mallikarjuna et al. 2011
3	ISATGR 5B	Synthetic autotetraploid	*A. magna x A. batizocoi*	*BB*	Shilpa et al. 2013; Mallikarjuna et al. 2011
4	ISATGR 9A	Synthetic amphidiploid	*A. batizocoi x A. cardenasii*	BA	Shilpa et al. 2013; Mallikarjuna et al. 2011
5	ISATGR 11A	Synthetic autotetraploid	*A. magna x A. valida*	BB	Shilpa Shilpa et al. 2013; Mallikarjuna et al. 2011
6	ISATGR 40A	Synthetic amphidiploid	*A. ipaensis x A. duranensis*	BA	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
7	ISATGR 90B	Synthetic autotetraploid	*A. kempff-mercadoi x A. stenosperma*	AA	Shilpa et al. 2013; Mallikarjuna et al. 2011
8	ISATGR 155	Autotetraploid	*A. diogoi x A. cardenasii*	*AA*	Shilpa et al. 2013; Mallikarjuna et al. 2011
9	ISATGR 168B	Synthetic amphidiploid	*A. valida x A. duranensis*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
10	ISATGR 278-18	Synthetic amphidiploid	*A. duranensis x A. batizocoi*	*AB*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
11	ISATGR 265-5	Synthetic amphidiploid	*A. kempff-mercadoi x A. hoehnei*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
12	ISATGR 268-5	Synthetic amphidiploid	*A. batizocoi x A. cardenasii*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011
13	ISATGR 10B	Synthetic autotetraploid	*A. magna x A. valida*	*BB*	Shilpa et al. 2013; Mallikarjuna et al. 2011
14	ISATGR 35A	Synthetic amphidiploid	*A. batizocoi x A. duranensis*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011
15	ISATGR 206B	Synthetic amphidiploid	*A. duranensis x A. valida*	*AB*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
16	ISATGR 91A	Synthetic autotetraploid	*A. duranensis × A. cardenasii*	*AA*	Shilpa et al. 2013; Mallikarjuna et al. 2011
17	ISATGR 154	Synthetic amphidiploid	*A. valida × A. duranensis*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017
18	ISATGR 48B	Synthetic amphidiploid	*A. valida × A. duranensis*	*BA*	Shilpa et al. 2013; Mallikarjuna et al. 2011; Sharma et al. 2017

1.4.3. Landraces and modern groundnut varieties

Landraces are a valuable source of genetic diversity and possess useful traits for breeding (Lopes et al. 2015; Corrado and Rao 2017). Landraces can be introduced in groundnut breeding programs to incorporate unique genes such as resistance to biotic and abiotic stresses; and quality attributes. Significant genetic variation for quality attributes such as oil, zinc and iron contents exist among groundnut landrace varieties (Yaw et al. 2008). Bolivian landrace varieties of groundnut revealed larger diversity with respect to seed color, seed size, seed weight, oleic and linoleic acid contents; and showed moderate to high level of resistance to late leaf spot (Husain and Mallikarjuna 2012). Mexican hirsuta groundnut landraces such as PI576633, PI576634, PI576635, PI576636, PI576637 and PI576638 were also identified to be superior in flavor and quality (Sanchez-Dominguez and Williams 1993). Many other sources of resistance to foliar diseases such as rust and late leaf spot were identified from South American landrace varieties (Singh and Nigam 2016). Several pure lines such as 48-7, 48-14, 48-15A, 48-21, 48-34, 48-35, 48-36, 48-37, 48-44, 48-45 and 48-70A with resistance to groundnut rosette disease were selections from landraces (Singh and Nigam 2016). In pigeon pea and chickpea, landraces or their selections were released directly as cultivated varieties Asthana et al. 1996; Remanadan 1996). Some cowpea landrace varieties were released for commercial production in India (Sharma B. 1996). Landrace varieties are rarely used in breeding programmes despite possessing useful attributes. Collection and strategic conservation of groundnut landrace varieties and their exploitation in breeding programmes will aid identification of useful genes/traits for breeding for improved grain yield, quality attributes, biotic and abiotic stress tolerance. Groundnut landrace varieties may also be useful for genetic mapping studies to unravel genetic control underlying of important traits (Varshney et al. 2013).

1.5. Breeding methods of groundnut

Groundnut improvement and cultivar development in SSA mainly depended on conventional breeding including, pure line selection, mass selection, pedigree breeding, single seed descent and backcross breeding methods (Okello et al. 2010; Janila et al. 2013). Various groundnut varieties have been developed through conventional breeding methods. For example, Serenut 5R, a high yielding, early maturing, resistant to groundnut rosette disease and late leaf spot was released in Uganda using bulk selection (Table 1.3). Babile-1 with the accession number ICGV-98412, released in Ghana and Ethiopia, is high yielding, medium maturing and moderately resistant to late leaf spot. It was bred at the International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, India (Table 1.3).

Genetic variability available in cultivated and wild *Arachis* have been extensively exploited through conventional breeding to develop improved varieties (Singh and Nigam 2016; Sharma et al. 2017). Genetic variation for important traits such as plant height, number of primary branches per plant, number of mature and immature pods per plant, kernel yield per plant, hundred seed weight, haulm yield per plant and dry pod yield per plant have been reported in groundnut. This is useful for phenotypic analysis and breeding in this crop (Kushwah et al. 2017; Hampannavar et al. 2018). Further, traits like plant height, pods per plant, 100-pods weight, shelling percentage, harvest index and pod yield per plant have high heritability and considerably higher genetic advance (Nath and Alam 2002; HajHussein et al. 2018). High heritability estimates and genetic advance is an indication that variation is attributable to a high degree of genetic effect and selection can be effective (Johnson et al. 1955).

Knowledge on degree of association between yield contributing characters and yield is very essential for development of high yielding genotypes in groundnut. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its component traits and also among various yield-related components (Faye et al. 2015; Mhlaba et al. 2018). Groundnut pod yield per plant exhibited significant positive correlation with grain yield per plant, number of kernel per plant, hundred kernel weight, number of pods per plant, harvest index and shelling percentage (Kushwah et al. 2017; Zongo et al. 2017a; Hampannavar et al. 2018). This information could help in formulating effective selection criteria in groundnut improvement programs for genetic improvement for grain yield.

In general, groundnut breeding in SSA is mostly dependent on limited selection in segregating generations resulting in low selection efficiencies. Consequently, a limited number of improved groundnut genotypes were developed and deployed. In addition, a conventional breeding requires extended time to develop varieties. It also depends on screening of large number of breeding populations under multi-location trials due to the high genotype and environment interaction effect (Ngirazi et al. 2015; Kebede and Getahun 2017). Therefore, integration of new breeding tools such as molecular markers and marker-assisted selection in groundnut breeding programs could enhance the precision and speedy development of improved groundnut cultivars.

Table 1.3. List of improved groundnut varieties with resistance to biotic and abiotic stress tolerance and desirable agronomic attributes reported globally.

Name	Pedigree	Traits	Country	Organization	Year of release	References
NuMex 01	NM Valencia A x Brantley	High oleic content	USA	New Mexico Agricultural State University	2013	Puppala and Tallury 2014
NemaTAM	A.cardenasii Krapov. and W.C. Gregory x A. diogoi Hoehne	Resistant to root-knot nematode	USA	Texas Agricultural Experiment Station	2002	Simpson et al. 2003
C724-19-15	C-99R X COAN	Resistant to root-knot nematode and tomato spotted wilt tospovirus	USA	USDA-ARS and Georgia Agricultural Experiment Station	2008	Holbrook et al. 2008
Tifguard	C-99R X COAN	Resistant to root-knot nematode and tomato spotted wilt tospovirus	USA	University of Georgia Coastal Plain Experiment Station	2007	Holbrook et al. 2008
TifGP-2		Resistant to root-knot nematode and tomato spotted wilt tospovirus	USA	USDA-ARS and Georgia Agricultural Experiment Station	2010	Holbrook et al. 2012
ICGV-91114	ICGV 86055 x ICGV 86533	Tolerant to rust and drought	India	ICRISAT	2006	ICRSAT 2012
"Webb" peanut	PI 667551	High-yielding, high-oleic fatty acid, nematode resistant	USA	Texas AgriLife Research	2001	Simpson et al. 2013
Golden	Mutant	Mutant with high yielding and *Cercospora* leaf spot resistant	India	Barani Agricultural Research Institute (BARI)	2002	Naeem-UD-Din et al. 2009
Binachinabadam-5	M6/250/54-20	Mutant with salinity tolerance		Bangladesh Institute of Nuclear Agriculture	2011	Azad et al. 2014
Huayu 22		Mutant with high yield, good quality, several diseases resistance, drought tolerant and wide adaptable	China	Shandong Peanut Research Institute	2003	Wu et al. 2006

Table 1.3. (Continued).

Name	Pedigree	Traits	Country	Organization	Year of release	References
Serenut 5R	ICGM 522 X RG 1	High yielding, early maturing, resistant to groundnut rosette disease resistant to late leaf spot	Uganda	National Semi-Arid Resources Research Institute	2010	Okello et al. 2016
CG-8	ICGV-SM 08501,	-	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-9	ICGV-SM 08503	-	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-10	ICGV-SM 01724	-	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-11	ICGV-SM 01731	-	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-13	ICGV-SM 99551	Short duration	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-14	ICGV-SM 99556	-	Malawi	ICRISAT	2014	Setimela et al. 2017
CG-12	ICGV-SM 01514	-	Malawi	ICRISAT	2014	Setimela et al. 2017
NARINUT 2015	ICGV-SM 01731	Rosette disease tolerant	Tanzania	ICRISAT	2015	Setimela et al. 2017
KUCHELE 2015	ICG 8326		Tanzania	ICRISAT	2015	Setimela et al. 2017
NACHI 2015	ICGV-SM 90704	-	Tanzania	ICRISAT	2015	Setimela et al. 2017
Serenut 6T	ICGV 93437 x ICGV-SM 93561	High-yielding, early maturing and resistant to groundnut rosette disease	Uganda	National Semi-Arid Resources Research Institute	2010	Okello et al. 2017
ICGV 91278	JL 24'/UF 71513-1	Aflatoxin resistant	India	ICRISAT	1999	Upadhyaya et al. 2001b
ICGV 9128	U 4-7-5/JL 24	Aflatoxin resistant	India	ICRISAT	1999	Upadhyaya et al. 2001b
ICGV 91284	J 11'/ICGV 86184	Aflatoxin resistant	India	ICRISAT	1999	Upadhyaya et al. 2001b

1.5.1. New and emerging tools for groundnut breeding

1.5.1.1. High-throughput automated phenotyping techniques

Plant phenotypic data collection with sufficient resolution and accuracy remains a major limiting factor for effective use of genomic data for crop improvement (Bai et al. 2016). In developing countries where groundnut yield is low, the breeding focus is to improve yield and tolerance to biotic and abiotic stress factors. Selection of groundnut genotypes using pod yield has been slow and yielded highly variable results as yield is affected by genotype by environment interactions (Luis et al. 2016), which causes difficulties in selecting genotypes with wide adaptation resulting in delayed cultivar release.

Crop breeding strategies for higher yield and disease tolerance can be accelerated through the use of high-throughput phenotyping (Shakoor et al. 2017). Instead of using high-throughput phenotyping tools directly in breeding programs, they may be more useful to enhance the efficiency of genomic tools during the establishment of marker-trait associations, genome-wide associations and training genomic selection models (Janila et al. 2016). Patrick et al. (2017) reported a rapid screening of tomato spot wilt disease resistance among 20 genotypes of groundnuts through the application of high-throughput phenotyping tool. High throughput phenotyping for total oil content in groundnut kernel through the application of single kernel near infrared spectrometry (NIRS) system determined as reproducible, robust, rapid, cost-effective, and non-destructive, and can be used in conjunction with high oleic fatty acid screening to provide for simultaneous phenotyping of total oil and high oleic acid contents (Awada et al. 2018; Deshmukh et al. 2020). Adoption of high-throughput automated technologies is hypothesized to result in faster development of well-adapted and high-performing cultivars (Awada et al. 2018). However, application of high-throughput phenotyping techniques in genetic improvement of groundnut and other crops are still very limited. This is probably because automated phenotyping is an emerging breeding approach and has not yet been adopted by plant breeders and crop improvement programmes (Awada et al. 2018).

1.5.1.2. Genomic tools

Molecular breeding refers to the technique of using DNA markers that are tightly linked to phenotypic traits to assist in a selection scheme for a particular breeding objective (Jaradat 2016). Molecular markers and genetic linkage maps are pre-requisites for molecular breeding (Varshney et al. 2009). Marker-assisted selection (MAS) refers to the selection of superior genotypes using molecular markers (Kumpatla 2012). Compared with conventional phenotypic selection, MAS is not influenced by environmental conditions because it detects the structural polymorphisms at molecular level. Further, MAS is cheaper and less labor-intensive, allows selection in off-season nurseries and has a potential to accelerate breeding process (Kumpatla 2012).

Due to low levels of molecular polymorphism among cultivated groundnut varieties, MAS in groundnut has not been used extensively compared with other major crops (Burow et al. 2013). Similarly, low levels of variability in cultivated groundnut have been reported using molecular markers (Bhagwat et al., 1997). The cultivated groundnut has been analyzed by several marker systems such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), single nucleotide polymorphism (SNPs) and simple sequence repeat markers (SSR) (Stalker and Mozingo 2001; Zhao et al. 2016). Currently, SSR markers are commonly used in groundnut genetic analysis and breeding due to their co-dominance, simplicity, high polymorphism, repeatability, multi-allelic nature and transferability within the genus *Arachis* (He et al. 2003; Pandey et al. 2012; Wang et al. 2018). Mondal and Badionnavar (2010) identified three and four SSR alleles that were found associated with rust and late leaf spot resistance in groundnut, respectively. About 376 highly informative SSR markers linked to resistance to early leaf spot, groundnut rosette disease, and rust and aflatoxin contamination across African cultivated groundnut varieties were identified useful to identify suitable parents for mapping populations or breeding (Kanyika et al. 2015). There is approximately 14 392 publicly available SSR markers in the *A. hypogeae* database (Wang et al. 2018). Recently, about 210 new SSRs were developed for *A. hypogaea* useful for genetic diversity analysis and cultivar development (Wang et al. 2018). In addition, SSR markers have been developed specifically for different *Arachis* species such as *A. duranensis, A. paensis* and *A. stenosperma* (Zhao et al. 2012).

Table 1.4 lists some molecular markers developed for groundnut breeding. Four SSR markers (e.g. IPAHM103, GM2079, GM1536 and GM2301) associated with groundnut leaf rust resistance were identified by Varshney et al. (2014). SSR markers pPGPseq-17F6, pPGPseq-2F05, pPGPseq-8E12, pPGPseq-13A10 and pPGPseq-16C6 are reportedly well-associated with rust resistance (Shoba et al. 2012). Zongo et al. (2017b) identified marker GM1911 associated to early leaf spot resistance in groundnut. Further, SSR markers, such as pPGPseq-2B10, pPGPseq-2F05, Ppgp13A7, PM

3751_{62}, pPGPseq5D5$_{220}$ and PM384$_{100}$ are also linked to late leaf resistance (Mace et al. 2006; Shoba et al. 2012). SSR markers such as SSR_F149451, Cer14, pPGP-seq2H08, SSR_DX508223 and SSR_FI500754 linked to plant growth habit and SSR markers PM50, SSR GW391728, SSR G0340377 and pPGP_seq2H08 liked seed size have been identified in groundnut. Two transposable elements, markers namely: TE 360 and TE 498, were found to be linked to rust resistance gene (Mondal et al. 2014). SSR marker, GM 1991 is reportedly linked to a drought tolerant QTL in groundnut (Guo et al. 2012). Chu et al. (2007) identified marker S197 as a reliable predictor for nematode resistance.

Other molecular tools such as diversity arrays technology (DArT) are useful in groundnut improvement programmes. Shasidhar et al. (2017) developed two genetic maps based on the DArT and diversity arrays technology sequencing (DArTseq) markers and identified genomic regions linked to groundnut oil content and fatty acids. However, genetic studies revealed low polymorphism and moderate level of genetic diversity among diploid and tetraploid groundnut genetic pool (Varshney et al. 2010) indicating utilization of DArT marker system may limit efficient genetic analysis of groundnut genetic resources for cultivar development (Pandey et al. 2012). Development of highly discriminative and informative DArT markers is useful for genetic analysis and breeding in groundnut.

MAS helps to develop ideal groundnut cultivar with inbuilt resistance and improved pod and kernel features (Mothilal 2012). Introgression of nematode resistance through an amphidiploid pathway into cultivated groundnut was successfully implemented using MAS and subsequently nematode resistant groundnut cultivar, NemaTAM, was developed (Holbrook et al. 2011). Marker-assisted backcrossing (MABC) has been commonly used in groundnut improvement for instance high oleic acid content and nematode resistant variety, 'Tifguard' was developed through the application of this technique (Tiwari et al. 2017). Introgression of rust resistance from 'GPBD 4' groundnut cultivar into susceptible varieties ICGV 91114, JL 24 and TAG 24 were employed through MABC which resulted in development of improved rust resistance groundnut lines (Varshney et al. 2014).

In developing countries including SSA, application of MAS in groundnut improvement is very limited. This is mainly due to lack of human capital and infrastructure (Janila et al. 2016). However, some successes have been reported. For example, high oleic acid content governing genes, *ahFAD2A* and *ahFAD2B,* were transferred from high-oleic parents (UF-85, Guat and Atete) to low-oleic commercially produced South African cultivars (e.g. Akwa, Kwarts and Harts) through the application of MAS (Mienie and Pretorius 2013). AFPL markers linked to resistance to groundnut rosette disease were successfully identified and mapped in South Africa (Herselman et al. 2004). In Malawi, two groundnut genotypes, RG1 and ICG 1291, were identified as resistant

to groundnut rosette disease using SSR markers (Chintu 2013). Selected advanced groundnut lines with different phenotypic attributes were characterized at molecular level using SSR markers in Ghana (Oteng-Frimpong et al. 2015). Integration of MAS into groundnut breeding programs in SSA will have greater implication on groundnut improvement in the future.

Marker-assisted backcrossing is routinely applied in breeding programs for gene introgression (Frisch and Melchinger 2005). MABC aims to transfer one or a few genes/QTLs of interest from agronomically inferior (donor parent) into a superior cultivar or elite breeding line (serving as the recurrent parent) to improve the targeted trait (Jiang, 2013). MABC was used to develop foliar fungal disease resistant lines (Varsheney et al. 2014; Janila et al. 2016) and high oleic lines in Spanish and Virginia bunch types (Janila et al. 2016). However, MABC is not the best approach to develop commercial varieties as compared to MAS which allows improvement of other desirable traits in addition to the target traits selected using markers.

MAS and MABC are not well-suited for analysis of quantitative traits (Sorrells 2015). In such cases, genomic selection is a promising breeding strategy for rapid improvement of quantitative traits. Genomic selection (GS) relies on development of selection models based on dense genetic markers distributed across the whole genome and phenotyping of a training population for selection of individuals with high genome-estimated breeding values in the breeding population (Resende et al. 2012). GS can therefore provide effective selection using polygenic traits with low heritability (Sun 2014).

In general, MAS has been useful in groundnut breeding. However, in order to develop sufficient genomic resources for groundnut, MAS has to be widely applied to identify markers linked to other important traits such as drought tolerance and aphid (*Aphis craccivora*) resistance which are becoming a major bottleneck for groundnut production in SSA. Thus, integration of MAS into groundnut breeding programs in the region will have greater implication on groundnut improvement in the future. In general, molecular markers developed specifically for groundnut provide opportunities to characterize groundnut genetic resources for biotic stress and abiotic stress constraints, agronomic attributes and grain quality traits. This will result in identification and selection of genetically unrelated genotypes possessing key attributes for strategic crossing to develop high-yielding genotypes with key farmer preferred traits and also for industrial purposes (Pandey et al. 2012). Further, to accelerate cultivar development in SSA, access to research funding and technology especially genomic tools will aid mapping of the groundnut genetic pool for accelerated selection and breeding.

Table 1.4. Some molecular marker systems developed for genetic analysis and breeding in groundnut

Marker name	Marker type	Marker sequence		
		Forward primer	Reverse primer	References
IPAHM103	SSR	GCATTCACCACCATAGTCCA	TCCTCTGACTTTCCTCCATCA	Varshney et al. 2014
GM1536	SSR	AAAGCCCTGAAAAGAAAGCAG	ATGCATTTGCAGGTTCTGGT	Varshney et al. 2014
GM2301	SSR	GTAACCACAGCTGGCATGAAC	CTTCAAGAACCCACCAACAC	Varshney et al. 2014
GM2079	SSR	GGCCAAGGAGAAGAAGAAAGA	GAAGGAGTAGTGGTGCTGCTG	Varshney et al. 2014
GM1991	SSR	GAAAATGATGCCGAGAAATGT	GGGGAGAGATGCAGAAAGAGA	Guo et al. 2012
GM 1911	SSR	CAGCTTTCTTTCAATTCATCCA	CACTTCGTGTTCTTCCTGCTC	Guo et al. 2012
TE 360	TEM	GGATATGATGCCCATAGCTGA	TGCTGACTACTTGCAATGCC	Mondal et al. 2014
TE 498	TEM	ATGACTTACATGTAGCAATTG	TGAAAGGAGTCAAAGGTCATG	Mondal et al. 2014
S197	RAPD	CTGTCGAACCATGGAAGAAGATCC	CCAACTTGATGGTAGAAGTATGCTT	Chu et al. 2007
AHCW0061	SSR	TCATGTGAATTTGTGGACGGT	CCAGGTTTTTGAGGTCCCTGA	Wang et al. 2018
AHCW0310	SSR	GTTCAAGGGCTGTGCATTGG	GGGTTCGACTCCCGTCTTAT	Wang et al. 2018
AHCW0545	SSR	ACAGAAGAAGAAACAGCGCG	TTCCGTCATGTGCTTCGGAA	Wang et al. 2018
AHCW0618	SSR	AAATTTGAGCACGCATCCCC	TGTCTTTTTCCTCGCCTTTGT	Wang et al. 2018
AHCW0700	SSR	TGGAAGTTTCACGGGACAGG	GTAGCAAGCTTCCCCACCAT	Wang et al. 2018
AHCW0768	SSR	GGACCCATTTTTGCAAGAGAGA	CGGATTGCAACATTGGCGAA	Wang et al. 2018
AHCW1250	SSR	ACAGCTGCCTCTTCTCTGTG	CCCACTCAAAATCGGATTTGGA	Wang et al. 2018
AHCW1510	SSR	TCCTGCACCATGACCATGAA	TGTTCGGCACCAATCTGTCA	Wang et al. 2018
AHCW1765	SSR	CGCTGGTCTGGCATTTAACG	AAGGGAGGAGGAGTTGGGTT	Wang et al. 2018
AHCW1862	SSR	TGTTCAGGGATGTGTTTGGACT	GGGCAAGCTCTTTAAACTGCA	Wang et al. 2018
Cer14	SSR	AGCTGCTTTGACCAGCCGGG	CGCAAGCTTCCTTGTAGATGGTGGT	Mondal et al. 2012
SSR_DX508223	SSR	GGATTAGGGTTATGAGTTAGGAAACAC	GCTGATGATTGGTTCGGGTAT	Bhad et al. 2016
SSR_FI500754	SSR	AAGTGGCAGAATCACAGATGG	AGGGTAGAGGTTGGAGAGAAGG	Bhad et al. 2016
SSR_FI499451	SSR	GTAAGCCACTCTATCACCCCAG	ACAGCCTCACAAATCCAAGAAT	Bhad et al. 2016
pPGPseq_2H08	SSR	TAAGTGGGGTGGGAGTGGAC	AGCAGTTTGCGTAAGCATTTG	Ferguson et al. 2004

Table 1.4. (Continued)

Marker name	Marker type	Marker sequence		
		Forward primer	Reverse primer	References
RGC 24	SSR	TTTGACGGTATGTGCTTTCTTG	TGCCACGACCAAACCAATC	Bhad et al. 2016
PM 50	SSR	CAATTCATGATAGTATTTTATTGGACA	CTTTCTCCTCCCCAATTTGA	Bhad et al. 2016
SSR_GW391728	SSR	TCATCATCTGCTAGGGTTATGG	GGTTCCACCTCTTGTCCAGTAT	Mondal et al. 2012
RS 5	SSR	TGATTGCCCGACTAACAA	GTGCCATGTATTTTACGGAT	Mondal et al. 2018
RS 25	SSR	CTACTAACCCTCCTAATGACCC	CTGAACTTGGTTTCATGGTT	Mondal et al. 2018
RS 42	SSR	CTTCAACTCTACCCTTCCCCTT	GGCTTCATTAACATGCTTTTCC	Mondal et al. 2018
RS 47	SSR	CGGGTTGAGAAATTGACTAA	TACAGATCACAGGGTACATCAG	Mondal et al. 2018
RS 50	SSR	GCCTTGTATTCTGTTAATGTCC	GACTCACTCTGACTTCACTAAGG	Mondal et al. 2018
RS 51	SSR	GTAAAAGGTTGAAGAGCAGAGT	CAGTGTCTTACGTTGTTCACAT	Mondal et al. 2018
RS 74	SSR	GAAACCTAACTCTCCAGAAGC	TTCATGGTCACAAATCACAC	Mondal et al. 2018
RS 78	SSR	ATGCTTCAAACTCCTCACTT	GTGGATCTGCATTATCGTTAG	Mondal et al. 2018
RS 103	SSR	TCCATATTCTTATGCCTTGC	TATAGTGCTCAATCTCCATCTG	Mondal et al. 2018

SSR, simple sequence repeat markers, *TEM*, Transposable element markers, *RAPD*, random amplified polymorphic DNA

1.5.1.2.1. Next generation sequencing (NGS)

NGS technologies are highly dependent on massive parallel sequencing, high resolution imaging, and complex algorithms to deconvolute signal data to generate sequence data. NGS technologies offer a wide variety of applications such as whole genome *de novo* and re-sequencing, transcriptome sequencing (RNA-seq), microRNA sequencing, amplicon sequencing, targeted sequencing, chromatin immuno precipitated DNA sequencing (ChIP-seq), and methylome sequencing (Kumpatla et al. 2012). Genotyping- by-sequencing and whole-genome resequencing, can lead to the development of molecular markers suited to studies of genetic relationships among breeding materials, genetic mapping of target genes and genome-wide association studies. This can facilitate selection of individuals with tolerance to climatic stress and resistance to pathogens causing substantial losses in agriculture (David and Repkova 2017). NGS technology has been applied for the identification of genes related to resistance to biotic stress in wild groundnut relatives (Brasileiro et al. 2014). For example, quantitative trait loci (QTLs) linked to leaf spot resistance were identified in groundnut through SNP-based next generation sequencing (Liang et al. 2017). Three different viruses from three families of forage groundnut (*A. pintoi*) were identified through the application of NGS (Sanchez et al. 2016). Complete chloroplast genome sequences of seven *Arachis* species were generated using NGS sequencing (Yin et al. 2017). The genetic relationship among groundnut genotypes can also be studied using NGS. In general, inclusion of NGS in groundnut breeding programs in SSA which currently rely mostly on conventional breeding methods will assist in rapid development of genomic tools for groundnut improvement and cultivar development.

1.5.2. Mutation breeding in groundnut

Groundnut has a narrow genetic base because of its monophyletic origin, limited gene flow due to ploidy barrier and self-pollination (Yusuf et al. 2017). Mutation breeding serves as an alternative approach to conventional plant breeding to increase genetic variability and could confer specific improvement without significantly altering phenotype expression (Kulthe and Kothekar 2011). Physical mutagens such as X-ray, gamma rays, β-rays, fast neutrons and chemical mutagens like, ethyl methane sulphonate, ethidium bromide, acryflavine, diethyl methane sulphonate (DES), N- nitroso-N-methylurea, N-ethyl–N-nitrosourea, ethylene imine and sodium azide have been successfully used to create genetic variability in groundnut (Kumari, 2008; Bhagwan and Akkiraju, 2015; Gunasekaran and Pavadai 2015; Habtamu 2016).

About 72 groundnut varieties have been developed through mutation breeding (Janila et al. 2013). Table 1.3 lists some improved groundnut varieties with resistance to biotic (e.g. leaf spot and aflatoxin) and abiotic stress (e.g. drought and salinity) tolerance and improved quality attributes (e.g. increased seed size, high oleic to linoleic ratio). Several of these varieties were developed using mutation breeding. For example, TG-37A and Golden groundnut mutants were developed and released in India. TG-37A is a semi-dwarf, compact pod setting, high yielding and with smooth pod surface, while variety Golden is high yielding and *Cercospora* leaf spot resistant. Mutants such as Huayu 22 and Fu 22, were released in China. Huayu 22 is high yielding, high quality and resistant to several diseases and with wide adaptation. Mutant variety Fu 22 is known for its tolerance against *A. flavus* (Maluszynski 2001).

Groundnut varieties with high oleic to linoleic acid ratio have become preferred by the groundnut industry due to their increased shelf life and improved health benefits (Chamberlin et al. 2011). Mondal and Badigannavar (2013) reported a groundnut mutant variety with 78% improvement in oleic acid content compared with its parental genotype. Similarly, Nadaf et al. (2009) reported high oleic to linoleic acid ratio in selected groundnut mutants. The first high oleic groundnut variety released in the world was SunOleic 95R, which was derived from a cross between a high oleic breeding line F435 and a component line 'Sunrunner' (Gorbet and Knauft 1997). Further, NuMex 01 is a high oleic acid Valencia groundnut variety developed by the New Mexico Agricultural State University (Puppala and Tallury 2014).

Significant genetic variability was created for morpho-physiological traits such as pod yield and related traits, and oil content of groundnut through gamma irradiation (Rashid et al. 2012). Similarly, Ahmed and Mohamed (2009) reported higher number of pods and seed yield per plant in groundnut mutants than their parents. Sui et al. (2015) reported that the use of Pingyangmycin-based *in vitro* mutagenesis in combination with directed screening with hydroxyproline is effective for development of potential drought-tolerant mutants of groundnut. Induced mutagenesis particularly through a combination of gamma rays and sodium azide was successful in developing mutants in groundnut with wide genetic variability (Mondal et al. 2007).

Increased pod yield, greater number of pods per plant, higher pod filling ability, increased pod size, resistance to foliar diseases and drought tolerance are important farmers' preferred traits of groundnut in SSA (Ntare et al. 2007; Ndjeunga et al. 2010). But due to the narrow genetic base of the crop, foliar diseases (e.g. rust and late leaf spot) cause significant yield losses (Kumari et al. 2014). In SSA, mutation breeding technology has been adopted in groundnut improvement programmes. For instance, groundnut yield has been improved with the aid of mutation breeding in Uganda (Bulafu 1991). In Egypt, groundnut mutants achieved higher pod yield, larger number of pods, higher seed set per plant and improved shelling percentage than their parents (Ahmed

and Mohamed 2009). Genetic variations induced by mutation represent a more efficient source of genetic variability than gene pools conserved by nature (Brock 1977). Thus, mutation breeding can be used as an alternative technique to induce genetic variation for desired characters. Thus, mutation breeding offers an alternative and novel approach for creating unique phenotypes which can be exploited for breeding. However, some challenges including access to mutation induction facilities limits the use of this technology for groundnut improvement in SSA. The low cost of other mutation breeding technologies such ethyl methane sulphonate mutagenesis (EMS) offers opportunities for groundnut improvement in the region. Approximately 3400 groundnut mutants have been developed using EMS delivering useful genetic variation in groundnut breeding (Knoll et al. 2011).

1.5.3. Rapid generation advancement

Rapid generation advancement (RGA) approach uses single seed descent as the breeding method in a small screen house or glass house space (Collard et al. 2017). Using RGA, many breeding programs in chickpea successfully take two generations per year i.e. one in the field during the crop season and the other in off-season either in greenhouse or in an off-season nursery (Gaur et al. 2007). In tomato, it was reported that RGA can produce a maximum of five generations per year compared to a maximum of three generations using conventional breeding methods (Bhattarai et al. 2009). In groundnut, RGA was used in breeding high oleic groundnut varieties in Spanish and Virginia Bunch varieties using controlled environment facilities that facilitated three cycles per year instead of two (ICRISAT 2017). The aim of RGA is to accelerate breeding cycles and breeding progress in many crops (Tanaka et al. 2016). Therefore, the method offers opportunities for rapid generation advancement to develop breeding populations for accelerated cultivar development (Bhattarai et al. 2009). The procedure is a cost effective and time saving method of breeding (Collard et al. 2017). The urgent need to develop superior and improved groundnut varieties for SSA requires accelerated methods such as RGA in cultivar development and release to boost production. The breeding procedure is reportedly cost effective and time saving (Collard et al. 2017) and should provide opportunities to accelerate groundnut breeding in the region.

Shuttle breeding uses diverse ecological environments to develop improved varieties with higher adaptability (Ortiz et al. 2007). Promising genotypes are grown simultaneously across different sites to select high-yielding genotypes (Ortiz et al. 2007). As a result, shuttle breeding can be used to develop drought tolerant, early-maturing groundnut varieties with high-yield, good seed quality, diseases and insect pest resistance and wide adaptability. In wheat (*Triticum aestivum* L.) shuttle breeding has been employed by the International Maize and Wheat Improvement Centre

(CIMMYT) to develop wheat genotypes possessing biotic and abiotic stress tolerance, high-yield potential and good end-user quality attributes for cultivation across diverse environments (Crespo-Herrera et al. 2018; Hernández-Espinosa et al. 2018). This is achieved through introduction of new and novel sources of genetic variation from wild species, landraces, and other sources of useful alleles (i.e. mutants) to develop well-adapted genotypes (Ortiz et al. 2007).

In SSA, groundnut breeding programmes can benefit from shuttle breeding for advancing the generations that can contribute to enhanced rate of genetic gain especially for yield. Further, development of efficient shuttle breeding method with RGA could help significantly to reduce groundnut breeding cycles in SSA. Despite these opportunities, limited collaborative research among groundnut breeders in SSA hinder accelerated cultivar development and release. There is a need for financial support by key groundnut producing countries in SSA for collaborative groundnut improvement that may accelerate breeding of highly-adapted and high-yielding genotypes in the region.

1.5.4. Single seed descent method in groundnut breeding

Genetic gains for key traits can be delayed due to the long breeding generation required in the traditional breeding methods. About 10-16 breeding generations are required for genetic advancement and to select desirable recombinants resulting from crosses (Saxena et al. 2017). Single Seed Descent (SSD) is most suitable for handling large segregating populations (Wells and Weiser 1989) and for accelerated cultivar development. SSD optimizes resources allocation without compromising on genetic variability and genetic advancement. It reduces time for cultivar development and saves cost associated with advancement of early generations (Sarutayophat and Nualsri 2010). SSD has been successfully used in groundnut breeding programs, where multiple generations per year have accelerated using the inbreeding process to advance fixed lines to multi-site evaluation trials (Holbrook and Culbreath 2008). In safflower (*Carthamus tinctorius* L.), SSD resulted in development of lines with higher yield and oil content producing compared with parental genotypes (Martinez et al. 1986). In pigeon pea [*Cajanus cajan* (L.) Millsp] development of RGA technology that integrates germination of immature seeds with single seed descent method resulted in about 3 to 4 generations advanced in 1 year (Saxena et al. 2017). In cowpea (*Vigna unguiculata* L. Walp) SSD allowed a more rapid generation than pedigree selection resulting in development of superior genotypes (Obisesan 1992). This method could be appropriate for groundnut breeding. There is a need for a standardized and efficient SSD protocol to accelerate cultivar development in SSA.

1.5.5. Genetic engineering and genome editing

Genetic engineering (i.e. recombinant DNA technology, gene modification, and gene therapy) refers to the process of inserting new genetic information into existing cells in order to modify a specific organism for the purpose of changing its characteristics (Nakashima 2018). Genetic engineering techniques such as the use of *Agrobacterium tumefaciens* mediated transformation and DNA-bombardment-mediated transformation are used as powerful tools to accelerate groundnut improvement (Shilpa et al. 2013). The success of genetic transformation depends on a reliable tissue culture regeneration system, gene construct(s), suitable vector(s) for transformation and efficient procedures to introduce desired genes into target plants (Banavath et al. 2018). Groundnut tissues such as leaf sections, cotyledonary nodes, longitudinal cotyledon halves, embryo axes, embryo leaflets, and hypocotyls have been used for genetic transformation (Holbrook et al. 2011).

Genetic engineering of groundnut is one of the potential options for improving abiotic stress tolerance and food safety (i.e. aflatoxin contamination) (Banavath et al. 2018). Resistance to several fungal diseases (late leaf spot and rust), virus diseases (bud necrosis and tomato spotted wilt virus) and insect pests (white grub, gram pod borer) have been achieved through the application of genetic engineering in groundnut (Shilpa et al. 2013). Table 1.5 summarizes some successful groundnut genetic transformation studies.

Genome editing is used to obtain new allelic forms which is targeted gene modification to obtain a generation of new allelic variants in the genomes of cultivated individuals (David and Repkova 2017). Various novel genome editing tools have been developed including, zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats/Cas9 (CRISPR/Cas9) (Kamburova et al. 2017). These tools make double-strand breaks (DSB) in DNA followed by repairing employing error-prone non-homologous end joining (NHEJ) or homology directed repair (HDR) mechanism which leads to mutation in specific location in the genome (Mishra and Zhao 2018). In groundnut, a TIR-NBS-LRR candidate gene for nematode resistance was transferred using CRISPR/Cas9 vector (Guimaraes et al. 2015). Groundnut allergy is a life-threatening food allergy. QTLs associated with aflatoxin resistance have been identified in groundnut (Guo et al. 2008). For hypoallergenic groundnuts to be safe for consumption, all genes coding for allergens can be silenced or removed resulting in aflatoxin free groundnuts, and genome editing offers an effective tool (Van de Wiel et al. 2017). Groundnut breeding programmes in SSA could hugely benefit from genetic engineering and genome editing technology to produce non-toxic groundnuts for consumption and increased trade.

1.6. Breeding for drought tolerance

Breeding for yield gains has been the major emphasis to enhancing groundnut productivity globally (Janila et al. 2016). Therefore, understanding yield enhancing agronomic and physiological traits is key for breeding. The important yield contributing parameters are pod yield per plant, number of pods per plant, shelling outturn, and 100-seed weight. Early maturity is an important trait in groundnut as it enables escape from late stress conditions such as drought and frost. Also, early maturity enables groundnut to to fit in multiple cropping systems (Janila and Nigam, 2013).

Relatively better progress in drought tolerance breeding has been achieved through selection of target physiological characters such as harvest index (HI), water use efficiency (WUE), specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) (Nigam *et al*., 2005). The SLA and SCMR have been found to be highly correlated with WUE (Nageswara Rao *et al*., 2001; Sheshshayee *et al*., 2006) and were used as surrogate traits for selection of genotypes with better WUE (Nigam *et al*., 2005; Lal *et al*., 2006; Sheshshayee *et al*., 2006). SLA and SCMR were found to be negatively correlated (Rao *et al*., 2001; Upadhyaya, 2005).

Significant genotypic variations for drought tolerance were reported in groundnut (Azevedo et al, 2010. According to Nageswara and Nigam (2003), two genetic enhancement approaches were developed and implemented simultaneously to enhance the adaptation to drought-prone environments. These are: (i) development of short-duration genotypes that can escape the end season drought and (ii) development of genotypes with superior yield performance in drought prone regions following conventional breeding approaches.

Genetic diversity study is a pre-requisite for breeding of new cultivars and population development. Phenotypic traits and marker technologies have been used to analyze genetic diversity and population structure in cultivated groundnut (Zheng et al. 2018). For example, Daudi et al. (2020) used phenotypic traits and simple sequence repeat (SSR) markers to select distinct and complementary groundnut genotypes for breeding rust resistance. The identification of genomic regions associated with drought tolerance would enable breeders to develop improved cultivars with increased drought tolerance using marker-assisted selection (Ribaut et al., 1996). During the past 10 years, molecular marker linkage maps were developed for groundnut followed by identification of markers and QTLs for target traits (Janila and Nigam, 2013).

1.6.1 Combining ability

Combining ability analysis helps to identify superior parents to be used in breeding programs or to identify promising cross combinations for cultivar development (Acquaah, 2007). Combining ability is the relative ability of a genotype to transmit its desirable performance to its progenies. Knowledge of the type of gene action involved in the expression of yield and yield components are essential to choose an appropriate breeding methodology to isolate desirable segregants in the later generations (Mothilal and Ezhil, 2010). Diallel mating design is an efficient method for the study of combining ability as well as the gene action involved. In diallel analysis Sprague and Tatum (1942) introduced the concept of general combining ability (GCA) effect and specific combining ability (SCA) effect. General combining ability is associated with genes which are additive in effects while SCA is attributed primarily due to deviations from the additive scheme caused by dominance and epistasis gene actions (Rojas and Sprague, 1952). Khute et al. (2018) reported significant general and specific combining abilities for pod yield, hundred seed weight, shelling percentage and harvest index in groundnut.

1.6.2. Genetic variability, heritability, genetic advance and correlation

Variability is the occurrence of differences among individuals due to varied genetic composition and/or the environment (Allard, 1960; Falconer and Mackay, 1996). Genetic improvement of any crop depends on the magnitude of genetic variability and the extent of heritability (Prabhu et al. 2017). According to Raje and Rao (2000) genetic variability is essential to realize response to selection as the estimates of genetic parameters of variation are specific for a particular population and environment. The phenotypic expression of the quantitative character may be altered by environmental stress that affect plant growth and development. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a population (Burton and Devane, 1953). Prabhu et al. (2017) reported the presence of wide spectrum of genetic variation for kernel yield per plant, pod yield per plant, plant height, and number of pods per plant, 100-pod weight, 100-kernel weight and shelling percentage.

According to Allard (1960), heritability in broad sense can be defined as the proportion of the total genetic variability to the total phenotypic variance. According to Falconer and Mackay (1996), heritability in narrow sense is defined as “the ratio of additive genetic variance to phenotypic variance”. Since broad sense heritability does not give a clear picture of

transmissibility of variation from generation to generation (because the genetic variation includes the fixable and non-fixable dominance and epistatic variation), its utilization is limited in crop improvement programs. In contrast, heritability in a narrow sense has predictive role to indicate the reliability of the phenotypic value as a guide to breeding value.

Heritability and correlations estimate among various agronomic, physiologic and and root traits are useful for planning suitable breeding strategies. Genetic advance (GA) measures the difference between genotypic values of generation obtained from the selected population over the mean value of the population. GA measures the expected genetic progress that would result from selecting the best performing genotype for a given character (Allard, 1960). High heritability and genetic advance estimates enhance selection gains (Johnson et al., 1955). Phenotypic correlations among traits are also important when simultaneous selection of multiple traits is to be carried out for quantitative traits under drought stress conditions (Painawadee, 2009).

Jain et al. (2016) reported pod yield per plant displaying significant positive association with kernel yield per plant, number of mature pods per plant, plant height, shelling percent and number of kernels per pod. Rao (2016) reported that pod yield correlated positively with kernel yield, number of pods per plant, hundred seed weight and SPAD chlorophyll meter reading (SCMR). RWC at 45 days after sowing correlated positively in all drought condition except under normal irrigated condition where the trait was negatively correlated with pod yield. Therefore, a better scope exists for this trait for improvement under drought or limited moisture condition in advanced breeding lines of groundnut (Savita et al. 2014).

1.7 Participatory rural appraisal

Participatory rural appraisal (PRA) is a set of participatory and multi-disciplinary research technique for assessing group and community resources, identifying and prioritizing problems and appraising strategies for solving them (Uddin and Anjuman 2013). It is a research/planning methodology in which a local community (with or without the assistance of outsiders) outlines issues that concern the population, prioritizes problems, evaluates options for solving the problem(s). In PRA, data collection and analysis are undertaken by local people, with researchers facilitating rather than controlling the process. PRA is therefore aimed at enabling local communities to conduct their own analysis and to plan and act (Abedi and Vahidi, 2011), so that, research would develop technologies preferred by farmers. PRA comprises different tools such as resource maps transect walks, semi-structured interviews, focus group discussions, timelines,

wealth ranking, proportional piling, seasonal calendars, Venn diagrams, and pair-wise ranking (Tesfay et al. 2014).

In conclusion, groundnut breeding in SSA is mainly dependent on limited phenotypic selection in segregating generations resulting in low selection efficiencies. Consequently, a limited number of improved groundnut genotypes were developed and deployed. To develop climate resilient, improved varieties with resistance to biotic and abiotic stress tolerance and quality attributes there is need to employ advanced techniques in the breeding processes. These include high-throughput and automated phenotyping techniques, rapid generation advancement, single seed descent approach, marker assisted selection, genomic selection, genetic engineering and genome editing. Integrating new breeding tools in the groundnut breeding programs will assist in rapid identification and selection of promising groundnut genotypes possessing useful agronomic attributes to facilitate development of genetically superior and improved cultivars to boost production in the region. Limited collaborative research and a lack of sustainable funding from groundnut producing countries hindered the progress of groundnut variety release in SSA. Moreover, breeding programs in SSA need to be well-equipped with both human capital and infrastructure through research collaboration and partnerships with potential institutes working on groundnut improvement.

Table 1.5. Summary of some successful groundnut genetic transformation studies.

Genotype	Explant	Transformation method	Promoter	Transgene	Selectable Marker	References
TMV-2	Embryo part	*Agrobacterium* mediated	*CaMV 35S*	Tobacco Chitinase	*npt-II*	Rohini et al. 2001
JL-24	Cotyledon	PROK II binary vector	*CaMV 35S*	*IPCVcp*	*npt-II*	Sharma et al. 2000
K6	IL	*Agrobacterium* mediated	*CaMV 35S*	*TSV-CP*		Mehta et al. 2013
k-134	DEC	*Agrobacterium* mediated	*CaMV 35S*	*TSV-CP*	*npt-II*	Mehta et al. 2013
New Mexico Valencia A	Cotyledon	*Agrobacterium* mediated	*CaMV 35S*	*vp1*	*Npt-II*	Qin et al. 2013
Georgia runner	E AX	Microprojectile bombardment	*ACT-2*	*Mer A*	GUS	Yang et al. 2003
BARI-2000	Cotyledon	*Agrobacterium* mediated	*CaMV 35S*	*AtNHX1 0029*	*npt-II*	Asif et al. 2011
J-11	Cotyledon	*Agrobacterium* mediated	*CaMV 35S*	*IPCVcp*	*npt-II*	Sharma et al. 2000
Florunner	E AX	*Agrobacterium* mediated	*CaMV 35S*	*tswv-np +gus+bar*		Brar et al., 1994
NC-7	Somatic embryo	*Agrobacterium* mediated	*CaMV 35S*	PStV CP4	*hph*	Partridge-Telenko et al. 2011

E AX, embryo axes, *DEC*, de-embryonated, *IL*, immature leaf, *CaMV*, Cauliflower mosaic virus, *ACT-2*, *Arabidopsis* thaliana.

1.8 References

Abedi M, Vahidi F. 2011. The importance of participatory rRural appraisal (PRA) in research. J. Appl. Environ. Biol. Sci. 1: 264-267.

Acquaah G. 2007. Principles of Plant Genetics and Breeding. Wiley- Blackwell, Oxford.

African Institute of Corporate Citizenship. 2016. Malawi Groundnut Outlook. TAURUS House Executive Offices City Centre, Along Convention Drive P/Bag 382 Lilongwe 3 Malawi

Ahmed MSH, Mohamed SMS. 2009. Improvement of groundnut (*Arachis hypogaea* L.) productivity under saline condition through mutation induction. World J Agric Sci. 5: 680-685

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons Inc. New York.

Amare K, Bushra F. 2012. Registration of BaHa-jidu and BaHa-gudo Groundnut (*Arachis hypogaea* L.) varieties. East Afr J Sci. 6: 79-80

Alemayehu C, Berhanu A, Mulugeta T, Abdi M, Tameru A, Helge S. 2014. Opportunities and constraints of groundnut production in selected drylands of Ethiopia. DCG Report No.74. Drylands Coordination Group

Asif MA, Zafar Y, Iqbal J, Iqbal MM, Rashid U, Ali GM, Arif A, Nazir F. 2011. Enhanced expression ofAtNHX1, in transgenic groundnut (*Arachis hypogaea* L.) improves salt and drought tolerance. Mol Biotechnol. 49: 250–256

Asthana AN, Ali M, Chaturvedi SK. 1996. Chickpea. In: Paroda RS, Chadha KL (eds.), 50 years of crop science research in India, Indian Council of Agricultural Research, New Delhi. pp. 287-296

Awada L, Phillips PWB, Smyth S.J. 2018. The adoption of automated phenotyping by plant breeders. Euphytica 214: 148

Azad MAK, Hamid MA, Yasmine F. 2014. Enhancing abiotic stress tolerance in groundnut through induced mutation. In: Tomlekova NB, Kozgar MI, Wani MR (eds) Mutagenesis: exploring genetic diversity of crops. pp. 331-346, Doi: https://doi.org/10.3920/978-90-8686-796-7_1

Azevedo NAD, Nogueira, RJMC, Melo FPA, Santos R. 2010. Physiological and biochemical responses of peanut genotypes to water deficit. J Plant Interact 5: 1-10.

Bagwan HV, Akkiraju PC. 2015. Effect of physical and chemical mutagens on rhizobium and study of mutated rhizobium activity on seed germination and antibiotic sensitivity. Int J Adv Res. 3: 1045-1056

Bai G, Ge Y, Hussain W, Baenziger PS, Graef G. 2016. A multi-sensor system for high throughput field phenotyping in soybean and wheat breeding. Comp Electr Agric. 128: 181-192

Banavath JN, Chakradhar T, Pandit V, Konduru S, Guduru KK, Akila CS, Podha and Puli COR. 2018. Stress inducible overexpression of AtHDG11 leads to improved drought and salt stress

tolerance in peanut (*Arachis hypogaea* L.). Front Chem. 2: 6: 34, Doi: https://doi.org/10.3389/fchem.2018.00034

Bhad PG, Mondal S, Badigannavar AMJ. 2016. Genetic diversity in groundnut (*Arachis hypogaea* L.) genotypes and detection of marker trait associations for plant habit and seed size using genomic and genic SSRs. Crop Sci Biotechnol. 19: 203-221, Doi: https://doi.org/10.1007/s12892-016-0060-1

Bhagwat A, Krishna TG, Bhatia CRJ. 1997. RAPD analysis of induced mutants of groundnut (*Arachis hypogaea* L.). J Genet. 76: 201-208, Doi: https://doi.org/10.1007/BF02932218

Bhattari SP, de la Pena RC, Midmore DJ and Palchamy K. 2009. In vitro culture of immature seed for rapid generation advancement in tomato. Euphytica 167: 23-30

Brar GS, Cohen BA, Vick CL, Johnson GW. 1994. Recovery of transgenic peanut (*Arachis hypogaea* L.) plants from elite cultivars utilizing ACCELL technology. Plant J. 5: 745-753

Brasileiro MAC, Guerra Araujo AC, Leal-Bertioli SC, Guimarães PM. 2014. Genomics and genetic transformation in *Arachis*. Int J Plant Biol Res. 2: 1017

Brock RD. 1977. Prospects and perspectives in mutation breeding. In: Muhammed A, Aksel R, von Borstel RC (eds) Genetic diversity in plants. Basic Life Sciences, Volume 8. Springer, Boston, MA

Busolo-Bulafu CM. 1991. Mutation breeding of groundnuts (*Arachis hypogaea* L.) in Uganda. International Atomic Energy Agency (IAEA): IAEA

Burow MD, Leal-Bertioli SC, Simpson CE, Ozias-Akins P, Chu Y, Denwar NN, Chagoya J, Starr JL, Moretzsohn MC, Pandey MK, Varshney RK, Corley Holbrook C, Bertioli DJ. 2013. Marker-assisted selection for biotic stress resistance in peanut. In: Varshney RK, Tuberosa R (eds) Translational genomics for crop breeding, Doi: https://doi.org/10.1002/9781118728475.ch8

Burton GW, Devane EH. 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal materials. Agron. J. 45: 487-488.

Cilliers AJ, Swanevelder CJ. 2003. The South African germplasm collection of groundnut, *Arachis hypogaea* L., and its utility. SA J. Plant Soil. 20: 93-96

Chamberlin KD, Melouk HA, Madden R, Dillwith JW, Bannore Y, El Rassi Z, Payton M. 2011. Determining the oleic/linoleic acid ratio in a single peanut seed: a comparison of two methods. Peanut Sci. 38: 78-84

Coulibaly MA, Ntare P, Gracen Danquah BR, Gracen VE, Kwadwo O. 2017. Groundnut production constraints and farmers' preferred varieties in Niger. Int J Innov Sci Eng Technol. 4: 2348 -7968

Chintu JMM. 2013. Breeding groundnut for resistance to rosette disease and its aphid vector, *Aphis craccivora* Koch in Malawi. PhD thesis. University of KwaZulu-Natal Pietermaritzburg, Republic of South Africa

Chu Y, Holbrook CC, Timper P, Ozias-Akins P. 2007. Development of a PCR-based molecular marker to select for nematode resistance in peanut. Crop Sci. 47: 841–847, Doi: https://doi.org/10.2135/cropsci2006.07.0474

Crespo-Herrera, LA, Crossa J, Huerta-Espino J, Vargas M, Mondal S, Velu G, Payne TS, Braun HJ, Singh RP. 2018. Genetic gains for grain yield in CIMMYT's semi-arid wheat yield trials grown in suboptimal environments. Crop Sci 58:1890-189, Doi: https://doi.org/10.2135/cropsci2018.01.0017

Collard BCY, Beredo JC, Lenaerts B, Mendoza R, Santelices R, Lopena V, Verdeprado H, Raghavan C, Gregorio GB, Vial L, Demont M, Biswas, PS, Iftekharuddaula KM, Rahman MA, Cobb JN and Mohammad Islam MR. 2017. Revisiting rice breeding methods—evaluating the use of rapid generation advance (RGA) for routine rice breeding. Plant Prod Sci. 20: 337–352, Doi: https://doi.org/10.1080/1343943X.2017.1391705

Corrado G, Rao R. 2017. Towards the genomic basis of local adaptation in landraces. Diversity 9: 51, Doi: https://doi.org/10.3390/d9040051

Daudi H, Shimelis H, Mathew I, Oteng-Frimpong R, Ojiewo C, Varshney RK. 2020. Genetic diversity and population structure of groundnut (*Arachis hypogaea* L.) accessions using phenotypic traits and SSR markers: implications for rust resistance breeding. Genet Resour Crop Evol 68: 581-604, Doi: https://doi.org/10.1007/s10722-020-01007-1

David V, Řepková J. 2017. Application of next-generation sequencing in plant breeding. Czech J Genet Plant Breed. 53: 89−96

Debele S, Ayalew A. 2015. Integrated management of *Cercospora* leaf spots of groundnut (*Arachis hypogaea* L.) through host resistance and fungicides in Eastern Ethiopia. Afr J Plant Sci. 9: 82-89, Doi: https://doi.org/10.5897/AJPS2014.1260

Deom CM, Kapewa T, Busolo-Bulafu CM, Naidu RA, Chiyembekeza AJ, Kimmins FM. 2006. Registration of ICG 12991 peanut germplasm line. Crop Sci 46: 481, Doi: https://doi.org/10.2135/cropsci2005.010

Deshmukh DB, Marathi B, Sudini HK, Variath MT, Chaudhari S, Manohar SS, Rani CVD., Pandey MK, and Pasupuleti J. 2020. Combining high oleic acid trait and resistance to late leaf spot and rust diseases in groundnut (*Arachis hypogaea* L.). Front Genet 11:514, Doi: https://doi.org/10.3389/fgene.2020.00514

Desmae H, Sones K. 2017. Groundnut cropping guide. Africa Soil Health Consortium, Nairobi. CAB International

Desmae H, Janila P, Okori P, Pandey MK, Motagi BN, Monyo E, Mponda O, Okello D, Sako D, Echeckwu C, Oteng-Frimpong R, Miningou A, Ojiewo C, Varshney RK. 2018. Genetics, genomics and breeding of groundnut (*Arachis hypogaea* L.). Plant Breed. 138:425–444

Falconer DS and Mackay TFC. 1996. Introduction to Quantitative Genetics 4th ed.Longman Group Limited, Malaysia. pp.464.

FAOSTAT. 2016. http: www.fao.org/faostat/en/#data/QC. (Accessed 16 July 2016)

FAOSTAT. 2018. http: www.fao.org/faostat/en/#data/QC. (Accessed 10 September 2018)

Faye I, Pandey MK, Hamidou F, Rathore A, Ousmane Ndoye O, Vadez V, Varshney RK. 2015. Identification of quantitative trait loci for yield and yield related traits in groundnut (*Arachis hypogaea* L.) under different water regimes in Niger and Senegal. Euphytica 206: 631-641, Doi: https://doi.org/10.1007/s10681-015-1472-6

Faye B, Webber H, Gaiser T, Diop M, Owusu-Sekyere JD, Naab JB. 2016. Effects of fertilization rate and water availability on peanut growth and yield in Senegal (West Africa). J Sustain Develop, 9: 111-131

Favero AP, Padua JG, Costa TS, Gimenes MA, Godoy IJ, Moretzsohn MC, Michelotto MD. 2015. New hybrids from peanut (*Arachis hypogaea* L.) and synthetic amphidiploid crosses show promise in increasing pest and disease tolerance. Genet Mol Res, 14: 16694-16703

Ferguson ME, Burrow MD, et al. (2004) Microsatellite identification and characterization in peanut (A. hypogaea L.). Theor Appl Genet, 108: 1064–1070.

Frisch M, Melchinger AE. 2005. Selection theory for marker-assisted backcrossing. Genetics 170: 909–917. doi: 10.1534/genetics.104.035451

Gaikpa DS, Akromah R, Asibuo JW, Appiah-Kubi Z, Nyadanu D. 2015. Evaluation of yield and yield components of groundnut genotypes under Cercospora leaf spots disease pressure. Int J Agron Agric. Res. 3: 66-75

Gaur PM, Srinivasan S, Gowda CLL, Rao BV. 2007. Rapid generation advancement in chickpea. J Agric Res, 3: 1-3

Gorbet DW, Knauft DA. 1997. Registration of 'SunOleic 95R' peanut. Crop Sci. 37: 1392

Guchi E. 2015. Stakeholders' perception about aflatoxin contamination in groundnut (arachis hypogaea L.) along the value chain actors in eastern Ethiopia. Int J Food Contam. 2: 1

Gunasekaran A, Pavadai P. 2015. Studies on induced physical and chemical mutagenesis in groundnut (*Arachis hypogia*). Int Lett Nat Sci. 8: 25-35

Guo BZ, Chen X, Dang P, Scully BT, Liang X, Holbrook CC, Jiujiang Yu and Culbreath AK. 2008. Peanut gene expression profiling in developing seeds at different reproduction stages during Aspergillus parasiticus infection. BMC Dev. Biol. 8:12

Guo Y, Khanal S, Tang S, Bowers JE, Heesacker AF, Khalilian N, Nagy ED, Zhang D, Taylor CA, Stalker HT, Ozias-Akins P, Knapp SJ. 2012. Comparative mapping in intraspecific populations uncovers a high degree of macrosynteny between A-and B-genome diploid species of peanut. BMC Genomics 13: 608. https://doi.org/10.1186/1471-2164-13-608

Guimaraes PM, Guimaraes LA, Morgante CV, Silva OB Jr, Araujo ACG, Martins ACQ, Saraiva MAP, Oliveira TN, Togawa RC, Leal-Bertioli SCM, Bertioli DJ, Brasileiro, ACM. 2015. Root transcriptome analysis of wild peanut reveals candidate genes for nematode resistance. PLoSONE 10: e0140937, Doi: https://doi.org/10.1371/journal.pone.0140937

Gulluoglu L, Basal H, Onat B, Kurt C, Arioglu H. 2016. The effect of harvesting on some agronomic and quality characteristics of peanut grown in the Mediterranean region of Turkey. Field Crops Res. 21: 224-232, Doi: https: 10.17557/tjfc.20186

HajHussein O, Assar AHB, Fraah ADM, Al Sir A. 2018. Variability heritability and genetic advance of some groundnut genotypes (*Arachis hypogaea* L.) under saline sodic soil. Ann Rev Res 1:1–5

Hampannavar MR, Khan H, Temburne BV, Janila P, Amaregouda A. 2018. Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.). J Pharm Phytochem. 7: 870-874

Habtamu A. 2016. Review paper on mutation breeding as applied in groundnut (*Arachis hypogea*e L.). Improv Gene Cell Therapy 1: 35-40

He G, Meng R, Newman M, Gao G, Pittman RN, Prakash CS. 2003. Microsatellites as DNA markers in cultivated peanut (*Arachis hypogaea* L.). BMC Plant Biol. 3: 3, Doi: https://doi.org/10.1186/1471-2229-3-3

Hernández-Espinosa, N, Mondal S, Autrique E, Gonzalez-Santoyo H, Cross J, Huerta-Espino J, Singh RP, Guzmán C. 2018. Milling, processing and end-use quality traits of CIMMYT spring bread wheat germplasm under drought and heat stress. Field Crops Res. 215:104-112

Herselman L, Thwaites R, Kimmins FM, Courtois B, van der Merwe PJA and Seal SE. 2004. Identification and mapping of AFLP markers linked to peanut (*Arachis hypogaea* L.) resistance to the aphid vector of groundnut rosette disease. Theor Appl Genet. 109: 1426 –1433. doi 10.1007/s00122-004-1756-z

Holbrook CC, Timper P, Culbreath AK, Kvien CK. 2008. Registration of 'Tifguard' peanut. J Plant Reg. 2: 92–94. doi: 10.3198/jpr2007.12.0662crc

Holbrook CC, Ozias-Akins P, Chu Y, Gou B. 2011. Impact of molecular genetic research on peanut cultivar development. Agronomy 1: 3-17. doi:10.3390/agronomy1010003

Holbrook, C. C., W. Dong, P. Timper, A. K. Culbreath, and C. K. Kvien. 2012. Registration of Peanut Germplasm Line TifGP-2, a nematode-susceptible sister line of 'Tifguard'. J Plant Reg. 6:208-211

Husain F, Mallikarjuna N. 2012. Genetic diversity in Bolivian landrace lines of groundnut (*Arachis hypogaea* L.). Ind J Genet Plant Breed. 72: 384-389

ICRISAT. 2012. Drought-tolerant groundnuts. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. 32 pp

ICRISAT. 2017. Food industry looks forward to commercialization of high-oleic groundnut varieties in India. Happening Newsletter, March No.1739

Janila P, Nigam SN, Pandey MK, Nagesh P, Varshney RK. 2013. Groundnut improvement: use of genetic and genomic tools. Front Plant Sci. 4: 1-16

Janila P, Variath MT, Pandey MK, Desmae H, Motagi BN, Okori P, Manohar SS, Rathnakumar AL, Radhakrishnan T, Boshou Liao B, Varshney RK. 2016. Genomic tools in groundnut breeding program: status and perspectives. Front Plant Sci. doi: 10.3389/fpls.2016.00289

Jaiswal JK, Levini LA, Dakora FD. 2017. Phylogenetically diverse group of native bacterial symbionts isolated from root nodules of groundnut (*Arachis hypogaea* L.) in South Africa. Syst Appl Microbiol. 40:215–226.

Jaradat AA. 2016. Breeding oilseed crops for climate change. Opportunities and constraints. In: Gupta SK (ed) Breeding oilseed crops for sustainable production London, UK, Academic Press, pp. 421-472

Jain S, Singh PB, Sharma PP. 2016. Correlation and path analysis in groundnut (*Arachis Hypogaea* L.). Int J Curr Res. 8: 35811-35813.

Janila P, Nigam SN. 2013. "Phenotyping for groundnut (*Arachis hypogaea* L.) improvement," in Phenotyping for Plant Breeding, eds S. K. Panguluri and A. A. Kumar (New York, NY: Springer Publishing), 129–16

Janila P, Nigam SN, Pandey MK, Nagesh P, Varshney RK. 2016. Groundnut improvement: use of genetic and genomic tools. Plant Sci 4: 1-16.

Jiang GA. 2013. Molecular markers and marker-assisted breeding in plants. In: Andersen SB (ed) Plant breeding from laboratories to fields (46-80). InTechOpen. https://doi.org/10.5772/3362

Johnson HW, Rodinson HF, Cronstrock RE. 1955. Estimation of genetic and environmental variability in soybeans. Agronomy J. 47: 314-318

Kamika I, Takoy LL. 2011. Natural occurrence of aflatoxin B1 in peanut collected from Kinshasa, Democratic Republic of Congo. Food Contam. 22: 1760-1746

Kanyika BTN, Davies D, Mweetwa AM, Kaimoyo E, Njung'e VM, Monyo ES, Siambi M, He G, Prakash CS, Zhao Y, de Villiers SM. 2015. Identification of groundnut (*Arachis hypogaea*) SSR markers suitable for multiple resistance traits QTL mapping in African germplasm. Electr J Biotechnol. 18: 61-67

Kamburova VS, Nikitina EV, Shermatov SE, Buriev ZT, Kumpatla SP, Emani C and Abdurakhmonov IY. 2017. Genome editing in plants: an overview of tools and applications. Hindawi Int J Agron. https://doi.org/10.1155/2017/7315351

Kebede A, Abady S, Endale E, Abdulahi J, Getahun A, Aliyi Robsa A, Yohanese Petros Y. 2017. Registration of 'Babile-1', 'Babile-2', and 'Babile-3' Groundnut Varieties. East Afr J Sci. 11: 59-64

Kebede A, Getahun A. 2017. Adaptability and stability analysis of groundnut genotypes using AMMI model and GGE-biplot. J Crop Sci Biotechnol. 20: 343-349, Doi: https://doi.org/10.1007/s12892

Khute SK, Rao SS, Painkra, P, Markam N. 2018. Combining Ability for Yield and Yield Components in Groundnut (Arachis hypogaea L.). Int J Curr Microbiol App Sci. 7: 2798-2804 Doi: https://doi.org/https://doi.org/10.20546/ijcmas.2018.702.340

Knoll JE, Ramos ML, Zeng Y, Holbrook CC, Chow M, Chen S, Maleki S, Bhattacharya A and Ozias-Akins P. 2011. TILLING for allergen reduction and improvement of quality traits in peanut (*Arachis hypogaea* L.). BMC Plant Biol. 11:81

Kumari V. 2008. Morphological and molecular characterization of induced mutants in groundnut. MSc Dissertation, University of Agricultural Sciences, Darwat, India

Kulthe MH, Kothekar VS. 2011. Effects of Sodium Azide on yield parameters of chickpea (*Cicer arietinum* L.). J Phytol 3: 39-42

Kumari V, Gowda MVC, Tasiwal V, Pandey MK, Bhat RS, Mallikarjuna N, Upadhyaya HD, Rajeev K, Varshney RK. 2014. Diversification of primary gene pool through introgression of resistance to foliar diseases from synthetic amphidiploids to cultivated groundnut (*Arachis hypogaea* L.). Crop J. 2: 110-119

Kumpatla SP, Buyyarapu R, Abdurakhmonov IY, Mammadov JA. 2012. Genomics-assisted plant breeding in the 21st Century: In Abdurakhmonov I (ed) Technological advances and progress, InTech. pp. 132-184

Kushwah A, Gupta S, Sharma SR, Pradhan K. 2017. Genetic variability, correlation coefficient and path coefficient analysis for yield and component traits in groundnut. Ind J Ecol. 44: 85-89

Liang Y, Baring M, Wang S, Septiningsih EM. 2017. Mapping QTLs for leaf spot resistance in peanut using snp-based next-generation sequencing markers. Plant Breed Biotechnol. 5:115–122, Doi: https://doi.org/10.9787/PBB.2017.5.2.115

Lopes MS, El-Basyoni I, Baenziger PS et al. 2015. Exploiting genetic diversity from landraces in wheat breeding for adaptation to climate change. J Exp Bot. 66: 3477–3486, Doi: https://doi.org/10.1093/jxb/erv122

Luis JM, Ozias-Akins P, Holbrook CC, Kemerait RC, Snider Jr. JL, Liakos V. 2016. Phenotyping peanut genotypes for drought tolerance. Peanut Sci. 43: 36–48Mallikarjuna N, Senthilvel S, Hoisington D. 2011. Development of new sources of tetraploid *Arachis* to broaden the genetic base of cultivated groundnut (*Arachis* hypogaea L.). Genet Resour Crop Evol. 58: 889. https:doi/10.1007/s10722-010-9627-8

Mace ES, Phong DT, Upadhyayaet HD al. 2006. SSR analysis of cultivated groundnut (*Arachis hypogaea* L.) germplasm resistant to rust and late leaf spot diseases. Euphytica 152: 317-330, Doi: https://doi.org/10.1007/s10681-006-9218-0

Magamba K, Matumba L, Matita G. et al. 2017. Aflatoxin risk management in commercial groundnut products in Malawi (Sub-Saharan Africa): a call for a more socially responsible industry. J Consum Prot Food Saf. 12: 309-316

Maluszynski M. 2001. Officially released mutant varieties – The FAO/IAEA Database. Plant Cell Tiss Organ Cult. 65:175- 177

Martinez JF, Gimenez JD, Jimenez A, Hernandez L. 1986. Use of the single seed descent method in breeding Safflower (*Carthamus tinctorius* L.). Plant Breed. 97: 364-367

Mastewal A, Sakhuja PK, Mashilla D. 2017. Evaluation of released and local groundnut varieties against groundnut rust (*Puccinia arachidis*) at Babile, Eastern Ethiopia. Open Acc J Agric Res. 2: 000123

Mehta R, Radhakrishnan T, Kumaret A et al. 2013. Coat protein-mediated transgenic resistance of peanut (*Arachis hypogaea* L.) to peanut stem necrosis disease through Agrobacterium-mediated genetic transformation. Ind J Virol. 24: 205-213, Doi: https://doi.org/10.1007/s13337-013-0157-9

Mhlaba ZB, Shimelis HA, Amelework B, Modi AT, Mashilo J. 2018. Variance components and heritability of yield and yield-related traits in tepary bean (*Phaseolus acutifolius*). S Afr J Plant Soil. Doi: https://doi.org/10.1080/02571862.2018.1487593

Michelotto MD, de Godoy IJ, dos Santos JF, Martins ALM, Leonardecz E, Favero AP. 2016. Identifying *Arachis* amphidiploids resistant to foliar fungal diseases. Crop Sci. 56: 1792-1798

Michelotto MD, de Godoy IJ, Pirotta MZ, dos Santos JF, Finoto EL, Favero AP. 2017. Resistance to thrips (*Enneothrips flavens*) in wild and amphidiploid *Arachis* species. PLoS ONE 12: e0176811

Mienie CMS, Pretorius AE. 2013. Application of marker-assisted selection for ahFAD2A and ahFAD2B genes governing the high-oleic acid trait in South African groundnut cultivars (*Arachis hypogaea* L.). Afr J Biotechnol. 12: 4283-4289

Minde I, Madzonga O, Kantithi G, Phiri K, Pedzisa T. 2008. Constraints, challenges, and opportunities in groundnut production and marketing in Malawi. Report No. 4

Mhlaba ZB, Shimelis HA, Amelework B, Modi AT, Mashilo J. 2018. Variance components and heritability of yield and yield-related traits in tepary bean (*Phaseolus acutifolius*). S Afr J Plant Soil. Doi: https://doi.org/10.1080/02571862.2018.1487593

Mondal S, Badigannavar AM, Kale DM, Murty GSS. 2007. Induction of genetic variability in a disease resistant groundnut breeding line. Newsletter, Founders day special issue 285

Mondal S, Badigannavar AM, D'Souza SF. 2010. Development of genic molecular markers linked to a rust resistance gene in cultivated groundnut (*Arachis hypogaea* L.). Euphytica 188: 163-173, Doi: https://doi.org/10.1007/s10681-011-0619-3

Mondal S, Badigannavar AM. 2013. A narrow leaf groundnut mutant, TMV2-NLM has a G to A mutation in AhFAD2A gene for high oleate trait. Ind J Genet. 73: 105-109, Doi: https://doi.org/10.5958/j.0019-5200.73.1.016

Mondal S, Hande P, Badigannavar AM. 2014. Identification of transposable element markers for a rust (*Puccinia arachidis* Speg.) resistance gene in cultivated peanut. J Phytopathol. 162: 548–552, Doi: https://doi.org/10.1111/jph.12220

Monyo ES, Njoroge SMC, Coe R, Osiru M, Madinda F, Waliyar F, Thakur RP, Chilunjika T, Anitha S. 2012. Occurrence and distribution of aflatoxin contamination in groundnuts (Arachis hypogaea L) and population density of *Aflatoxigenic aspergilli* in Malawi. Crop Protec. 42: 149-155

Monyo ES, Varshney RK. 2016. Seven seasons of learning and engaging smallholder farmers in the drought-prone areas of sub-Saharan Africa and South Asia through Tropical Legumes, 2007–2014. ICRISAT, Patancheru

Motagi BN, Vabi MB, Ajeigbe HA, Echekwu CA, Mohammed SG. 2016. Designing effective groundnut breeding strategies through farmers-breeder interactions in Northern Nigeria.

2nd International Conference on Drylands (12th – 16th December 2016). ICRISAT, Patancheru, India. pp 248 – 249

Mothilal A. 2012. Groundnut. In: Gupta S (ed) Technological innovations in major world oil crops, Volume 1. Springer, New York, NY. https://doi.org/10.1007/978-1-4614-0356-2_13

Mothilal A, Ezhil A. 2010. Combining ability analysis for yield and its components in groundnut (Arachis hypogaea L.). Electron J Plant Breed. 1:162-166

Muitia A. 2011. Farmer perceptions and genetic studies of rosette disease in groundnut (*Arachis hypogaea* L.) in northern Mozambique. PhD thesis, University of KwaZulu-Natal, South Africa

Nadaf HL, Kaveri SB, Madhusudan K, Motagi BN. 2009. Induced Genetic variability for yield and yield components in peanut (*Arachis hypogaea* L.). In: Shu QY (ed) Induced Plant Mutations in the Genomics Era. Food and Agriculture Organization of the United Nations (FAO). Rome. pp 346-348

Naeem-UD-Din AM, Gul SSK, Iqbal S, Muhammad FH. 2009. High yielding groundnut (*Arachis hypogea* L.) variety "Golden". Pak J Bot. 41: 2217-2222

Nagy ED, Chu Y, Guo Y et al. 2010. Recombination is suppressed in an alien introgression in peanut harboring Rma, a dominant root-knot nematode resistance gene. Mol Breed. 26: 357-370

Nakashima K et al. 2018. Application of biotechnology to generate drought-tolerant soybean plants in Brazil: development of genetic engineering technology of crops with stress tolerance against degradation of global environment. In: Kokubun M, Asanuma S (ed) Crop production under stressful conditions. Springer, Singapore. https://doi.org/10.1007/978-981-10-7308-3_7

Nath UK, Alam MS. 2002. Genetic variability, heritability and genetic advance of yield and related traits of groundnut (*Arachis hypogaea* L.). J Biol Sci. 2: 762-764

Ndjeunga J, Ntare BR, Abdoulaye A, Ibro A, Zarafi MA, Cisse Y, Moutari A, Kodio O, Echekwu CA, Mohammed SG, Micko I. 2010. Farmer preferences for groundnut traits and varieties in West Africa: Cases of Mali, Niger and Nigeria. Working paper Series no. 27. Working paper. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India

Ngirazi NS, Manjeru P, Ncube B. 2017. Assessment of genotype x environment interaction and pod yield evaluation of groundnut (*Arachis hypogaea* L.) genotypes in Zimbabwe. Afr J Plant Sci. 11: 54-60

Nigam SN, Chandra S, Sridevi KR, Bhukta M, Reddy A.G.S. et al. 2005. Efficiency of physiological trait-based and empirical selection approaches for drought tolerance in groundnut. Ann. Applied Biol. 146: 433-439.

Njoroge SMC, Matumba L, Kanenga K. et al. 2017. Aflatoxin B1 levels in groundnut products from local markets in Zambia Mycotoxin Res. 33: 113

Ntare B, Ndjeunga R, Waliyar J, Kodio F, Echekwu O, Kapran CA et al. 2007. Farmer participatory evaluation and dissemination of improved groundnut varieties in West Africa. ICRISAT. pp 36

Obisesan IO. 1992. Evaluation of pedigree and single seed descent selection methods for cultivar development in cowpea (*Vigna unguiculata* L. Walp). Plant Breed. 108: 162-168

Okello DK, Biruma M, Deom CM. 2010. Overview of groundnuts research in Uganda: Past, present and future. Afr J Biotechnol. 9: 6448-6459

Okello DK, Deom CM, Puppala N, Monyo E, Bravo-Ureta B. 2016. Registration of 'Serenut 5R' Groundnut. J Plant Reg. 10: 115–118

Okello DK, Ugen MA, Tukamuhabwa P, Ochwo-Ssemakula M, Odong TL, Adriko J, Kiconco F, Male A and Deom CM. 2017. Molecular diagnostics of groundnut rosette disease agents in Uganda: Implications on epidemiology and management of groundnut rosette disease. J of Plant Breed Crop Sci. 9, 63–70, Doi: https://doi.org/10. 5897/JPBCS2016.0630

Okello DK, Deom CM, Puppala N, Monyo E, Bravo-Ureta B. 2018. Registration of 'Serenut 6T' Groundnut. J Plant Reg. 12:43-47

Oteng-Frimpong R, Sriswathi M, Ntare BR, Dakora FD. 2015. Assessing the genetic diversity of 48 groundnut (*Arachis hypogaea* L.) genotypes in the Guinea savanna agro-ecology of Ghana, using microsatellite-based markers. Afr J Biotechnol. 14: 2484-2493, Doi: https://doi.org/10.5897/AJB2015.14770

Ortiz R, Trethowan R, Ferrara GO et al. 2007. High yield potential, shuttle breeding, genetic diversity, and a new international wheat improvement strategy. Euphytica 157: 365-384, Doi: https://doi.org/10.1007/s10681-007-9375-9

Pandey MK, Monyo E, Ozias-Akins P, Liang X, Guimarães P, Nigam SN et al. 2012. Advances in *Arachis* genomics for peanut improvement. Biotechnol Adv. 30: 639–651, Doi: 10.1016/j.biotechadv.2011.11.001

Painawadee M, Jogloy S, Kesmala T, Akkasaeng C, Patanothai A. 2009. Heritability and correlation of drought resistance traits and agronomic traits in peanut (*Arachis hypogaea* L.). Asian J Plant Sci. 8: 325-334.

Partridge-Telenko DE, Hu J, Livingstone DM, Shew BB, Phipps PM, Grabau EA. 2011. Sclerotinia blight resistance in Virginia-type peanut transformed with a barley oxalate oxidase gene. Phytopathol. 101: 786-793

Patrick A, Pelham S, Culbreath A, Holbrook CC, de Godoy IJ, Li C. 2017. High throughput phenotyping of tomato spot wilt disease in peanuts using unmanned aerial systems and multispectral imaging. IEEE Instr Measur Mag. 20: 4-12

Prabhu R, Manivannan N, Mothilal A, Ibrahim SM. 2017. Variability analysis for yield, yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). Int J Pure App Biosci. 5: 206-214.

Puppala N, Tallury SP. 2014. Registration of 'NuMex 01' high oleic Valencia peanut. J Plant Reg. 8: 127–130, Doi: https://doi.org/10.3198/jpr2013.11.0070crc

Qin H, Gu Q, Kuppu S, Sun L, Zhu X, Mishra N, Hu R, Shen G, Zhang J, Zhang Y, Zhu L et al. 2013. Expression of the Arabidopsis vacuolar H+-pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. Plant Biotechnol Rep 7: 345-355

Rao, NRC, Talwar HS, Wright GC. 2001. Rapid assessment of specific leaf area and leaf nitrogen in peanut (*Arachis hypogaea* L.) using a chlorophyll meter. J. Agron Crop Sci. 189: 175-182.

Rao T. 2016. Genetic variability, correlation and path coefficient analysis under drought in groundnut (*Arachis hypogaea* L.). Legum Res., 39: 319-322

Raje RS and Rao SK. 2000. Genetic parameters of variation for yield and its components in mungbean (*Vigna radiata* [L.] Wilc.) over environments. Legum Res., 23: 211-216.

Rojas BA, Sprague GF. 1952. A comparison of various components in corn yield traits. General and specific combining ability and their interaction with locations and years. Agron J. 44: 462-466

Rashid JA, Alam MS, Moniruzzaman M, Salim M, Azad MAK, Nat UK. 2012. Genetic study of groundnut (*Arachis hypogaea* L.) mutants for their yield attributes and oil content. Bangl J Progr Sci Technol. 10: 181-186

Remanandan P. 1996. Landraces of the primitive pigeonpea yield economic benefit and contribute to sustainability. Diversity 12:58

Resende MFR, Muzon JP, Acosta JJ et al. 2012. Accelerating the omestication of trees using genomic selection: accuracy of prediction models across ages and environments. New Phytol. 193: 617–624, Doi: https://doi.org/10.1111/j.1469-8137.2011.03895.x

Rohini VK, Rao KS. 2001. Transformation of peanut (*Arachis hypogaea* L.) with tobacco chitinase gene: variable response of transformants to leaf spot disease. Plant Sci. 160: 889–898, Doi: https://doi.org/10.1016/S0168-9452(00)00462-3

Savita SK, Kenchanagoudar PV, Nadaf HL. 2014. Genetic variability for drought tolerance in advanced breeding lines of groundnut (Arachis hypogaea L.). Karnataka J Agric Sci., 27: 116-120.

Sanchez-Dominguez S, Williams DE. 1993. Results of a recent plant exploration in Mexico to collect the hirsuta peanut. Proc Amer Peanut Res Educ Soc. 25: 35

Sanchez PAG, Mesa HJ, Montoya MM. 2016. Next generation sequence analysis of the forage peanut (*Arachis pintoi*) virome. Rev Fac Nac Agron. https://doi.org/10.15446/rfna.v69n2.59133

Saxena K, Saxena RK, Varshney RK. 2017. Use of immature seed germination and single seed descent for rapid genetic gains in pigeonpea. Plant Breed. 136: 954– 957

Setimela P, Prasanna BM, Worku M, Okori P. 2017. Variety release and registration of public bred varieties and land races. SADC Technical Meeting 13-17 November 2017. CIMMYT, Mexico

Sharma B. 1996. Other pulses. In: Paroda RS, Chadha KL (eds.), 50 years of crop science research in India, Indian Council of Agricultural Research, New Delhi. pp. 297-317

Sharma K, Anjaiah V. 2000. An efficient method for the production of transgenic plants of peanut (*Arachis hypogaea* L.) through agrobacterium tumefaciens-mediated genetic transformation. Plant Sci. 159: 7-19, Doi: https://doi.org/10.1016/S0168-9452(00)00294-6

Shakoor N, Lee S, Mockler TC. 2017. High throughput phenotyping to accelerate crop breeding and monitoring of diseases in the field. Curr Opinion Plant Biol. 38:184-192

Sharma NH, Bisen P, Dhakar TR, Bhumica Singh B, Jain S. 2017. Diversity assessment among groundnut (*Arachis hypogaea* L.) genotypes using RAPD Markers. Ind J Ecol. 44: 838-842

Sharma S, Pandey MK, Sudini HK, Upadhyaya HD, Varshney RK. 2017. Harnessing genetic diversity of wild *Arachis* species for genetic enhancement of cultivated peanut. Crop Sci. 57: 1121-1131. doi:10.2135/cropsci2016.10.0871

Shasidhar Y, Vishwakarma MK, Pandey MK, Janila P, Variath MT, Surendra SM, Nigam SN, Guo B and Rajeev K. Varshney RK 2017. Molecular mapping of oil content and fatty acids using dense genetic maps in groundnut (*Arachis hypogaea* L.). Front Plant Sci. 8: 794, Doi: https:// doi.org/10.3389/

Sheshshayee MS, Bindumadhava H, Prasad TG, Udayakumar M, Wright GC, Nigam SN. 2006. Leaf chlorophyll concentration relates to transpiration efficiency in peanut. Ann. Applied Biol., 148: 7-15.

Shilpa K, Sunkad G, Kurella S, Marri S, Padmashree K, Jadhav DR et al. 2013. Biochemical composition and disease resistance in newly synthesized amphidiploid and autotetraploid peanuts. Food Nutr Sci. 4: 169–176, Doi: https://doi.org/10.4236/fns.2013.42024

Simpson, CM, Star JL, Church GT et al. 2003. Registration of NemaTAM peanut. (Registrations of cultivar). Crop Sci. 43: 1561

Simpson CE, Starr JL, Baring MR, Burow MD, Cason JM, Wilson JN. 2013. Registration of 'Webb' Peanut. J. Plant. Reg. 7:265-268

Singh AK. 1986. Utilization of wild relatives in the genetic improvement of *Arachis hypogaea* L. 8. Synthetic amphidiploids and their importance in interspecific breeding. Theor Appl Genet. 72: 433-439

Singh AK, Nigam SN. 2016. Arachis gene pools and genetic improvement in groundnut. In: Rajpal VR, Rao S, Raina S (eds) Gene pool diversity and crop improvement, sustainable development and biodiversity, Volume 10. Springer International Publishing Switzerland. Doi: https://doi.org/10.1007/978-3-319-27096-8

Shoba D, Manivannan N, Vindhiyavarman P, Nigam SN. 2012. SSR markers associated for late leaf spot disease resistance by bulked segregant analysis in groundnut (*Arachis hypogaea* L.) Euphytica 188: 265-272, Doi: https://doi.org/10.1007/s10681-012-0718-9

Sorrells ME. 2015. Genomic selection in plants: empirical results and implications for wheat breeding. In: Ogihara Y, Takumi S Handa H (eds) Advances in wheat genetics: From genome to field. Springer, Tokyo, Doi: https://doi.org/10.1007/978-4-431-55675-6_45

Sprague GF, Tatum LA. 1942. General versus specific combining ability in single crosses of corn. J Am Soc Agron., 34, 923- 932.

Stalker HT, Mozingo LG. 2001. Molecular markers of *Arachis* and marker-assisted selection. Peanut Sci. 28: 117-123

Sui J, Wang Y, Wang P, Qiao L, Sun S, Hu X et al. 2015. Generation of peanut drought tolerant plants by Pingyangmycin-mediated in vitro mutagenesis and hydroxyproline-resistance screening. PLoSONE 10: e0119240.doi:10.1371/ journal.pone.0119240

Sun C, van Raden PM, Cole JB, O'Connell JR. 2014. Improvement of prediction ability for genomic selection of dairy cattle by including dominance effects. PLoSONE 9: e103934. https://doi.org/10.1371/journal.pone.0103934

Tallury SP, Isleib TG, Copeland SC, Rosas-Anderson P, Balota M, Singh D, Stalker H T. 2014. Registration of two multiple disease-resistant peanut germplasm lines derived from *Arachis cardenasii* Krapov. & W.C. Gregory, GKP 10017. J Plant Reg. 8:86-89

Tanaka J, Hayashi T, Iwata H. 2016. A practical, rapid generation-advancement system for rice breeding using simplified biotron breeding system. Breeding Sci. 66: 542-551

Teerawat S, Charassri N. 2010. The efficiency of pedigree and single seed descent selections for yield improvement at generation 4 (F4) of two yardlong bean populations. Kasetsart J. (Natural Science) 44: 343–352

Tesfay G, Gebresamuel G, Gebretsadik A, Gebrelibanos A, Gebremeskel Y, Hagos T. 2014. Participatory Rural Appraisal Report: Raya Azebo *Woreda*, Tigray Region. Cascape Working Paper 2.6.5.

Tiwari S, Tripathi MK, Kumar N, Tomar RS, Joshi E, Tiwari R, Gupta R, Singh AK. 2017. Improvement of groundnut for fatty acids using marker assisted breeding approaches. Int J Pure Appl Biosci. 5: 59-63. https://dx.doi.org/10.18782/2320-7051.5952

Uddin MN, Anjuman N. 2013. Participatory rural appraisal approaches: an overview and an exemplary application of focus group discussion in climate change adaptation and mitigation strategies. Int J Agril Res Innov Tech., 3:72-78

Upadhyaya HD, Ferguson ME, Bramel PJ. 2001a. Status of the *Arachis* germplasm collection at ICRISAT. Peanut Sci. 28: 89-96

Upadhyaya HD, Nigam SN, Mehan VK, Reddy AGS, Yellaiah N. 2001b. Registration of Aspergillus flavus seed infection resistant peanut germplasm ICGV 91278, ICGV 91283, and ICGV 91284 Registration by CSSA. Crop Sci. 41:599-600

Upadhyaya HD, Bramel PJ, Ortiz R, Singh S. 2002. Developing a mini core of peanut for utilization of genetic resources. Crop Sci. 42: 2150–2156

Upadhyayaa HD, Mallikarjuna Swamyb BP, Kenchana Goudarb PV, Kullaiswamy BY, Singha S. 2005. Identification of diverse groundnut germplasm through multie-nvironment evaluation of a core collection for Asia. Field Crops Res. 93: 293–299

Upadhyaya HD, Dwivedi SL, Vadez V, Hamidou F, Singh S, Varshney RK, Liao B. 2014. Multiple resistant and nutritionally dense germplasm identified from mini core collection in peanut. Crop Sci. 54:679-693

Van de Wiel CCM, Schaart JG, Lotz LAP, Smulders MJM. 2017. New traits in crops produced by genome editing techniques based on deletions. Plant Biotechnol Rep. 11: 1–8, Doi: https://doi.org/10.1007/s11816-017-0425-z

Variath MT, Janila P. 2017. Economic and Academic Importance of Peanut. In: Varshney R, Pandey M, Puppala N (eds) The peanut genome. Compendium of plant genomes. Springer, Cham, Doi: https://doi.org/10.1007/978-3-319-63935-2_2

Varshney RK, Bertioli DJ, Moretzsohn MC et al. 2009. The first SSR-based genetic linkage map for cultivated groundnut (*Arachis hypogaea* L.). Theor Appl Genet. 118: 729-39, Doi: https://doi.org/10.1007/s00122-008-0933-x

Varshney RK, Gowda MVC, Radhakrishnan T, Pandey MK, Gautami B, Sujay V, et al. 2010. Development and application of genomic resources for molecular breeding in groundnut (*Arachis hypogaea* L). Proc: The 3rd International Conference on Plant Molecular Breeding (ICPMB), 5–9th September. Beijing, China

Varshney RK, Mohan SM, Gaur PM, Gangarao NVPR, Pandey MK,Bohra A, Sawargaonkar SL, Chitikineni A, Kimurto PK, Janila P et al. 2013. Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-aridtropics. Biotechnol Adv. 31:1120–1134

Varshney RK, Pandey MK, Janila P, Nigam SN, Sudini H, Gowda MVC, Sriswathi M, Radhakrishnan T, Manohar SS, Nagesh P. 2014. Marker-assisted introgression of a QTL region to improve rust resistance in three elite and popular varieties of peanut (*Arachis hypogaea* L.). Theor Appl Genet. 127: 1771-1781, Doi: https://doi.org/10.1007/s00122-014-2338-3

Vindhiyavarman P, Nigam SN, Janila P, Vaidhyalingan M, Manivannan N, Saravanan S, Meenakumari B, Gopalakrishnan C and Kennedy J S. 2014. A new high yielding Spanish bunch groundnut variety CO7 (ICGV 00351) for the drought prone areas of Tamil Nadu. Electr J Plant Breed. 5: 192-196

Waliyar F, Hassan H, Bonkoungou S. 1994. Sources of resistance to *Aspergillus flavus* and aflatoxin contamination in groundnut genotypes in West Africa. Plant Dis. 78: 704-708

Waliyar F, Kumar KVK, Diallo M, Traore A, Mangala UN, Upadhyaya HD and Sudini H. 2016. Resistance to pre-harvest aflatoxin contamination in ICRISAT's groundnut mini core collection. Eur J Plant Pathol. 145: 901-913

Wang H, Lei Y, Yan L, Wan L, Cai Y, Yang Z, Lv J, Zhang X, Xu C, Liao B. 2018. Development and validation of simple sequence repeat markers from *Arachis hypogaea* transcript sequences. Crop J. 6: 172 – 180, Doi: https://doi.org/10.1016/j.cj.2017.09.007

Wells WC, Weiser GC. 1989. Additive genetic variance within populations derived by single-seed descent and pod-bulk descent. Theor Appl Genet. 78: 365-368, Doi: https://doi.org/10.1007/s10681-007-9375-9

Wu L, Chen J, Shi Y, Miao H, Hu W, Qi W, Chen X. 2006. Breeding of Huayu 22 by 60Co γ-rays mutagenesis combined with hybridization. Acta Agric Nucl Sinica. 20: 309-311

Yang H, Nairn J, Ozias-Akins P. 2003. Transformation of peanut using a modified bacterial mercuric ion reductase gene driven by an actin promoter from *Arabidopsis thaliana*. J Plant Physiol. 160: 945–952

Yaw AJ, Richards A, Safo-Kantanka O, Adu-Dapaah, HK, Ohemeng-Dapaah S and Agyeman A. 2008. Chemical composition of groundnut, *Arachis hypogaea* (L.) landraces. Afr J of Biotechnol, 7: 2203-2208.

Yin D, Wang Y, Zhang X, Ma X, He X, Zhang J. 2017. Development of chloroplast genome resources for peanut (*Arachis hypogaea* L.) and other species of *Arachis* Sci Rep. 7: 11649, Doi: https://doi.org/10.1038/s41598-017-12026-x

Yusuf Z, Zeleke H, Mohammed W, Hussein S, Hugo A. 2017. Genetic progress for yield, yield components and other agronomic characters of groundnut (*Arachis Hypogea* L.) cultivars in eastern Ethiopia. Int J Plant Breed Crop Sci. 4: 237-242

Zhao Y, Prakash CS, He G. 2012. Characterization and compilation of polymorphic simple sequence repeat (SSR) markers of peanut from public database. MC Res Notes 5:362

Zhao Y, Zhang C, Chen H Yuan M, Nipper R, C S Prakash CS, Zhuang W, He G.2016. QTL mapping for bacterial wilt resistance in peanut (*Arachis hypogaea* L.). Mol Breed. 36: 13

Zongo A, Nana AT, Sawadogo M, Konate AK, Sankara P, Ntare BR, Desmae H. 2017a. Variability and correlations among groundnut populations for early leaf spot, pod yield, and agronomic traits. Agronomy 7: 52. Doi: https://doi.org/10.3390/agronomy7030052

Zongo A, Khera P, Sawadogo M, Shasidhar Y, Sriswathi M, Vishwakarma MK, Sankara P, Ntare BR, Varshney RK, Pandey MK and Desmae H. 2017b. SSR markers associated to early leaf spot disease resistance through selective genotyping and single marker analysis in groundnut (*Arachis hypogaea* L.). Biotechnol Rep. 15: 132–137

Chapter 2

Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding

---

Abstract

Groundnut (*Arachis hypogaea* L.) is an important food and cash crop globally. The eastern region of Ethiopia is known for its groundnut production despite the low productivity attributable to diverse biotic and abiotic stresses and socioeconomic constraints. The objective of this study was to assess farmers' perceived production constraints, variety choice, and preferred traits of groundnut in eastern Ethiopia to guide future groundnut variety development and release. Participatory rural appraisal studies were conducted in two major groundnut-producing districts (Babile and Fedis) in eastern Ethiopia. Data were collected through a semi-structured questionnaire, transect walks, and focus group discussions. All respondent farmers widely cultivated local or outdated, introduced varieties because of a lack of seed of modern groundnut cultivars. Ninety percent of respondents reported drought stress, mainly occurring during the flowering stage, as the leading constraint to groundnut production. Other groundnut production constraints, included poor soil fertility (reported by 88% of respondents), lack of access to improved seed (67%), pre-harvest diseases (59.5%), use of low yielding varieties (52.5%), inadequate access to extension services (41.5%), limited access to credit (21.5%), and limited availability of improved varieties (18.5%). Farmer-preferred traits, included high shelled yield (reported by 27.67% of respondents), early maturity (16.84%), and tolerance to drought stress (13.67%), market value (11.17%), good grain quality (10%), adaptability to local growing conditions (5.8%), and resistance to diseases (5.17%). Therefore, the aforementioned production constraints and farmer-preferred traits are key drivers that need to be integrated into groundnut breeding and variety release programs in eastern Ethiopia.

Keywords: *Arachis hypogaea*, participatory rural appraisal, seed system, soil fertility

---

This chapter was published in the Journal of Crop Improvement. Seltene Abady, Hussein Shimelis and Pasupuleti Janila (2019). Farmers 'perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding. 1-17. doi: 10.1080/15427528.2019.1625836

2.1. Introduction

Groundnut or peanut (*Arachis hypogaea* L.; 2n = 4x = 40) is one of the major food and oil seed crops in the world. It is an annual legume crop that is predominantly self-pollinated. Groundnut is a rich source of oil (45-56%), protein (25-30%), carbohydrates (9.5-19.0%), minerals (P, Ca, Mg and K) and vitamins (E, K and B) (Gulluoglu et al. 2016). It is used in intercropping or crop rotation systems because of its ability to improve soil fertility through atmospheric nitrogen fixation (Ajeigbe et al. 2014). Globally, groundnut is cultivated on 27.66 million ha, with an annual total production of 43.98 million tons (FAOSTAT 2018). The leading groundnut producing countries in the world are India (20.97%), China (16.35%), Nigeria (9.68%) and Sudan (8.37%) (FAOSTAT 2018).

In Ethiopia, groundnut is commonly produced for food, cash income and animal feed. It is solely grown by smallholder farmers under dryland conditions in the lowland and drought-prone areas of the country. The national mean yield is 1.796 tons/ha, and the total area under groundnut production is 80,841.57 ha (CSA 2018). In the country, groundnut is largely produced in the Oromia Region, constituting 59.2% of the total national production, followed by Benishangul-Gumuz (24.83%), Amhara (7.43%), Harari (3.29%) and Southern Nation and Nationalities People (1.29%) regions (CSA 2018). The eastern parts of Ethiopia, encompassing Babile, Fedis and Gursum, are the leading groundnut-producing zones (Chala et al. 2013; Guchi et al. 2014). Babile and Fedis districts are characterized by low and erratic, poorly distributed rainfall. Further, fungal diseases, such as early leaf spot (*Cercospora arachidicola)*, late leaf spot (*Phaeoisariopsis personata*) and rust (*Puccinia arachidis*) are the major factors limiting groundnut production in these agro-systems. A limited number of introduced groundnut varieties were released for cultivation in the country (MoANRs, 2016). For instance, Babile-1 and Babile-2, with a relatively high pod yield and moderate resistance to leaf spot disease, were released in 2016. However, these varieties are late maturing and low yielding, and were not bred for drought tolerance. Therefore, there is need to develop groundnut varieties with tolerance to abiotic and biotic stresses that are adapted for cultivation under rainfed and drought-affected agro-ecologies.

Understanding farmer- and market-preferred traits and identification and prioritization of their production constraints are crucial to enhance the adoption rate of improved varieties among farmers and their value chains (Nigam et al. 2005; Daudi et al. 2018). Participatory rural appraisal (PRA) is a multidisciplinary tool that is reportedly effective in capturing farmers' perceptions regarding their production constraints, variety choice and trait preferences (Banla et al. 2018; Amelework et al. 2016). It enables farmers to conduct their own analysis, plan and take action. PRA studies have been successfully used in Togo and Tanzania to guide crop breeding programs through pinpointing production challenges and market- and farmer-preferred quantitative and qualitative traits of groundnut (Banla et al. 2018; Daudi et al. 2018). Banla et al. (2018) identified, through participatory assessment, leaf spot diseases, rosette and groundnut bud necrosis as key

production constraints to groundnut in Togo. Daudi et al. (2018) reported the major groundnut production constraints to be diseases, insect pests, drought and non-availability of improved varieties in Tanzania. In Ethiopia, sorghum researchers used PRA tools and indicated the important sorghum production constraints to be moisture stress, insect pests, *Striga*, shortage of agricultural land, poor soil fertility, diseases, and lack of improved varieties with farmer-preferred traits (Amelework et al. 2016; Derese et al. 2017; Mengistu et al. 2018). However, in the major groundnut-production belts of eastern Ethiopia, there is no recent study documenting farmers' perceived production constraints, and market- and farmer-preferred traits. Up-to-date and well-described production constraints and prioritized traits of groundnut are key drivers for developing new cultivars. This should enable release of high-performing cultivars possessing suitable product profiles relevant to farmers and their value chains. Therefore, the objective of the current study was to assess farmers' perceived production constraints, variety choice and preferred traits of groundnut to guide breeding of drought-tolerant and high-yielding varieties adapted to the eastern Ethiopia agro-ecologies.

2.2. Material and methods

2.2.1. Description of the study areas

The study was carried out in 2018 in two selected districts of eastern Ethiopia, viz., Babile (9^0 13' 09'' N latitude and 42^0 19' 25'' E longitude; 1642 meters above sea level) and Fedis ($9^0$07'N Latitude and $42^0$4'E Longitude; 1702 meters above sea level) (Figure 2.1). Babile is situated some 35 km away from Harar and about 555 km east of Addis Ababa. The district has a total area of 3,169.06 km^2 (Musa et al. 2016) and a population of 115,229 (CSA 2013). It has a predominantly well-drained sandy loam soil that is ideal for groundnut production. The rainfall distribution of the area is bimodal, with the main rain (locally referred to as *Meher* rain) received during July to October and short rain (locally known as *Belg* rain) during March to May (Anteneh 2017). The mean annual maximum and minimum temperatures are 28.1^0C and 15.5^0C, respectively, with the total annual rainfall ranging from 507 to 984 mm. Rainfall distribution at Fedis is also bimodal. Fedis has a total area of 1,105.02 km^2 (Musa et al. 2016) and a population of 135,532 (CSA, 2013). The mean annual maximum and minimum temperatures in Fedis are 27.8^0C and 8.8^0C, respectively, with a total annual rainfall of 659.2 mm (Anteneh, 2017).

2.2.2 Sampling procedures

A multi-stage sampling technique was implemented to ensure good representativeness of groundnut grower households in the study areas. In the first stage, the districts of Babile and Fedis were selected from the Oromia region (eastern Hararghe zone) on the basis of their current high levels of groundnut production. In the second stage, four peasant associations (PAs), viz., Ifa, Tula, Bishan Babile and Likale were selected from Babile and two PAs, viz., Balina Arba and

Tuta Balina were selected from Fedis district. Twenty-five farmers were selected in each peasant association on the basis of their experience in groundnut production. This provided a total of 150 farmers for face-to-face interviews. Furthermore, four focus group discussions (FGDs) were held, two in Babile district and two in Fedis district. Each FGD comprised 12 to 15 participants, representing farmers, district extension experts and developmental agents (DAs). During the FGDs, four DAs and one district extension expert were involved in each district. A checklist was prepared for the FGDs, which focused mainly on groundnut production constraints, uses, groundnut variety preference and marketing aspects.

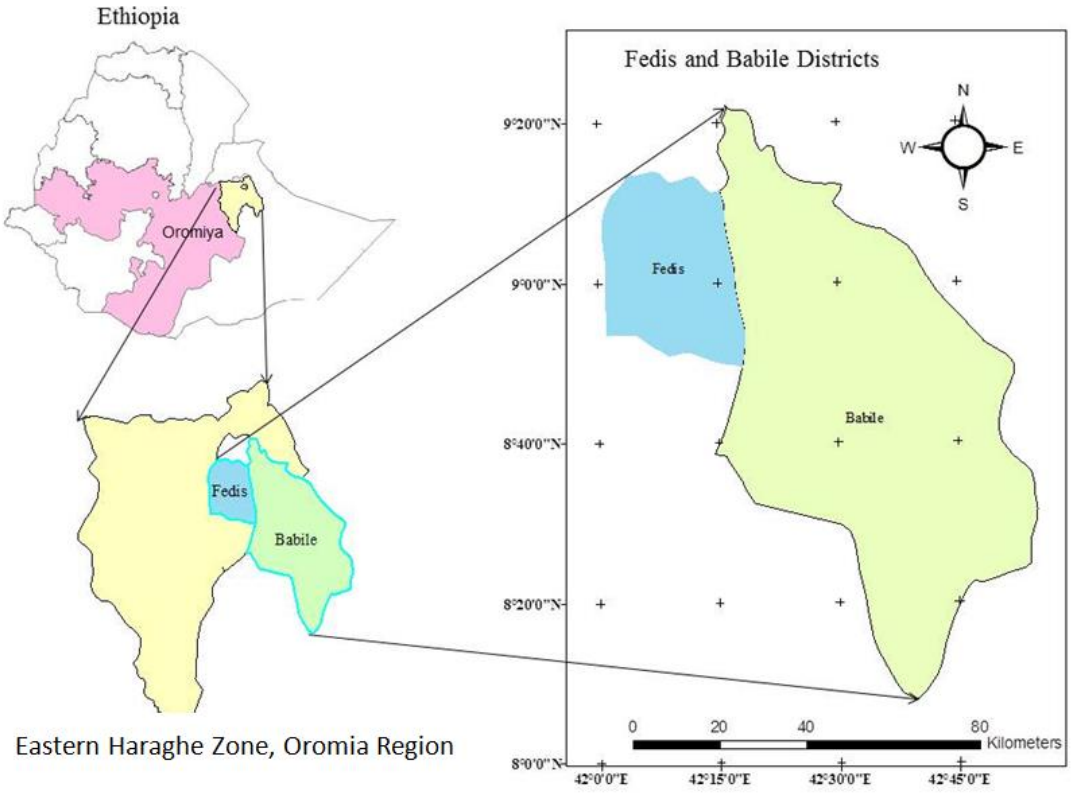


Figure 2.1. Map of Ethiopia showing the study sites.

2.2.3. Data collection

Data were collected using a semi-structured questionnaire, transect walks and FGDs. DAs and district extension experts facilitated the FGDs and data collection. Data were collected on demographic descriptors (e.g., gender, education status, and farm size), groundnut farming system, and farmers' knowledge about improved groundnut varieties, constraints to groundnut production, market access, and varietal trait preference.

2.2.4. Data analysis

Both qualitative and quantitative data were coded and analyzed using the Statistical Package for the Social Sciences software version 22 (SPSS 2013). Data were subjected to analysis using the cross-tabulation procedure and descriptive statistics, such as frequencies and percentages, were determined. Further, Chi-square and t-test analyses were conducted to determine statistical significance among the test parameters across districts.

2.3. Results and discussion

2.3.1. Socio-economic descriptions of households

The present study highlighted the socio-economic characteristics of groundnut farmers in eastern Ethiopia using the variables, gender, age, family size, education level and farm size (Table 2.1). Out of the 150 farmers interviewed, 16.5% were women and 83.5% men. There was a highly significant difference ($p<0.01$; $\chi^2 = 12.91$) in gender representation between the two districts. Participation of women in groundnut production was relatively higher in Babile district (29%) compared with Fedis (4%). Among the respondent farmers, 56.5% were between 31 and 50 years of age, indicating that groundnut production was dominated by middle-aged adults. About 35.5% of the respondents were categorized as young adults (Table 2.1).

There was a significant difference ($p < 0.05$; $\chi2 = 8.559$) in family size between the two districts (Table 2.1). In Babile, 57% of the respondents had a family size of 6 to 9 individuals, whereas in Fedis, 52% of respondents had a family size of ≤5 individuals. About 54% of the respondents had 1 to 5 grade education, 4.5% had 6 to 8 grade education, and the rest of the farmers (41.5%) had no formal education (Table 2.1). Due to the low level of education in the study areas, agricultural service providers need to communicate with the farmers using vernacular language in transmitting the latest technical knowledge or new technologies for their rapid adoption. This concurs with the findings of Daudi et al. (2018) in Tanzania.

About 74.5% of respondents owned a farm of < 2 ha, whereas 24.5% owned a farm of 2 to 3.5 ha and 1% owned a farm of > 3.5 ha. In both districts, groundnut was the third most important food

and cash crop in the area after sorghum and maize, the key food security crops in the study areas (Figure 2.2). During the FGDs, farmers explained that they used a low amount of inorganic fertilizers for cereal crops grown after groundnut, due to its ability to fix valuable nitrogen into the soil.

Table 2.1. Demographic and socio-economic information about the farmers in the study areas.

		District							
		Babile†		Fedis‡					
Variable	Category	Frequency	Percent	Frequency	Percent	%mean	*df*	χ^2	*P value*
Gender	Male	71	71	48	96	83.5	1	12.91	0.000
	Female	29	29	2	4	16.5			
Age (year)	18-30	29	29	21	42	35.5	2	4.121	0.127
	31-50	59	59	27	54	56.5			
	>50	12	12	2	4	8			
Family size	≤5	33	33	26	52	42.5	2	8.559	0.014
	6-9	57	57	24	48	52.5			
	≥10	10	10	0	0	5			
Education status	Illiterate	39	39	22	44	41.5	2	5.962	0.051
	1-5	60	60	24	48	54			
	≥6	1	1	4	8	4.5			
Farm land size (ha)	<2	67	67	41	82	74.5	2	4.154	0.125
	2-3.5	31	31	9	18	24.5			
	>3.5	2	2	0	0	1			

†No. number of respondents at Babile = 100, df = degrees of freedom, χ^2 = Chi square, p = probability,
‡No. of respondents at Fedis = 50

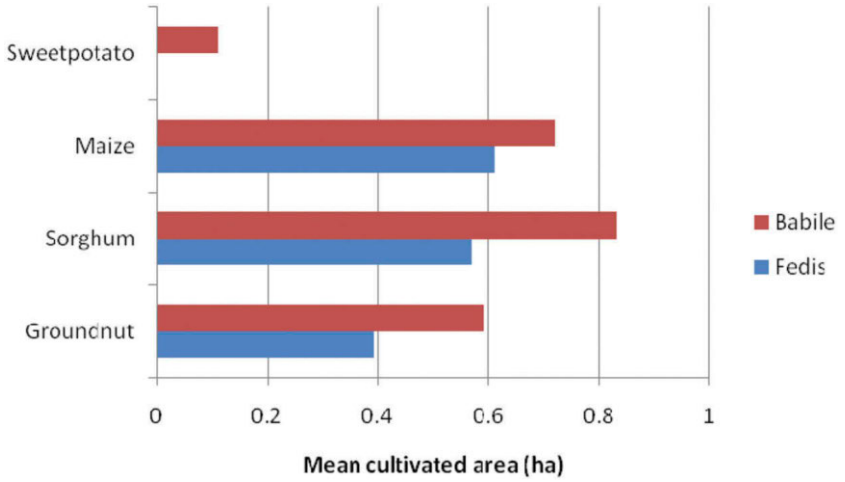


Figure 2.2. Mean cultivated land (ha) allocated for major food and cash major crops grown during the 2017/18 cropping season in the study areas.

2.3.2. Roles of farmers in groundnut farming and marketing

The roles of farmers in various groundnut farming and marketing activities are summarized in Table 2.2. Selection of suitable seed is one of the most important agronomic practices in groundnut production. In the study areas, limited numbers of local or improved varieties were available. Consequently, the respondent farmers did not have options in selecting a suitable variety for production. Farmers practiced mass selection among the available landrace varieties. Results revealed that seed selection was mainly done by men (reported by 68.7% of respondents); participation by women was substantially less (31.3%). During the study period, groundnut production fields were mainly prepared by men (78%); by women (9.3%), by children (1.3%), by men and women (4.7%), by men and children (2%), by women and children (2%), and by men, women and children (2.7%). Hand weeding in groundnut is commonly done twice in a cropping season; 28% of men and 10.7% of women participated in this practice during the study period.

In the present study, women were also involved in key groundnut post-harvest activities, such as shelling (42% of respondents), fumigation of storage facility (82%) and storing (43.3%). Groundnut shelling is the most challenging postharvest operation. This activity was left to women and children in the study areas. Hand shelling keeps the rate of kernel breakage low compared with mechanical shelling. However, hand shelling is labor-intensive, time-consuming and leads to sore thumb syndrome or painful wounds on fingers when large quantities are handled (Gitau et al. 2013). In this regard, farmers in the study areas desired efficient and affordable shellers.

During groundnut harvesting, men, women and children were involved in both study areas. Groundnut pod shelling was done largely by women and children, who accounted for 68.7% of this activity. In the study areas, groundnut is mostly sold unshelled, while a limited amount is sold shelled. Farmers in the study area used shelled groundnut for home consumption, planting and selling in the local market. Results indicated that groundnuts were sold mostly by men (reported by 63.3% of respondents) and women (32.6%). In addition, children (2%), men and women (0.7%), men and children (0.7%) and men, women and children (0.7%) were engaged in groundnut selling. The main marketplace for groundnuts was Harar city for the Fedis district, which is located about 24 km away from Fedis. Similarly, groundnut farmers in Babile district sold their produce in Babile town and Harar city. During the study period, 100 kg of unshelled groundnut were sold [500 Birr (about 18 USD)]. The low groundnut price in the study areas was attributable to poor market access and a lack of storage and processing facilities or value addition. Often, farmers accessed market information from neighbors and nearby farmers.

Table 2.2. Roles of farmers in various groundnut farming and marketing activities (%) in both study areas.

Role	Men	Women	Children	Men and women	Men and children	Women and children	Men, women and children
Seed selection	68.7	31.3	0	0	0	0	0
Land preparation	78.0	9.3	1.3	4.7	2	2	2.7
Planting	52	9.3	0	25.3	0	13.3	0
Fertilizer application	35.3	24.6	2.7	22.7	0	14.7	0
Weeding	28	10.7	0	35.3	2	0	24
Harvesting	22.6	0	0	0.7	0	2	74.7
Shelling	8.0	42	8.7	0	0	18.0	23.3
	9.3	82.0	0	2	0	6.7	0
Storing	46.0	43.3	0	10.7	0	0	0
Selling	63.3	32.6	2	0.7	0.7	0	0.7

2.3.3. Groundnut cropping system and production status

Table 2.3 contains a summary of perceptions by farmers about their soil type, fertility status and type of fertilizer used in groundnut production during the 2017/2018 cropping season. It was noted that the predominant soil types in the study areas were sandy, sandy loam, silty clay loam and clay soils, reported by 35.5, 55%, 8.5% and 1% of respondents, respectively. There was a highly significant difference ($p<0.01$; $\chi^2 = 92.487$) in soil type between the two districts. In Babile, 67% of agricultural land was sandy, whereas in Fedis, most of the soil type (96%) was sandy loam. The fertility status of groundnut production area could be regarded as good (30%), medium (48%)

and poor (22%) based on farmer-perception and field observations through transect walks. Most of the respondents (66%) used inorganic fertilizers for groundnut production. Among the farmers that used inorganic fertilizers, 93.7% used urea and 6.3% used diammonium phosphate (DAP). Farmers who used fertilizers indicated obtaining better pod yield (Figure 2.3). Depending on soil tests, side application of calcium (Ca) in the form of gypsum at 250-500 kg/ha during peak flowering stage could enhance unshelled groundnut yield (Prasad et al. 2010). Calcium is an important nutrient for groundnut because of its ability to improve pod filling. Therefore, further research is needed to determine the optimum rate of Ca for improving groundnut yield and quality and fertilizer-use efficiency.

Farmers in Babile district used a seed rate of 90 kg/ha, whereas a seed rate of 94 kg/ha was used in Fedis because of frequent dry spells and poor seed germination. The seed rates used by farmers are in agreement with the national recommendation, which is between 60-110 kg/ha (Amare et al. 2017). A t-test showed a highly significant difference ($p<0.01$) in unshelled yields between the two districts. Higher mean unshelled yield was recorded in Babile (1375 kg/ha) compared with Fedis district (1301 kg/ha) (Table 2.4). However, the yields reported by farmers in both districts were lower than the mean national yield of 1796 kg/ha in the same year (CSA 2018). According to the respondent farmers, 94% of groundnut was cultivated as a sole crop and 6% was intercropped with sorghum. Almost all groundnut growers (97%) practiced crop rotation with sorghum; a small proportion used maize (3%) instead of sorghum.

Understanding production status of a particular crop in a given area is useful for generating information on how and why the crop is replaced by other crops (i.e., reduced production status) or replacing other crops (increased status). In addition, this issue may also be related to other factors, such as market demand and access, utilization and production constraints, which may affect the production status of the crop. In the present study, 54% respondents perceived that groundnut production areas had remained constant, 16% indicated that area increased; while the remainder, 30%, indicated that production area had decreased (Table 2.5). The perceptions were further explored through FGDs. Fifty-four percent of the respondents reported that groundnut production remained constant because of increased number of family members and a lack of agricultural land. Under this circumstance, farmers would need to maximize their groundnut productivity through the utilization of inputs like improved varieties and other recommended agronomic practices. Fan et al. (2012) reported an increased total groundnut production in China that was mainly attributable to increased yield per unit area rather than expansion in the cultivated area. Idoko and Sabo (2014) suggested that small-scale groundnut producers could have increased their production capacity if technology packages and capital were made available to them. Availability of seeds of resource-use efficient cultivars and adoption of integrated crop management technologies, together with enabling policy

environment, can contribute to acceleration and stabilization of groundnut production (Upadhyaya and Dwivedi 2015). Further, farmers reported that the main reasons for reduced production area were several biotic and abiotic stress factors, and socioeconomic constraints, such as poor market linkages.

Table 2.3. Farmers' perception about soil type, soil fertility status, fertilizer use and type in groundnut production in the study areas.

		District							
		Babile		Fedis					
Variable	Category	Frequency	Percent	Frequency	Percent	%mean	df†	χ^2	P value
Soil type	Sandy	67	67	2	4	35.5	3	92.487	0.000
	Silty clay loam	17	17	0	0	8.5			
	Sandy loam	14	14	48	96	55			
	Clay	2	2	0	0	1			
Soil fertility status	Poor	14	14	15	30	22	2	6.023	0.049
	Medium	50	50	23	46	48			
	Good	36	36	12	24	30			
Fertilizer application	Yes	78	78	27	54	66	1	9.143	0.002
	No	22	22	23	46	34			
Fertilizer type	Urea	71	91.03	26	96.3	93.675	1	0.792	0.374
	DAP†	7	8.97	1	3.7	6.335			

†*df* = degrees of freedom, χ^2 = Chi square, *p* = probability, DAP = Diammonium phosphate

Table 2.4. Comparison of groundnut production management practices and yield potential in the study areas.

Management practices and yield	Babile					Fedis				
	Mean	SD†	Std. Error	*df*	*t*-value	Mean	SD†	Std. Error	*df*	*t*-value
Seed rate (kg/ha)	90.97	14.83	1.48	99	61.355**	94.24	26.28	3.72	49	25.357**
Urea fertilizer (kg/ha)	44.44	24.69	2.93	70	15.168**	61.73	33.73	6.62	25	9.331**
DAP‡ fertilizer (kg/ha)	42.86	12.20	4.61	6	9.295**	50.00	.00[a]	.00	-	-
Yield (kg/ha)	1375.63	344.94	34.49	99	39.881**	1301.20	479.46	67.81	49	19.190**

SD = standard deviation, Std. Error = standard error, *df* = degrees of freedom, DAP = Diammonium Phosphate, ** denote highly significant difference at p<0.01 probability level.

†SD = standard deviation

‡DAP = Diammonium phosphate

-denotes t value was computed because the standard deviation is 0

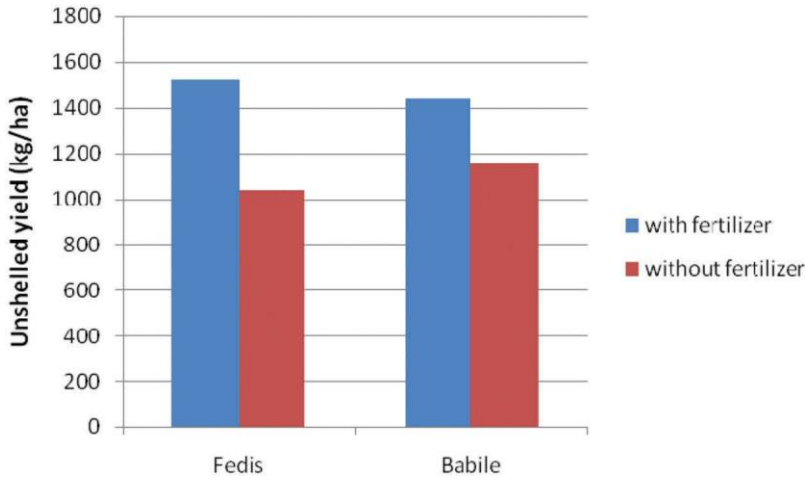


Figure 2.3 Comparison of unshelled groundnut yields (kg/ha) with and without fertilizer use in 2018 cropping season in Fedis and Babile areas.

Table 2.5. Farmers' groundnut cropping system and perceptions on production trends.

		District				
		Babile†		Fedis‡		
Variable	Category	Frequency	Percent	Frequency	Percent	%mean
Cropping system	Sole cropping	94	94	47	94	94
	Intercropping	6	6	2	6	6
Groundnut rotation with	Sorghum	98	98	48	96	97
	Maize	2	2	2	4	3
Groundnut production status	Constant	48	48	30	60	54
	Increasing	26	26	3	6	16
	Decreasing	26	26	17	34	30

†No. of respondents at Babile = 100 and ‡No. of respondents at Fedis = 50

2.3.4. Farmers' awareness about groundnut varieties

Farmers were not aware of improved groundnut varieties in their areas. About 75.5% of the farmers reported a lack of information about improved varieties. Farmers in the study areas continuously cultivated three groundnut varieties, i.e., Oldhale, Sartu and Roba. About 13% of the respondents used variety Roba. Roba (ICG 7794) is a large-seeded and late-maturing groundnut variety. It is an introduced variety, released in 1989, for cultivation in high rainfall areas in Ethiopia (MoANRs 2016). Oldhale and Sartu are landrace groundnut varieties. Oldhale has an upright growth habit, while Sartu is with a runner or prostrate growth form. During the FGD, a few female farmers in Babile mentioned using Roba to process groundnut butter. About 44.5% of the respondents grew variety, Oldhale, whereas 42.5% of the farmers grew Sartu. During FGD, participants explained that Oldhale was used for its good oil quality and grain yield potential. Based on seed size, farmers made selections and found three sub-groups of the variety Oldhale: large, medium and small. Farmers used large seeds of this variety for production, with the expectation that large seeds provided better shelled yield. Farmers used small and medium size seeds of the same variety for household oil processing.

In the study areas, groundnut is mainly consumed in a roasted form and large-seeded groundnuts are highly preferred for this purpose. Farmers in the study areas classified Sartu as early maturing and Oldhale as medium maturing varieties; these were highly preferred for their relatively better drought tolerance. Based on FGD and transect walks, it was noted that groundnut varieties in the study areas were susceptible to root rot and leaf spot diseases.

Chi-square analysis revealed the presence of a significant difference between the two districts for groundnut seed sources ($p<0.05$; $\chi^2 = 19.95$) (Table 2.6). Because of low access to seeds of improved varieties, 42% of the farmers used groundnut seed obtained from other farmers, whereas 37.5% used own farm-saved seed. About 7% of farmers used seed received from research centers (National Groundnut Research Program of Haramaya University and Fedis Agricultural Research Centers), 10.5% sourced seed through government extension program and 3% received seed from non-government organizations (NGOs), such as Self Help, the Hararghe Catholic Secretariats (HCS) and Catholic Relief Service (CRS). In the study areas, there were no private or government groundnut seed enterprises. Consequently, farmers could not get access to seeds of improved groundnut varieties. In the present study, the adoption rate of improved varieties was low (13%). This implies that unless the seed system in these areas is improved, farmers will continue to use local unimproved varieties. Govindaraj et al. (2009) reported 65% yield increase in groundnut because of the adoption of improved varieties. Therefore, sustainable groundnut production and productivity can be ensured through the development of improved varieties and supply of quality seeds to the farmers. Access to quality seed needs to be enhanced

by involving all stakeholders, including government institutions, NGOs, farmer cooperatives and unions.

During the FGD, farmers mentioned that, because of various production constraints, groundnut yields had declined during the past years. For instance, more than 85% farmers reported a lack of access to improved groundnut varieties. About 47.5% of the respondents participated in training on groundnut technology transfer. Three quarters (74) of farmers were involved in technology transfer, of which 29% and 26% participated in farmers' field days and on-farm trial activities, respectively (Table 2.6). In this study, farmer training centers were the best source of information and technology transfer option, followed by attendance at farmers' field days and on-farm trials. Therefore, the linkage between technology provider institutes and extension service providers was encouraging, which needs to be strengthened further. Furthermore, demonstration of improved varieties at farmer training centers has to be sustainably implemented.

Table 2.6. Farmers' awareness about improved groundnut varieties, seed sources and participation in technology transfer activities (%).

		District							
		Babile		Fedis					
Variable	Category	Frequency	Percent	Frequency	Percent	%mean	*df*	χ^2	*P* value
Seed source	Farmers saved	45	45	15	30	37.5	4	19.95	0.001
	Government Extension	3	3	9	18	10.5			
	NGOs†	2	2	2	4	3			
	Research Centers	14	14	0	0	7			
	Other farmers	36	36	24	48	42			
Information about improved varieties	Yes	19	19	15	30	24.5	1	2.301	0.129
	No	81	81	35	70	75.5			
Variety grown	Roba	22	22	2	4	13	2	39.51	0.000
	Sartu	17	17	34	68	42.5			
	Oldhale	61	61	14	28	44.5			
Participation in technology transfer	Yes	53	53	21	42	47.5	1	1.614	0.204
	No	47	47	29	58	52.5			
Method of technology transfer	On-farm trial activities	16	30.19	4	19.05	24.62	3	7.054	0.07
	Invited to farmers field day	8	15.09	9	42.86	28.98			
	FTC‡	27	50.94	8	38.10	44.52			
	Learning from other farmers	2	3.77	0	0.00	1.89			

†df = degrees of freedom, χ^2 = Chi square, p = probability; FTC = Farmers Training Center; NGOs = non-government organizations

‡FTC = Farmers Training Center

2.3.5. Rainfall pattern

In the study areas, groundnut is cultivated only under rainfed conditions and the crop stand is often prone to drought stress, notably at the flowering stage. Table 2.7 contains a summary of the frequency of drought stress, susceptible growth stage of groundnut and farmers' drought-coping mechanism. There was a non-significant difference ($p>0.05$; $\chi^2 = 5.479$) in frequency of drought stress between the two districts. About 42.5%, 45.5% and 12% of the respondents mentioned drought occurred in groundnut production once every year, once every 2 years and once every 3 years, respectively. Results showed that 83% of drought stress occurred during the main cropping season (July to October) and 17% during the offseason production (March to May). A large majority of the respondents (80.5%) reported that drought stress occurred during the flowering stage, whereas 12% and 7.5% of the respondents reported drought stress being critical during seedling and pod-filling stages, respectively. Meisner and Karnok (1992) reported 49% and 37% unshelled yield reduction in groundnut because of drought stress during peak flowering and early pod-filling stages, respectively. Girdthai et al. (2010) reported that terminal drought stress or end-of-season drought reduced unshelled yield by 35%. In the study areas, the main rainfall is expected between mid-March and early-April, during which farmers plant groundnut. Delayed rainfall and poor distribution, such as extending up to May, are often associated with drought stress and subsequent crop failures. As a drought-stress-coping mechanism, 48.5% of the farmers replaced groundnut with other food security crops, such as sorghum and maize; 32.5% of the farmers resorted to planting an early-maturing groundnut variety (e.g., variety Sartu), 19% of the respondents grew a relatively drought-tolerant groundnut variety, Oldhale.

Table 2.7. Farmers' experience regarding of drought stress in groundnut production and their coping mechanism.

		District							
		Babile†		Fedis‡					
Variable	Category	Frequency	Percent	Frequency	Percent	%mean	*df*	χ^2	*P* value
Frequency of drought stress	Every 1 year	47	47	19	38	42.5	2	5.479	0.065
	Every 2 years	47	47	22	44	45.5			
	Every 3 years	6	6	9	18	12			
Drought season	*Belg* (march to May)	70	70	48	96	83	1	13.427	0.000
	Meher (July to October)	30	30	2	4	17			
Growth stage affected by drought	Seedling	12	12	6	12	12	2	8.462	0.015
	Flowering	73	73	44	88	80.5			
	Grain feeling	15	15	0	0	7.5			
Copping mechanism of drought	Early maturity variety	47	47	9	18	32.5	2	12.123	0.002
	Drought tolerant variety	16	16	11	22	19			
	Replace with other crop	37	37	30	60	48.5			

†No. df = degrees of freedom, χ^2 = Chi square, p = probability, number of respondents at Babile = 100
‡No. of respondents at Fedis = 50

2.3.6. Constraints to groundnut production

In the study areas, groundnut production was constrained by various biotic and abiotic stresses (Table 2.8). There was a nonsignificant difference ($P>0.05$; $\chi^2 = 16.315$) in production constraints between the two districts. Farmers identified the major groundnut production constraints as follows: drought stress (90% of respondents), poor soil fertility (88%), poor supply of improved seed (67%), pre-harvest diseases (e.g., root rots and leaf spots) (59.5%), low-yielding varieties (52.5%), poor access to extension services (41.5%), poor access to credit (21.5%) and limited availability of improved varieties (18.5%). Appendix 2.1 summarizes the historical weather data of the study areas, for main cropping seasons, between May and October (1985-2016). Depending on the availability of rainfall, groundnut is planted at the beginning of May. The

rainfall trend indicates that the study areas receive low rainfall in the month of June and this period coincides with flowering stage of groundnut which agrees with farmers experiences recorded during the PRA study.

Farmers in the study area reported poor soil fertility as the next yield-limiting factor in groundnut production. Anteneh (2017) reported low soil fertility status as one major abiotic constraint to sustainable groundnut production in the same study areas, which agrees with the present study. Groundnut diseases, such as root rot and leaf spot, are among the most important biotic factors that limit groundnut production. As a good disease-management practice, farmers grew groundnut in rotation with cereal crops like sorghum (Table 2.5). However, more effective disease control options, such as the use of resistant varieties, ensured sustainable groundnut production. Farmers in the study areas recycled groundnut seeds of the same variety year after year. This practice is conducive to disease build-up and reduces seed germination percentage, viability and vigor, which significantly affect the performance of the crop. Extremely low seed replacement rate is one of the hindrances to introducing high-yielding varieties (Singh and Singh, 2016). Thus, effective strategies need to be developed to enhance the seed replacement rate of the crop.

Conversely, farmers in Fedis district reported *Orobanche* spp. being noxious weeds. *Orobanche* weeds may cause 5-100% yield loss in oilseed crops, especially in the arid and warmer areas (Habimana et al. 2014). Because *Orobanche* control through hand weeding is laborious and not fully effective hence application of herbicides is recommended to enhance production and productivity.

Table 2.8. Farmer- perceived constraints to groundnut production in eastern Ethiopia (%).

Production constraints	District		mean	df	χ^2	P value
	Babile	Fedis				
Drought stress	88	92	90	15	16.315	0.361
Poor soil fertility	78	98	88			
Poor supply of improved seed	64	70	67			
Pre-harvest diseases	67	52	59.5			
Low yielding varieties	51	54	52.5			
Low access to extension services	37	46	41.5			
Low access to credit	15	28	21.5			
Limited availability of improved varieties	23	14	18.5			
Undesired improved varieties	21	16	18.5			
Post-harvest diseases	10	24	17			
Limited agricultural lands	13	20	16.5			
Lack of appropriate storage facility	10	20	15			
Limited availability of inorganic fertilizers	14	12	13			
High cost of seed	11	14	12.5			
Insect pests	15	8	11.5			
High cost of commercial fertilizers	8	12	10			

df = degrees of freedom, χ^2 = Chi square, *p* = probability

2.3.7. Farmer-preferred traits of groundnut variety

There was a nonsignificant difference ($p>0.05$; $\chi^2 = 10.891$) in farmer-preferred traits of groundnut variety between the two districts. Farmer-preferred traits were high shelled yield (reported by 27.67% of respondents), early maturity (16.84%), tolerance to drought stress (13.67%), market value (11.17%), good grain quality (10%), adaptability to local growing conditions (5.8%), and resistance to diseases (5.17%). (Table 2.9). Though 90% of respondents mentioned that drought is a major constraint to groundnut production in the study areas, farmers preferred to grow high yielding (27.67%) and early maturing (16.84%) varieties compared to drought tolerance (10%). During the FGD, farmers indicated that large seed, uniform seed size, and tan to red kernel color were market-preferred traits, with price premium. Further, farmers preferred to grow groundnut varieties with upright growth habit rather than runner types because of their being unsuitable for intercropping.

Table 2.9. Farmer-preferred traits of a groundnut variety in the study areas.

Trait	District								
	Babile		Fedis						
	Frequency	Percentage	Frequency	Percentage	% mean	Rank	df	χ^2	*P* value
High Yield	74	24.67	46	30.67	27.67	1	9	10.89	0.283
Good Seed quality	38	12.67	11	7.33	10	5			
Early maturity	57	19	22	14.67	16.84	2			
Drought tolerance	38	12.67	22	14.67	13.67	3			
Resistance to field insect pests	8	2.67	3	2	2.34	10			
Resistance to diseases	11	3.66	10	6.67	5.17	7			
Resistance to storage pests	9	3	9	6	4.5	8			
Marketability	39	13	14	9.33	11.17	4			
Best adaptability	17	5.67	9	6	5.84	6			
Good biomass	9	3	4	2.67	2.84	9			

df = degrees of freedom, χ^2 = Chi square, *p* = probability

2.4. Conclusions

In the present study, farmers identified drought stress, poor soil fertility, poor seed supply systems, pre-harvest diseases (root rot and leaf spot), low yielding varieties, limited access to extension services, low access to credit and limited availability of improved varieties as the major groundnut production constraints. Among the identified production constraints, recurrent drought was reported by the majority of the respondents to significantly reduce unshelled groundnut yield across the study areas. Farmers cultivated unimproved landraces and few obsolete and late-maturing introduced varieties. The present study found that farmers sought high-yielding and well-adapted modern groundnut varieties for production under drought stress, poor soil fertility and diseases. Results also indicated a lack of sustainable groundnut seed system in the region. There is a need to strengthen formal, semi-formal, and private seed systems to sustain the supply of new varieties in the region. The study identified the following farmer-preferred traits: high shelled yield, early maturity, drought tolerance, market value, good seed quality and adaptability to local growing conditions and resistance to diseases. Therefore, groundnut breeding programs should consider and integrate the production constraints and farmer-preferred traits during the development of improved varieties. This would enhance the production and productivity of groundnut in eastern Ethiopia.

2.5. References

Ajeigbe, H.A., F. Waliyar, C.A. Echekwu, K. Ayuba, B.N. Motagi, D. Eniayeju, and A. Inuwa. 2014. A farmer's guide to groundnut production in Nigeria. Patancheru 502 324, Telangana, India: International Crops Research Institute for the Semi-Arid Tropics. P. 36

Amare, K. and B. Feysal. 2012. Registration of BaHa-jidu and BaHa-gudo groundnut (*Arachis hypogaea* L.) varieties. East African Journal of Sciences 6:79-80

Amare, K., A. Seltene, E. Daniel, A. Jemal, G. Adissu, R. Aliyi, and P. Yohanese. 2017. Registration of 'Babile-1', 'Babile-2', and 'Babile-3' groundnut varieties. East African Journal of Sciences 11: 59-64

Amelework, B.A., H.A. Shimelis, P. Tongoona, F. Mengistu, M.D. Laing, and D.G. Ayele. 2016. Sorghum production systems and constraints, and coping strategies under drought-prone agro-ecologies of Ethiopia. South African Journal of Plant and Soil 33 (3) 207-217, Doi: https://doi.org/10.1080 /02571862.2016.1143043

Anteneh, A. 2017. Development of environmental friendly bioinoculate for peanut (*Arachis hypogea* L.) production in eastern Ethiopia. Environmental Systems Research 6:23. doi:10.1186/s40068-017-0100-y

Banla, E.M., D.K. Dzidzienyo, I.E. Beatrice, S.K. Offei, P. Tongoona, and H. Desmae. 2018. Groundnut production constraints and farmers' trait preferences: a pre-breeding study in Togo. Journal of Ethnobiology and Ethnomedicine 14:75. Doi: https://doi.org/10.1186/s13002-018-0275-y

Central Statistical Agency (CSA). 2013. Population projection of Ethiopia for all regions at woreda level from 2014 – 2017. CSA, Addis Ababa

Central Statistical Agency (CSA). 2018. Agricultural sample survey 2017/18: Report on area and production of major crops (private peasant holdings, main season), Vol.1. CSA, Addis Ababa

Chala A., A. Mohammed, A. Ayalew, and H. Skinne. 2013. Natural occurrence of aflatoxins in groundnut (*Arachis hypogaea* L.) from eastern Ethiopia. Food Control 30:602-605, Doi: https://doi.org/10.1016/j.foodcont.2012.08.023

Daudi, H., H. Shimelis, M. Laing, P. Okori, & O. Mponda (2018): Groundnut productioconstraints, farming systems, and farmer-preferred traits in Tanzania. Journal of Crop Improvement. Doi: https://doi.org/10.1080/15427528.2018.1531801

Derese, S.A., H. Shimelis, M. Laing & F. Mengistu. 2017. The impact of drought on sorghum production, and farmer's varietal and trait preferences, in the north eastern Ethiopia: implications for breeding. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science. Doi: https://doi.org/10.1080/09064710.2 017.1418018

Fan, M., J. Shen, L. Yuan, R. Jiang, X. Chen, W.J. Davies, and F. Zhang. 2012. Improving crop productivity and resource use efficiency to ensure food security and environmental quality in China. Journal of Experimental Botany 63: 13–24, Doi: https://doi.org/10.1093/jxb/err248

FAOSTAT. 2018. Food and Agriculture Organization of the United Nations Database of agricultural production. FAO Statistical Databases. Available at *http*: www.fao.org/faostat/ (accessed 25 Feb. 2019)

Girdthai, T., S. Jogloy, N. Vorasoot, C. Akkasaeng, S. Wongkaew, C.C. Holbrook, and A. Patanothai. 2010. Associations between physiological traits for drought tolerance. Plant Breeding. 129: 693-699, Doi: https://doi.org/10.1111/j.1439-0523.2009.01738.x

Gitau, A.N., P. Mboya, B.N.K. Njoroge, and M. Mburu. 2013. Optimizing the performance of a manually operated groundnut (*Arachis hypogaea*) decorticator. Open Journal of Optimization 2:26-32, Doi: https://doi.org/10.4236/ojop.2013.21004

Govindaraj, G., G.D.S. Kumar, and M.S. Basu. 2009. Benefits of imporved groundnut technologies to resource-poor farmers: A participatory approach. Agricultural Economics Research Review 22:355-360

Guchi, E., A. Ayalew, M. Dejene, M. Ketema, B. Asalf, and C. Fininsa. 2014. Occurrence of *Aspergillus species* in groundnut (*Arachis hypogaea* L.) along the value chain in different agro-ecological zones of eastern Ethiopia. Journal of Applied & Environmental Microbiology 2: 309-317, Doi: https://doi.org/10.12691/jaem-2-6-7

Gulluoglu, L., H. Bakal, B. Onat, C. Kurt, and H. Agrioglu. 2016. The effect of harvesting on some agronomic and quality characteristics of peanut grown in the Mediterranean region of Turkey. Turkish Journal of Field Crops 21: 224-232, Doi: https://doi.org/10.17557/tjfc.20186

Habimana,S., A. Nduwumuremyi, J.D. Chinama, 2014. Management of orobanche in field crops-A review. Journal of Soil Science and Plant Nutrition 14:43-62, Doi: https://doi.org/10.4067/S0718-951620140 05000004

Idoko, M.D. and E. Sabo. 2014. Challenges in groundnut production and adoption of groundnut production technology information packages among women farmers. Agriculture and Biology Journal of North America 5: 252-258, Doi: https://doi.org/10.5251/abjna.2014.5.6.252.258

Meisner, C. A., and K.J. Karnok. 1992. Peanut root response to drought stress. Agronomy Journal 84: 159-65, Doi: https://doi.org/10.2134/agronj1992.00021962008400020007x

Mengistu G., H. Shimelis, M. Laing, and D. Lule. 2018. Assessment of farmers' perceptions of production constraints, and their trait preferences of sorghum in western Ethiopia: implications for anthracnose resistance breeding. Acta Agriculturae Scandinavica, Section B — Soil & Plant Science. Doi: https://doi.org/10.1080/09064710.20 18.1541190

Ministry of Agriculture and Natural Resources (MoANRs). 2016. Crop Variety Register Issue No. 19. Plant Variety Release. Protection and Seed Quality Control Directorate. MoANRs, Addis Ababa

Musa H.A., M.M. Hiwot, A. Seltene, M. M. Wendmagegn, and K. Amare, 2016. Adoption of improved groundnut seed and its impact on rural households' welfare in Eastern Ethiopia. Cogent Economics and Finance. 4:1268747, Doi: https://doi.org/10.1080 /23322039.2016.1268747

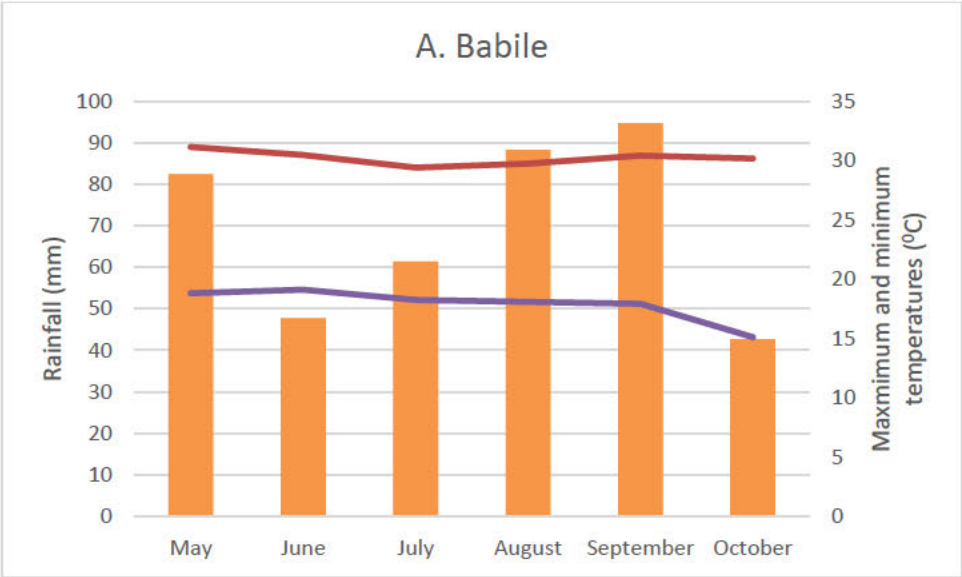
Nigam, S.N., R. Aruna, D.Y. Giri, T.Y. Reddy, K. Subramanyam, B.R.R. Reddy, and K.A. Kareem. 2005. Farmer participatory varietal selection in groundnut – A success story in Anantapur, Andhra Pradesh, India. International *Arachis* Newsletter (25):13-15

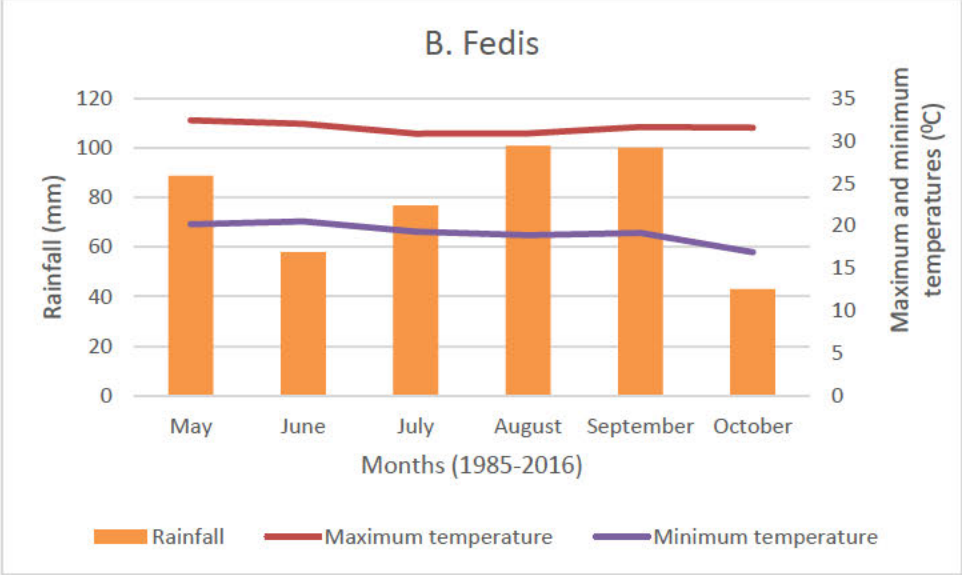
Prasad, P. V. V. and V.G. Kakani, and H.D. Upadhyaya. 2010. Growth and production of groundnut. In: Soils, Plant growth and crop production. Encyclopedia of Life Support Systems (EOLSS), Developed under the Auspices of the UNESCO, Oxford UK. Pp. 1-26

Singh, R.P. and S. Singh. 2016. Optimizing seed replacement rates In Jharkhand: Present scenario, challenges and opportunities. Jharkhand Journal of Development and Management Studies 14: 6987-7007

SPSS 2013. IBM SPSS Statistics for Windows, Version 22.0. Armonk, NY: IBM Corp

Upadhyaya, H.D., and S.L. Dwivedi. 2015. Global perspectives on groundnut production, trade, and utilization: constraints and opportunities. In: national seminar on technologies for enhancing oilseeds production through NMOOP, January 18-19, 2015, PJTSAU, Hyderabad





Appendix 2.1. Monthly mean rainfall, minimum and maximum temperatures of (A) Babile and (B) Fedis districts during the main groundnut production season of May to October 1985 to 2016.

Chapter 3

Assessment of the diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield, and oil and haulm quantity and quality under moisture stress conditions

---

Abstract

Recurrent drought is the main factor limiting groundnut yield, oil and fodder quality. Breeding and deployment of drought tolerant and high yielding genotypes with quality attributes is essential to meet the requirements of the food and feed sectors. The objective of this study was to determine drought tolerance, kernel and fodder yield and quality amongst diverse groundnut genotypes for direct production or breeding. One hundred genotypes were evaluated at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)/India during 2018/19 and 2019/20 under drought-stressed (DS) and non-stressed (NS) conditions using a 10 x 10 alpha lattice design with two replications. Data were collected on kernel yield (KY), oil content (OC), oil yield (OY), protein content (PC), palmitic acid content (PAC), stearic acid content (SAC), oleic acid content (OAC) and linoleic acid content (LAC), haulm yield (HY) and fodder quality parameters such as the contents of dry matter (DM), ash, nitrogen (NC), neutral detergent fiber (NDFDM), acid detergent fiber (ADFDM), acid detergent lignin (ADLDM), *in vitro* digestibility (IVOMD) and metabolizable energy (ME). Data were subjected to parametric and non-parametric statistical analyses. Combined analysis of variance revealed significant ($P< 0.05$) genotype differences for all assessed traits. Genotype × water regime interaction effects were significant for KY, OC, ash content, NC, NDFDM and ADLDM. Kernel yield positively and significantly ($P<0.05$) correlated with oil yield ($r = 0.99$), LAC ($r = 0.13$), ash ($r = 0.32$), NDFDM ($r = 0.54$) under DS condition. Haulm yield was positively and significantly ($P<0.05$) correlated with OC ($r = 0.24$), NDFDM ($r = 0.19$), ADFDM ($r = 0.18$) and ADLDM ($r = 0.17$) under DS condition. Cluster analysis grouped the test genotypes into 12 distinct genetic groups. The study identified genotypes, ICGV 10178, ICGV 01260, ICGV 06175 and ICGV 10379, with high kernel and haulm yields, and CGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063, with high oleic acid content. Further, genotypes, ICGV 7222, ICGV 10143, ICGV 6040, ICGV 03042, ICGV 06175, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, were selected with relatively better drought tolerance. The selected genotypes are recommended for further breeding and variety release under drought-stressed environments.

Keywords: Abiotic stress, *Arachis hypogaea*; drought tolerance, fatty acids, fodder quality

---

This chapter has been published in Crop Science, 2021; 1–18. https://doi.org/10.1002/csc2.20483

3.1. Introduction

Groundnut (*Arachis hypogaea* L., 2n = 4x = 40) is an important oilseed crop with multiple uses in the food and feed sectors. It is cultivated in diverse agro-ecologies including the semi-arid tropics and sub-tropical regions globally. Groundnut is mainly cultivated as a source of vegetable oil for local, regional and international markets (Ojiewo et al. 2020). Further, groundnut kernels are eaten raw, roasted, boiled or processed into groundnut butter (Janila et al. 2016). The oil content of groundnut kernels varies from 45 to 56% (Sarvamangala et al. 2011; Bishi et al. 2013; Yol et al. 2017). Groundnut oil is one of the premium cooking oils for its stability at high temperatures and higher smoke point conditions compared with soybean and rapeseed oils (Choe and Min, 2007). Groundnut kernels contain macro-and micro-nutrients such as calcium (920 mg/kg), magnesium (1690 mg/kg), potassium (7054 mg/kg), iron (46mg/kg) and Zinc (33mg/kg) (Nigam, 2014). The kernels are also rich in vitamins (e.g. vitamins E, K and B) and protein (~25%) (Sarvamangala et al. 2011; Janila et al. 2014). The main fatty acids present in groundnut are oleic acid (80%), linoleic acid (~40%) and palmitic acid (5 to 10%) (Bishi et al. 2013). It also consists of minor fatty acids such as stearic, arachidic, eicosenoic, behenic, lignoceric and gadoleic acids each accounting between 1 to 3% of the total fatty acid (Andersen et al. 1998). Groundnut genotypes with oleic acid content $\geq$ 78% are referred to as high oleic genotypes and possess oil with longer shelf life (Janila et al. 2018a; Deshmukh et al. 2020). The high auto-oxidative stability nature of oleic acid is a key factor attributing to the extended shelf life of the oil (Nawade et al. 2018). Groundnut oil with high linoleic acid content is prone to oxidation, which result in unpleasant odor and taste, and reduced shelf-life (Shasidhar et al. 2020). Therefore, high oleic acid/linoleic acid ratio is a desired quality parameter to enhance the shelf-life of groundnut oil. Developing groundnut genotypes with high oleic acid is a key breeding objective for human health, product quality and to access the lucrative market opportunities (Nawade et al. 2018).

Groundnut haulm serves as an important feed source for livestock in fresh or dry forms. This is essential in the crop-livestock farming systems such as in Ethiopia and other arid and semi-arid regions where grazing lands are limited (Oteng-Frimpong et al. 2017; El-Sabagh et al. 2019; Abady et al. 2019). Reportedly, the haulm contains protein ranging from 8–15%, lipid (1–3%), minerals (9 = 17%) and carbohydrates (38–45%) (Janila et al. 2016). These attributes make groundnut haulm as a quality fodder source for supplementing the diet of livestock. Key quality parameters of the haulm include the contents of nitrogen, *in vitro* organic matter digestibility and metabolized energy (Joshi et al. 2019). *In vitro* organic matter digestibility is the proportion of organic matter that is digested in the ruminant digestive tract. Metabolizable energy is the net energy available for animal growth or reproduction after fecal and urinary energy loss (Samireddypalle et al. 2017). Conversely, carbohydrate components such as high neutral detergent fiber, acid detergent fiber, and acid detergent lignin have negative impact on haulm

quality due to their indigestibility (Samireddypalle et al. 2017). Neutral detergent fiber includes all cell wall components and acid detergent fiber. Acid detergent fiber corresponds to cellulose and lignin contents (Mertens, 2000).

Due to its multiple uses and relatively higher drought tolerance, groundnut is grown in the mixed crop-livestock production systems in sub-Saharan Africa and Asia, mainly by small-holder farmers. These agro-ecosystems are drought-prone where land, water and natural pastures are becoming increasingly scarce (Abady et al. 2019). Drought stress caused by low precipitation is the leading cause of the decline of natural grazing lands resulting in high livestock mortality. For example, Tanzania livestock mortality, herd value and income losses attributed to drought accounted for 5, 4 and 31%, respectively (Ahmed et al. 2019). Similarly, small-holder farmers in some parts of Ghana reported chronic water shortages for both human and livestock due to drought (Ngcamu and Chari, 2020). Drought stress occurring during the reproductive growth stage is most devastating and can lead to a yield loss reaching up to 33% (Pereira et al. 2016; Carvalho et al. 2017). Therefore, it is an overriding consideration to develop and deploy dual-purpose groundnut cultivars with high kernel and haulm yields and associated quality parameters with drought tolerance. In the past there was no dedicated groundnut breeding program that aimed at breeding genotypes with high kernel and haulm yields with quality attributes under drought stress environments.

Groundnut exhibits extensive phenotypic and genotypic diversity (Upadhyaya et al. 2005; Pandey et al. 2012; Ren et al. 2014; Zheng et al. 2018). Moreover, marked variation for drought tolerance has been reported in groundnut germplasm collections (Hamidou et al. 2012; Falke et al. 2019; Oteng-Frimpong et al. 2019). These present opportunities to develop fit-for-purpose genotypes for food and feed with drought tolerance. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in India maintains the world's largest collection of groundnut germplasm which has essential sources for genetic variation with desirable attributes for breeding. The groundnut genetic resources at ICRISAT mainly comprise of the Spanish (sub-species *fastigiata*) and Virginia (sub-species *hypogaea*) market types. Many of these genotypes possess desirable agronomic traits which can be exploited to designing new groundnut cultivars (Singh and Nigam, 2016). Therefore, the diverse groundnut germplasm collections can be sourced and rigorously evaluated for drought tolerance and kernel and fodder yield, and associated quality traits to select unique genotypes for breeding. In light of the above background, the objective of this study was to determine the response of diverse groundnut genotypes for drought tolerance, kernel and fodder yield and quality for direct production or breeding.

3.2. Material and methods

3.2.1. Plant materials, site description and experiment design

One hundred groundnut genotypes acquired from ICRISAT/Patancheru, India, were used for the study. The majority of these genotypes are currently used in the groundnut breeding program in Ethiopia, and the remaining lines were recently developed by ICRISAT. The list of the genotypes with pedigree information is shown in Table 3.2. Of these genotypes, 70 belonged to the subsp. *fastigiata* var. *vulgaris and 30 to the* subsp. *hypogaea* var. *hypogaea.* The genotypes were selected based on desirable traits, including drought tolerance, resistance to foliar diseases such late leaf spot and rust, high oil and oleic acid contents, and being early-to-medium maturing. The genotypes (Appendix 3.1) were evaluated under drought-stressed (DS) and non-stressed (NS) conditions at ICRISAT (latitude, 17.51^0N, longitude, 78.27^0E and altitude 545 m) during 2018/2019 and 2019/2020 post-rainy seasons (December to May) using a 10 x 10 alpha lattice design with two replications. Seeds of each genotype were sown in 4 rows of 4-meter-long with 30 cm between rows and 10 cm between plants. The field was maintained with regular irrigation until flowering for NS and DS treatments, after which irrigation was withdrawn for the DS treatment to induce moisture stress. For the NS treatment, sufficient irrigation was supplied until physiological maturity. Other agronomic practices were carried out following the standard guideline for groundnut production (Janila et al. 2018b). Table 3.1. Presents weather data during field trials. The mean minimum and mean maximum temperatures during 2018/19 and 2019/20 were 18.86/34.28 and 19.45/33.39 C^0, respectively.

Table 3.1. Monthly weather data during the field trial at ICRISAT/India (2018/19 and 2019/20 post-rainy seasons).

Year	Month	Rainfall (mm)	Tmax (^{0}C)	Tmin (^{0}C)	RHmax (%)	RHmin (%)
2018/19	December	2.75	26.97	14.45	95.52	54.00
	January	0.29	29.03	12.31	95.35	41.39
	February	0.09	32.44	17.63	86.54	43.03
	March	0	36.84	20.3	80.19	36.71
	April	1.08	39.39	23.48	68.60	25.93
	May	0.93	41.03	25.01	56.75	20.81
Mean		0.86	34.28	18.86	80.49	36.98
2019/20	December	0	28.23	15.79	92.26	69.05
	January	0.07	29.75	16.39	90.58	61.9
	February	0.05	31.48	16.87	86.86	53.41
	March	0	34.72	20.24	84.23	50.23
	April	0.7	37.52	22.77	77.57	23.23
	May	0.51	38.64	24.61	79.19	50.06
Mean		0.22	33.39	19.45	85.12	51.31

Tmax = average maximum temperature, Tmin = average minimum temperature, RHmax = average maximum relative humidity, RH min = average minimum relative humidity

Table 3.2. Descriptions of the groundnut genotypes used for genetic diversity analysis.

Serial number	Genotype	Pedigree	Trait	Drought tolerance	Origin	Market type	Sub-species	Breeding history
1	ICGV 16667	ICGV 06110 x (ICGV 06110 x Sun Oleic 95-R) F1P2-BC1F1P3-P9-P4-P5-P1-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
2	ICGV 93128	(ICGMS 42 x Kadiri 3) F_2-B1-B2-B2-B2-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
3	ICGV 95066	(ICGV 86388 x ICGV 86029) F4-B1-B1-B2	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
4	ICGV 96174	{[(Florigiant x NCAc17090) x (Dh-3-20 x PI259747)] x ICGV 88312} F_2-SSD(2)-B2-B1(2)-B2-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
5	ICGV 97087	{(Florigiant x NCAc 17090)x[(Dh3-20 x PI259747)x ICGV 88312]} F2-SSD-SSD-B2-B1(6)	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
6	ICGV 98077	[(ICGV 86185 x ICGV 86743) x Kadiri 134] F2-SSD-SSD-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
7	ICGV 01279	(ICGV 92069 x ICGV 93184) F2-SSD-B3-B1-B2-B3-B1-B1-B1-P3-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
8	ICGV 03042	{ICGV 99160 x [ICGV 93124 x (LI x ICGS 44)]} F2-SSD-SSD-B1-B1-B1	HO	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
9	ICGV 06039	[(ICGV 92069 x ICGV 93184) x (NC Ac 343 x ICGV 86187)S23] F2-SSD-SSD-P4-P1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
10	ICGV 06040	[(ICGV 92069 x ICGV 93184) x (NC Ac 343 x ICGV 86187)S23] F2-SSD-SSD-P5-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
11	ICGV 07010	(ICGV 00043 x ICGV 00064) F2-SSD-SSD-P6-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
12	ICGV 10143	(ICGV 01274 x ICGV 05063) F2-SSD-SSD-P8-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
13	ICGV 11422	(ICGV 01274 x ICGV 04124) F2-SSD-SSD-P1-B1-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
14	ICGV 11396	(ICGV 99159 x ICGV 95047) F2-SSD-SSD-P11-B1-B1-B1-B1-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
15	ICGV 11418	(ICGV 01274 x ICGV 05063) F2-SSD-SSD-P7-B1-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
16	ICGV 91223	[ICGV 87165 x (ICG 9516 x ICGS 30)] F2-B1-B1-B1-B1-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
17	ICGV 94118	[(J 11 x CS 52) x ICGV 86015] F2-B1-B1-B1-B2-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
18	ICGV 99019	(ICGV 94118 x ICGV 92209) F2-SSD(S)-B5-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
19	ICGV 00162	(259-2 x ICGV 93197) F2-P14-B1-B1-B2-B2-B1(SB)	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL

Table 3.2. Continued

Serial number	Genotype	Pedigree	Trait		Origin	Market type	Sub-species	Breeding history
20	ICGV 00211	(ICGV 94118 x ICGV 93388) F_2-P5-B1-B1-B1-B1-B1(SB)	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
21	ICGV 00187	(ICGV 94118 x ICGV 92267) F_2-P21-B1-B1-B1-B1-B1(SB)	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
22	ICGV 00213	(ICGV 94118 x ICGV 93427) F_2-P23-B1-B1-B1-B1-B1(SB)	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
23	ICGV 06146	[(ICGV 92069 x ICGV 93184) x (ICGV 96246 x 92 R/75)] F_2-SSD-SSD-P12-B1-B2-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
24	ICGV 07120	[{[(86187x86350)x(Florix17090)]x(Dh.3-20xPI259747)} x [ICGV 87121 x ICGV 87853)xICGV 92023]] F2-B1-SSD-P8-B1-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
25	ICGV 10178	(ICGV 04078 x ICG 10889) F_2-SSD-SSD-SSD-P1-B1-B1-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
26	ICGV 11380	(ICGV 07106 x ICGV 86590) F-SSD-SSD-SSD-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
27	ICGV 14001	(ICGV 06142 x ICGV 07075) F_2-SSD-SSD-P9-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
28	ICGV 14030	(ICGV 06142 x ICGV 06282) F_2-SSD-SSD-P31-B1-B1	FDR	unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
29	ICGV 86015	(ICGS 44 x TG 2E) F_2-B1-B2-B1	EM	EM	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
30	ICGV 93260	(ICGS 11 x ICG 4728) F_2-B1-B1-B1-B1-B1A-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
31	ICGV 93261	(ICGS 11 x ICG 4728) F_2-B1-B1-B1-B1-B1A-B1-B1-B1RF-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
32	ICGV 92121	(Ah 7827 x ICGS 11) F_2-B1-B1-B3-B1-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
33	ICGV 99241	(ICGV 87290 x ICGV 87846) F_2-P29-B1-B1-B1-B2-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
34	ICGV 00351	(ICGV 87290 x ICGV 87846) F_2-P63-B1-B1-B1-B3-B1-B1-B1-B1-B1(SB)	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
35	ICGV 01260	(ICGV 92113 x ICGV 86300) F_2-P1-B1-B1-B1-B1-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
36	ICGV 01265	(ICGV 94148 x ICGV 91123) F_2-SSD-SSD-B4-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
37	ICGV 13200	{TAG 24-P2 x [TAG 24-P2 x (TAG 24-P2 x GPBD 4-P1_26-1)]} $BC2F_1$P2-P11-B1-B2-B1	FDR	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
38	ICGV 07220	[(ICGV 92069 x ICGV 93184)SIL 4 x (ICGS 44 x ICGS 76)] F2-SSD-SSD-P5-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL

Table 3.2. Continued

Serial number	Genotype	Pedigree	Trait		Origin	Market type	Sub-species	Breeding history
39	ICGV 07222	[(ICGV 92069 x ICGV 93184)SIL 4 x (ICGS 44 x ICGS 76)] F_2-SSD-SSD-P19-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
40	ICGV 13317	(ICGV 07225 x JAL 13) F_2-SSD-SSD-P14-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
41	ICGV 13254	(ICGV 07223 x ICGV 07405) F_2-SSD-SSD-P1-B1-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
42	ICGV 181026	((ICGV 06142 x Sun Oleic 95R) X Sunoleic 95-R)-P5-P1-P1-P2-P1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
43	ICGV 15073	(ICGV 06420 × Sun Oleic 95R)F1P3-BC1F1P14-P3-P4-P9-P6-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
44	ICGV 15074	(ICGV 06420 × Sun Oleic 95R)F1P3-BC1F1P14-P3-P4-P9-P8-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
45	ICGV 15083	(ICGV 06420 × Sun Oleic 95R)F1P3-BC1F1P14-P3-P5-P10-P3-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
46	ICGV 15019	(ICGV 06420 × Sun Oleic 95R)F2P191-P3-P7-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
47	ICGV 06420	(ICGV 87846 x ICGV 99240)F2-P1-B1-B1-B1-B1-B1-B1-B1-B3		Unknown				
48	ICGV 05155	(ICGV 99160 x ICGV 99240) F2-B3-P6-B1-B3-B2-B1-B1-B1-B1	HO	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
49	ICGV 16688	ICGV 06110 x (ICGV 06110 x Sun Oleic 95-R) F1P2-BC1F1P3-P9-P4-P32-P1-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
50	ICGV 03043	{ICGV 99160 x [ICGV 93124 x (LI x ICGS 44)]} F2-SSD-SSD-B3-B1-B1	HO	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
51	ICGV 00350	(ICGV 87290 x ICGV 87846) F_2-P63-B1-B1-B1-B1-B2-B1-B1-B1-B1(SB)	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
52	ICGV 86590	(X14-4-B-19-B x PI 259747) F_2-B2-B1-B1-B1-B1-B2	FDR	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
53	ICGV 02266	(ICGV 94143 x ICGV 94136) F_2-B1-B1-B1-B1-B1	DR	DR	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
54	ICGV 13189	{ICGV 91114-P1 x [ICGV 91114-P1 x (ICGV 91114-P1 x GPBD 4-P1_13-1)]} BC2F1P3-P1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
55	ICGV 13207	{TAG 24- P3 x [TAG 24-P3 x (TAG 24-P3 x GPBD 4-P1_27-1)]} BC2F1P2-P2-B2-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
56	ICGV 14421	(ICGV 91114-P1 x GPBD 4-P2-16-7) F_2-P13-P29-B2-B2-B1-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
57	ICGV 13219	{JL 24- P1 x [JL 24- P1 x (JL 24-P1 x GPBD 4-P1_19-5)]} BC2F1P1-P6-B1-B2-B1	DT	DT	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL

Table 3.2. Continued.

Serial number	Genotype	Pedigree	Trait		Origin	Market type	Sub-species	Breeding history
58	GPBD 4	KRG 1 x ICGV 86855	FDR	Unknown	Karnataka, India	Spanish bunch	*fastigiata*	Cultivar
59	ICGV 86031	(F 334 A-B-14 x NC Ac 2214) F2-B1-B3-B2-B3-B2-B3	MD	MD	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
60	ICGV 16686	ICGV 06110 x (ICGV 06110 x Sun Oleic 95-R) F1P2-BC1F1P3-P9-P4-P28-P2-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
61	ICGV 16005	(ICGV 06420 × Sun Oleic 95R) F2P411-P2-P9-P29-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
62	ICGV 171013	ICGV 07368 x (ICGV 07368 x Sun Oleic 95-R) F1P1-BC1F1P39-P3-P1-P2-P5-P2-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
63	ICGV 171026	(ICGV 00350 x SO 95R)F2 SSD-SSD-SSD-SSD-P18-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
64	ICGV 171039	ICGV 06110x[ICGV 06110x{ICGV 06110x(ICGV 06110 x SO 95R)}]-BC3F1P4-P17-P7-P1-B1-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
65	ICGV 171046	ICGV 06142x[ICGV 06142x{ICGV 06142x(ICGV 06142 x SO 95R)}]-BC3F1P96-P14-P2-P3-B1-B1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
66	ICGV 181017	((ICGV 06142 x Sun Oleic 95R) x Sunoleic 95-R)-P4-P4-P1-P1-P1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
67	ICGV 181063	(ICGV 02266 x ICGV 15059)-P2-P1-P1-P1-P1-P1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
68	ICGV 98412	[(ICGV 88361 x ICGV 88390)x(ICGV 88438 x ICG 5240)F1] F_2-SSD-B3-B1-B2-B1-B2-B1-B1	CON	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	Cultivar
69	ICGV 181489	(ICGV 00351 x Sun Oleic 95R)-14-1-1-1-1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
70	ICGV 181490	(DH 86 x Sun Oleic 95R)-5-1-1-1-1-B1	HOA	Unknown	ICRISAT, Hyderabad	Spanish bunch	*fastigiata*	ABL
71	ICGV 92054	[ICGV 87137 x (ICGS 21 x ICGS 50)F5] F_2-B1-B1-B1VB-B2SB-B2-B1VB	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
72	ICGV 93162	[ICGV 86187 x (JL 24 x Robut 33-1)] F_2-B1-B1-B1-B2-B1-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
73	ICGV 95111	(ICGV 88308 x ICGMS 42) F_2-SSD-SSD-SSD-B2SB-B1-B2-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
74	ICGV 96165	(CSMG 84-1 x ICGS 76) F_2-SSD-SSD-SSD-B4-B1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
75	ICGV 97115	(ICGV 88308 x CSMG 84-1) F_2-SSD-B1-B1-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
76	ICGV 98184	(ICGV 91061 x ICGV 86015) F_2-SSD-SSD-B1NI-B1-B1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL

Table 3.2. Continued.

Serial number	Genotype	Pedigree	Trait		Origin	Market type	Sub-species	Breeding history
77	ICGV 01491	[(ICGV 88414 x USA 63) x ICGV 95172] F_2-SSD-B2-B1-P1-B1-B2-B1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
78	ICGV 03287	(ICGV 99229 x ICGV 97245) F_2-P21-P3-P1-B1	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
79	ICGV 05057	{[ICGV 86015 x (B4 x ICGMS 2)] x (ICGV 92035 x ICGV 93128)} F_2-SSD-SSD-B1-B1-B1-B1-B1-B1-B1-B2	MD	MD	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
80	ICGV 06175	(ICGV 99052 x ICGV 00241) F_2-B1-SSD-P1-B1-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
81	ICGV 00064	{[ICGV 88312 x (B4 x ICGV 86885)] x [(JL 24 x ICG(FDRS) 4) x JL 24]} F_2-SSD-SSD-SSD-B1-B1-B2(VB)	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
82	ICGV 00246	(ICGV 93222 x ICGV 92209) F_2-P6-B1-B1-B2-B1-B1(VB)	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
83	ICGV 97150	{[([(JH 60 x PI 259747)-F2-B1-B1-B2-B2-B1-B1 x NC Ac 17133]F_2-B2-B2-B1-B1-B1 x J 11)x NC Ac 343]x ICGV 86003} F_2-B1-B1-B1-B1-B1-B1-B1-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
84	ICGV 98385	(91/57-2 x PI 270806) F_2-P13-B1-B1-B2-B1-B2-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
85	ICGV 96266	(ICGV 86577 x ICGV 86594) F_2-B1-B1-B2-B1-B2-B1-B1-B1-B1-B1-B1-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
86	ICGV 14224	(ICGV 06184 x ICGV 07076) F_2-SSD-SSD-P4-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
87	ICGV 14232	[(ICGV 00037 x ICGV 00038) x ICGV 06184] F_2-SSD-SSD-P2-B1-B1	FDR	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
88	ICGV 07262	[(ICGV 92069 x ICGV 93184)SIL 4 x (ICGS 44 x ICGS 76)] F_2-SSD-SSD-P13-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
89	ICGV 07247	[(ICGV 92069 x ICGV 93184)SIL 4 x (ICGS 44 x ICGS 76)] F_2-SSD-SSD-P12-B1-B1-B1	DT	DT	ICRISAT, Hyderabad Hydrabad	Virginia bunch	*hypogaea*	ABL
90	ICGV 10371	{{[(ICGV 87121 x ICGV 87853) x ICGV 93023] x ICGV 99160}B1 x [ICGV 87846 x (ICGV 87290 x ICGV 87846)]B1VB}} F_2-SSD-SSD-P2-B1-B1-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
91	ICGV 10373	{{[(ICGV 87121 x ICGV 87853) x ICGV 93023] x ICGV 99160}B1 x [ICGV 87846 x (ICGV 87290 x ICGV 87846)]B1VB}} F_2-SSD-SSD-P2-B1-B2-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
92	ICGV 10379	(ICGV 03115 x ICGV 91114) F_2-SSD-SSD-P7-B1-B1-B1-B1-B1	DT	DT	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
93	ICGV 15094	(ICGV 06420 × Sun Oleic 95R)F1P8-BC1F1P28-P3-P6-P25-P10-B1	HOA	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL

Table 3.2. Continued.

Serial number	Genotype	Pedigree	Trait		Origin	Market type	Sub-species	Breeding history
94	ICGV 87846	(CS 9 x ICGS 5) F_2-B1-B2-B2-B1	DT	DT	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	Cultivar
95	ICGV 86699	CS 29/1-B2-B1	FDR	Unknown		Virginia bunch	*hypogaea*	ABL
96	GG 20	GAUGG 10 x Robust 33-1	MD	MD	Gujarat, India	Virginia bunch	*hypogaea*	Cultivar
97	ICGV 171007	ICGV 06110 x (ICGV 06110 x Sun Oleic 95-R) F1P2-BC1F1P11-P7-P1-P6-P2-P2-B1	HOA	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
98	ICGV 171027	(ICGV 03042 X SO 95R)F_2 SSD-SSD-SSD-SSD-P8-B1	HOA	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
99	ICGV 181006	((ICGV 06420 x Sun Oleic 95R) x Sunoleic 95-R)-P1-P15-P1-P2-P1	HOA	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL
100	ICGV 181033	((ICGV 03042 x Sun Oleic 95R) x ICGV 03042)-2-1-1-1-1	HOA	Unknown	ICRISAT, Hyderabad	Virginia bunch	*hypogaea*	ABL

DT = drought tolerant, Con = confectionery, FDR = foliar disease resistant, MD = medium maturity, EM = early maturity, MDR = multiple disease resistant, HO = high oil content, HOA = high oleic acid content, ABL = advanced breeding line

3.2.2. Data collection

Data were collected on kernel and haulm yields from each plot and converted to tons per hectare (t ha^{-1}). Oil yield in t ha^{-1} (OY = oil content in % x kernel yield in t ha^{-1}), the contents of total oil (OC), total protein (PC), palmitic acid (PAC), stearic acid (SAC), oleic acid (OAC) and linoleic acid (LAC) of the kernels were estimated using near infrared spectroscopy-NIRS (XDS monochromator, FOSS Analytical AB, Sweden) (Deshmukh et al., 2020). Data on dry haulm yield was collected and expressed in t ha^{-1}. Briefly, the haulm samples were collected at physiological maturity by cutting from above-ground at the soil surface followed by oven drying at 70 ^{0}C for three days. Subsequently, haulm weights were recorded and the samples were ground into powder for NIRS analysis. The haulm fodder quality analysis was conducted at the International Livestock Research Institute (ILRI) based at ICRISAT/India. Haulm fodder quality parameters including the contents of dry matter (DM), ash, neutral detergent fiber (NDFDM), acid detergent fiber (ADFDM), acid detergent lignin (ADLDM), and *in vitro* digestibility (IVOMD) and metabolizable energy (ME) were estimated using a NIRS using a FOSS Forage Analyzer 5000 with software package WinISI II (Kadim et al. 2005). Nitrogen was determined using the Kjeldahl method (Da Silva et al. 2016).

3.2.3. Data analysis

Data were subjected to analysis of variance using SAS version 9.3 Software (SAS Institute Inc., 2011). Differences between treatment means were determined using the least significant difference (LSD) test at 5% significance level. Heritability in a broad-sense (H^2) was calculated according to Allard (1960) using the following formulae:

$$H^2=\frac{\sigma^2 g}{\sigma^2 p}\ x\ 100\%$$

Where, $\delta^2 g$ and $\delta^2 p$ are genotypic variance and phenotypic variance, respectively.

Stress tolerance index (STI) was calculated to select high kernel and haulm yielding genotypes under DS and NS conditions using the following formula (Fernandez, 1992):

$$STI = (Yp * Ys)/ (\bar{Y}p)^2$$

Where, Ys = yield of genotypes under DS condition; Yp = yield of genotypes under NS condition, and $\bar{Y}p$ = mean yield of test genotypes under NS condition.

Pearson correlation coefficients were performed using SAS software to determine the level of association among the assessed traits. Principal component (PC) analysis was performed using JMP software (SAS Institute Inc., Cary, NC, 1989-2019). PC bi-plots were constructed to determine association among traits and groundnut genotypes to aid simultaneous selection of genotypes with multiple traits. Hierarchical cluster analysis based on Ward method was computed using JMP Trail 15 version software to determine genetic groupings of the test genotypes. For sub-species comparison, the mean values for the two sub-species were statistically compared using a t-test at 5% level of significance. Boxplots were constructed using the GGPUBR package in R version 4.0 (R Core Team, 2020).

3.3. Results

3.3.1. Effects of genotypes, water regimes and seasons on kernel and haulm yields, oil content and haulm quality parameters

Combined analysis of variance revealed highly significant ($p<0.05$) genotype differences for kernel yield, oil content and fatty acids contents (Table 3.3). Significant genotype by water regime interaction effect was recorded for kernel yield and oil content. Genotype x year interaction effect was significant for all traits except stearic acid content, whereas genotype × water regime × year interaction effect was significant for all traits except palmitic acid content. Analysis of variance revealed highly significant ($p<0.05$) genotype differences for haulm yield and quality parameters. Also, significant genotype × water regime interaction effect was noted for nitrogen, neutral detergent fiber and acid detergent lignin. Genotype × year interaction effect was significant for ash, neutral detergent fiber, and acid detergent lignin, whereas genotype × water regime × year interaction effect was significant for haulm yield, ash, acid detergent lignin, *in vitro* organic matter digestibility and metabolizable energy.

Table 3.3. Mean squares and significant test among 100 groundnut genotypes evaluated for kernel yield, oil content and fatty acid compositions, and haulm yield and quality attributes across 2018/19 and 2019/20 post-rainy seasons under drought-stressed and non-stressed conditions.

		Kernel yield, oil content and fatty acid compositions							
Source of variation	df	KY	OC	OY	PC	PAC	SAC	OAC	LAC
Year (Y)	1	74.55**	373.46**	14.20**	350.05**	0.041ns	85.02**	15.61ns	51.03ns
Water regime (WR)	1	186.61**	357.04**	46.48**	898.93**	11.06*	32.31**	1487.74**	2138.93**
Genotype (G)	99	0.58**	21.02**	0.14**	10.68**	20.11**	0.61**	774.97**	547.64**
Rep(Year)	2	2.01**	82.27**	0.69**	114.23**	5.61*	6.34**	60.65ns	266.49**
Block(Year*Rep)	36	0.15ns	3.91ns	0.03ns	4.23ns	0.73ns	0.077ns	37.708ns	22.25ns
G*WR	99	0.26*	6.78*	0.07*	3.17ns	0.81ns	0.15	35.13ns	24.22ns
G*Y	99	0.30**	5.85*	0.07**	6.06*	1.46*	0.16ns	51.41*	36.01*
G*WR*Y	100	0.44**	11.36**	0.17**	8.10**	0.95ns	0.30**	47.25*	37.31*
Error	362	0.15	4.52	0.039	3.81	0.95	0.15	35.68	25.45

Haulm yield and quality parameters										
Source	df	HY	DM	Ash	NC	NDFDM	ADFDM	ADLDM	IVOMD	ME
Year (Y)	1	174.03**	722.36**	208.75**	13.02**	3600.71**	56.56**	31.04**	708.05**	16.96**
Water regime (WR)	1	678.03**	4.08**	519.04**	6.04**	62.94**	112.34**	5.94**	282.77**	18.57**
Genotype (G)	99	6.11**	0.14*	2.93**	0.06**	7.00*	5.49*	0.32*	3.33**	0.09**
Rep(Year)	2	47.99**	0.79*	8.07*	0.10*	7.14ns	30.78*	1.01*	19.33**	0.65**
Block(Year*Rep)	36	2.62*	0.05ns	2.03ns	0.03ns	5.01ns	5.09ns	0.28ns	2.23*	0.06*
G*WR	99	1.62ns	0.08ns	2.50*	0.04*	6.69*	4.53ns	0.27*	1.85ns	0.05ns
G*Y	99	1.68ns	0.10ns	2.13*	0.03ns	5.42*	4.07ns	0.29*	1.86ns	0.05ns
G*WR*Y	100	5.17**	0.10ns	2.68**	0.02ns	4.33ns	4.92*	0.50**	2.17*	0.06*
Error	362	1.52	0.09	1.54	0.02	4	3.54	0.2	1.52	0.2

df = degrees of freedom, KY = kernel yield, OC = oil content, OY = oil yield, PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, HY = haulm yield, DM = dry matter, N = nitrogen, NDFDM = Neutral detergent fiber, ADFDM = acid detergent fiber, ADLDM = acid detergent lignin, IVOMD = *in vitro* organic matter digestibility, ME = metabolizable energy. * = significant at 5% level of significance, ** = significant at 1% level of significance, ns = non-significant.

3.3.2. Performance of groundnut genotypes for kernel yield, oil content and fatty acids composition under non-stressed and drought-stressed conditions

Mean performance of the assessed groundnut genotypes for kernel yield, oil content and fatty acid composition under DS and NS conditions in the 2018/19 and 2019/20 post-rainy seasons are presented in Table 3.4. Highly significant ($p < 0.001$) genotype differences were recorded for kernel yield under NS and DS conditions. Under DS condition, the highest kernel yield was recorded for ICGV 06040 (1.2 t ha^{-1}), ICGV 7222 (1.17 t ha^{-1}), ICGV 01260 (1.14 t ha^{-1}), ICGV 10178 (1.11 t ha^{-1}), ICGV 06175 (1.1 t ha^{-1}) and ICGV 10373 (1.07 tha^{-1}). Genotypes, ICGV 10143, ICGV 7222, ICGV 03042, ICGV 06039, ICGV 98412, ICGV 14001 and ICGV 06040, were high-yielding (>2 t ha^{-1}) under NS condition.

For oil content, highly significant ($p < 0.001$) differences were recorded among the test genotypes under both conditions. Under DS condition, the highest oil content was recorded for, ICGV 10379 (53.9%), ICGV 00064 (52.8%), ICGV 86699 (52.07%), ICGV 95111 (51.97%) and ICGV 96266 (51.14%). Genotypes ICGV 98385, ICGV O1279, GPBD 4, and ICGV 00246, recorded high oil content of > 50% under NS condition. Highly significant ($p < 0.001$) genotype differences were recorded for oil yield under both conditions. Under DS condition, the highest oil yield was recorded for, ICGV 6040 (0.58 t ha^{-1}), ICGV 10178 (0.54 t ha^{-1}), ICGV 01260 (0.54 t ha^{-1}), ICGV 7222 (0.53 t ha^{-1}), ICGV 10373 (0.52 t ha^{-1}) and ICGV 06175 (0.52 t ha^{-1}). Genotypes ICGV 10143, ICGV 06039, ICGV 7222, ICGV 03042, ICGV 14001 and ICGV 06040 recorded high oil yield (> 1.2 t ha^{-1}) under NS condition. Significantly higher protein content (> 30%) was recorded in genotypes, ICGV 11380, ICGV 171007, ICGV 181490 and ICGV 171046, under DS condition, whereas genotypes, ICGV 06146, ICGV 13219, ICGV 14030 and ICGV 10143, recorded high protein content (>28%) under NS condition.

Palmitic acid content differed significantly among the assessed groundnut genotypes under both conditions. Under DS condition, the highest palmitic acid content was recorded for ICGV 00187 (13.76%), ICGV 13254 (13.54%), ICGV 00213 (13.39%), ICGV 06040 (13.31%) and ICGV 96165 (13.29%). Under NS condition, genotypes ICGV 00187, ICGV 96165 and ICGV 94118 had the highest contents of palmitic acid (> 14%). For stearic acid content, the highest value was recorded for ICGV 00213 (3.66%), ICGV 98412 (3.58%), ICGV 96174 (3.54%) and ICGV 00187 (3.5%) under DS condition, whereas genotypes ICGV 94118, ICGV 98412, GG 20 and ICGV 13254 recorded high concentrations (>3%) under NS condition. Highly significant ($p<0.001$) genotype differences were observed for oleic acid content under both conditions. The highest oleic acid content was recorded for ICGV 181026 (71.64%), ICGV 15019 (71.16%), ICGV 181017 (70.65%), ICGV 181063 (69.68%) and ICGV 16667 (68.89%) under DS condition, whereas ICGV 181026, ICGV 181017, ICGV 171027, ICGV 16688 and ICGV 15074 recorded high oleic acid content (> 69%) under NS condition. Highly significant ($p <0.001$) genotype differences were observed for linoleic acid. Under DS condition, genotypes, ICGV 181026, ICGV 181017, ICGV 15019, ICGV 181063, ICGV 16667, ICGV 171046 and ICGV 171026, expressed low linoleic acid content (< 13%) under NS condition. High broad-sense heritable values (>80%) were recorded for oleic, linoleic and palmitic acid contents under both water conditions. Low to medium H^2 values were observed for oil and protein contents under both moisture conditions (Table 3.4). Medium heritability values at 49% and 51% were estimated for kernel yield under NS and DS conditions, in that order.

Table 3.4. Mean values for kernel yield, protein content and fatty acid compositions of 100 groundnut genotypes evaluated under drought-stressed (DS) and non-stressed (NS) conditions in 2018/19 and 2019/20 post-rainy seasons.

Serial number	Genotypes	KY (t ha^{-1})		OC (%)		OY (t ha^{-1})		PC (%)		PAC (%)		SAC (%)		OAC (%)		LAC (%)	
		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
1	ICGV 16667	0.5	1.47	48.33	49.15	0.24	0.72	25.97	25.46	8.67	9.36	2.59	2.12	68.89	61.3	11.75	19.24
2	ICGV 93128	0.37	1.73	46.28	47.04	0.17	0.81	29.31	26.65	12.53	12.39	2.76	2.57	48.01	46.69	28.63	30.61
3	ICGV 95066	0.79	1.4	48.87	48.67	0.39	0.68	27.93	25.56	12.08	12.88	2.9	2.45	44.39	40.62	33.64	36.56
4	ICGV 96174	0.41	1.23	45.55	48.27	0.19	0.59	28.47	24.19	11.79	12.57	3.54	3.07	47.12	41.06	28.98	35.32
5	ICGV 97087	0.73	1.2	49.87	50.43	0.36	0.61	29.31	25.59	12.9	13.34	2.87	1.97	57.49	55.19	22.96	25.67
6	ICGV 98077	0.37	1.29	47.56	49.04	0.18	0.63	26.29	25.08	12.66	12.99	2.85	2.28	39.57	37.61	37.79	40.23
7	ICGV 01279	0.51	1.76	50.81	52.65	0.26	0.93	27.63	24.13	12.77	13	3.03	2.67	44.99	39.94	31.61	37.28
8	ICGV 03042	0.94	2.52	47.79	49.59	0.45	1.25	25.96	24.45	12.65	13.33	2.66	2.18	42.39	35.77	34.85	41.12
9	ICGV 06039	0.85	2.51	47.84	51.93	0.41	1.30	28.88	24.42	13.11	13.54	3.27	2.78	40.22	36.27	34.66	40.04
10	ICGV 6040	1.2	2.36	48.63	51.99	0.58	1.23	27.8	26.87	13.31	13.33	2.99	2.76	40.61	37.68	35.52	38.87
11	ICGV 07010	0.68	1.92	46.25	46.86	0.31	0.90	27.97	25.81	12.18	12.85	2.68	2.47	44.58	37.44	32.18	39.56
12	ICGV 10143	1	2.89	45.41	49.19	0.45	1.42	30.16	28.27	12.22	12.99	2.89	2.45	44.53	37.65	32.11	39.28
13	ICGV 11422	0.26	1.24	48.35	49.4	0.13	0.61	25.9	24.16	13.24	12.98	2.89	2.11	38.46	38.34	37.06	38.73
14	ICGV 11396	0.37	2.1	49.93	49.42	0.18	1.04	27.34	25.02	12.99	12.64	3.05	2.21	41.4	38.01	34	39.04
15	ICGV 11418	0.42	1.46	48.19	48.7	0.20	0.71	26.37	24.74	12.88	13.23	2.93	2.26	40.71	37.5	36.03	38.86
16	ICGV 91223	0.41	1.51	45.01	46.68	0.18	0.70	28.8	25.23	11.6	11.8	3.04	2.46	46.64	42.95	31.06	35.74
17	ICGV 94118	0.73	1.77	46.59	48.06	0.34	0.85	29.25	26.15	12.88	14	3.08	3.25	42.57	35.92	33.61	38.07
18	ICGV 99019	0.75	1.99	47.47	47.68	0.36	0.95	27.12	26.14	13.21	13.61	3.18	2.65	41.05	38.19	34.7	37.92
19	ICGV 00162	0.52	1.25	46.8	47.51	0.24	0.59	29	27.02	12.57	12.86	2.94	2.57	44.96	38.71	32.04	38.52
20	ICGV 00211	0.64	1.95	49.48	49.69	0.32	0.97	27.5	24.97	12.73	12.58	2.76	2.43	40.27	39.11	36.87	39.11
21	ICGV 00187	0.68	1.26	45.24	49.32	0.31	0.62	28.63	24.96	13.76	14.05	3.5	3.15	40.81	37.48	32.93	37.31
22	ICGV 00213	0.59	1.71	45.82	47.69	0.27	0.82	28.19	26.56	13.39	13.82	3.66	3.02	42.27	35.61	32.73	38.73
23	ICGV 06146	0.85	1.47	47.81	48.79	0.41	0.72	29.48	30.3	12.23	12.64	2.92	2.88	44.82	40.53	32.56	37.62
24	ICGV 07120	0.84	1.32	48.04	47.93	0.40	0.63	26.84	26.89	12.63	13.2	3.06	2.52	40.86	41.04	35.67	35.57
25	ICGV 10178	1.11	1.46	48.62	47.09	0.54	0.69	25.76	24.47	13.2	13.45	2.96	2.7	38.97	36.43	37.01	39.04
26	ICGV 11380	0.91	2.16	47.22	51.42	0.43	1.11	31.87	26.34	12.31	12.08	3.01	2.66	46.36	42.2	31.43	37.03
27	ICGV 14001	0.81	2.37	46.68	52.1	0.38	1.23	28.57	25.45	12.18	12.38	2.67	2.55	42.36	40.21	34.23	38.6
28	ICGV 14030	0.52	2.15	48.7	49.64	0.25	1.07	28.96	28.55	12.33	12.19	2.98	2.61	44.66	40.41	32.93	37.7
29	ICGV 86015	0.58	1.87	47.22	46.77	0.27	0.87	26.15	24.8	11.8	11.94	2.87	2.41	50.53	45.02	27.57	32.96
30	ICGV 93260	0.57	2.28	43.14	46.12	0.25	1.05	28.6	25.11	11.56	12.03	2.63	2.75	48.04	43.57	29.91	34.23
31	ICGV93261	0.71	1.88	41.66	41.78	0.30	0.79	29.62	27.13	10.96	12.04	2.72	2.08	50.8	44.81	27.13	32.44
32	ICGV 92121	0.89	1.58	44.91	48.58	0.40	0.77	28.98	28.09	11.88	12.57	2.9	2.44	46.93	38.75	30.06	38.05
33	ICGV 99241	0.91	1.76	48.99	51.59	0.45	0.91	24.43	23.01	12.78	12.82	2.93	2.59	40.51	36.52	36.08	41.1
34	ICGV 00351	0.62	1.6	49.25	49.91	0.31	0.80	25.63	25.16	12.51	12.1	2.73	2.04	40.04	41.6	37.72	36.68
35	ICGV 01260	1.14	1.72	47.31	47.12	0.54	0.81	27.75	26.46	12.39	12.72	3.04	2.81	44.61	42.35	32.58	35.16
36	ICGV 01265	0.76	1.62	46.07	47.46	0.35	0.77	27.86	24.55	12.1	11.8	2.64	1.96	43.49	44.27	34.09	34.8

Table 3.4. Continued.

Serial number	Genotypes	KY (t ha^{-1})		OC (%)		OY (t ha^{-1})		PC (%)		PAC (%)		SAC (%)		OAC (%)		LAC (%)	
		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
37	ICGV 13200	0.94	1.55	47.74	49.8	0.45	0.77	27.16	27.55	11.53	11.37	2.79	2.6	46.37	45.2	31.79	34.2
38	ICGV 7220	0.3	2	46.65	48.85	0.14	0.98	29.61	27.01	12.95	12.76	2.97	2.59	42.07	38.84	33.73	37.84
39	ICGV 7222	1.17	2.64	45.5	49.1	0.53	1.30	30.28	27.05	12.49	13.05	2.71	2.41	44.78	37.85	32.25	39.19
40	ICGV 13317	0.75	2.35	47.75	50.36	0.36	1.18	27.85	25.93	12.94	13.71	2.69	2.69	41.16	35.52	34.62	40.31
41	ICGV 13254	0.55	1.99	46.05	49	0.25	0.98	27.25	24.49	13.57	13.12	3.43	3.16	41.84	41.35	32.33	34.6
42	ICGV 181026	0.53	1.74	47.35	50.08	0.25	0.87	27.95	26.26	8.32	6.68	2.18	1.92	71.64	76.03	10.11	7.62
43	ICGV 15073	0.74	1.31	49.86	49.33	0.37	0.65	27.38	26.52	8.97	9.45	2.63	2.16	66.64	59.59	13.99	20.34
44	ICGV 15074	0.67	1.97	47.84	50.65	0.32	1.00	27.2	26.63	9.22	8.28	2.63	2.28	64.24	69.09	15.42	12.93
45	ICGV 15083	0.88	2.06	48.76	48.94	0.43	1.01	28.5	25.75	8.9	8.71	2.89	1.83	66.5	63.85	14.13	16.36
46	ICGV 15019	0.82	1.68	43.84	44.25	0.36	0.74	29.76	25.42	7.86	7.84	2.11	1.51	71.16	68.46	10.62	13.46
47	ICGV 6420	0.77	1.82	50.3	51.51	0.39	0.94	25.79	23.59	12.68	13.08	2.75	2.23	39.62	35.94	37.54	41.42
48	ICGV 5155	0.6	1.83	49.12	51.78	0.29	0.95	27.38	24.43	12.41	11.85	2.89	2.27	41.48	41.87	35.34	37.4
49	ICGV 16688	0.73	1.79	46.54	50.05	0.34	0.90	28.84	25.32	9.07	8.05	2.71	2.27	66.01	69.65	14.32	12.66
50	ICGV 03043	0.71	1.9	48.64	49.55	0.35	0.94	27.4	25.46	12.87	13.14	2.71	2.2	38.58	35.81	38.07	41.73
51	ICGV 00350	0.71	2.04	48.09	48.37	0.34	0.99	26.88	23.22	12.12	13.15	2.59	2.26	40.74	37.38	36.43	39.79
52	ICGV 86590	0.76	1.49	45.04	46.36	0.34	0.69	27.98	26.14	11.6	12.18	3	2.7	43.47	38.51	34.58	39.94
53	ICGV 02266	0.88	1.68	45.75	48.53	0.40	0.82	28.16	25.78	12.13	12.67	3	2.56	49.63	41.42	26.93	35.61
54	ICGV 13189	0.78	2.02	46.66	47.62	0.36	0.96	29.11	26.85	11.88	11.76	2.63	2.23	46.77	44.54	31.35	34.53
55	ICGV 13207	0.72	1.37	45.77	48.01	0.33	0.66	27.33	26.11	12.23	11.99	2.78	2.59	44.17	40.68	32.45	37.83
56	ICGV 14421	0.96	2.19	45.65	50.87	0.44	1.11	28.06	25.98	11.77	12.61	2.18	2.39	43.94	39.64	34	39.05
57	ICGV 13219	0.62	1.08	48.41	49.7	0.30	0.54	29.92	28.58	12.45	13.19	2.93	2.72	42.69	38.85	34.65	38.13
58	GPBD 4	0.48	1.28	48.62	52.52	0.23	0.67	26.86	25.26	10.73	11.71	2.95	2.56	50.69	44.03	28.86	36.18
59	ICGV 86031	0.52	1.4	48.44	48.71	0.25	0.68	26.74	26.25	13.23	13.45	2.53	2.27	36.7	36.15	39.52	39.81
60	ICGV 16686	0.66	1.6	49.5	48.75	0.33	0.78	27.5	25.33	9.52	11.11	2.77	2.78	61.72	52.86	18.18	24.44
61	ICGV 16005	0.52	1.56	47.18	49.41	0.25	0.77	27.41	23.97	8.44	7.72	2.36	2.24	67.56	68.47	13.06	14.65
62	ICGV 171013	0.84	1.61	47.3	44.85	0.40	0.72	27.52	25.81	9.71	8.51	2.67	1.52	59.74	67.87	19.56	13.7
63	ICGV 171026	0.76	1.26	46.93	47.49	0.36	0.60	27.86	24.84	8.5	8.94	2.8	2.31	67.76	64.5	12.79	16.17
64	ICGV 171039	0.82	1.77	46.23	51.68	0.38	0.91	28.58	24.31	10.33	8.31	2.53	1.95	57.03	66.91	22.63	15.72
65	ICGV 171046	0.99	1.4	46.25	51.01	0.46	0.71	30.44	26.6	8.61	8.39	2.89	2.86	67.91	64.82	12.38	16.65
66	ICGV 181017	0.9	1.49	47.6	47.72	0.43	0.71	29.65	28.22	8.2	8	2.58	2.01	70.65	72.12	10.2	8.72
67	ICGV 181063	0.52	0.8	45.84	45.97	0.24	0.37	29.32	26.57	8.13	8.47	2.99	2.4	69.68	66.5	10.76	14.67
68	ICGV 98412	0.68	2.42	46.14	44.64	0.31	1.08	28.18	27.57	11.44	11.65	3.58	3.23	46.21	44.36	30.51	32
69	ICGV 181489	0.45	0.88	49.88	48.97	0.22	0.43	25.67	25.91	8.57	8.49	2.52	2.02	65.42	66.62	15.95	14.57
70	ICGV 181490	0.89	1.7	46.05	46.26	0.41	0.79	30.67	28.11	9.27	9.37	2.87	2.56	64.39	64.39	15.2	15.37
71	ICGV 92054	0.58	1.02	48.8	48.82	0.28	0.50	27.21	24.87	11.57	11.7	2.89	2.37	43.19	45.35	33.99	33.21
72	ICGV 93162	0.53	1.38	46.92	48.72	0.25	0.67	29.38	24.81	11.7	12.09	2.74	2.47	47.13	46.54	29.95	31.36
73	ICGV 95111	0.82	1.07	51.97	50.99	0.43	0.55	28.49	26.75	11.35	12.7	2.63	2.25	66.11	57.03	16.27	25.23

Table 3.4. Continued

Serial		KY (t ha^{-1})		OC (%)		OY (t ha^{-1})		PC (%)		PAC (%)		SAC (%)		OAC (%)		LAC (%)	
number	Genotype	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
74	ICGV 96165	0.61	1.24	48.05	48.9	0.29	0.61	26.52	25.46	13.29	14.04	2.08	1.77	51.72	45.6	26.87	32.43
75	ICGV 97115	0.56	1.23	48.79	49.34	0.27	0.61	26.92	25.22	12.19	12.81	2.87	2.59	48.27	38	29.36	38.26
76	ICGV 98184	0.65	1.33	49.27	49.13	0.32	0.65	26.89	23.8	12.6	12.84	3.02	2.14	44.19	43.48	34.08	35.8
77	ICGV 01491	0.51	1.14	46.74	47.01	0.24	0.54	28.78	26.47	12.11	13.06	3.01	2.45	46.63	39.95	29.67	37.14
78	ICGV 03287	0.63	1.47	48.51	49.19	0.31	0.72	26.73	25.33	12.71	13.47	2.91	2.43	42.85	37.53	34.26	39.34
79	ICGV 05057	0.52	1.43	47.43	50.44	0.25	0.72	28.14	25.81	12.42	12.9	2.7	2.63	45.82	41.94	31.75	36.88
80	ICGV 06175	1.1	2.09	46.87	50.45	0.52	1.05	28.34	24.27	12.56	12.95	2.47	2.22	45.25	38.23	32.41	39.17
81	ICGV 00064	0.8	1.34	52.8	50.39	0.42	0.68	27.2	26.45	12.03	12.84	2.83	2.6	56.12	52.19	26.66	27.57
82	ICGV 00246	0.63	1.32	47.67	52.11	0.30	0.69	28.33	23.94	12.75	13.11	2.93	2.67	42.36	40.1	34.02	37.53
83	ICGV 97150	0.32	0.76	48.58	49.5	0.16	0.38	26.34	25.13	12.3	12.93	2.41	2.1	53.04	49.59	25.93	30.4
84	ICGV 98385	0.29	1.07	50.11	52.83	0.15	0.57	26.04	23.88	12.53	12.76	2.56	2.34	53.56	49.95	25.95	31.44
85	ICGV 96266	0.47	0.9	51.14	51.2	0.24	0.46	25.21	24.42	12.17	12.06	2.96	2.48	51.98	55.61	26.89	25.91
86	ICGV 14224	0.73	1.92	48.15	50.27	0.35	0.97	29.6	26.25	12.88	12.6	2.72	2.93	44.26	40.61	33.74	36.95
87	ICGV 14232	0.83	1.56	48.23	52	0.40	0.81	27.57	24.55	11.78	12.63	3.13	3.01	44.72	41.48	32.78	36.69
88	ICGV 7262	0.6	1.58	46.9	48.14	0.28	0.76	30.15	27.84	11.88	13.17	2.94	2.18	43.88	43.75	33.58	33.49
89	ICGV 7247	0.58	2	47.55	48.92	0.28	0.98	28.33	25.65	12.52	12.64	2.96	1.98	41.69	44.31	34.68	34.31
90	ICGV 10371	0.62	1.46	49.73	50.31	0.31	0.73	26.88	24.64	12.65	11.8	2.47	2.44	42.56	48.51	35.25	30
91	ICGV 10373	1.07	1.65	48.53	50.19	0.52	0.83	27.57	25.96	12.67	12.13	2.63	2.17	43.69	50.61	33.77	28.71
92	ICGV 10379	0.76	1.94	53.9	49.16	0.41	0.95	26.02	23.99	10.62	12.81	2.89	2.37	56.41	41.27	23.46	35.81
93	ICGV 15094	0.42	1.16	47.71	50.06	0.20	0.58	28.97	26.1	9.57	10.84	2.66	2.32	60.22	50.21	19.25	29.55
94	ICGV 87846	0.67	1.88	49.59	51.41	0.33	0.97	25.42	25.52	12.83	12.88	3.01	3.08	42.27	41.84	34.98	35.9
95	ICGV 86699	0.57	1.23	52.07	47.45	0.30	0.58	25.24	27.27	11.43	11.66	3.17	2.31	59.3	52.21	20.96	27.41
96	GG 20	0.55	2.16	48.78	48.15	0.27	1.04	27.96	27	11.21	12.16	3.27	3.2	50.97	43.17	27.27	34.03
97	ICGV 171007	0.42	1.31	45.41	47.75	0.19	0.63	31.12	28.01	10.45	10.13	2.92	2.65	57.87	57.56	20.01	22.38
98	ICGV 171027	0.6	1.28	48.78	50.4	0.29	0.65	28.07	24.96	8.67	8.35	3.19	2.04	66.59	71.42	13.49	10.69
99	ICGV 181006	0.41	1.42	47.88	50.94	0.20	0.72	28.32	25.31	10.13	9.55	2.54	2.03	58.36	64.17	20.69	17.75
100	ICGV 181033	0.87	2.13	49.15	48.47	0.43	1.03	27.84	27.82	9.26	9.48	2.72	1.98	61.9	65.47	18.06	16.23
Mean		0.68	1.65	47.75	49.09	0.33	0.81	27.9	25.78	11.62	11.86	2.84	2.43	49.57	46.84	28.39	3.66
H^2 (%)		51.37	49.28	57.17	67.21	48.8	48.69	43.87	23.9	80.1	86.6	51.04	53.13	89.1	92.42	89.57	92.28
P-value		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
SED		0.23	0.5	1.93	2.13	0.11	0.24	1.74	2.01	0.98	0.97	0.31	0.46	6.02	5.96	4.93	5.13
LSD (5%)		0.32	0.69	2.68	2.96	0.15	0.33	2.43	2.8	1.36	1.35	0.43	0.63	8.4	8.31	6.87	7.15
CV (%)		33	30	4.03	4.33	34.82	29.76	6.25	7.8	8.41	8.16	11.07	18.76	12.15	12.73	17.36	16.19

KY = kernel yield, OC = oil content, OY = oil yield, PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, DS = drought-stressed, NS = non-stressed, H^2 = heritability in the broad-sense, P = probability level, SED = Standard error of the mean differences, LSD = Least significant difference, CV = coefficient of variation.

3.3.3. Performance of groundnut genotypes for haulm yield and quality parameters

Mean performance of groundnut genotypes for haulm yield and quality parameters under DS and NS conditions are presented in Table 3.5. Significant genotype differences were observed among the test genotypes for haulm yield under both conditions. Appendix 3.1 shows the field performormance of test genotypes under DS and NS condition. Under DS condition, the highest haulm yield was recorded for ICGV 01260 (7.79 t ha^{-1}), ICGV 96165 (7.29 t ha^{-1}), ICGV 171027(6.88 t ha^{-1}), ICGV 96266 (6.71 t ha^{-1}) and ICGV 14232 (6.51 t ha^{-1}), whereas genotypes ICGV 01491, ICGV 181006, ICGV 00211 and ICGV 97115 recorded high haulm yield > 8.5 t ha^{-1}) under NS condition.

Higher broad-sense heritability value (70%) was recorded for haulm yield under NS condition, whereas low heritability value (36%) was recorded under DS condition. Under NS condition, higher nitrogen contents were recorded for genotypes, ICGV 93162 (2.94%), ICGV 171007 (2.91%) and ICGV 99019 (2.84%), whereas genotypes, ICGV 01491, ICGV 171007, ICGV 171039 and ICGV 05057, recorded high nitrogen contents of > 3% under DS condition. Significantly ($p<0.001$) higher ash contents were recorded for ICGV 86015 (18.36%), ICGV 96165 (17.18%), ICGV 14232 (17.15%), ICGV 14421 (16.27%) and ICGV 7220 (15.95%) under DS condition. Highly significant ($p<0.001$) differences were recorded among groundnut genotypes for neutral detergent fiber under DS condition. Under DS condition, the lowest neutral detergent fiber was recoded for genotypes, ICGV 86015 (32.03%), ICGV 96165 (34.29%), ICGV 14232 (37.04%) and ICGV 00187 (37.23%). Significant ($p <0.05$) genotype differences were observed for acid detergent fiber and acid detergent lignin under DS condition. The highest acid detergent fiber was noted for ICGV 03043 (31.93%), ICGV 00211 (31.4%), ICGV 171013 (31.3%) and ICGV 16667 (31.24%), whereas genotypes, ICGV 171039, ICGV 181033, ICGV 13200, ICGV 14030 and ICGV 13219, recorded low acid detergent fiber contents of <27% under DS. High acid detergent lignin contents were recorded for ICGV 181489 (5.56%), ICGV 16667 (5.54%), ICGV 00211 (5.46%), ICGV 03043 (5.43%) and ICGV 171013 (5.43%), whereas genotypes, ICGV 171039 (4.21%), ICGV 14030 (4.24%), ICGV 181033 (4.36%), ICGV 171046 (4.38%) and ICGV 13219 (4.39%), recorded low acid detergent lignin of <5% under DS condition. Groundnut genotypes differed significantly ($P <0.05$) for *in vitro* organic matter digestibility under DS condition. The highest *in vitro* organic matter digestibility was recorded for GG 20 (63.52%), ICGV 171007 (63.43%), ICGV 14030 (63.41%), ICGV 86031 (63.23%) and ICGV 13219 (63.07%) under DS condition. Significant genotype differences were observed among the genotypes for metabolizable energy under both conditions. Under DS condition, high metabolizable energy values were recorded for GG 20 (63.52%), ICGV 171007 (63.43%), ICGV 14030 (63.41%), CGV 86031(63.23%) and CGV 13219 (63.07%).

Table 3.5. Mean values for haulm yield and fodder quality parameters of 100 groundnut genotypes evaluated under drought-stressed (DS) and non-stressed (NS) conditions in 2018/19 and 2019/20 post-rainy seasons.

serial number	Genotypes	HY (t ha^{-1})		DM (%)		Ash (%)		NC (%)		NDFDM (%)		ADFDM (%)		ADLDM (%)		IVOMD (%)		ME (%)	
		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
1	ICGV 16667	5.67	7.71	91.57	91.32	13.66	12.25	2.52	2.7	37.65	35.98	31.24	27.34	5.54	4.91	61.39	62.95	8.69	8.85
2	ICGV 93128	5.4	6.2	91.35	91.05	14.46	11.84	2.99	2.67	33.76	36.33	27.40	27.46	4.71	4.83	61.61	63.02	8.47	8.92
3	ICGV 95066	4.88	7.52	91.26	91.29	13.69	12.08	3	2.62	33.86	35.86	26.81	28.17	4.50	5.06	62.53	63.83	8.7	9.06
4	ICGV 96174	4.66	7.88	91.46	91.49	13.20	11.81	2.61	2.62	38.85	36.84	30.92	27.97	5.26	4.87	60.47	62.72	8.45	8.85
5	ICGV 97087	5.47	8.84	91.43	91.48	14.29	13.44	2.73	2.38	36.53	37.53	30.16	30.16	4.94	5.26	61.59	61.57	8.56	8.72
6	ICGV 98077	6.14	7.6	91.84	91.65	15.02	12.31	2.96	2.72	36.33	36.03	29.41	27.83	5.03	4.87	59.98	62.76	8.18	8.81
7	ICGV 01279	5.63	7.06	91.52	91.46	15.03	12.73	2.96	2.74	34.98	35.40	28.89	27.28	4.77	4.75	60.52	62.28	8.31	8.72
8	ICGV 03042	5.17	6.31	91.39	91.48	13.49	12.58	2.7	2.46	39.19	37.25	30.96	29.39	5.42	5.35	59.95	61.72	8.33	8.68
9	ICGV 06039	3.82	5.63	91.50	91.34	14.07	12.71	2.76	2.51	35.96	36.63	29.52	28.42	4.97	5.00	61.07	62.39	8.48	8.86
10	ICGV 6040	5.59	6.29	91.39	91.30	13.58	12.79	2.81	2.61	36.05	35.51	27.66	27.05	4.54	4.47	61.02	62.44	8.5	8.78
11	ICGV 07010	5.6	6.43	91.54	91.40	14.18	12.42	2.72	2.5	36.09	36.94	29.35	27.97	4.94	4.99	61.7	62.05	8.59	8.81
12	ICGV 10143	4.45	6.42	91.44	91.42	15.07	12.80	2.65	2.54	36.13	36.68	30.17	29.61	5.04	5.30	59.52	62.52	8.26	8.87
13	ICGV 11422	6	8.23	91.69	91.53	14.39	12.77	2.77	2.6	35.39	36.35	29.07	27.95	4.97	4.83	61.65	62.14	8.53	8.71
14	ICGV 11396	5.54	7.45	91.48	91.48	15.16	12.16	2.67	2.5	35.11	38.05	29.15	29.02	4.76	5.18	61.56	61.11	8.51	8.61
15	ICGV 11418	5.59	8.26	91.45	91.42	13.90	12.06	2.71	2.66	36.60	35.37	29.58	27.25	4.81	4.94	61.03	63.18	8.47	8.9
16	ICGV 91223	3.8	6.7	91.35	91.31	13.98	11.55	2.85	2.53	35.67	37.30	28.99	28.42	4.99	5.05	61.47	62.68	8.56	8.92
17	ICGV 94118	3.97	7.61	91.27	91.44	14.86	12.20	2.68	2.66	36.29	34.99	30.80	27.94	5.15	5.20	60.63	62.96	8.42	8.93
18	ICGV 99019	5.68	7.79	91.47	91.40	12.88	12.58	2.76	2.84	36.37	33.82	28.02	25.67	4.77	4.37	60.81	63.8	8.49	8.95
19	ICGV 00162	4.67	6.94	91.46	91.36	12.54	12.72	2.57	2.63	39.00	35.38	30.02	27.80	5.14	4.90	60.46	62.68	8.53	8.85
20	ICGV 00211	4.66	8.61	91.44	91.44	14.19	12.95	2.63	2.48	37.69	37.75	31.40	29.59	5.46	5.35	59.92	60.69	8.33	8.56
21	ICGV 00187	4.67	6.09	91.49	91.27	14.84	11.51	2.93	2.58	33.34	37.23	27.51	27.92	4.63	4.91	61.23	62.83	8.47	8.93
22	ICGV 00213	4.6	6.69	91.35	91.46	13.57	12.12	2.91	2.64	34.77	34.63	27.32	26.65	4.68	4.84	61.09	63.42	8.53	9
23	ICGV 06146	3.95	4.7	91.43	91.34	12.29	11.52	2.74	2.48	36.33	37.43	27.32	28.94	4.65	5.29	61.82	62.27	8.7	8.9
24	ICGV 07120	5.89	6.1	91.56	91.51	13.88	12.07	2.74	2.69	37.35	36.41	29.63	26.95	4.88	4.64	60.6	62.9	8.42	8.87
25	ICGV 10178	6.28	7.41	91.52	91.55	13.18	12.31	2.51	2.59	39.41	36.62	31.09	28.43	5.20	5.07	60.38	62.7	8.46	8.85
26	ICGV 11380	3.54	5.55	91.39	91.35	13.07	12.01	2.79	2.63	36.05	37.12	28.32	28.58	4.62	5.03	61.79	62.39	8.64	8.85
27	ICGV 14001	4.69	6.22	91.52	91.55	13.97	12.28	2.62	2.53	36.64	37.71	30.20	29.89	4.98	5.57	61.41	62.53	8.57	8.87
28	ICGV 14030	3.76	5.47	91.28	91.43	12.78	11.93	2.9	2.41	34.58	38.66	26.68	30.05	4.24	5.40	63.41	61.77	8.89	8.83
29	ICGV 86015	3.79	5.68	91.35	91.52	18.36	11.97	2.74	2.62	32.03	35.67	29.83	27.36	4.49	4.81	60.08	62.62	8.22	8.84
30	ICGV 93260	3.09	6.51	91.43	91.42	15.45	12.26	2.91	2.6	34.31	37.15	28.50	28.50	4.56	5.02	61.14	62.72	8.42	8.89
31	ICGV93261	3.9	5.08	91.42	91.43	13.26	12.50	2.87	2.67	36.32	35.33	27.97	27.38	4.82	4.82	62.11	62.64	8.64	8.81

Table 3.5. Continued.

serial number		HY (t ha^{-1})		DM (%)		Ash (%)		NC (%)		NDFDM (%)		ADFDM (%)		ADLDM (%)		IVOMD (%)		ME (%)	
		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
32	ICGV 92121	6.26	7.27	91.32	91.63	12.89	11.94	2.83	2.72	36.85	35.71	28.05	26.58	4.59	4.80	62.7	63.55	8.78	8.93
33	ICGV 99241	6.35	8.28	91.58	91.27	12.47	12.19	2.78	2.57	35.63	36.58	26.78	28.60	4.39	5.27	62.88	63.07	8.78	8.99
34	ICGV 00351	5.31	5.89	91.62	91.54	12.51	11.80	2.72	2.53	38.52	37.49	29.74	28.47	5.10	5.23	61.14	62.42	8.56	8.89
35	ICGV 01260	7.79	7.66	91.74	91.55	12.50	12.26	2.57	2.62	38.80	35.49	30.24	27.08	5.19	4.74	60.26	62.65	8.46	8.81
36	ICGV 01265	4.94	6.06	91.57	91.26	12.78	12.31	2.76	2.56	36.65	36.00	28.18	27.78	4.72	4.81	61.83	63.41	8.68	8.97
37	ICGV 13200	4.15	4.3	91.37	91.34	14.54	12.49	2.85	2.68	33.53	35.27	26.63	27.35	4.40	4.82	62.2	62.68	8.65	8.81
38	ICGV 7220	3.59	5.34	91.47	91.06	15.94	12.97	2.63	2.47	34.53	37.39	30.11	28.90	4.76	4.89	60.27	61.64	8.3	8.70
39	ICGV 7222	5.08	5.04	91.76	91.31	13.43	13.86	2.71	2.62	36.27	34.61	28.15	27.23	4.84	4.46	60.85	61.77	8.5	8.59
40	ICGV 13317	4.9	6.27	91.54	91.71	14.57	12.24	2.76	2.64	36.11	36.46	30.11	28.64	4.99	5.15	60.15	63.17	8.33	8.92
41	ICGV 13254	4.8	7.95	91.40	91.41	13.41	11.52	2.88	2.52	34.47	37.59	27.27	28.79	4.72	5.30	61.18	62.9	8.53	8.97
42	ICGV 181026	4.42	7.61	91.40	91.47	13.90	11.94	2.76	2.54	34.71	36.71	27.89	28.40	4.54	5.00	62.4	62.94	8.68	8.93
43	ICGV 15073	4.93	7.48	91.34	91.40	13.42	12.86	2.86	2.58	36.78	36.38	28.61	28.35	4.69	5.01	61.46	62.44	8.52	8.76
44	ICGV 15074	4.23	7.23	91.68	91.40	12.24	12.74	2.84	2.47	36.96	37.24	28.13	28.72	4.80	5.18	62.11	61.98	8.7	8.77
45	ICGV 15083	4.92	7.98	91.67	91.81	13.83	10.24	2.65	2.46	37.46	38.36	29.90	28.94	5.05	5.73	60.79	62.29	8.48	8.94
46	ICGV 15019	4.41	7.68	91.12	91.62	14.92	12.97	2.85	2.53	35.95	36.76	28.97	29.17	4.66	5.24	59.7	61.55	8.23	8.67
47	ICGV 6420	5.05	7.95	91.69	91.37	12.73	12.64	2.75	2.60	38.30	34.93	29.42	27.27	5.11	4.70	61.52	62.82	8.59	8.87
48	ICGV 5155	5.6	5.41	91.47	91.38	13.21	12.74	2.61	2.55	38.28	36.86	30.73	28.18	5.41	4.95	60.81	61.63	8.5	8.70
49	ICGV 16688	5.7	7.77	91.70	91.61	13.27	12.15	2.76	2.50	36.55	37.58	28.73	28.85	4.67	5.16	61.68	62.62	8.58	8.86
50	ICGV 03043	5.23	6.52	91.43	91.35	14.60	13.06	2.63	2.54	39.11	35.97	31.93	27.85	5.43	4.83	59.56	62.2	8.25	8.76
51	ICGV 00350	4.61	7.08	91.70	91.20	13.98	12.65	2.80	2.58	37.18	35.28	29.72	26.83	4.92	4.55	61.45	63.39	8.53	8.97
52	ICGV 86590	4.89	7.87	91.57	91.38	13.72	11.96	2.94	2.59	35.92	36.68	28.19	28.45	4.67	5.16	61.59	63.35	8.5	9.00
53	ICGV 02266	3.99	6.66	91.74	91.45	14.28	12.16	2.92	2.64	34.97	36.52	27.79	27.64	5.01	4.84	61.26	62.85	8.47	8.86
54	ICGV 13189	3.4	5.32	91.22	91.26	12.70	12.09	2.69	2.46	37.54	35.24	29.42	26.60	5.15	4.59	62.52	64.14	8.84	9.11
55	ICGV 13207	2.66	3.54	91.44	91.35	14.16	13.49	2.58	2.52	35.32	35.90	29.45	28.66	4.99	5.06	60.94	61.9	8.6	8.76
56	ICGV 14421	3.88	5.99	91.45	91.23	16.28	12.33	2.67	2.47	34.30	36.84	29.66	28.75	4.80	5.36	60.91	62.74	8.43	9.00
57	ICGV 13219	3.72	4.32	91.37	91.18	13.38	12.45	2.74	2.46	34.47	36.65	26.74	27.82	4.39	5.15	63.07	62.21	8.86	8.85
58	GPBD 4	3.47	6.15	91.51	91.43	14.43	11.99	2.83	2.55	34.40	37.49	27.45	28.04	4.44	4.92	62.3	62.55	8.6	8.85
59	ICGV 86031	3.73	5.75	91.53	91.42	12.84	12.14	2.86	2.74	36.22	34.69	28.47	25.91	4.80	4.66	63.23	63.54	8.85	8.93
60	ICGV 16686	5.81	7.45	91.44	91.41	13.30	12.03	2.76	2.58	36.80	36.07	28.79	27.91	4.68	4.97	61.21	63.38	8.5	8.96
61	ICGV 16005	4.67	6.99	91.81	91.73	13.43	11.68	2.83	2.54	34.70	37.43	27.91	28.64	4.81	5.18	62.46	62.41	8.68	8.83

Table 3.5. Continued.

		HY (t ha^{-1})		DM (%)		Ash (%)		NC (%)		NDFDM (%)		ADFDM (%)		ADLDM (%)		IVOMD (%)		ME (%)	
serial number		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
62	ICGV 171013	4.69	4.61	91.46	91.20	13.74	12.83	2.70	2.61	38.55	35.97	31.30	28.38	5.43	4.87	60.58	62.74	8.47	8.90
63	ICGV 171026	5.49	7.08	91.26	91.31	14.91	12.59	2.76	2.60	34.18	36.26	28.42	27.66	4.50	4.70	61.77	62.67	8.51	8.83
64	ICGV 171039	4.34	6.22	91.36	91.44	14.04	12.26	3.07	2.55	34.12	37.89	26.05	28.43	4.21	4.88	62.28	61.78	8.6	8.69
65	ICGV 171046	4.09	6.33	91.44	91.26	14.47	12.38	2.76	2.61	33.65	36.27	27.53	27.63	4.38	4.84	62.37	62.82	8.69	8.87
66	ICGV 181017	5.51	8.5	91.50	91.49	11.88	12.26	2.68	2.55	37.70	36.89	28.98	28.97	4.86	5.24	62.49	63.02	8.81	8.93
67	ICGV 181063	5.23	8.03	91.53	91.43	13.17	11.91	2.75	2.63	37.07	36.75	29.48	28.09	4.96	4.99	62.01	63.08	8.62	8.88
68	ICGV 98412	5.75	6.8	91.37	91.48	12.93	12.70	2.88	2.51	36.47	36.50	28.14	29.01	4.63	5.37	61.74	61.74	8.55	8.75
69	ICGV 181489	6.06	7.92	91.59	91.47	13.57	12.53	2.70	2.65	37.45	36.97	30.86	28.70	5.56	5.17	61.19	62.66	8.5	8.82
70	ICGV 181490	4.51	5.49	91.45	91.23	13.13	13.43	2.84	2.45	37.16	35.98	29.13	27.85	4.96	4.77	61.3	62.4	8.54	8.83
71	ICGV 92054	5.39	7.57	91.80	91.43	13.56	12.55	2.88	2.61	35.32	37.20	27.96	29.37	4.59	5.12	62.01	62.18	8.62	8.72
72	ICGV 93162	6.47	7.38	91.97	91.46	13.16	11.81	2.73	2.94	38.51	36.29	30.85	26.34	5.34	4.64	61.1	63.58	8.5	8.92
73	ICGV 95111	5.77	7.94	91.78	91.49	13.30	12.22	2.83	2.58	35.50	37.47	28.57	28.90	4.87	5.18	62.54	61.85	8.71	8.75
74	ICGV 96165	7.29	6.88	92.06	91.55	17.18	13.23	2.77	2.72	32.86	34.29	29.68	27.03	4.76	4.83	60.48	62.66	8.29	8.80
75	ICGV 97115	5.03	8.55	91.69	91.37	14.26	11.52	2.80	2.68	35.60	36.46	29.64	28.24	5.06	5.36	61.3	62.99	8.51	8.94
76	ICGV 98184	6.11	6.49	92.05	91.11	15.73	12.35	2.65	2.51	35.20	38.55	30.70	29.56	4.93	5.24	61.04	61.24	8.44	8.69
77	ICGV 01491	5.38	9.42	91.59	91.57	13.30	12.00	3.10	2.77	35.43	37.35	27.73	28.43	4.68	5.09	62.78	62.75	8.68	8.79
78	ICGV 03287	5.02	6.85	91.86	91.58	14.37	12.33	2.75	2.53	36.98	38.36	29.79	29.41	5.13	5.32	59.98	62.12	8.27	8.77
79	ICGV 05057	5.17	6.52	91.70	91.50	14.00	12.33	3.03	2.66	34.57	36.60	27.38	28.79	4.60	5.10	62.19	62.74	8.58	8.82
80	ICGV 06175	5.09	6.92	91.66	91.58	13.34	11.41	2.69	2.54	36.90	38.83	29.61	29.31	5.11	5.21	60.80	60.87	8.53	8.59
81	ICGV 00064	6.3	7.75	91.79	91.68	15.22	12.92	2.84	2.72	34.86	35.57	28.99	28.22	4.82	5.14	61.23	62.35	8.42	8.73
82	ICGV 00246	5.28	6.81	91.58	91.46	12.51	12.69	2.63	2.61	36.73	36.38	28.70	28.77	4.87	5.07	61.64	62.62	8.66	8.79
83	ICGV 97150	5.54	7.9	91.65	91.50	15.07	12.01	2.77	2.78	35.28	35.77	30.13	27.33	4.95	4.93	60.95	63.23	8.43	8.89
84	ICGV 98385	5.49	8.23	91.58	91.39	13.41	12.24	2.85	2.71	36.41	36.00	29.32	28.54	4.93	5.18	61.72	62.92	8.59	8.89
85	ICGV 96266	6.71	7.65	91.91	91.63	15.33	11.56	2.75	2.68	34.68	36.46	29.74	28.00	4.81	5.05	61.36	63.45	8.47	8.98
86	ICGV 14224	5.83	7.23	91.71	91.28	14.46	11.80	2.70	2.66	36.51	36.85	30.57	28.17	4.97	5.01	60.22	61.53	8.35	8.69
87	ICGV 14232	6.51	6.66	91.87	91.33	17.15	12.75	2.64	2.67	33.18	37.04	30.81	28.70	4.93	4.95	59.90	61.83	8.21	8.69
88	ICGV 7262	5.07	6.1	91.52	91.39	13.97	12.79	2.67	2.54	35.83	36.34	29.30	28.72	4.92	5.20	60.71	60.91	8.49	8.60
89	ICGV 7247	4.6	7.2	91.74	91.33	14.38	12.30	2.84	2.61	35.03	37.39	28.04	29.44	4.69	5.25	61.31	62.38	8.48	8.86
90	ICGV 10371	4.88	6.8	91.83	91.35	13.31	11.60	2.79	2.6	36.77	38.66	29.49	29.21	5.25	5.33	60.64	61.96	8.46	8.75
91	ICGV 10373	5.83	7.11	91.96	91.51	12.80	12.29	2.65	2.63	38.54	37.95	30.37	30.29	5.34	5.67	60.37	61.21	8.42	8.65
92	ICGV 10379	5.73	8.03	91.93	91.60	14.49	11.68	2.83	2.62	35.79	37.82	29.13	29.06	4.90	5.23	61.56	62.27	8.51	8.79
93	ICGV 15094	5.27	7.79	91.74	91.40	12.43	11.32	2.85	2.66	36.56	38.31	28.54	29.48	4.98	5.32	62.42	62.52	8.73	8.90

Table 3.5. Continued.

		HY (t ha^{-1})		DM (%)		Ash (%)		NC (%)		NDFDM (%)		ADFDM (%)		ADLDM (%)		IVOMD (%)		ME (%)	
serial number		DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
94	ICGV 87846	5.26	8.1	91.63	91.33	13.49	12.08	2.82	2.57	35.52	37.92	28.25	29.16	4.71	5.15	61.44	62.08	8.53	8.80
95	ICGV 86699	5.53	7.09	91.65	91.49	14.58	12.20	2.79	2.7	34.59	36.98	29.24	28.34	4.74	5.08	62.00	63.35	8.62	8.93
96	GG 20	6.02	7.43	91.82	91.53	12.24	12.14	2.87	2.75	35.52	35.10	27.25	26.95	4.50	4.92	63.52	63.76	8.88	8.99
97	ICGV 171007	4.89	6.81	91.92	91.57	13.98	12.45	3.09	2.91	33.86	34.10	27.06	26.25	4.40	4.44	63.43	64.51	8.77	9.04
98	ICGV 171027	6.88	7.36	91.60	91.49	13.84	11.49	2.78	2.52	35.91	39.12	28.33	29.27	4.60	5.26	61.59	61.49	8.52	8.68
99	ICGV 181006	5.18	8.95	91.81	91.58	13.00	11.79	2.67	2.72	38.85	36.63	31.09	28.89	5.34	5.28	60.45	63.81	8.44	8.99
100	ICGV 181033	5.62	7.73	91.82	91.44	13.60	12.24	2.93	2.68	34.14	36.39	26.23	28.16	4.36	5.06	61.96	63.08	8.6	8.88
Mean		5.08	6.92	91.57	91.42	13.89	12.28	2.78	2.6	36.04	36.5	28.99	28.24	4.86	5.03	61.37	62.56	8.53	8.84
H^2 (%)		69.72	36.41	15.38	5.03	35.89	7.93	44.44	35.5	32.61	10.65	22.78	8.91	21.42	14.29	46.1	41.18	50	41.41
P-value		<0.001	<0.001	0.06	0.29	<0.001	0.19	<0.001	<0.001	<0.001	0.11	0.003	0.16	0.012	0.06	0.002	0..008	<0.001	0.001
SED		1.09	1.49	0.34	0.25	1.44	0.93	0.16	0.15	2.16	1.88	2.11	1.67	0.47	0.42	1.41	1.16	0.22	0.18
LSD (5%)		1.53	2.08	0.48	0.35	2.09	1.3	0.22	0.2	3.01	2.62	2.94	2.33	0.67	0.59	1.96	1.62	0.3	0.24
CV (%)		21.62	21.58	0.37	0.28	10.42	7.61	5.93	5.62	5.99	5.13	7.27	5.93	9.84	8.45	2.29	1.85	2.59	2.06

HY = haulm yield, DM = dry matter, NC = nitrogen, NDFDM = neutral detergent fiber, ADFDM = acid detergent fiber, ADLDM = acid detergent lignin, IVOMD = in vitro organic matter digestibility, ME = metabolizable energy, DS = drought-stressed, NS = non-stressed, H^2 = heritability in the broad-sense, SED = Standard error of the mean differences, LSD = Least significant difference, CV = coefficient of variation.

3.3.4. Comparison of groundnut (*Arachis*) sub-species for kernel and haulm yields, and quality parameters

Comparison of groundnut (*Arachis*) sub-species (i.e., *fastigiata and hypogaea*) for kernel and haulm yields, and kernel and fodder quality under DS and NS conditions are presented in Figure 3.1. Significant ($p<0.05$) differences were recorded between the two sub-species for kernel yield with *fastigiata* recoding higher kernel yield. Under both conditions, significant differences were observed between the two sub-species for oil content. Sub-species *hypogaea* recorded high mean oil content of 48.87% and 49.75% under DS and NS conditions compared to sub-species *fastigiata.* There were non-significant differences between the two sub-species for protein, palmitic acid, stearic acid, oleic acid and linoleic acid contents under both conditions. Significantly ($p<0.001$) higher haulm yields were recorded for sub-species *hypogaea* under DS (mean = 5.64 t ha^{-1}) and NS (mean = 7.44 t ha^{-1}) compared to sub-species *fastigiata.* Sub-species *hypogaea* recorded significantly higher dry matter content of 91.77% than sub-species *fastigiata* under DS condition. Ash content showed non-significant differences between the two *Arachis* sub-species under both conditions. Under NS condition, significant ($p<0.05$) differences were recorded between the two sub-species for nitrogen content with sub-species *hypogaea* recording higher mean nitrogen content of 2.80%. For neutral detergent fiber and acid detergent fiber, non-significant sub-species differences in mean values were observed under both water conditions. Sub-species *hypogaea* had high mean value for acid detergent lignin (5.12%) compared to a lower value of 4.99% for sub-species *fastigiata* under NS condition. For in vitro organic matter digestibility and metabolizable energy, non-significant differences were detected between the two sub-species under both water conditions.

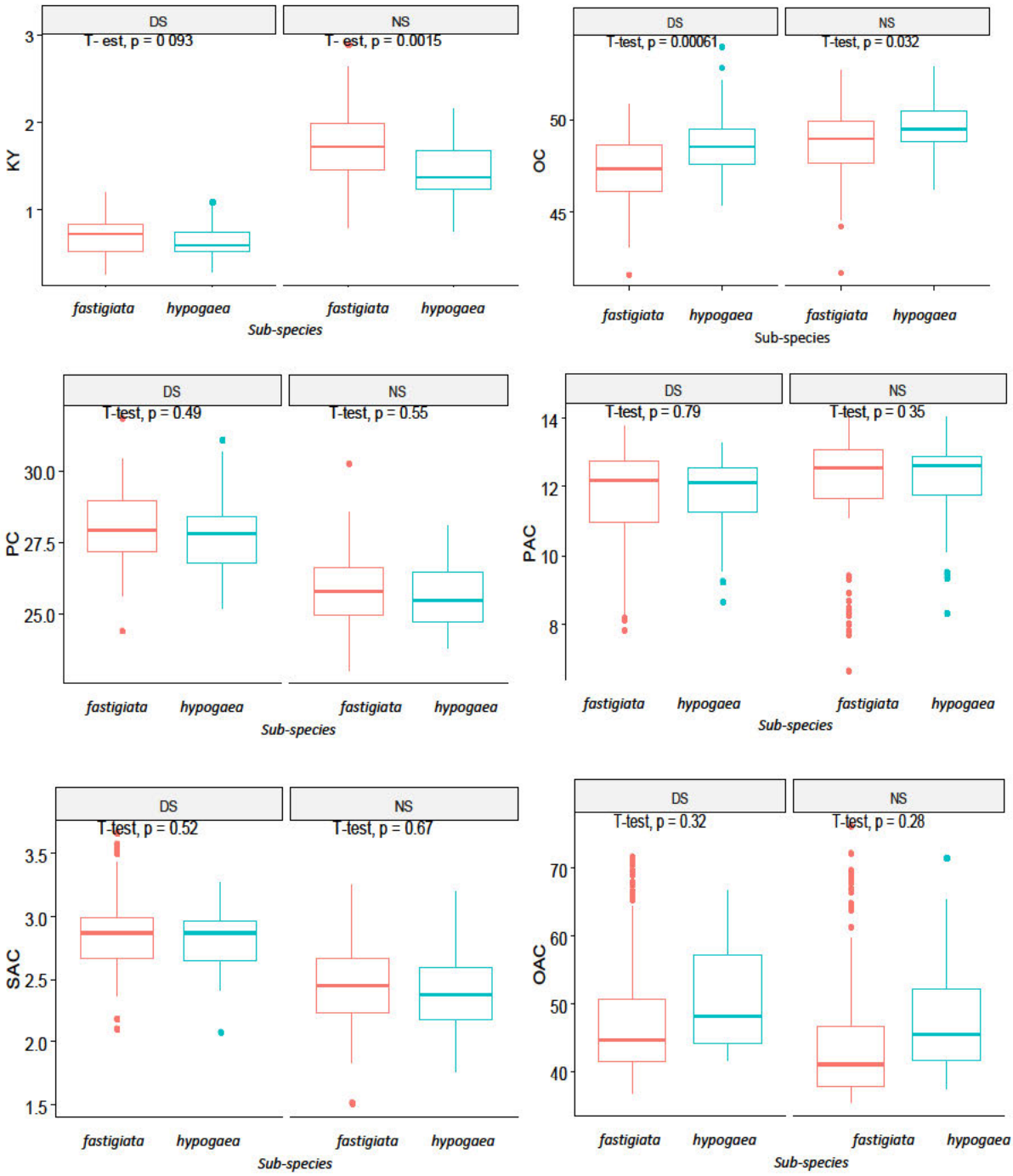


Figure 3.1. Mean response of groundnut (Arachis) sub-species for kernel and haulm yields, and kernel and fodder quality parameters under drought-stressed (DS) and non-stressed (NS) conditions evaluated during 2018/19 and 2019/20 post-rainy seasons at the International Crops Research Institute for the Semi-Arid, India. KY = kernel yield, OC = oil content, PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, HY = haulm yield, DM = dry matter, NC = nitrogen content, NDFDM = neutral detergent fiber, ADFDM = acid detergent fiber, ADLDM = acid detergent lignin, IVOMD = in vitro organic matter digestibility, ME = metabolizable energy.

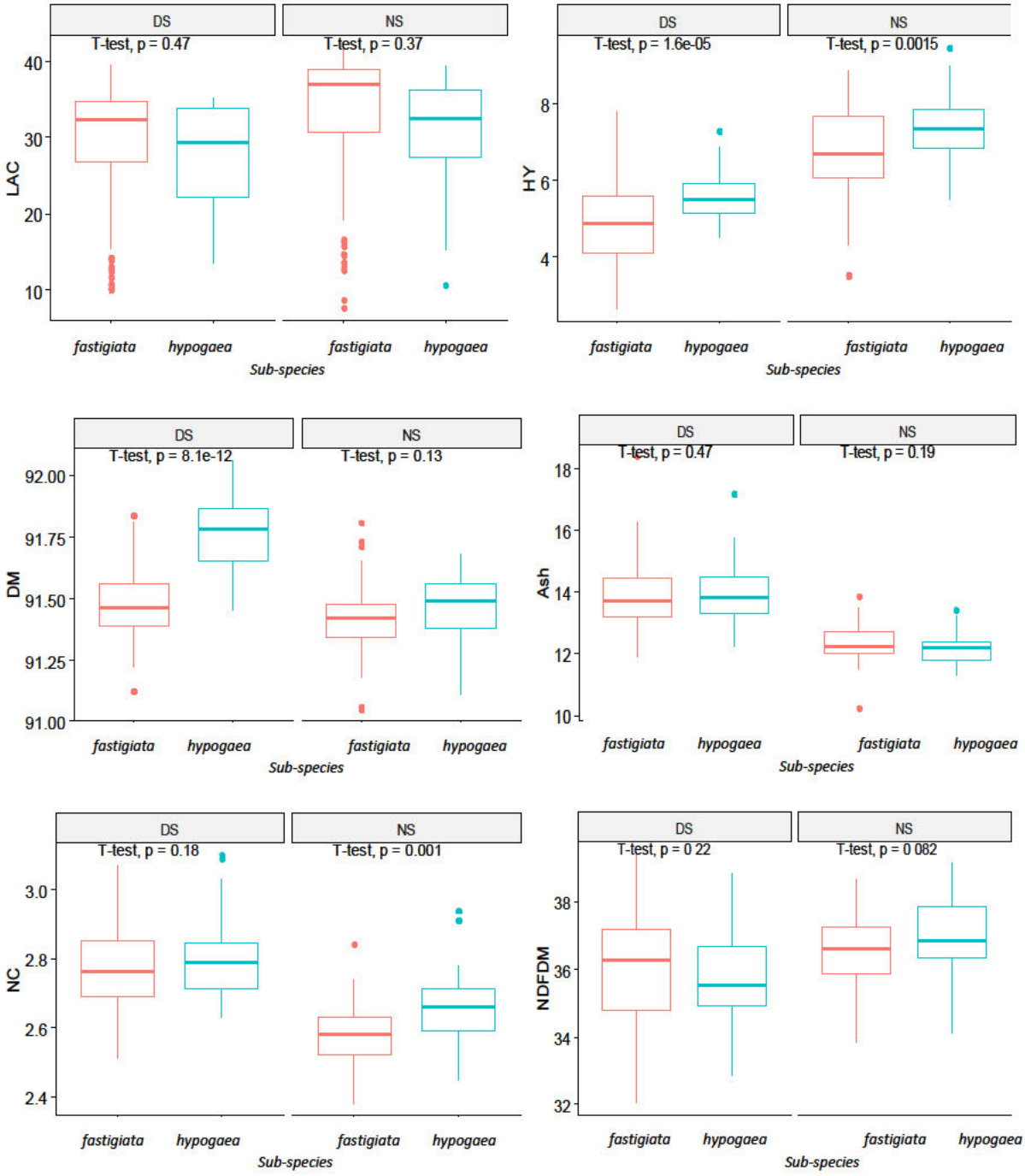


Figure 3.1. Continued.

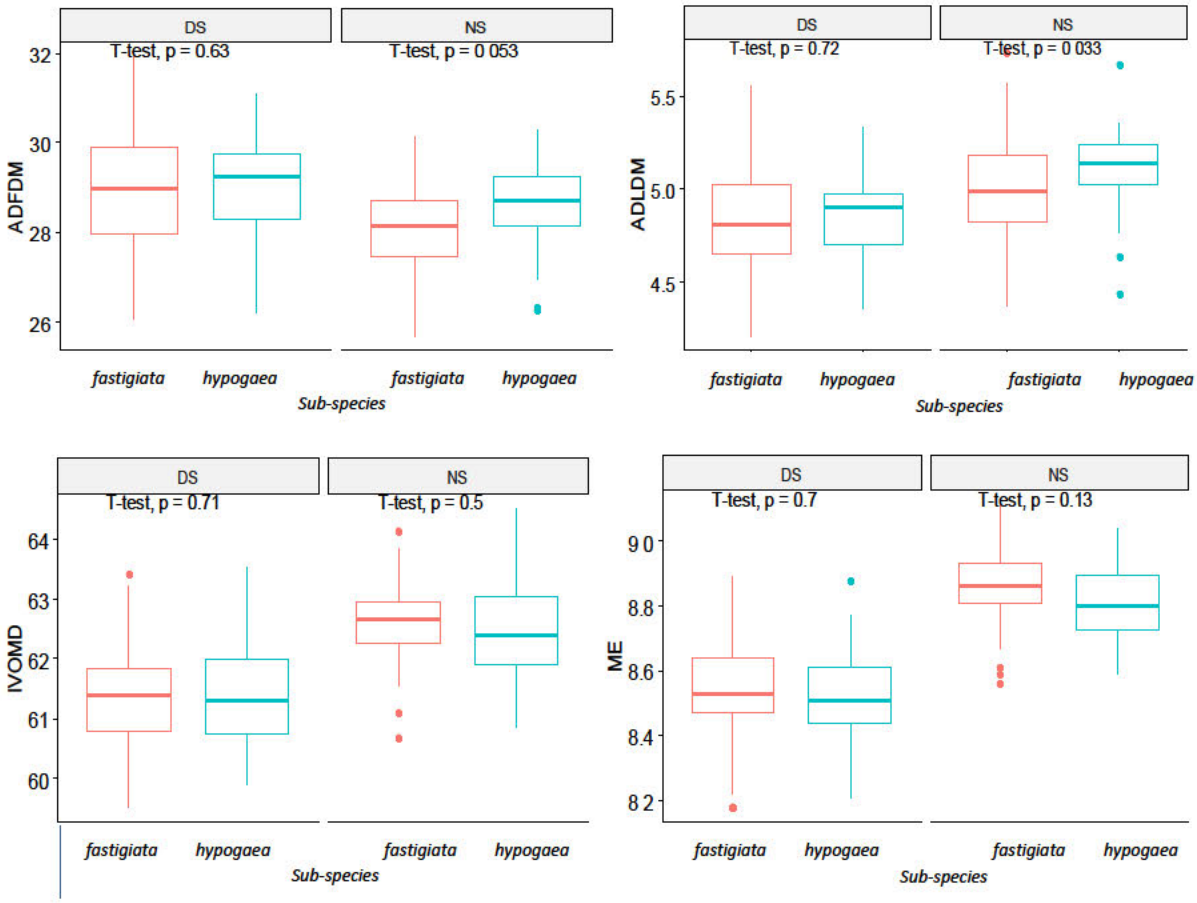


Figure 3.1. Continued.

3.3.5. Drought stress tolerance

Stress tolerance index (STI) of the assessed groundnut genotypes is presented in Table 3.6. The STI was used to identify genotypes that can provide high yields under both stressed and non-stressed conditions (Fernandez, 1992). Higher stress tolerance index values for kernel yield were recorded for ICGV 7222 (STI = 1.14), ICGV 10143 (1.06), ICGV 6040 (1.04), ICGV 03042 (0.87) and ICGV 06175 (0.85). For haulm yield, groundnut genotypes such as ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491 recorded higher STI values of > 1 indicating the stable performance of the genotypes under both conditions.

Table 3.6. Stress tolerance index (STI) of 100 groundnut genotypes based on kernel yield (KY) and haulm yield (HY) evaluated under drought-stressed and non-stressed conditions in 2018/19 and 2019/20 post-rainy seasons.

Serial number	Genotypes	STI		Serial number	Genotypes	STI	
		KY	HY			KY	HY
1	ICGV 16667	0.27	0.91	51	ICGV 00350	0.53	0.68
2	ICGV 93128	0.24	0.70	52	ICGV 86590	0.42	0.80
3	ICGV 95066	0.41	0.77	53	ICGV 02266	0.54	0.55
4	ICGV 96174	0.19	0.77	54	ICGV 13189	0.58	0.38
5	ICGV 97087	0.32	1.01	55	ICGV 13207	0.36	0.20
6	ICGV 98077	0.18	0.97	56	ICGV 14421	0.77	0.49
7	ICGV 01279	0.33	0.83	57	ICGV 13219	0.25	0.34
8	ICGV 03042	0.87	0.68	58	GPBD 4	0.23	0.45
9	ICGV 06039	0.78	0.45	59	ICGV 86031	0.27	0.45
10	ICGV 6040	1.04	0.73	60	ICGV 16686	0.39	0.90
11	ICGV 07010	0.48	0.75	61	ICGV 16005	0.30	0.68
12	ICGV 10143	1.06	0.60	62	ICGV 171013	0.50	0.45
13	ICGV 11422	0.12	1.03	63	ICGV 171026	0.35	0.81
14	ICGV 11396	0.29	0.86	64	ICGV 171039	0.53	0.56
15	ICGV 11418	0.23	0.96	65	ICGV 171046	0.51	0.54
16	ICGV 91223	0.23	0.53	66	ICGV 181017	0.49	0.98
17	ICGV 94118	0.48	0.63	67	ICGV 181063	0.15	0.88
18	ICGV 99019	0.55	0.92	68	ICGV 98412	0.61	0.82
19	ICGV 00162	0.24	0.68	69	ICGV 181489	0.15	1.00
20	ICGV 00211	0.46	0.84	70	ICGV 181490	0.56	0.52
21	ICGV 00187	0.32	0.59	71	ICGV 92054	0.22	0.85
22	ICGV 00213	0.37	0.64	72	ICGV 93162	0.27	1.00
23	ICGV 06146	0.46	0.39	73	ICGV 95111	0.32	0.96
24	ICGV 07120	0.41	0.75	74	ICGV 96165	0.28	1.05
25	ICGV 10178	0.60	0.97	75	ICGV 97115	0.25	0.90
26	ICGV 11380	0.72	0.41	76	ICGV 98184	0.32	0.83
27	ICGV 14001	0.71	0.61	77	ICGV 01491	0.21	1.06
28	ICGV 14030	0.41	0.43	78	ICGV 03287	0.34	0.72
29	ICGV 86015	0.40	0.45	79	ICGV 05057	0.27	0.70
30	ICGV 93260	0.48	0.42	80	ICGV 06175	0.85	0.74
31	ICGV93261	0.49	0.41	81	ICGV 00064	0.39	1.02
32	ICGV 92121	0.52	0.95	82	ICGV 00246	0.31	0.75
33	ICGV 99241	0.59	1.10	83	ICGV 97150	0.09	0.91
34	ICGV 00351	0.36	0.65	84	ICGV 98385	0.11	0.94
35	ICGV 01260	0.72	1.25	85	ICGV 96266	0.16	1.07
36	ICGV 01265	0.45	0.63	86	ICGV 14224	0.52	0.88
37	ICGV 13200	0.54	0.37	87	ICGV 14232	0.48	0.91
38	ICGV 7220	0.22	0.40	88	ICGV 7262	0.35	0.65
39	ICGV 7222	1.14	0.53	89	ICGV 7247	0.43	0.69
40	ICGV 13317	0.65	0.64	90	ICGV 10371	0.33	0.69
41	ICGV 13254	0.40	0.80	91	ICGV 10373	0.65	0.87
42	ICGV 181026	0.34	0.70	92	ICGV 10379	0.54	0.96
43	ICGV 15073	0.36	0.77	93	ICGV 15094	0.18	0.86
44	ICGV 15074	0.49	0.64	94	ICGV 87846	0.46	0.89
45	ICGV 15083	0.67	0.82	95	ICGV 86699	0.26	0.82

Table 3.6. Continued

		STI				STI	
Sr. No.	Genotypes	KY	HY	Sr. No.	Genotypes	KY	HY
46	ICGV 15019	0.51	0.71	96	GG 20	0.44	0.93
47	ICGV 6420	0.52	0.84	97	ICGV 171007	0.20	0.70
48	ICGV 5155	0.40	0.63	98	ICGV 171027	0.28	1.06
49	ICGV 16688	0.48	0.92	99	ICGV 181006	0.21	0.97
50	ICGV 03043	0.50	0.71	100	ICGV 181033	0.68	0.91

3.3.6. Relationships between kernel and haulm yields, and oil and haulm quality parameters under non-stressed and drought-stressed conditions

Pearson correlation coefficients showing relationships among kernel yield and haulm yields, and kernel and haulm quality parameters among the 100 groundnut genotypes evaluated under drought-stressed (DS) and non-stressed (NS) conditions are presented in Tables 3.7. Under DS condition, kernel yield was positively correlated ($p<0.001$) with oil yield ($r = 0.99$) and negatively and significantly correlated ($P < 0.05$) with stearic acid content ($r = 0.63$). Oil content exhibited positive and significant correlations with oil yield ($r = 0.12$), oleic acid content ($r = 0.12$). Kernel yield poorly and positively correlated with haulm yield ($r = 0.14$), but negatively correlated with dry matter ($r = 0.76$), nitrogen content ($r = 0.53$), *in vitro* organic matter digestibility ($r = 0.37$) and metabolizable energy ($r = 0.33$). Contrastingly, kernel yield positively and significantly correlated with ash content ($r = 0.32$), neutral detergent fiber ($r = 0.54$), acid detergent fiber ($r = 0.18$) and acid detergent lignin ($r = 0.46$). Haulm yield was positively correlated with oil yield ($r = 0.15$) and negatively correlated with nitrogen content ($r = 0.20$), *in vitro* organic matter digestibility ($r = 0.13$) and metabolizable energy (0.12), and positive correlation with neutral detergent fiber ($r = 0.19$), acid detergent fiber ($r = 0.18$), and acid detergent lignin ($r = 0.17$).

Under NS condition, kernel yield exhibited positive correlations with oil yield ($r = 0.98$), protein content ($r = 0.11$) and linoleic acid content ($r = 0.15$). Oil content exhibited low and positive correlation with oil yield ($r = 0.14$), stearic acid content (0.19) and linoleic acid content (0.18). Haulm yield exhibited positive correlation with oil content (0.31), dry matter content ($r = 0.54$), ash content ($r = 0.4$), nitrogen content ($r = 0.4$), metabolizable energy ($r = 0.4$) and *in vitro* organic matter digestibility ($r = 0.43$). Positive correlations were recorded between nitrogen content and *in vitro* organic matter digestibility ($r = 0.67$), nitrogen content and metabolizable energy ($r = r = 0.51$) and *in vitro* organic matter digestibility and metabolizable energy ($r = 0.94$). Positive correlations were observed between nitrogen content and *in vitro* organic matter digestibility ($r = 0.72$), nitrogen content and metabolizable energy ($r = 0.56$) and *in vitro* organic matter

digestibility and metabolizable energy (r = 0.95). Positive correlation were recoded between neutral detergent fiber and acid detergent fiber (r = 0.62), neutral detergent fiber and acid detergent lignin (r = 0.84) and acid detergent fiber and acid detergent lignin (r = 0.79). Positive correlation were observed between neutral detergent fiber and acid detergent fiber (r = 0.5), neutral detergent fiber and acid detergent lignin (r = 0.5) and acid detergent fiber and acid detergent lignin (r = 0.85).

Table 3.7. Pearson correlation coefficients among kernel and haulm yields, kernel and fodder quality parameters in 100 groundnut genotypes evaluated under drought-stressed (upper diagonal) and non-stressed (lower diagonal) conditions in 2018/19 and 2019/20 post-rainy seasons.

Traits	KY	OC	OY	PC	PAC	SAC	OAC	LAC	HY	DM	Ash	NC	NDFDM	ADFDM	ADLDM	IVOMD	ME
KY		0.04ns	0.99**	0.03ns	-0.02ns	-0.63**	-0.05ns	0.13*	0.14*	-0.76**	0.32**	-0.53**	0.54**	0.18*	0.46**	-0.37**	-0.32**
OC	-0.03ns		0.12*	-0.48**	-0.03ns	-0.04ns	0.12*	-0 05ns	0.24**	-0.02ns	0.07ns	-0.14*	0.10*	0.13*	0.13*	-0.08ns	-0.09ns
OY	0.98**	0.14*		-0.01ns	-0.03ns	-0.62**	-0.04ns	0.13*	0.15*	-0.76**	0.33**	-0.54**	0.54**	0.19*	0.46**	-0.37**	-0.33**
PC	0.11*	-0.62**	0.01		-0.07ns	0.11*	0.07ns	-0.10*	-0.21**	0.01ns	-0.02ns	0 06ns	-0.05ns	-0 06ns	-0.11*	0.05ns	0 04ns
PAC	0.08ns	0.06ns	0.09	-0.08ns		0.13*	-0.89**	0.87**	0.02ns	0.03ns	0.08ns	-0.04ns	-0.02ns	0.06ns	0.04*	-0.14*	-0.13*
SAC	-0.04ns	0.19*	-0 01	0.04ns	0 28**		-0.13*	0.02ns	-0.08ns	0.68**	-0.30**	0.44**	-4.08	-0 22**	-0.49**	0.31**	0 28**
OAC	-0.15*	-0.11*	-0.17	0.16*	-0.89**	-0.32**		-0 98**	0.02ns	0.04ns	-0.04ns	0.10ns	-0.07ns	-0 07ns	-0.09ns	0.18*	0.15*
LAC	0.15*	0.18*	0.18	-0.21**	0 86**	0.24**	-0.99**		-0.01ns	-0.12*	0.08ns	-0.16*	0.13*	0.10*	0.15*	-0.22**	-0.18*
HY	-0.02ns	0.33**	0.04	-0.44**	-0.07ns	0.03ns	0.05ns	-0 04ns		0.01ns	0.03ns	-0.20**	0.19*	0.18*	0.17*	-0.13*	-0.12*
DM	-0.23**	0.46**	-0.15	-0.49**	-0.04ns	0.30**	-0.04ns	0.05ns	0.54**		-0.40**	0 53**	-0.58**	-0.16*	-0.45**	0.40**	0 39**
Ash	0.03ns	-0.17*	0.0002	0.18**	0 05ns	-0.07ns	-0.01ns	0.01ns	-0.19**	-0.26**		-0.33**	-0.08ns	0.33**	0.13*	-0.53**	-0.71**
NC	-0.23**	0.24**	-0.18	-0.27**	0 04ns	0.23**	-0.03ns	0.02ns	0.40**	0.56**	-0.09ns		-0.70**	-0.72**	-0.73**	0.67**	0 51**
NDFDM	0.17*	-0 31**	0.11	0.34**	-0.05ns	-0.26**	0.09ns	-0 08ns	-0.40**	-0.69**	-0.15**	-0.76**		0.62**	0.84**	-0.57**	-0.39**
ADFDM	-0.07ns	0.01ns	-0 07	0.04ns	-0.06ns	0.04ns	0.07ns	-0 07ns	-0.04ns	0.06ns	-0.05ns	-0.49**	0.50**		0.79**	-0.74**	-0.63**
ADLDM	-0.03ns	-0 01ns	-0 03	0.06ns	-0.04ns	0.001ns	0.06ns	-0 05ns	-0.01ns	0.03ns	-0.28**	-0.46**	0.50**	0.85**		-0.66**	-0.49**
IVOMD	-0.2*	0.3**	-0.13	-0.4**	-0.03ns	0.2**	-0.004ns	-0 003ns	0.43**	0.63**	-0.26**	0.72**	-0.78**	-0.41**	-0.39**		0 94**
ME	-0.15**	0.30**	-0 09	-0.35**	-0.03ns	0.25**	-0.02ns	0.01ns	0.40**	0.63**	-0.40**	0 56**	-0.67**	-0 27**	-0.20**	0.95**	

KY = Kernel yield, OC = Oil content, OY = oil yield, PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, HY = haulm yield, DM = dry matter, NC = nitrogen, NDFDM = neutral detergent fiber, ADFDM = acid detergent fiber, ADLDM = acid detergent lignin, IVOMD = *in vitro* organic matter digestibility, ME = metabolizable energy.

3.3.7. Principal component and bi-plot analyses

Principal component analysis for the assessed traits among 100 groundnut genotypes revealed five and six principal components (PCs) with Eigen values greater than one under DS and NS condition, respectively. The principal component accounted for 79.4% and 82.5% of the total phenotypic variation under drought-stressed and non-stressed conditions, respectively (Table 3.8). Under DS condition, PC1 positively correlated with acid detergent fiber, acid detergent lignin and neutral detergent fiber and negatively correlated with *in vitro* organic matter digestibility and metabolizable energy which accounted for 25.7% of total variation. Oleic acid content positively correlated with PC2, whereas palmitic acid content, linoleic acid content and stearic acid content negatively correlated with PC2 which accounted for 17.4% of total variation. Kernel yield, oil yield and protein content positively correlated with PC3 which accounted for 14.1% of total variation. Oil content and haulm yield positively correlated with PC4 which accounted for 12% of total variation. Kernel yield and oil yield positively correlated with PC5 which accounted for 10.2% of total variation.

Under NS condition, neutral detergent fiber, acid detergent fiber and acid detergent lignin positively correlated with PC1 whereas nitrogen content negatively correlated with PC1 which accounted for 24.4% of total variation. Kernel yield, oil yield, palmitic acid content, stearic acid content and linoleic acid content positively correlated with PC2, whereas oleic acid content negatively correlated with PC2 which accounted for 21.7% of total variation. PC3 positively correlated with haulm yield and negatively correlated with protein content and ash content and both traits accounted for 13% of total variation. PC4 positively correlated with metabolizable energy which accounted for 9.7% of total variation. PC5 positively correlated with dry matter which accounted for 7.6% of total variation. PC6 positively correlated with dry matter content and negatively correlated with oil content which accounted for 6.1% of total variation.

The relationship between groundnut genotypes and assessed traits based on principal component bi-plots under drought-stressed and non-stressed conditions are presented in Figure 3.2. Smaller angles between dimension vectors in the same direction indicated high correlation of the variables in terms of discriminating genotypes. Genotypes that are good in a particular trait were plotted closer and furthest to the vector line. Under DS condition, genotypes, ICGV 93162, ICGV 10373, ICGV 01260, ICGV 10379, ICGV 10178, ICGV 05155, ICGV 03042 and ICGV 96174, were grouped based on high neutral detergent fiber, acid detergent fiber, acid detergent lignin and dry matter, high haulm, oil yield and kernel yields (Figure 3.2 A). Genotypes, ICGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063 excelled with high oleic acid content. Genotypes ICGV 171007, ICGV 181063, ICGV 171039, ICGV 181039, ICGV 93261, GPBD 4, and ICGV 13219, were grouped and possessed high metabolizable energy, *in vitro* organic matter digestibility, nitrogen and protein contents.

Under NS condition, genotypes, ICGV 7220, ICGV 06039, ICGV 05155, ICGV 03287, ICGV 06175, ICGV 14001, ICGV 00211 and ICGV 11396, were grouped recording high kernel yield, oil yield and oil content (Figure 3.2B). Genotypes, ICGV 181017, ICGV 181026, ICGV 181063, ICGV 181489, ICGV 181006, ICGV 16005 and ICGV 15083, were grouped based on high dry matter content, haulm yield and oleic acid content. Genotypes, ICGV 171007, ICGV 13189, ICGV 99019, ICGV 86031 and ICGV 86590, ICGV 86699, were excelling in nitrogen content, metabolizable energy, *in vitro* organic matter digestibility and protein content.

Table 3.8. Principal component scores, Eigen values, variances of kernel yield, oil and haulm fodder quality parameters among 100 groundnut genotypes evaluated under drought-stressed and non-stressed conditions in the 2018/19 and 2019/20 post-rainy seasons.

	Drought-stressed					Non-stressed					
Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
KY	0.11	0.16	**0.75**	0.02	**0.62**	0.07	**0.63**	-0.35	0.52	0.43	0.06
OC	0.22	0.13	-0.44	**0.55**	0.31	0.24	0.23	0.36	-0.10	0.30	**-0.52**
OY	0.14	0.17	**0.70**	0.10	**0.67**	0.11	**0.65**	-0.29	0.49	0.47	-0.02
PC	-0.37	0.05	**0.49**	-0.40	-0.18	-0.14	-0.05	**-0.49**	0.29	-0.43	0.45
PAC	0.48	**-0.80**	0.09	0.19	0.01	-0.41	**0.72**	0.41	-0.19	-0.11	0.14
SAC	0.00	**-0.48**	0.10	0.17	-0.09	-0.37	**0.42**	0.25	0.25	-0.26	0.01
OAC	-0.48	**0.81**	-0.20	-0.18	0.09	0.42	**-0.80**	-0.34	0.07	0.11	-0.10
LAC	0.49	**-0.79**	0.19	0.20	-0.06	-0.39	**0.81**	0.35	-0.09	-0.10	0.07
HY	0.32	0.24	-0.35	**0.45**	0.36	0.15	-0.40	**0.58**	-0.05	0.34	0.15
DM	0.24	0.13	-0.47	0.37	0.29	0.19	-0.29	0.39	0.10	**0.43**	**0.59**
Ash	0.22	-0.24	-0.47	**-0.67**	0.38	-0.13	0.27	**-0.58**	-0.54	0.18	0.08
NC	**-0.66**	-0.34	-0.24	0.02	0.13	**-0.63**	-0.36	0.29	-0.16	0.23	0.18
NDFDM	**0.54**	0.44	0.38	0.36	-0.39	**0.86**	0.10	0.26	0.12	-0.22	-0.10
ADFDM	**0.85**	0.35	-0.07	-0.15	-0.21	**0.89**	0.20	0.14	0.05	-0.15	0.05
ADLDM	**0.78**	0.38	0.04	0.07	-0.35	**0.78**	0.09	0.33	0.26	-0.18	0.17
IVOMD	**-0.83**	-0.04	-0.01	0.45	-0.10	**-0.73**	-0.45	0.16	0.39	0.03	-0.12
ME	**-0.70**	0.07	0.22	0.54	-0.23	-0.54	-0.35	0.18	**0.61**	-0.16	-0.22
Eigenvalue	4.37	2.95	2.39	2.04	1.74	4.14	3.69	2.21	1.66	1.30	1.03
Proportion variance (%)	25.71	17.36	14.08	12.00	10.22	24.38	21.68	13.02	9.74	7.64	6.09
Cumulative variance (%)	25.71	43.06	57.14	69.13	79.35	24.38	46.06	59.07	68.81	76.45	82.54

KY = Kernel yield (t ha^{-1}), OC = Oil content, OY = oil yield (t ha^{-1}), PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, HY = haulm yield, DM = dry matter, NC = nitrogen, NDFDM = neutral detergent fiber, ADFDM = acid detergent fiber, ADLDM = acid detergent lignin, VOMD = *in vitro* organic matter digestibility, ME = metabolizable energy.

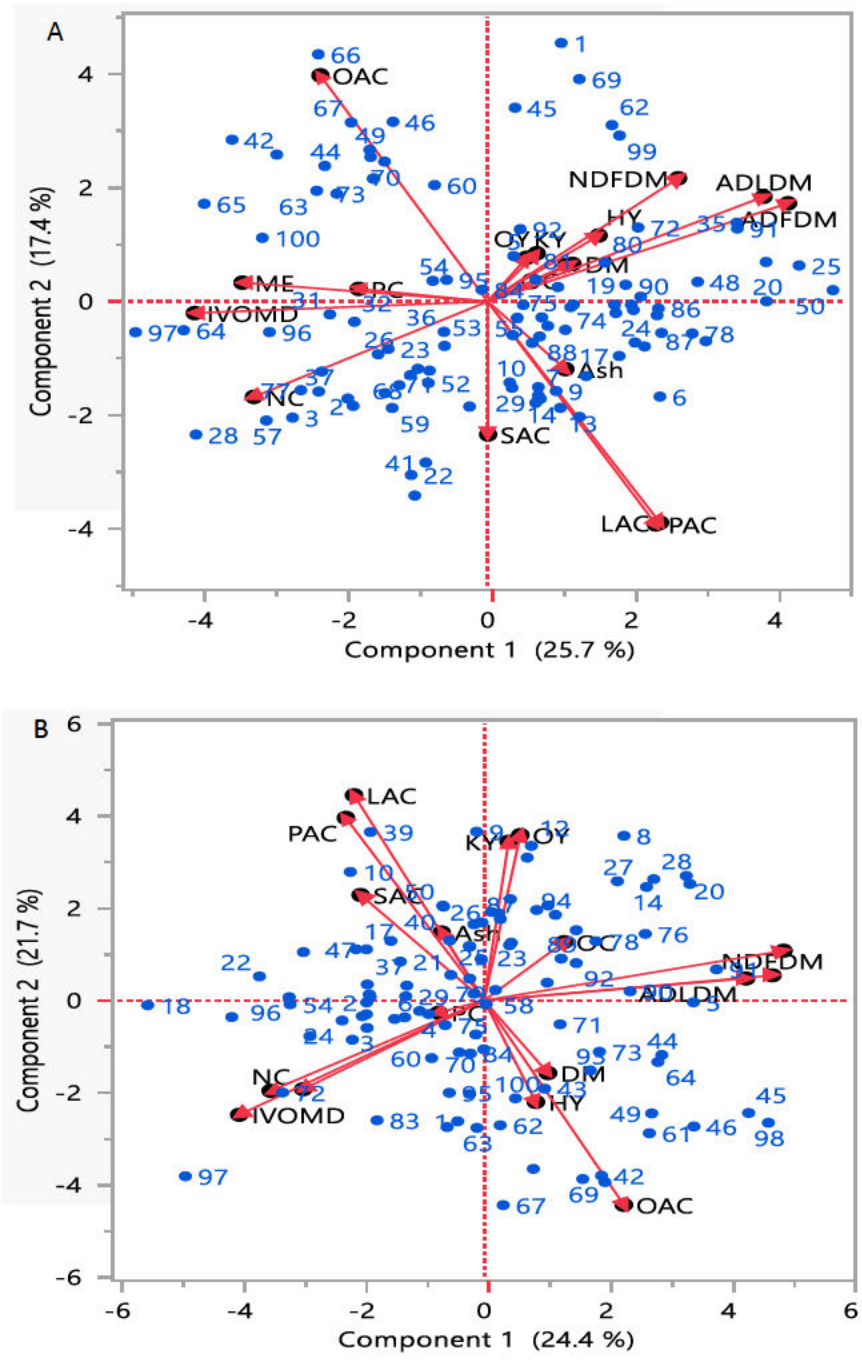


Figure 3.2. Principal components bi-plot showing the relationship between assessed traits among 100 groundnut genotypes under drought-stressed (A) and non-stressed (B) conditions evaluated across the 2018/19 and 2019/20 post-rainy seasons at the International Crops Research Institute for the Semi-Arid Tropics, India. KY = Kernel yield, OC = Oil content, OY = oil yield, PC = protein content, PAC = palmitic acid content, SAC = stearic acid content, OAC = oleic acid content, LAC = linoleic acid content, HY = haulm yield, NC = nitrogen, IVOMD = *in vitro* organic matter digestibility, ME = metabolizable energy. See code of genotypes in Table 3.2.

3.3.8. Cluster analysis among groundnut genotypes based on kernel and haulm yields, and kernel and fodder quality parameters

Cluster analysis showing the grouping of 100 groundnut genotypes based on kernel and haulm yields, and kernel and fodder quality traits are summarized in Table 3.9 and Figure 3.3. The test genotypes were allocated into 12 genetic groups. Cluster 11 and 12 comprised of high kernel and oil yielding genotypes with a mean of 1.72 t ha^{-1} and 0.84 t ha^{-1}. Genotypes with high oil content (> 49.5%) were grouped in clusters 8 and 12. Clusters 1 and 2 comprised of high oleic groundnut genotypes with mean values of 65.57 and 66%, respectively. Conversely, clusters 1 and 2 consisted of genotypes with lower linoleic acid contents of < 16%. Genotypes with high nitrogen content, *in vitro* organic matter digestibility and metabolizable energy were grouped in clusters 4 and 5. Genotypes with higher haulm yield possessing good haulm fodder qualities were grouped in cluster 6. In this cluster, genotypes, ICGV 01490, ICGV 96266, ICGV 93162, ICGV 98077, ICGV 11422 and ICGV 11418, recorded the highest mean haulm yield (≥ 6.5 t ha^{-1}), nitrogen content (≥ 2.75%), *in vitro* organic matter digestibility (≥ 62%) and metabolizable energy (≥ 8.5%).

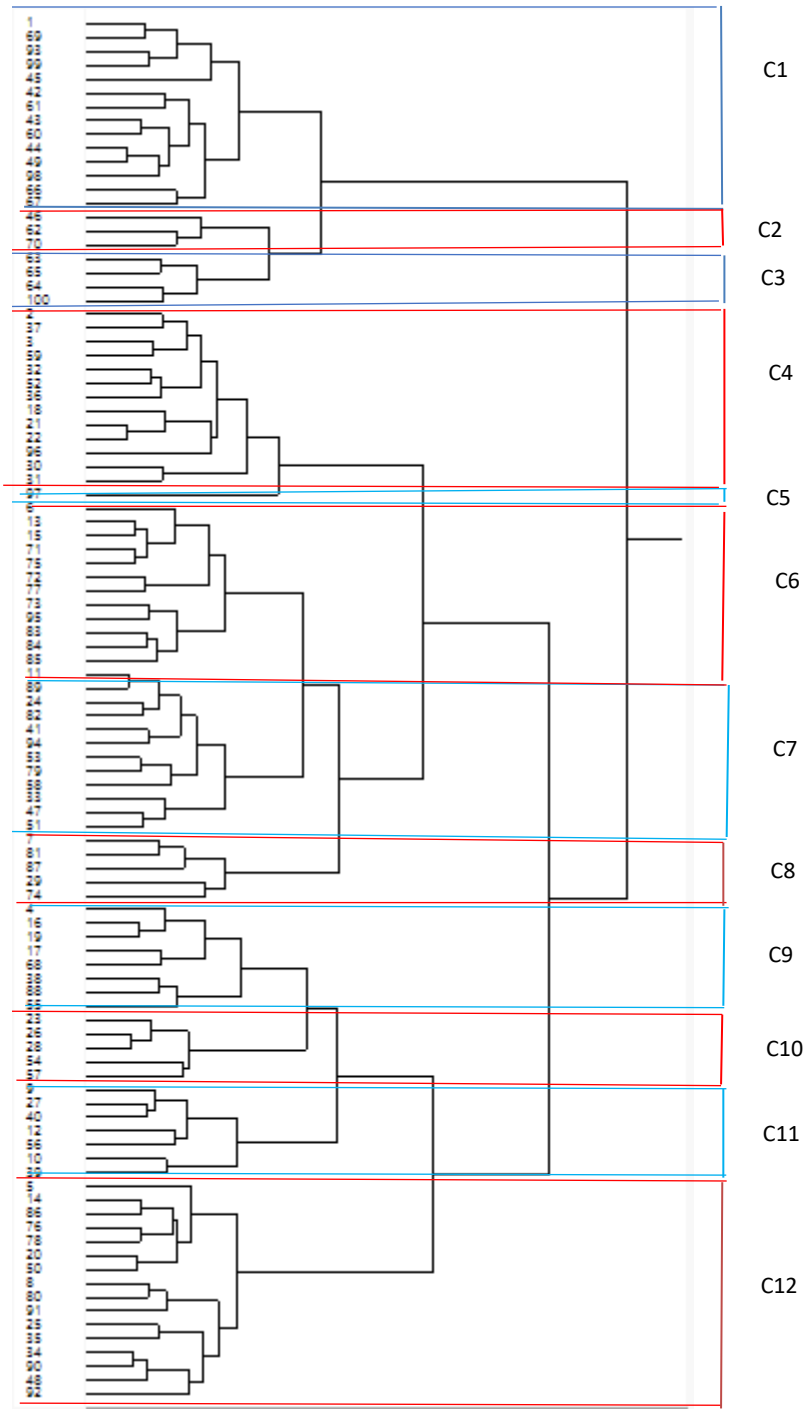


Figure 3.3. Hierarchical clustering using Ward's method showing groupings of 100 groundnut genotypes assessed based on kernel and haulm yields, and kernel and fodder quality parameters under drought-stressed and non-stressed conditions when genotypes were assessed in the 2018/19 and 2019/20 post-rainy seasons at the International Crops Research Institute for the Semi-Arid Tropics, India. See code of genotypes in Table 3.2. C = stand for cluster number

Table 3.9. Grouping of 100 groundnut genotypes evaluated under drought-stressed and non-stressed conditions across 2018/19 and 2019/20 post-rainy seasons.

Cluster	Number of genotypes	Name/designation of genotypes
1	14	ICGV 16667, ICGV 181026, ICGV 15073, ICGV 15074, ICGV 15083, ICGV 16688 ICGV 16686, ICGV 16005, ICGV 181017, ICGV 181063, ICGV 181489, ICGV 15094 ICGV 171027, ICGV 181006
2	3	ICGV 15019, ICGV 171013, ICGV 181490
3	4	ICGV 171026, ICGV 171039, ICGV 171046, ICGV 181033
4	13	ICGV 93128, ICGV 95066, ICGV 99019, ICGV 00187, ICGV 00213, ICGV 93260 ICGV93261, ICGV 92121, ICGV 01265, ICGV 13200, ICGV 86590, ICGV 86031, GG 20
5	1	ICGV 171007
6	12	ICGV 98077, ICGV 11422, ICGV 11418, ICGV 92054, ICGV 93162, ICGV 95111 ICGV 97115, ICGV 01491, ICGV 97150, ICGV 98385, ICGV 96266, ICGV 86699
7	12	ICGV 07010, ICGV 07120, ICGV 99241, ICGV 13254, ICGV 6420, ICGV 00350 ICGV 02266, GPBD 4, ICGV 05057, ICGV 00246, ICGV 7247, ICGV 87846
8	5	ICGV 01279, ICGV 86015, ICGV 96165, ICGV 00064, ICGV 14232
9	8	ICGV 96174, ICGV 91223, ICGV 94118, ICGV 00162, ICGV 7220, ICGV 13207 ICGV 98412, ICGV 7262
10	5	ICGV 06146, ICGV 11380, ICGV 14030, ICGV 13189, ICGV 13219
11	7	ICGV 06039, ICGV 6040, ICGV 10143, ICGV 14001, ICGV 7222, ICGV 13317 ICGV 14421
12	16	ICGV 97087, ICGV 03042, ICGV 11396, ICGV 00211, ICGV 10178, ICGV 00351 ICGV 01260, ICGV 5155, ICGV 03043, ICGV 98184, ICGV 03287, ICGV 06175 ICGV 14224, ICGV 10371, ICGV 10373, ICGV 10379

3.4. Discussion

Groundnut is a key legume crop for food and feed in crop-livestock farming systems. : It is one of the main sources of cash for small-holder farmers in arid and semi-arid parts of sub-Saharan Africa and Asia. Despite the multiple uses of groundnut, breeding for drought tolerance, high kernel and haulm yields, and quality traits have been largely ignored in groundnut improvement programmes. As a result, genotypic variation of groundnut germplasm for kernel and haulm yields, and kernel and haulm quality parameters remain largely unknown, limiting selection and development of dual-purpose groundnut cultivars for kernel and haulm production in smallholder crop-livestock systems.

The present study found significant variations in kernel and haulm yields, kernel and fodder quality parameters and drought tolerance among genetically distinctive groundnut genotypes (Table 3.3). The significant genotype differences observed among the studied groundnut genotypes for kernel and haulm yields, and quality traits allowed selection of suitable dual-purpose genotypes (Table 3.3). Also, genotype x water regime x year interaction effect was significant for kernel and haulm yields, indicating that the performance of the assessed genotypes varied across seasons and water conditions (Table 3.3). Groundnut genotypes, ICGV

7222, ICGV 10143, ICVG 06040, ICGV 03042, and ICGV 06175, were selected with marked drought tolerance and possessing high stress tolerance index values for kernel yield (Table 3.6). Also, genotypes, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, recorded high STI values for haulm yield. The stable yield performance of these genotypes in the two environments suggests that these genotypes can be used in groundnut breeding to exploit their drought tolerance and yield potentials.

Agronomic traits such as kernel and haulm yields are key attributes for selection and development of dual-purpose groundnut cultivars (Pande et al. 2005). In the present study, genotypes, ICGV 10143, ICGV 7222, ICGV 6040, ICGV 03042 and ICGV 06039, were high kernel and oil yielders (Table 3.4). Also, genotypes, ICGV 01490, ICGV 96266, ICGV 93162, ICGV 98077, ICGV 11422 and ICGV 11418, were the highest haulm yielders and possessed better fodder quality traits such as nitrogen content, *in vitro* organic matter digestibility and metabolizable energy (Table 3.5). Moreover, genotypes such as ICGV 10178, ICGV 01260, ICGV 06175 and ICGV 10379 produced both high kernel and haulm yields and therefore making them ideal candidates for production in mixed crop-livestock farming systems (Tables 3.4 and 3.5). In addition, kernel and haulm quality traits such as high oil, protein and oleic acid contents, reduced neutral detergent fiber, acid detergent fiber, acid detergent lignin and higher nitrogen content, *in vitro* organic matter digestibility and metabolizable energy are distinguishing traits for selection of groundnut genotypes for production (Samireddypalle et al. 2017; Nigam, 2014). Genotypes, ICGV 06146, ICGV 11380, ICGV 14030, ICGV 13189 and ICGV 7222, recorded high protein contents (Table 3.4). Genotypes, ICGV 1279, ICGV 6420, ICGV 5155, ICGV 97087 and ICGV 99241, were best performers with high oil content, whereas CGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063 were identified as high oleic acid genotypes (Table 3.4). All the test genotypes that recorded higher oleic acid content under both conditions showed lower linoleic acid content (<13%). Low oleic to linoleic ratio enhances the stability and shelf-life of groundnut oil and other groundnut derived products (Achola et al. 2017). Genotypes, ICGV 92121, ICGV 86590, ICGV 93161, ICGV GG 20 and ICGV 171007, had high nitrogen content, *in vitro* organic matter digestibility, metabolizable energy and the lowest mean neural detergent fiber, acid detergent fiber and acid detergent lignin under both drought-stressed and non-stressed conditions. The present study identified divergent parental lines for groundnut breeding for enhanced kernel and haulm yields, and kernel and fodder quality. Genotypes, ICGV 7222, ICGV 10143, ICGV 6040, ICGV 03042, ICGV 06175, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, possessing drought tolerance are recommended for cultivar development under drought stress environments (Table 3.6).

Comparison across sub-species for kernel and haulm yields, and quality traits revealed that the Virginia bunch (sub-species *hypogaea*) recorded slightly higher values for several traits including

oil content, oleic acid content, haulm yields, dry matter, nitrogen content, acid detergent fiber and acid detergent lignin (Figure 3.1). These allowed identification of genotypes with desirable kernel quality, haulm yield and fodder quality. The Spanish bunch groundnuts have higher oil content than other types of groundnuts including Virginia bunch groundnut (Nigam, 2014). The highest mean oil content recorded for Virginia sub-species (Figure 3.1) is probably due to the long intercrosses between the two sub-species. Therefore, groundnut genotypes belonging to the Virginia bunch types are useful genetic resources for the development of high oil groundnut cultivars. Also, Virginia bunch groundnuts are late maturing than Spanish bunch groundnuts (Krapovickas and Gregory, 1994). The high haulm yields recorded by the Virginia sub-species may offer opportunity to improve biomass production. Despite a lack of statistical significance difference, Virginia sub-species comprised of genotypes with high oleic acid content but low linoleic acid content compared to the Spanish sub-species. These imply that the variability within the Virginia sub-species for majority of the assessed traits can be exploited through selection for developing high oleic groundnut cultivars.

Associations of kernel and haulm yields, and quality is key to designing breeding strategies for development of dual-purpose groundnut genotypes. Under DS condition, oil content exhibited low and positive correlation with oil yield, oleic acid content, suggesting selection for higher oil content result in improved oil yield and oleic acid content. Haulm yield exhibited positive and significant correlation with oil yield and oil content under drought-stressed and non-stressed conditions, suggesting that these traits can be simultaneously improved via selection. Haulm quality traits such as nitrogen content, in vitro organic matter digestibility and metabolizable energy exhibited negative relationships with haulm yield under drought-stressed condition (Table 3.7). Contrastingly, these traits showed positive correlations with haulm yield under non-stressed condition, underlying the causal role of water deficit contributing to the trade-off between haulm quality traits and haulm yield (Table 3.7). This limits simultaneous selection and improvement of the of haulm yield and quality traits under drought-stressed condition. Drought stress affects the symbiotic nitrogen fixation capacity of the crop, and consequently leads to reduced nitrogen content, haulm digestibility and this results in low metabolizable energy (Blümmel et al. 2012).

In the present study, positive and significant correlations were exhibited between nitrogen content and *in vitro* organic matter digestibility, nitrogen content and metabolizable energy, and *in vitro* organic matter digestibility and metabolizable energy under both water conditions (Table 3.7). Further, these traits influence haulm quality. Negative and significant correlations were detected with the indigestible haulm quality traits such as neutral detergent fiber, acid detergent fiber and acid detergent lignin under both conditions. This suggests that nitrogen content, *in vitro* organic matter digestibility and metabolizable energy can be simultaneously improved through

selection. Nitrogen content is an important haulm quality trait which influences kernel yield due remobilization of nitrogen resources to pods (Blümmel et al. 2012). Under DS condition, negative correlations displayed between nitrogen content with kernel and haulm yields suggests the effect of drought on groundnut biomass and kernel yield production with consequences on the source-sink relationship for nitrogen.

Selecting of genotypes based on multiple traits enables enhancing genetic gains. Under DS condition, the principal component analysis indicated high contribution and strong association of neutral detergent fiber, acid detergent fiber, acid detergent lignin and haulm yield to the first principal component (Table 3.8 and Figure 3.2). Oleic acid content and metabolizable energy correlated with the second principal component, suggesting these traits have much influence during selection and can be simultaneously selected and improved. Under NS condition, neutral detergent fiber, acid detergent fiber, acid detergent lignin, oil content, kernel yield, oleic acid content were main contributors in the first principal component (Table 3.7 and Figure 3.2). These traits can also be simultaneously selected for breeding.

3.5. Conclusions

Well-characterized groundnut germplasm collection is essential to select unique genotypes with drought-tolerance, high kernel, oil and haulm yield and quality. The study revealed the presence of marked genetic variability among the tested groundnut genotypes for the measured traits which can be exploited in groundnut breeding. Kernel and haulm yields were not inversely related. Low correlation between kernel yield and haulm yield under drought-stressed and non-stressed condition, suggests independent selection and improvement of the two traits. Strong correlations among the haulm quality traits in both moisture conditions provide an opportunity for breeding of these traits in parallel and developing high haulm fodder quality under drought-stressed and non-stressed conditions. The following genotypes: ICGV 10178, ICGV 01260, ICGV 06175 and ICGV 10379 expressed high kernel and haulm yields, and CGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063 had higher oleic acid content. Further, genotypes, ICGV 7222, ICGV 10143, ICGV 6040, ICGV 03042, ICGV 06175, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, were relatively drought tolerant. The above genotypes are recommended for production or breeding drought-stress tolerant groundnut varieties with high kernel and fodder yields and quality attributes.

3.6. References

Abady, S., Shimelis, H. and Janila, P. 2019. Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding. *Journal of Crop Improvement* 33, 504-521. https://doi.org/10.1080/ 154275 28.2019. 1625836

Achola, E., Tukamuhabwa, P., Adriko, J., Edema, R., Mwale, S. E., Gibson, P., and Okello, D. K. 2017. Composition and variation of fatty acids among groundnut cultivars in Uganda. *African Crop Science Journal* 25, 291-299

Ahmed, H., Yoder, J., de Glanville, W., Davis, A., Kibona, T.J., Mmbaga, B.T., Lankester, F., Swai, F.E., and Cleaveland, S. 2019. Economic burden of livestock disease and drought in northern Tanzania. *Journal of Development and Agricultural Economics* 11, 140-151

Andersen, P.C., Hill, K., Gorbet, D.W., and Brodbeck, B.V. 1998. Fatty acid and amino acid profiles of selected peanut cultivars and breeding lines. *Journal of Food Composition and Analysis* 11, 100-111

Bishi, S.K., Kumar, L., Dagla, M.C., Mahatma, M.K., Rathnakumar, A.L., Lalwani, H.B., and Misra, J.B. 2013. Characterization of Spanish peanut germplasm (*Arachis hypogaea* L.) for sugar profiling and oil quality. *Industrial Crops and Products* 51, 46-50

Blümmel, M., Ratnakumar, P., and Vadez, V. 2012. Opportunities for exploiting variations in haulm fodder traits of intermittent drought tolerant lines in a reference collection of groundnut (*Arachis hypogaea* L.). *Field Crops Research* 126, 200–206

Carvalho, M.J., Vorasoot, N., Puppala, N., Muitia, A. and Jogloy, S. 2017. Effects of terminal drought on growth, yield and yield components in Valencia peanut genotypes. *SABRAO Journal of Breeding and Genetics* 49, 270-279

Choe, E. and Min, B.D. 2007. Chemistry of deep-fat frying oils. *Journal of Food Science* 72, 77-86

Da Silva, T. E., Detmann, E., Franco M de, O., Nobre, P. M. N., and Rocha, G. C. 2016. Evaluation of digestion procedures in Kjeldahl method to quantify total nitrogen in analyses applied to animal nutrition. *Acta Agriculturae Scandinavica. Section A-Animal Science* 38, 45–51. https://doi.org/10.4025 /actascianimsci. v38i 1.29171

Deshmukh, D.B., Marathi, B., Sudini, H.K., Variath, M.T., Chaudhari, S., Manohar, S.S., Rani, C.V.D., Pandey, M.K., and Pasupuleti, J. 2020. Combining high oleic acid trait and resistance to late leaf spot and rust diseases in groundnut (*Arachis hypogaea* L.). *Frontiers in Genetics* 11:514. https://doi.org/10.3389/fgene.2020.00514

Dwivedi, S.L., Nigam, S.N., Nageswara, R.R.C., Singh, U., and Rao, K.V.S. 1996. Effect of drought on oil, fatty acids and protein contents of groundnut (*Arachis hypogaea* L.) seeds. *Field Crops Research* 48, 125-133

EL. Sabagh, A., Hossain, A., Barutcular, C., Gormus, O., Ahmad, Z., Hussain, S., Islam, M., Alharby, H., Bamagoos, A., Kumar, N., Akdeniz, A., Fahad, S., Meena, R.S., Abdelhamid, M., Wasaya, A., Hasanuzzaman, M., Sorour S., and Saneoka, H. 2019. Effects of drought stress on the quality of major oilseed crops: Implications and possible mitigation strategies—A review. *Applied Ecology and Environmental Research* 17, 4019–4043. https://doi.org/ 10.15666/aeer/1702_40194043

Falke, A.B., Hamidou, F., Halilou, O., and Harou, A. 2019. Assessment of groundnut elite lines under drought conditions and selection of tolerance associated traits. *Advances in Agriculture* 2019, 1-10. https://doi.org/10.1155/2019/3034278

Fernandez, G.C.J. 1992. Effective selection criteria for assessing plant stress tolerance. Proceedings of the International Symposium on Adaptation of Vegetables and other Food Crops in Temperature and Water Stress, August 13-16, 1992, Shanhua, Taiwan, pp: 257-270

Hamidou, F., Ratnakumar, P., Halilou, O., Mponda, O., Kapewa, T., Monyo, E., Faye, I., Ntare, B.R., Nigam, S.N., Upadhyaya, H.D., and Vadez, V. 2012. Selection of intermittent drought tolerant lines across years and locations in the reference collection of groundnut (*Arachis hypogaea* L.). *Field Crops Research* 126,189-199

Hashim, I.B., Koehler, P.E., Eitenmiller, R.R., and Kvien, C.K. 1993. Fatty acid composition and tocopherol content of drought stressed Florunner peanuts. *Peanut Sci*ence 20, 21-24

Janila, P., Nigam, S.N., Pandey, M.K., Nagesh, P., and Varshney, R.K. 2013. Groundnut improvement: use of genetic and genomic tools. *Frontiers in Plant Science* 4: 1-16. https://doi.org/10.3389/fpls.2013.00023

Janila, P., Nigam, S. N., Abhishek, R., Kumar, V. A., Manohar, S. S., and Venuprasad, R. 2014. Iron and zinc concentrations in peanut (*Arachis hypogaea* L.) seeds and their relationship with other nutritional and yield parameters. *Journal of Agricultural Science* 153, 975–994. https://doi.org/10.1017/S0021859614000525

Janila, P., Variath, M.T, Pandey, M.K., Desmae, H., Motagi, B.N., Okori, P., Manohar, S.S., Rathnakumar, A.L., Radhakrishnan, T., Boshou, L.B., and Varshney, R.K. 2016. Genomic tools in groundnut breeding program: status and perspectives. *Frontiers in Plant Science* 7:289. https://doi.org/10.3389/fpls.2016.00289

Janila, P., Radhakrishnan, T., Murali T. V., Bera, S.K., Dobariya, K.L., Nigam, S.N., Varshney, R. K., Pandey, M. K., Manohar, S. S., Manivannan, N., and Vasanthi, R.P. 2018a. High oleic peanuts for Asia and Africa to meet the needs of the food processing industries. Case study. Science forum, Stellenbosch, South Africa

Janila, P., Manohar, S., Deshmukh, D., Chaudhari, S., Papaiah, V., and Variath, M.T. 2018b. Standard operating procedures for groundnut breeding and testing. Documentation ICRISAT

JMP®, Version *15.1*. SAS Institute Inc., Cary, NC, 1989-2019.

Joshi, A.K., Kumar, U., Mishra, V.K., Chand, R., Chatrath, R., Naik, R., Biradar, S., Singh, R.P., Budhlakoti, N., Devulapalli, R., and Blümmel, M. 2019. Variations in straw fodder quality and grain–Straw relationships in a mapping population of 287 diverse spring wheat lines. *Field Crops Research* 243, 107627

Kadim, I.T., Mahgoub, O., Al-Marzooqi, W., and Annamalai, K. 2005. Prediction of crude protein, extractable fat, calcium and phosphorus contents of broiler chicken carcasses Using Near-infrared Reflectance Spectroscopy. *Asian-Australasian Journal of Animal Sciences* 8, 1036-1040

Krapovickas A, Gregory W. 1994. Taxonomía del género *Arachis* (*Leguminosae*). Bonplandia 8:1–186

Mertens, D.R. 2000. Interpretation of forage analysis reports. In 30th National alfalfa symposium. Las Vegas, NV

Nawade, B., Mishra, G. P., Radhakrishnan, T., Dodia, S. M., Ahmad, S., Kumar, A., and Kundu, R. (2018). High oleic peanut breeding: Achievements, perspectives, and prospects. *Trends in Food Science & Technology* 78, 107–119. https://doi.org/10.1016/j.tifs.2018.05.022.

Ngcamu, B.S., and Chari, F., 2020. Drought influences on food insecurity in Africa: A Systematic literature review. *International Journal of Environmental Research and Public Health* 2020, 1-17. https://doi.org/10.3390/ijerph17165897

Nigam S.N., Chandra, S., Sridevi, R. K., Bhukta, M., Reddy, A.G.S., Rachaputi, R.N., Wright, G.C., Reddy, P.V., Deshmukh, M.P., Mathur, R.K., Basu, M.S., Vasundhara, S., Varman, V.P., and Nagda, A.K. 2005. Efficiency of physiological trait based and empirical selection approaches to drought tolerance in groundnut. A*nnals of Applied Biology* 146, 155–162

Nigam, S.N. 2014. Groundnut at a glance. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. Pp 121

Nigam, S.N., and Blummel, M. 2010. Cultivar-dependent variation in food-feed-traits in groundnut (*Arachis hypogaea* L.). *Animal Nutrition and Feed Technology* 10S, 39-48

Ojiewo, C.O., Janila, P., Bhatnagar-Mathur, P., Pandey, M.K., Desmae, H., Okori, P., Mwololo, J., Ajeigbe, H., Njuguna-Mungai, E., Muricho, G., Akpo, E., Gichohi-Wainaina, W.N., Variath, M.T., Radhakrishnan, T., Dobariya, K.L., Bera, S.K., Rathnakumar, A.L., Manivannan, N., Vasanthi, R.P., Kumar, M.V.N., and Varshney, R.K. 2020. Advances in crop improvement and delivery research for nutritional quality and health benefits of groundnut (*Arachis hypogaea* L.). *Frontiers in Plant Science* 11:29. https://doi.org/10.3389/fpls.2020.00029

Oteng-Frimpong, R., Konlan, S.P., and Denwar, N.N. 2017. Evaluation of selected groundnut (*Arachis hypogaea* L.) lines for yield and haulm nutritive quality traits. *International Journal of Agronomy* 2017, 1-9

Oteng-Frimpong, R., Baba Y.K., Danful, R., Akromah, R., Wireko-Kena, A., and Forson, S. 2019. Modeling groundnut (*Arachis hypogaea* L.) performance under drought conditions.

Journal of Crop Improvement 33, 125-144. https://doi.org/10.1080/15427528.2018.1542363

Pande, S., Upadhyaya, H.D., Narayana, R.J., Lakshmi, R.P., and Parthasarathy, R. 2005. Promotion of integrated disease management for ICGV 91114, a dual-purpose, early maturing groundnut variety for rainfed areas. Information BulletinNo. 68. Technical report. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India. Pp 28

Pandey, M.K., Monyo, E., Ozias-Akins, P., Liang, X., Guimarães, P., Nigam, S.N., Upadhyaya, H.D., Janila, P., Zhang, X., Guo, B., Cook, D.R., Bertioli, D.J., Michelmore, R., and Varshney, R.K. 2012. Advances in *Arachis* genomics for peanut improvement. *Biotechnology Adv*ances 30, 639–651. https://doi.org/10.1016/j. biotechadv.2011.11.001

Paul, P.J., Samineni, S., Sajja, S.B., Rathore, A., Das, R.R., Chaturvedi, S.K., Lavanya, G.R., Varshney, R.K., and Gaur, P.M. 2018. Capturing genetic variability and selection of traits for heat tolerance in a chickpea recombinant inbred line (RIL) population under field conditions. *Euphytica* 2018, 214–227

Pereira, J.W.L., Albuquerque, M.B., Melo Filho, P.A., Nogueira, R.J.M.C., Lima, L.M., and Santos, R.C. 2016. Assessment of drought tolerance of peanut cultivars based on physiological and yield traits in a semiarid environment. *Agricultural Water Management* 166, 70–76

R Core Team 2020. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/

Ren, X. Jiang, H., Yan, Z., Chen, Y., Zhou, X., Huang, L., Lei, Y., Huang, J., Yan, L., Qi, Y., Wei, W., and Liao, B. 2014. Genetic diversity and population structure of the major peanut (*Arachis hypogaea* L.) cultivars grown in China by SSR markers. *PLoS One* 9(2): e88091. https://doi.org/10.1371/ journal. pone.0088091

Samireddypalle A., Boukar O., Grings E., Fatokun C.A., Kodukula P., Devulapalli R., Okike I., and Blümmel, M. 2017. Cowpea and groundnut haulms fodder trading and its lessons for multidimensional cowpea improvement for mixed crop livestock systems in West Africa. *Frontiers in Plant Science* 8:30. https://doi.org/10.3389/fpls.2017.00030

Sarvamangala, C., Gowda, M.V.C., and Varshney, R.K. 2011. Identification of quantitative trait loci for protein content, oil content and oil quality for groundnut (*Arachis hypogaea* L.). *Field Crops Research* 122, 49-59

SAS Institute 2011. SAS/STAT User's Guide 9.3. Cary, NC: SAS Institute

Shasidhar, Y., Variath, M.T., Vishwakarma, M.K., Manohar, S.S., Gangurde, S.S., Sriswathi, M., Sudini, H.K., Dobariya, K.L., Bera, S.K., Radhakrishnan, T., Pandey, M.K., Janila, P., and Varshney, R.K. 2020. Improvement of three popular Indian groundnut varieties for foliar disease resistance and high oleic acid using SSR markers and SNP array in marker-assisted backcrossing. *The Crop Journal* 8, 1-15

Sharma, J. R. 1998. Statistical and biometrical techniques in plant breeding. New Age International (P) Limited Publishers, New Delhi, PP. 432

Singh, A. K., and Nigam, S.N. 2016. *Arachis* gene pools and genetic improvement in groundnut. In: Rajpal VR, Rao SM, Raina *SN* (eds.) Gene pool diversity and crop improvement, sustainable development and biodiversity. https://doi.org/10.1007/978-3-319-27096-8_2

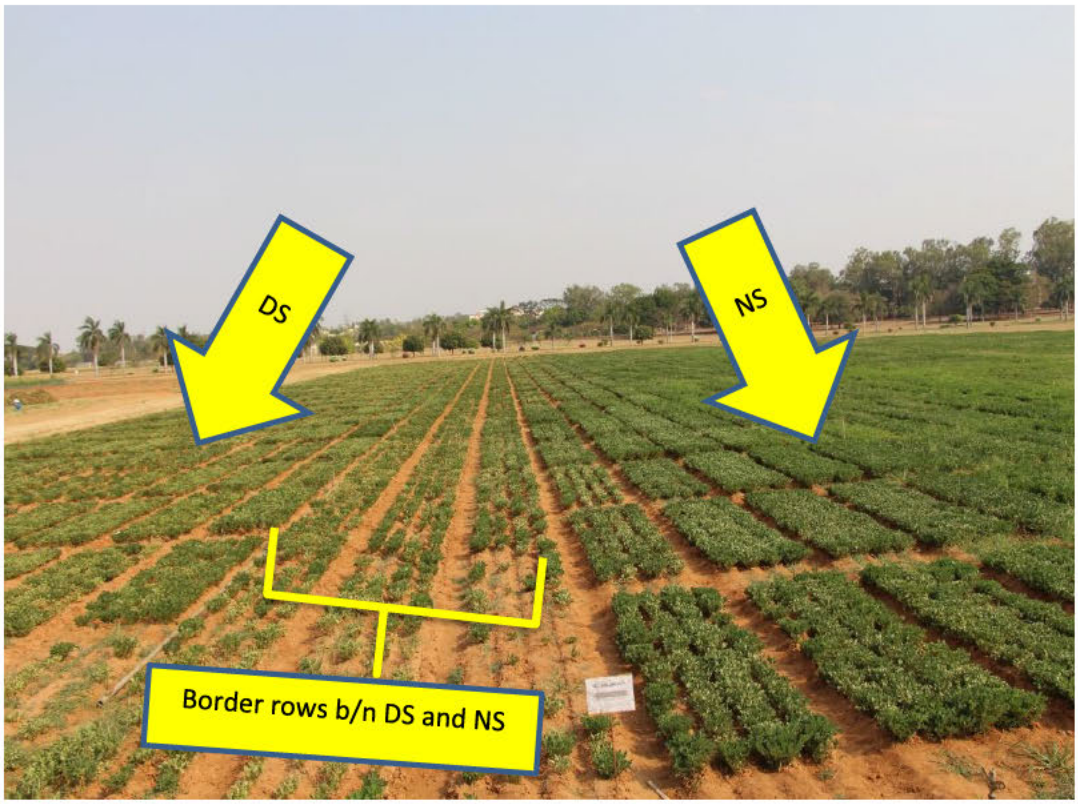
Singh, P., and Narayanan, S.S. 2017. Biometrical techniques in plant breeding. Kalyani Publishers, New Delhi, India

Songsri, P. Jogloy, S., Vorasoot, N., Akkasaeng, C., Patanothai, A., and Holbrook, C.C. 2008. Root distribution of drought resistant peanut genotypes. *Journal of Agronomy and Crop Science* 194, 92-103

Upadhyaya, H.D., Swamy, B.P.M., Goudar, P.V.K., Kullaiswamy, B.Y., and Singh, S. 2005. Identification of diverse groundnut germplasm through multienvironment evaluation of a core collection for Asia. *Field Crops Research* 93, 293-299

Yol, E., Ustun R., Golukcu, M., and Uzun, B. 2017. Oil content, oil yield and fatty acid profile of groundnut germplasm in Mediterranean climates. *Journal of the American Oil Chemists' Society* 94, 787–804. https://doi.org/ 10.1007/s11746-017-2981-3

Zheng, Z., Sun, Z., Fang, Y., Qi, F., Liu, H., Miao, L., Du, P., Shi, L., Gao, W., Han, S., Dong, W., Tang, F., Cheng, F., Hu, H., Huang, B., and Zhang, X. 2018. Genetic diversity, population structure, and botanical variety of 320 global peanut accessions revealed through tunable genotyping-by-sequencing. *Scientific Reports 8:14500.* https://doi.org/10.1038/s41598-018-32800-9



Appendix 3.1. Performance of groundnut genotypes under drought-stressed (DS) and non-stressed (NS) conditions in 2019/20 post-rainy season at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)-India.

Chapter 4

Assessment of the genetic diversity and population structure of groundnut germplasm collections using phenotypic traits and SNP markers: implications for drought tolerance breeding

---

Abstract

Profiling the genetic composition and relationships among groundnut germplasm collections are essential for breeding of new cultivars. The objectives of this study were to assess the genetic diversity and population structure among 100 groundnut genotypes using agronomic traits and high density single nucleotide polymorphism (SNP) markers. The genotypes were evaluated for agronomic traits and drought tolerance at the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)/India across two seasons. Ninety-nine of the test genotypes were profiled with 16, 363 SNP markers. Pod yield per plant (PY), seed yield per plant (SY) and harvest index (HI) were significantly ($p < 0.05$) affected by genotype × environment interaction effects. Genotypes, ICGV 07222, ICGV 06040, ICGV 01260, ICGV 15083, ICGV 10143, ICGV 03042, ICGV 06039, ICGV 14001, ICGV 11380 and ICGV 13200, exhibited higher pod yield under both drought-stressed and non-stressed conditions. PY exhibited significant ($p \leq 0.05$) correlation with SY, HI and total biomass (TBM) under both test conditions. Twelve and 18% of the test genotypes attained physiological maturity at 100 and 110 days after sowing, respectively. These early maturing genotypes can be selected for drought tolerance breeding. In the principal component analysis, PY, SY, HSW, SHP and HI were contributed maximum variability for yield under the two water regimes. Hence, selection of these traits could be successful for screening of groundnut genotypes under drought-stressed and non-stressed conditions. Model-based population structure analysis grouped the studied genotypes into three sub-populations. However, cluster analysis resolved the collections into 5 clusters based on pedigree, selection history, and market type. Cluster III and Cluster V consisted of the Spanish bunch types, late leaf spot (*Phaeoisariopsis personata)* and rust (*Puccinia arachidis*) resistant, and drought-tolerant genotypes. Analysis of molecular variance revealed that 98% of the total genetic variation was attributed to among individuals, while only 2% of the total variance was due to variation among the subspecies. The genetic distance between the Spanish bunch and Virginia bunch types ranged from 0.11 to 0.52. Genotypes, ICGV 13189, ICGV 95111, ICGV 14421, and ICGV 171007, were selected for further breeding based on their wide genetic divergence. Data presented in this study will guide groundnut cultivar development emphasizing economic traits and adaptation to water-limited agro-ecologies including in Ethiopia.

Key words: *Arachis hypogaea*; population genetics; genetic diversity, single nucleotide polymorphisms

4.1. Introduction

Groundnut (*Arachis hypogaea* L., AABB, 2n = 4x = 40) is an important oilseed legume crop providing various products worldwide. Groundnut is a self-pollinated allotetraploid crop derived from natural hybridization involving two diploid species, *A*. *duranensis* (A genome), and *A*. *ipaensis* (B genome) followed by polyploidization (Bertioli et al. 2016). Cultivated groundnut is classified into two subspecies viz. *hypogaea* (without floral axes on the main stem) and *fastigiata* (with floral axes arising from the main stem) (Zhang et al. 2017). Subspecies *hypogaea* has spreading growth habit with side branches procumbent to decumbent and a long growth cycle. In contrast, subspecies *fastigiata* has a more erect growth habit with side branches erect to procumbent and has a shorter growth cycle (Krapovickas and Gregory 1994). There are four market types of the cultivated groundnut viz., Virginia (*A. hypogaea* subsp. *hypogaea* var. *hypogaea*), runner (*A. hypogaea subsp. hypogea var. hirstu*), Spanish (*A.hypogaea* subsp. *fastigiata* var. *vulgaris),* and Valencia (*A.hypogaea* subsp. *fastigiata* var. *fastigaita*) (Nigam, 2014; Janila et al. 2016). Virginia type of groundnuts have the largest kernels and account for most of the groundnuts roasted and processed. Runners have uniform kernel sizes and are mostly used for groundnut butter. Spanish groundnuts have smaller kernels covered with reddish-brown skin and have a higher oil content than the other types of groundnuts. Valencia types of groundnuts usually have three or more small kernels in a pod and are covered in a bright-red skin. Valencia types are sweet and are generally preferred for fresh use as boiled groundnuts (Nigam SN. 2014). Groundnut kernels are rich sources of oil, protein, carbohydrate, minerals (e.g. P, Ca, Mg, and K), and vitamins (E, K, and B) (Gulluolu et al. 2016). Groundnut kernels with high oleic acid increase oil stability and confer health benefits (Gangadhara and Nadaf 2016). Groundnut haulm is used for animal feed. Also, groundnut improves soil fertility through nitrogen fixation.

In Ethiopia, groundnut has been used for food, edible oil extraction, and animal feed. The national mean yield is 1.796 ton/ha, and the total area under groundnut production is 80,841.57 ha (CSA 2018). In the last decade, groundnut production and yield have increased by two-fold in the country (FAOSTAT, 2018). Local demand for groundnut is increasing due to the emerging groundnut processing factories. Currently, smallholder farmers account for the bulk of production under rainfed conditions in the lowland and drought-prone areas of the country. Drought stress occurring during the flowering stage is a leading constraint to groundnut production in these production areas (Abady et al. 2019). The yield reduction due to drought stress is highly variable depending on genotype, timing, intensity, and duration (Falke et al. 2019). Drought stress during the reproductive phase can drastically reduce groundnut yield (Pereira et al. 2016). Terminal drought can cause 33% pod yield loss in groundnut (Carvalho et al. 2017). Although several introduced groundnut varieties have been released for cultivation in the country, none of them

are well-adapted or drought tolerant. This has rendered low production and productivity of groundnut in sub-Sharan Africa including Ethiopia.

Breeding groundnut for drought tolerance is an effective strategy to alleviate the impact of drought stress. Groundnut improvement for drought tolerance has achieved significant milestones (Pande et al. 2005; Vindhiyavarman et al. 2014). For example, ICGV 00351, a cross derivative from ICGV 87290 x ICGV 87846, was developed and released for cultivation in drought-prone areas of India (Vindhiyavarman et al. 2014). Similarly, ICGV 91114, an early maturing and drought tolerant cultivar, derived from a cross between ICGV 86055 x ICGV 86533 using the bulk pedigree method was developed at ICRISAT, India. Though conventional breeding played an important role in the release of drought-tolerant groundnut varieties, the breeding progress is slow (Janila et al. 2016). This is due to the narrow genetic base among the cultivated groundnuts (Nigam 2014). Introgression of genes from wild species into the cultivated groundnut is difficult due to the ploidy differences. In addition, the negative effects of linkage drag associated with genes from wild relatives often present a challenge to yield gain (Oteng-Frimpong et al. 2019; Janila et al. 2016). Yield and yield-related traits, including pod weight, shelling percentage, hundred seed weight, and the proportion of matured pods, are the most widely used traits in groundnut improvement (Janila et al. 2016; Wang et al. 2018). Ravi et al. (2011) confirmed the complex and quantitative nature of drought tolerance in groundnut. Other traits such as specific leaf area, chlorophyll content, biomass production, and harvest index have been used as surrogate traits for drought tolerance in groundnut (Nigam et al. 2005; Jongrungklang et al. 2008; Vadez and Ratnakumar 2016; Oteng-Frimpong et al. 2019).

Based on cross-compatibility, groundnut genetic resources are classified into four gene pools. The primary gene pool, includes landraces, cultivars, and wild *A. monticola* which is cross-compatible with *A. hypogaea*. The secondary gene pool consists of diploid species from the genus *Arachis*, which have cross-compatibility with *A. hypogaea*. The tertiary gene pool includes section *Procumbentes, which* are cross-compatible with diploid *Arachis* species. The quaternary gene pool includes *Arachis* species, which are partially cross-compatible with section *Arachis* (Nigam 2014; Singh and Nigam 2016). Previous findings indicated that the primary gene pool in the groundnut could be considered as the main source of genes for drought tolerance (Dutra et al. 2018; Desmae et al. 2017; Janila et al. 2016; Varshney et al. 2009).

Profiling the genetic composition and relationships among groundnut germplasm collections are essential for breeding of new cultivars. Earlier studies used phenotypic traits and marker technologies to analyze genetic diversity and population structure in cultivated groundnut (Zheng et al. 2018). SSR markers have been extensively used for assessing the genetic diversity of groundnut germplasm (Pandey et al. 2012; Wang et al. 2018). For example, 146 polymorphic

simple sequence repeat (SSR) revealed five heterotic groups among 196 groundnut cultivars (Ren et al. 2014). However, SSR markers cannot sufficiently explain the polymorphism in groundnut germplasm due to their extensive repetitive genomic content (Zheng et al. 2018). The single nucleotide polymorphisms (SNP) are increasingly becoming popular markers of choice due to their high genome abundance, ease of discovery, and the extremely high-throughput genotyping at a low cost per data point, with lower genotyping error rates (Singh and Singh, 2015; You et al. 2018; Adu et al. 2018). An Affymetrix SNP array with 58,000 SNP positions has been developed and deployed to study genetic diversity and population structure in groundnut (Otyama et al. 2019). Studies on genetic diversity of improved groundnut germplasm are needed to aid drought tolerance breeding for Ethiopia or genetic analysis. There is a lack of information regarding the local groundnut diversity to guide the regional breeding program. Consequently, production, utilization, and improvement of the crop are highly restricted. Thus, the objectives of this study were to assess the genetic diversity and population structure among improved groundnut genotypes using phenotypic traits and high density single nucleotide polymorphism (SNP) markers.

4.2. Material and Methods

4.2.1. Plant materials and study site

The study evaluated 100 improved groundnut genotypes comprising of diverse advanced breeding lines acquired from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in India (Chapter 3, Table 3.2). The 100 genotypes were evaluated during 2018/19, 2019, 2019/20 post-rainy and rainy seasons at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. Weather data for 2018/19 and 2019/20 post-rainy seasons' field trails were presented in Chapter 3. Tables 3.1 and 4.1 summarizes weather data during field trial in 2019.

4.2.2. Experimental design

One hundred genotypes were evaluated at ICRISAT/India during 2018/19 and 2019/20 under drought-stressed (DS) and non-stressed (NS) conditions using a 10 x 10 alpha lattice design with two replications as described in Chapter 3 under section 3.2.1. The 100 genotypes were also evaluated under field condition at ICRISAT/India in 2019 rainy season using alpha lattice design with 10 blocks each containing 10 entries. Seeds of each genotype were sown in two rows of four meters. Five plants were harvested from each genotype at 100, 110, 120 and 130 days

after sowing to determine the maturity duration of the test genotypes. Pod maturity can be determined either by the sound produced by the pods when they are pressed or by observing the inner pod wall which will turn blackish in mature pods.(Hamidou et al. 2012).

Table 4.1. Monthly weather data during the field trial at ICRISAT/India in 2019

Year	Month	Rainfall (mm)	Tmax (^{0}C)	Tmin (^{0}C)	RHmax (%)	RHmin (%)
2019	June	36	34.12	23.08	88.2	55.6
	July	79.5	31.88	22.78	86.42	62.16
	August	193.4	29.91	22.11	89.26	70.22
	September	294	29.67	21.59	94.3	81
	October	55.4	30.53	20.87	94.3	79.81
Mean		131.66	31.222	22.086	90.496	69.758

Tmax = average maximum temperature, Tmin = average minimum temperature, RHmax = average maximum relative humidity, RH min = average minimum relative humidity

4.2.3. Data collected

The following phenotypic traits were described in Chapter 3, were considered for this study. Days to 50% flowering (DF) were recorded by counting the number of days from sowing to the time when 50% of the total plant stand had reached flowering. Soil plant analysis development (SPAD) chlorophyll meter reading (SCMR) was recorded at 80 days after sowing from three trifoliates of each plant between 8:00 to 9:30 am. The SCMRs were recoded using Minolta SCMR-502 m (Tokyo, Japan) and the reading was taken as described by Nageswara Rao et al. (2001). Leaf area was measured using leaf area scanner and leaves were oven-dried at 80 ^{0}C for 48 hours. Specific leaf area (SLA) was calculated based on the formula suggested by Rao et al. (2001) as follows:

SLA = Leaf area (cm^2)/Leaf dry weight (g)

Leaflets of five plants were collected and stored in sealed plastic bags and transport to the laboratory for fresh weight measurement. After the fresh weight measurements, the samples were soaked in distilled water for 8 hours and accordingly saturated weights were recorded. Leaf relative water content (LRWC) was calculated according to the formula given by Gonzalez and Gonzalez, 2001:

$$LRWC = \frac{\text{fresh weight-dry weight}}{\text{Saturated weight-dry weight}} \times 100$$

Plant height (PH, expressed in cm) was measured from ten randomly sampled and tagged plants from the soil surface to the tip of the main stem. Number of primary branches (PB) was recorded as the average number of primary branches from the ten plants. Pod yield per plant (PY, expressed in g $plant^{-1}$) was recoded as the average pod weight of ten sample plants. Shelling

percentage (SHP, expressed in %) for each genotype was calculated from a random sample of pods weighing 200 g, as the proportion of shelled seed weight to the total weight of the unshelled pods. Seed yield per plant (SY, expressed in g plant^{-1}) was estimated as the product of pod yield per plant and shelling percentage. Total biomass per plant (TBM, expressed in g plant^{-1}) was recorded as the mean total biomass weight of ten sample plants during physiological maturity of the crop. Harvest index (HI) was computed as a ratio of pod weight to total biomass (Mukhtar et al. 2013).

The following phenotypic data were collected to determine the maturity duration of the test genotypes: total number of pod per plant, number of matured pods per plant and subsequently percentage of mature pods per plant were calculated at 100, 110 and 120 days after sowing.

4.2.4. Phenotypic data analysis

Analysis of variance was performed using SAS version 9.3 Software. Phenotypic and genotypic coefficients of variation were computed as per the methods suggested by Burton and Devane (1953):

Genotypic variance (σ^2_g) = $\frac{(msg-\text{mse})}{r}$; Environmental variance (σ^2_e) = mse,

Where, msg and mse are the mean sum of squares for the genotypes and error in the analysis of variance, respectively; r is the number of replications.

The phenotypic variance was estimated as the sum of the genotypic and environmental variances:

$\sigma^2_{ph} = \sigma^2_g + \sigma^2_e$

Genotypic coefficients of variability (GCV) and phenotypic coefficients of variability (PCV) were calculated according to the formulae of Singh and Chaundary (1977):

GCV = (σ_g/grand mean) x 100; PCV = (σ_{ph} /grand mean) x 100

Where, σ_g and σ_{ph} are genotypic and phenotypic standard deviations, respectively.

Heritability in a broad sense (H^2) was calculated as per the following formula (Allard 1960):

$H^2 = \frac{\sigma 2g}{\sigma 2p} \; x \; 100$

The genetic advance for selection intensity (k) at 5% (2.06) was estimated by the following formula (Johnson *et al*. 1955):

$EGA = k * \sigma_{ph} * h_b^2$

Where, EGA represents the expected genetic advance under selection; σ_{ph} is the phenotypic standard deviation; h_b^2 is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was estimated following the procedure of Johnson *et al*. (1955):
GAM = (EGA/grand mean) * 100.

Decision for maturity duration was made based on the increase in pod yield per plant and percentage of matured pods per plant >70% (Janila and Nigam 2013). Pearson correlation was computed using SAS software. Principal component analysis was carried out using JMP Version 15.1 Software with mean observation of all the traits.

4.2.5. Genotyping

The genotypes were grown under field conditions at ICRISAT, Hyderabad, India. The genomic DNA was extracted from leaves of three weeks old seedlings at the Center of Excellence in Genomics and Systems Biology at ICRISAT. The DNA was extracted using the modified cetyl trimethyl ammonium bromide (CTAB) method (Mace et al. 2003). DNA was quantified by loading 1 ml on the 0.8% agarose gel containing 10 ml ethidium bromide (10 mg/ml) and run at 80 V for 30-45 min. The agarose gel was documented under UV transilluminator. The DNA quality and concentration were estimated using NanoDrop Spectrometry (UV 160 A, Japan). Haplotype-based genotyping using 48 k SNP Array was conducted at the University of Georgia, Tifton, United States (Clevenger et al. 2018).

4.2.6. Data analysis

The SNP data were analyzed using the Axiom analysis suite (Thermo Fisher Scientific Inc, 2018). SNP markers with more than 20% of missing data and the minor allele frequencies lower than 0.05 were eliminated, resulting in 16,363 SNP markers, which were used for further analysis (Mathew et al. 2019). Ninty-nine genotypes were used after the data imputation. The genotype data filtering was performed using TASSEL version 5.2.61 Software (Bradbury et al. 2007). Genetic dissimilarity, minor allele frequency (MAF), observed gene diversity, polymorphic information content (PIC), and inbreeding coefficients were determined using GenALEx Version 6.5 Software (Peakall and Smouse 2012). Analysis of molecular variance was performed using GenALEx version 6.5 Software to estimate fixation (F_{ST}) values and to partition molecular variance within sub-

species and among subspecies of cultivated groundnut. The genetic differentiation parameter (PhiPT) was used to measure the similarity of pairwise genotypes from the entire collection. Phi'PT represents the proportion of PhiPT relative to the maximum variability proportion attainable PhiPTmax calculated as PhiPT/PhiPTmax (Nadia et al. 2019). The genetic relationship among the genotypes was constructed based on the unweighted paired group method with arithmetic mean (UPGMA) using TASSEL Software. The pairwise genetic distance matrix between 99 genotypes was analyzed using TASSEL Software. Kinship matrix and 3D-principal component analysis were generated using the GAPIT program in R software (Lipka et al. 2012). The pattern of population structure and detection of admixture were inferred using a Bayesian model-based clustering algorithm implemented in STRUCTURE version 2.3.4 (Pritchard et al. 2000). The length of the burn-in period and Markov Chain Monte Carlo (MCMC) were set at 10,000 iterations (Evanno et al. 2005). The K value was set between 1 and 10 to generate the number of subpopulations in the genotypes. Twenty runs were performed for each K-value, to obtain an accurate estimation of the number of populations. Delta K values were calculated, and the appropriate K value was determined by the Evanno et al. (2005) method using the STRUCTURE Harvester program (Earl and von Holdt 2012).

4.3. Results

4.3.1. Analysis of variance

Analysis of variance for 13 phenotypic traits of 100 groundnut genotypes evaluated under drought-stress and non-stressed conditions are presented in Table 4.2. Under drought-stressed condition, the ANOVA revealed significant ($p<0.05$) difference among genotypes for plant height (cm), SCMR, specific leaf area ($cm^2\ g^{-1}$) and shelling percentage, and highly significant ($p<0.001$) for days to 50% flowering, number of primary branch, leaf relative water content, haulm weight ($g\ plant^{-1}$), hundred seed weight (g), pod weight ($g\ plant^{-1}$), total biomass weight ($g\ plant^{-1}$) and harvest index (%). Under non-stressed condition, the result revealed non-significant differences for SCMR and SLA; significant ($p<0.05$) difference for number of primary branches and highly significant difference for the rest of the tested traits. Non-significant difference for genotype by year interaction was recorded for SCMR and SLA under both moisture stress conditions.

4.3.2. Genetic variation among groundnut genotypes

All the measured traits showed a wider range of values under both moisture conditions except days to 50% flowering (48-53) (Table 4.3). The highest pod yield per plant under drought-stressed

condition was recorded by ICGV 01260 (8.57g), ICGV 06040 (8g), ICGV 06175 (7.51g), ICGV 07222 (7.2g) and ICGV 10178 (7.12g) (Appendix 4.1.), whereas ICGV 98412 (16.21g), ICGV 07222 (15.93g) and ICGV 10143 (15.49g) were under non-stressed condition. (Appendix 4.2). Phenotypic coefficient of variation (PCV) values was higher than genotypic coefficient of variation (GCV) for all the measured traits (Table 4.3). Under drought-stressed condition, the highest GCV and PCV were observed for PY (32.93% and 42.71%) followed by HI (31.97% and 38.48%) and TBM (27.49% and 31.62%), while SHP (22.33% and 24.91%), HSW (17.37% and 20.61%) and HI (26.28% and 31.54%) were recorded under non-stressed condition. The highest heritability in abroad sense (H^2) was observed for TBM (75.6%) followed by HI (69.15%) and PDW (59.43%) under drought-stressed condition. Under non-stressed condition, high H^2 values were recorded for SHP (80%), HSW (71.04%) and HI (69%). Genetic advance as percent of mean (GAM) ranged from 0.65% to 70% under drought-stressed condition and 0.33% to 45% under non-stressed condition.

4.3.3. Maturity determination of groundnut genotypes

In the present study, 12, 18, 45 and 25% of the test genotypes attained physiological maturity at 100, 110, 120 and 130 days after sowing (DAS) in that order (Appendix 4.3). The lowest maturity duration (100 DAS) was exhibited by Spanish bunch groundnut genotypes. Among the genotypes which recorded 110 DAS, 93% of the genotypes belongs to Spanish bunch type. The results indicate that Virginia bunch type groundnuts are late maturing compared to the Spanish bunch type.

4.3.4. Association of traits

Pearson correlation among the studied traits is summarized in Table 4.4. The correlation result revealed that harvest index and total biomass per plant were positively and significantly associated with pod yield per plant under both drought-stressed and non-stressed condition. Under drought-stressed condition, PY showed significant ($p \leq 0.05$) correlation with SY (r = 0.97), HI (r = 0.92), TBM (r = 0.55) and SHP (r = 0.38), HSW (r = 0.36), LRWC (r = 0.26) and SLA (r = 0.13), while under non-stressed condition, PY exhibited significant ($p \leq 0.05$) correlation with SY (r = 0.93), HI (r = 0.81) and TBM (r = 0.35). The following traits revealed significant ($p \leq 0.05$) correlations: SHP and HSW (r = 0.48), PH and SHP (r = 0.36), LRWC and HSW (r = 0.47) under drought-stressed and DF and PB (r = 0.45), DF and HLM (r = 0.24) under non-stressed condition.

4.3.5. Principal component (PC)

The first five PCs with Eigen value greater than one accounted for 75.59% and 77.70% of the total phenotypic variability exhibited by the studied traits under drought-stressed and non-stressed conditions, respectively (Table 4.5). DF, PH and HI were the main contributing traits in PC1 under

both moisture conditions and; HLM and TBM in PC2 under drought stress condition and PY and TBM under non-stressed condition. PY was one of the main contributing traits in PC1 under drought-stressed condition and in PC2 under non-stressed condition.

Table 4.2. Analysis of variance showing mean square values due to year, replications (Rep), blocks (Blk), genotypes (Geno), and genotype for year and error 13 phenotypic traits among 100 groundnut genotypes across two seasons evaluated under drought-stressed and non-stressed conditions.

Mean squares												
Drought-stressed							Non-stressed					
traits	Year	Rep(year)	Blk(year*Rep)	Geno	Geno*year	Error	Year	Rep(year)	Blk(year*rep)	Geno	Geno*year	Error
DF	10826.40**	9.03*	1.17ns	3.48**	2.20**	1.01	14137**	20.29**	2.60*	3.37**	2.45*	253.82
PH	11509**	9.95^{NS}	7.63*	7.13*	5.49^{NS}	4.27	21744**	192.66**	6.31^{NS}	26.07**	12.77*	7.92
PB	42.45**	9.52*	3.28*	4.77**	1.7^{NS}	1.68	244**	10.23^{NS}	2.39^{NS}	7.84*	4.12^{NS}	4.46
SCMR	2218.02**	112.58^{NS}	109.22^{NS}	124.42*	106.43^{NS}	87.57	2.13^{NS}	120.27*	19.42^{NS}	35.55^{NS}	15.45^{NS}	14.62
LRWC	11391**	45.39^{NS}	209.80ns	146.58**	125.66^{NS}	214.4	11392**	709.52**	98.31^{NS}	239.03**	224.79**	67.15
SLA	1647.28*	200.18^{NS}	209.98ns	206.51*	173.13^{NS}	164.2	1647*	1145*	114^{NS}	228^{NS}	236^{NS}	241.29
Hualm	117.84*	165.59**	30.06**	38.08**	21.23*	11.48	6275**	566**	32.51^{NS}	57.55**	32.36^{NS}	26.89
PY	3586**	29.57**	1.50^{NS}	6.48**	4.46**	1.65	1114**	107**	11.97^{NS}	21.78**	14.32*	8.27
SHP	4043.68**	146.34^{NS}	36.58ns	45.28*	40.52^{NS}	48.33	4044**	9.20^{NS}	11.64^{NS}	103.31**	100.26**	11.25
SY	1120.52**	4.00*	0.75^{ns}	2.23**	1.48**	0.68	126.93**	33.33**	4.55 ^{NS}	9.1**	6.05**	3.07
HSW	1228**	23.18^{NS}	16.89ns	26.23**	24.18^{NS}	19.3	1228**	96.59**	10.08^{NS}	52.68**	52.32**	8.92
TBM	5950**	161.52**	32.85*	98.17**	76.14**	13.64	2102**	1043**	65.72^{NS}	65.37*	58.39ns	49.35
HI	38776**	340.56**	19.22^{NS}	89.52**	41.60**	16.33	17532**	165.81*	33.31^{NS}	155.52**	56.41**	28.08

Rep = replications, Blk = no of blocks, trt = number of treatment, DF = days to 50% flowering, PH = plant height (cm), PB = number of primary branches per plant, SCMR = SPAD chlorophyll meter reading, LRWC = leaf relative water content, SLA = specific leaf area ($cm^2\ g^{-1}$), Hualm = haulm weight (g $plant^{-1}$), PY = pod yield (g $plant^{-1}$), SHP = shelling percentage, SY = seed yield (g/ plant, HSW = hundred seed weight (g), TBM = Total biomass (g $plant^{-1}$), HI = harvest index (%), NS = non-significant, *, ** significant at the 5% and 1% probability level, respectively

Table 4.3. Genetic parameters for 13 phenotypic traits evaluated across two seasons evaluated under drought-stressed and non-stressed conditions.

Traits	WR	Gmean	SE	Ve	Vg	Vp	H2	GVC	PCV	EGA	GAM
DF	DS	50.23	1	1.01	1.24	2.25	55.01	2.21	2.98	169.8	3.38
	NS	50.51	1.25	1.56	0.91	2.47	36.71	1.88	3.11	118.74	2.35
PH	DS	14.14	2.06	4.27	1.54	5.81	26.55	8.79	17.05	131.85	9.32
	NS	18.73	2.81	7.92	9.08	16.99	53.41	16.08	22.01	453.56	24.22
PB	DS	8.01	1.29	1.68	1.54	3.23	47.82	15.51	22.43	176.96	22.09
	NS	8.87	2.11	4.46	1.69	6.15	27.51	14.66	27.96	140.51	15.84
SCMR	DS	47.83	9.35	87.57	18.43	105.99	17.38	8.97	21.52	368.7	7.71
	NS	47.94	3.82	14.62	10.46	25.09	41.72	6.75	10.45	430.42	8.98
LRWC	DS	56.34	14.64	214.4	16.09	230.49	6.98	7.12	26.95	218.33	3.88
	NS	69.12	8.19	67.15	85.94	153.09	56.14	13.41	17.89	1430.86	20.69
SLA	DS	124.18	12.81	164.24	21.13	185.38	11.4	3.7	10.96	319.76	2.57
	NS	130.51	15.53	241.29	3.31	244.6	1.35	1.39	11.98	43.57	0.33
HAULM	DS	18.61	3.38	11.48	13.3	24.78	53.67	19.6	26.75	550.41	29.58
	NS	36.14	5.18	26.89	15.33	42.22	36.3	10.83	17.98	485.92	13.45
PY	DS	4.72	1.28	1.65	2.42	4.06	59.43	32.93	42.71	246.82	52.29
	NS	10.78	2.87	8.27	6.75	15.03	44.94	24.11	35.96	358.84	33.29
SHP	DS	50.77	6.95	14.88	0.63	15.51	4.05	1.56	7.76	32.89	0.65
	NS	56.21	3.35	11.25	46.03	57.28	80.36	12.07	13.46	1252.88	22.29
SY	DS	2.5	0.82	0.68	0.72	1.4	51.43	33.94	47.33	175	70.00
	NS	6.04	1.75	3.07	3.02	6.09	49.59	28.77	40.85	251.48	41.64
HSW	DS	22.93	4.39	2.93	3.47	6.4	54.2	8.12	11.03	282.41	12.32
	NS	26.93	2.98	8.92	21.88	30.8	71.04	17.37	20.61	812.17	30.16
TBM	DS	23.65	3.69	13.64	42.27	55.91	75.6	27.49	31.62	1164.46	49.24
	NS	36.14	7.02	49.35	8.01	57.36	13.96	7.83	20.96	217.87	6.03
HI	DS	18.92	4.04	16.33	36.6	52.92	69.15	31.97	38.45	1036.29	54.77
	NS	30.38	5.29	28.08	63.72	91.8	69.41	26.28	31.54	1370	45.1

DF = days to 50% flowering, PH = plant height (cm), PB = number of primary branches per plant, SCMR = SPAD chlorophyll meter reading, LRWC = leaf relative water content, SLA = specific leaf area ($cm^2\ g^{-1}$), Hualm = haulm weight (g $plant^{-1}$), PY = pod yield (g $plant^{-1}$), SHP = shelling percentage, SY = seed yield (g/ plant, HSW = hundred seed weight (g), TBM = Total biomass (g $plant^{-1}$), HI = harvest index (%), WR = water regime.

Table 4.4. Pearson' s correlation coefficient (r) showing association of 13 phenotypic traits of 100 groundnut genotypes evaluated across two seasons under drought-stresses (upper diagonal) and non-stressed (lower diagonal) conditions.

	DF	PH	PB	SCMR	HLM	PY	TBM	HI	SHP	HSW	LRWC	SLA	SY
DF	1	-0.88**	-0.12*	0.21**	-0.01ns	-0.81**	-0.41**	-0.81**	-0.43**	-0.35**	-0.36**	-0.12*	-0.11ns
PH	0.09ns	1	0.17*	-0.24**	0.12*	0.78**	0.43**	0.77**	0.36**	0.31**	0.32**	0.19*	0.0002ns
PB	0.47**	0.31*	1	-0.03ns	0.15*	0.15*	0.19*	0.11*	-0.01ns	0.04ns	0.06ns	-0.07ns	-0.19ns
SCMR	0.09ns	-0.09ns	-0.16ns	1	-0.001ns	-0.2**	-0.08ns	-0.21**	-0.07ns	-0.027ns	-0.07ns	-0.041ns	-0.12ns
Haulm	0.24*	0.38**	0.39**	-0.06ns	1	0.14*	0.67**	-0.17*	0.02ns	-0.005ns	0.01ns	0.1ns	-0.009
PY	-0.2*	-0.08ns	-0.08ns	0.05ns	-0.22*	1	0.55**	0.92**	0.38**	0.36**	0.28**	0.13*	0.97**
TBM	0.12ns	0.32*	0.34*	-0.03ns	0.84**	0.35*	1	0.25**	0.22**	0.12*	0.21**	0.10*	0.34*
HI	-0.31*	-0.29*	-0.31*	0.01ns	-0.72**	0.81**	-0.24*	1	0.37**	0.37**	0.29**	0.12*	0.78**
SHP	0.17ns	-0.11ns	0.01ns	0.09ns	-0.3*	0.18ns	-0.19ns	0.25*	1	0.48**	0.48**	0.17*	0.54**
HSW	0.14ns	-0.1ns	0.10ns	-0.09ns	-0.06ns	0.17ns	0.04ns	0.17ns	-0.07ns	1	0.47**	0.36**	0.3*
LRWC	-0.03ns	-0.0005ns	-0.01ns	-0.09ns	-0.05ns	-0.05ns	-0.07ns	0.008ns	-0.05ns	0.36*	1	0.19*	-0.03ns
SLA	0.001ns	-0.03ns	-0.1ns	-0.10ns	-0.07ns	0.025ns	-0.05ns	0.1ns	0.14ns	0.05ns	-0.07ns	1	-0.05ns
SY	-0.11ns	-0.09ns	-0.05ns	0.06ns	-0.3*	0.93**	0.24*	0.79**	0.52**	0.21*	0.3*	0.09ns	1

DF = days to 50% flowering, PH = plant height (cm), PB = number of primary branches per palnt, SCMR = SPAD chlorophyll meter reading, Haulm = haulm weight (g plant^{-1}), PY = pod yield (g plant^{-1}), TBM = Total biomass (g plant^{-1}), HI = harvest index (%), SHP = shelling percentage, SLA = specific leaf area (cm^2 g^{-1}), LRWC = leaf relative water content HSW = hundred seed weight (g), SY = seed yield (g plant^{-1}), NS = non-significant, *, ** significant at the 5% and 1% probability level, respectively

Table 4.5. Principal component scores, Eigen values, variances of 13 phenotypic traits among 100 groundnut genotypes evaluated under drought-stressed and non-stressed conditions across two seasons.

Drought-stressed						Non-stressed				
Traits	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5
DF	-0.40	0.41	0.04	0.53	-0.24	-0.30	0.49	-0.34	0.14	-0.42
PH	-0.11	0.18	-0.06	-0.50	-0.22	-0.40	0.36	0.18	-0.13	0.07
PB	-0.44	0.31	0.02	0.49	0.06	-0.40	0.60	-0.03	0.05	-0.42
SCMR	-0.24	0.06	-0.24	0.11	0.83	0.12	-0.11	0.02	0.80	0.46
LRWC	0.10	-0.13	0.68	0.38	0.04	0.31	0.53	-0.48	-0.01	0.13
SLA	-0.12	0.23	0.57	-0.58	0.08	0.20	0.18	-0.30	-0.59	0.52
HAULM	-0.49	0.81	0.07	-0.06	-0.03	-0.75	0.45	0.30	0.02	0.26
PY	0.78	0.56	-0.19	-0.03	0.09	0.70	0.32	0.62	-0.02	-0.05
SHP	0.62	0.06	0.24	0.27	-0.31	0.54	0.46	-0.48	0.21	0.00
SY	0.84	0.52	-0.12	0.04	0.01	0.81	0.45	0.36	0.05	-0.05
HSW	0.42	0.08	0.69	0.00	0.34	0.24	0.50	-0.45	0.03	0.18
TBM	-0.17	0.94	0.00	-0.07	0.01	-0.33	0.62	0.64	0.01	0.22
HI	0.91	-0.01	-0.23	0.08	0.08	0.91	-0.07	0.27	-0.10	-0.18
Eigenvalue	3.42	2.52	1.50	1.36	1.03	3.57	2.41	1.99	1.09	1.04
Proportion variance (%)	26.34	19.36	11.53	10.44	7.92	27.45	18.51	15.33	8.38	8.03
Cumulative variance (%)	26.34	45.70	57.23	67.67	75.59	27.45	45.96	61.29	69.67	77.70

DF = days to 50% flowering, PH = plant height (cm), PB = number of primary branches per plant , SCMR = SPAD chlorophyll meter reading, LRWC = leaf relative water content, SLA = specific leaf area ($cm^2\ g^{-1}$), Hualm = haulm weight (g $plant^{-1}$), PY = pod yield (g $plant^{-1}$), SHP = shelling percentage, SY = seed yield (g/ plant, HSW = hundred seed weight (g), TBM = Total biomass (g $plant^{-1}$), HI = harvest index (%), PC = principal component.

4.3.6. Genetic variability of 99 groundnut genotypes using SNP markers

Table 4.6 summarizes the diversity indices of 99 groundnut genotypes. The genetic dissimilarity (diversity) (GD) ranged from 0 to 0.5, with a mean of 0.1. The polymorphic information content (PIC) value varied from 0 to 0.38, with a mean of 0.08 per locus. The minor allele frequency ranged from 0 to 0.5, with a mean of 0.08. The lowest and highest observed gene diversity recorded were 0.02 and 0.11, respectively. The inbreeding coefficient (F) ranged from -0.09 to 0.77, with a mean of 0.39.

Table 4.6. Diversity indices statistics of the 99 groundnut genotypes based on 16 363 SNP markers.

	Genetic parameters				
Statistics	GD	PIC	MAF	Ho	F
Minimum	0	0	0	0.02	-0.09
Maximum	0.5	0.38	0.5	0.11	0.77
Mean	0.1	0.08	0.08	0.06	0.39

GD = genetic dissimilarity, PIC = polymorphic information content, MAF = minor allele frequency, Ho = observed gene diversity, F = inbreeding coefficient

4.3.7. Cluster analysis of 99 groundnut genotypes

The UPGMA clustering method grouped the 99 groundnut genotypes into five clusters based on pedigree, selection history and market type (Figure 4.1, Table 4.7). A detailed description of the genotypes used in this study is presented in Table 3.2. Cluster I consisted of 53 genotypes which are high oleic acid and drought-tolerant genotypes. Cluster III consisted of seven genotypes. These genotypes have foliar disease resistance, and all except ICGV 93261 and ICGV 93260 are descendants to the variety GPBD 4. Groundnut variety except ICGV 93261 and ICGV 93260. The last two genotypes are full-sib lines derived from a cross between ICGS 11 and ICG 4728. Cluster V consisting of five genotypes, including ICGV 99241, ICGV 00350, ICGV 00351, and ICGV 181489. These genotypes are drought tolerant advanced breeding lines. In cluster V the following genotypes were allocated: ICGV 03042 and ICGV 05155 which are high oil content genotypes, with the same half-sib family selection history and having a common ancestor, ICGV 99160 and half-sib lines grouped. Similarly, full-sib lines, including ICGV 7222 and ICGV 7220; ICGV 93260 and ICGV 93261 and; ancestor, ICGV 99160, and half-sib line grouping in Cluster I, cluster III and cluster IV, respectively (Figure 4.1).

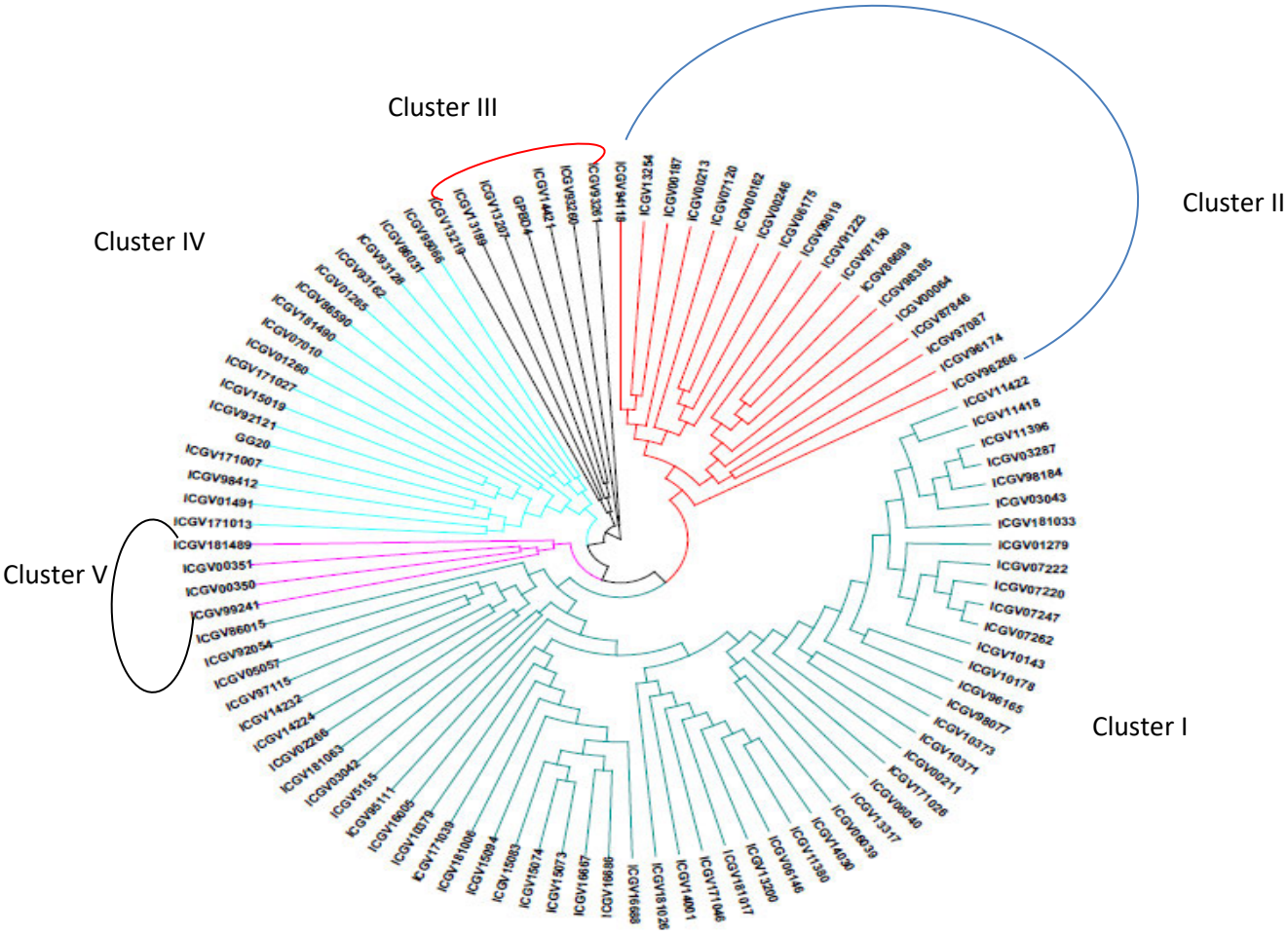


Figure 4.1. Unweighted pair group method with arithmetic mean (UPGMA) showing the genetic relationship among 99 groundnut genotypes using 16 363 SNP markers.

Table 4.7. Summary of unweighted pair group method with arithmetic mean clustering method providing five clusters among 99 groundnut genotypes using SNP markers.

Cluster	No of genotypes	Genotype percentage
I	53	53.53
II	18	18.12
III	7	7.07
IV	17	17.17
V	4	4.04

4.3.8. Genetic relationship among the 99 groundnut genotypes

The genetic distance (GD) ranged from 0.11 to 0.52, with a grand mean of 0.34 (Figure 4.2). Twenty percent of the test genotypes had GD that ranged between 0.4 to 0.52, while 71% had a GD that ranged from 0.21 to 0.39 (Figure 4.2). The GD within the two subspecies, *vulgaris* and *hypogaea*, were similar. The lowest GD (0.11) was observed between ICGV 10371 and ICGV 10373. These two genotypes are categorized under Virginia (var. *vulgaris* subspecies *hypogaea*), and they have good resistance to late leaf spot and rust. The pedigree of these two genotypes revealed common parentage involving ICGV 87846, and with similar selection history. The highest GD (0.52) was observed between ICGV 95111 and ICGV 13189. These genotypes were derived from different genetic backgrounds. ICGV 95111 is a medium maturing genotype and belongs to the Virginia bunch market class and was derived from a cross between ICGV 88308 x ICGSMS 42, whereas ICGV 13189 is a drought-tolerant genotype which belongs to the Spanish (var. *fastigiata* subspecies *vulgaris*) market class. It was derived from a cross between ICGV 91114 x GPBD-4.

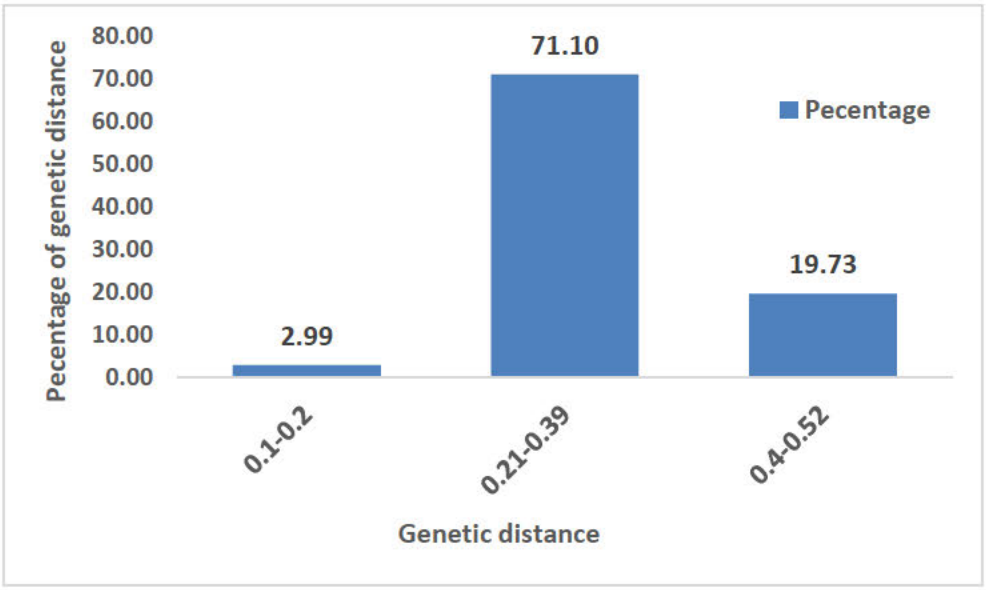


Figure 4.2. Percentage distribution of pairwise genetic distance for 99 groundnut genotypes with 16,363 SNPs.

4.3.9. Population structure, principal component, and kinship analyses

Based on the Evanno method, the best K was estimated to be 3 (Figure 4.3a), showing three subpopulations (Figure 4.3b). The population structure analysis revealed three main subpopulations with 32% (32/99) of admixture genotypes (Appendix 4.4). Allocation into clusters was done at 70% ancestry. Sub-populations 1, 2, and 3 comprised of 24, 22, and 21 genotypes, respectively. Subpopulation 1 included 83% Spanish bunch, subpopulation II had 36% Virginia bunch, and subpopulation III consisted of 81% Spanish bunch. Table 4.8 summarized the allele frequency divergence among subpopulations and expected heterozygosity between the genotypes within the same subpopulations. The highest allele frequency divergence (0.0566) was recorded between subpopulations 1 and 3, followed by subpopulations 2 and 3 with 0.052, while the lowest allele frequency divergence (0.0508) was recorded between subpopulations 1 and 2. The expected heterozygosity among genotypes within the three subpopulations ranged between 0.01 (subpopulation 3) and 0.08 (subpopulation 2) with an average of 0.047.

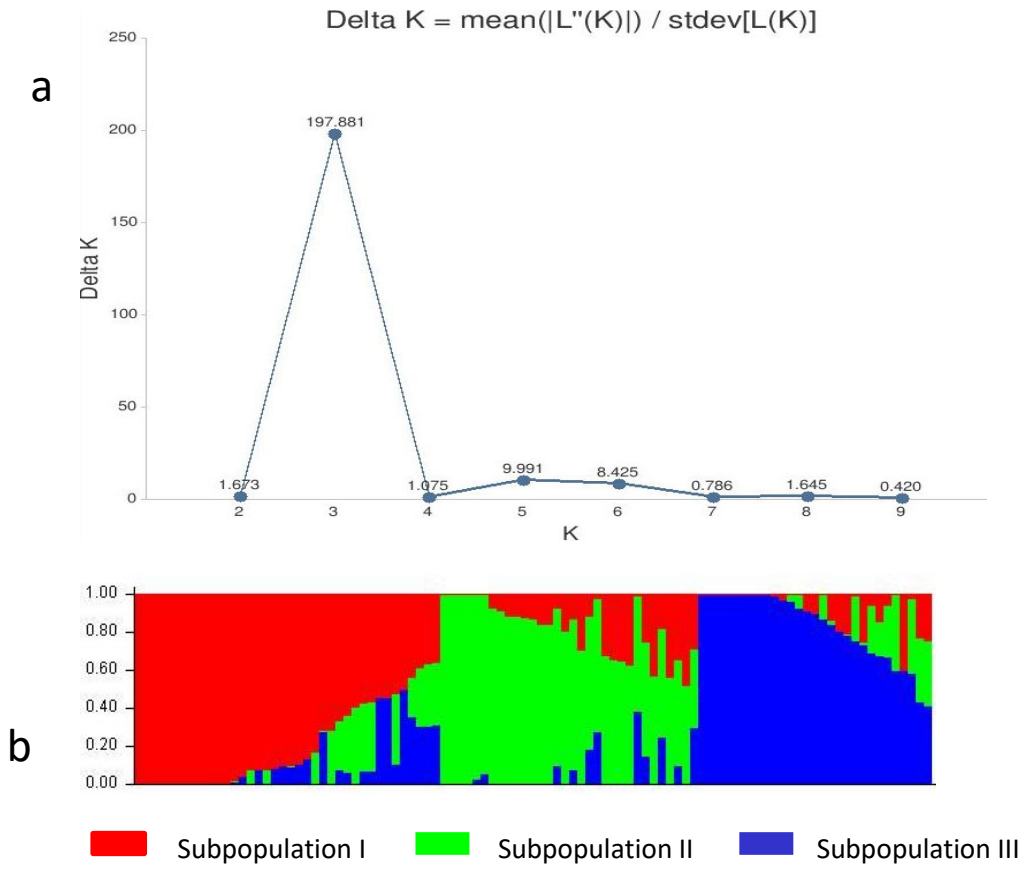


Figure 4.3. Population structure analysis of 99 groundnut genotypes; (a) Delta K showing the number of populations; (b) Bar plot of population sorted by kinship matrix.

Table 4.8. Allele frequency divergence among sub-populations and expected heterozygosity (average distance) between genotypes within the same subpopulations.

	Allele frequency divergence among subpopulations		
	I	II	III
I		0.0508	0.0566
II			0.052
	Expected heterozygosity within subpopulations		
	I	II	III
	0.052	0.08	0.01

I = subpopulation 1, II = subpopulation 2 and III = subpopulation 3

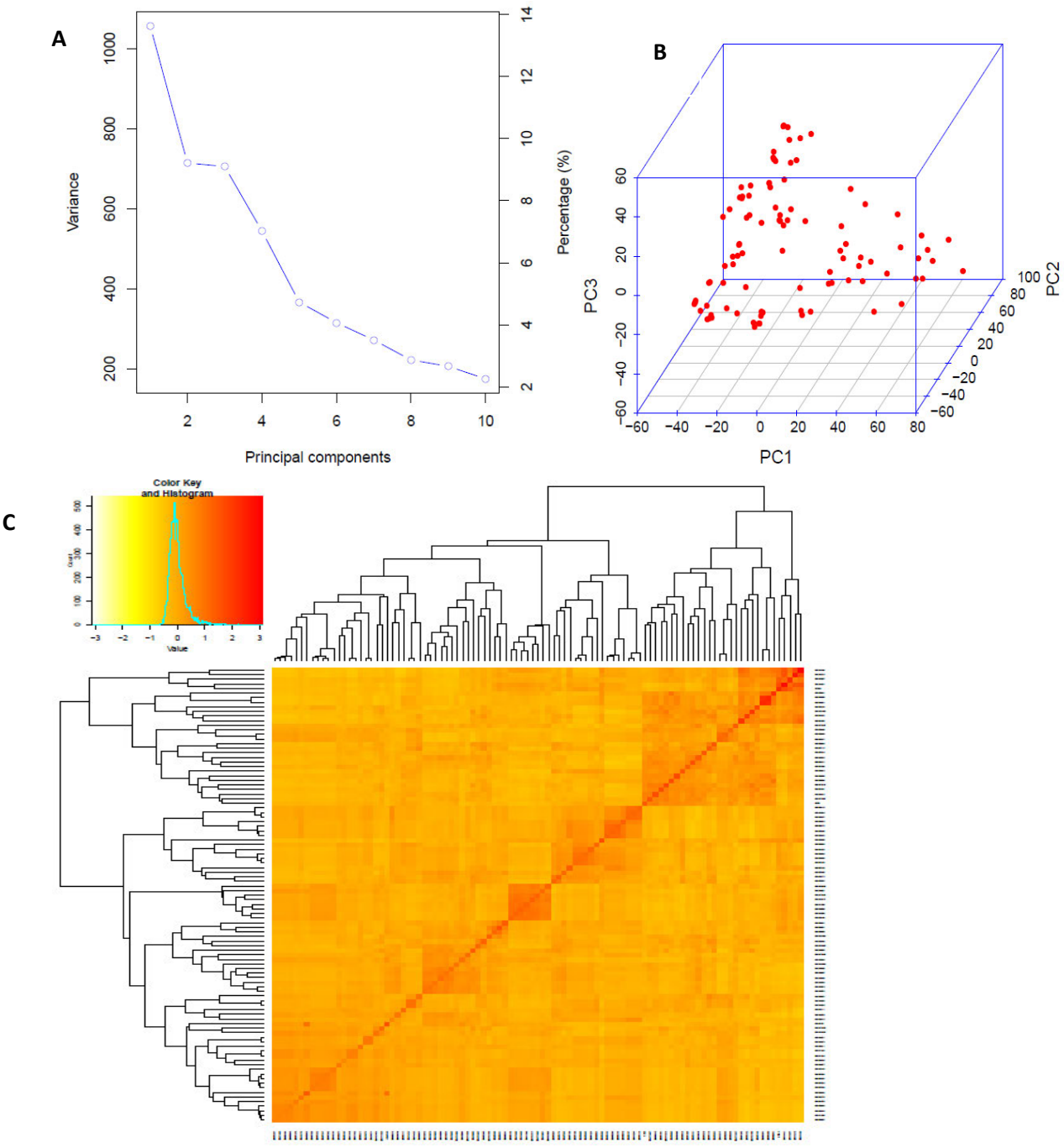


Figure 4.4. Principal component and Kinship analysis of 99 groundnut genotypes based on 16 363 SNPs with minor allele frequency >0.05 using the first three principal components. Note: **(A)** The first three principal components accounting for 32% of the variation, as indicated in the scree plot, (**B**) The 3D-principle components stratifying the genotypes into five distinct clusters and (**C**) the kinship matrix showing the relationship among the genotypes. The kinship matrix is displayed as a heat map, where red indicates the highest correlation between pairs of individuals, and yellow indicates the lowest correlation. The kinship matrix shows two main clusters and five sub-clusters.

4.3.10. Genetic differentiation

The analysis of molecular variance (AMOVA) revealed that 98% of the total genetic variation was attributed to among individuals, while only 2% of the total variance was due to variation among the subspecies (Table 4.9). The overall PhiPT value was 0.016 (with a PhiPT max of 0.887 and Phi'PT of 0.018) with an associated permutation P-value <0.05.

Table 4.9. Analysis of molecular variance based on two subspecies using 16,363 SNP markers in 99 groundnut genotypes.

Source	df	SS	MS	Est. Var.	%
Among sub-species	1	1547.995	1547.995	14.799	2%
Within sub-species	97	90123.419	929.107	929.107	98%
Total	98	91671.414		943.907	100%

Note: df = degrees of freedom, SS = sum of square, MS = mean square, Est. Var. = estimated variance.

4.4. Discussion

4.4.1. Genotypic variation and performance of test genotypes for phenotypic traits

This study evaluated the genetic diversity presented among 100 diverse genotypes of groundnut using phenotypic traits and SNP markers as a preliminary step to identify suitable parental lines for drought tolerance breeding. Analysis of variance revealed significant differences among the genotypes for all the measured traits under drought-stressed and non-stressed conditions except SCMR and SLA under non-stressed condition, indicating the presence of genetic variability for most of the traits among the tested genotypes. Similar findings were reported by Zongo et al. (2017), Zaman et al. (2011) and Ratnakumar and Vadez (2011). PY, SY and HI were affected by genotype x season interaction under both moisture conditions. In this study, drought stress reduced PY, SY, HI by 44%, 40% and 63%, respectively. Pereira et al. (2016) reported 32%, 41% and 31% losses in that order.

The knowledge of existing variability and degree of association between yield contributing characters and their relative contribution in yield is essential for developing high yielding genotypes in groundnut (Zaman et al. 2011). A wide range of variation was recorded for most of the traits. Estimation of GCV and PCV revealed high values for PY, SY, HI, TBM, SHP and HSW under both moisture stress conditions, suggesting the presence of considerable variation among the tested genotypes. High H^2 coupled with high GAM indicates variation is attributed to high

degree of additive effect and selection would be more effective (Johnson et al. 1955). High H^2 and GAM values were recorded for TBM, PY, SY, HI, SHP and HSW under the two water regimes. The study selected genotypes, ICGV 07222, ICGV 06040, ICGV 01260, ICGV 15083, ICGV 10143, ICGV 03042, ICGV 06039, ICGV 14001, ICGV 11380 and ICGV 13200, with high PY under drought stressed and non-stressed condition.

Identification of early maturing groundnut genotypes is one most common breeding strategy to avoid late season droughts. Early maturity is a relative term and its range vary from country to country (Nigam et al. 2014). For example, In Ethiopia a groundnut variety which, can attain physiological maturity up to 120 days duration, after sowing can be considered as early maturing variety. In the present, 75% of the test genotypes attain physiological maturity between 100 and 120 days after sowing (DAS), of which 12 and 18% of the genotypes attain maturity at 100 and 110 DAS in that order. These early maturing genotypes can be selected for drought tolerance breeding.

4.4.2. Association studies

Positive and strong association between SY, HI, TBM, HSW and SHP with pod yield revealed the importance of these characters in determining yield under drought-stress environment. DF showed negative and strong correlation with PY and other economic traits such as HI and HSW under drought-stressed condition, suggesting early flowering provides a promising strategy for the development of drought-adapted groundnut cultivars. Similar finds were reported by Zongo et al. 2017. Linear regression reveals contribution of independent variable to the total variation in response traits such as seed yield per plant (Paul et al. 2018). The results identified PY, HI and SHP as main contributors to the total variation in SY under both moisture conditions, suggesting these traits could be considered for the development of high yielding groundnut cultivars under drought stress and non-stressed condition. PCA used to identify large contributing traits to the total variation in a population under given environment. PY, SY, HSW, SHP and HI were contributed maximum variability for yield under the two water regimes. Hence, selection of these traits will be successful for screening of groundnut genotypes under drought-stressed and non-stressed conditions.

4.4.3. Genetic diversity estimates based on the SNP markers

Information on genetic diversity and genetic relationships helps to minimize the risk of using closely related parents which may lead to genetic ‘bottlenecks’ in improvement programs (Suvi et al. 2019). The current study utilized 16,363 SNP markers to elucidate the genetic diversity of

99 groundnut genotypes. Genetic dissimilarity was adopted to measure the genetic divergence among genotypes (Silva et al. 2016). In this study, genetic dissimilarity ranged from 0 to 0.5, with an average of 0.1. Similarly, low genetic diversity (0.11) was reported by Ren et al. (2014). Moretzsohn et al. (2004) reported that cultivated groundnut presents a relatively low genetic variation when using random amplified polymorphic DNAs (RAPDs), amplified fragment length polymorphisms (AFLPs) and restriction fragment length polymorphisms (RFLPs) marker system. The polymorphism information content (PIC) value is used to measure a genetic marker's usefulness for linkage analysis (Elston 2005). In this study, PIC value varied from 0 to 0.38, with an average of 0.08. This value was relatively lower than a previously reported PIC value of 0.70 when using SSR markers (Varshney et al 2009). This may be attributed to the smaller number of accessions used in the present study (99) than the earlier study (189 accessions) or the difference the markers used.

The inbreeding coefficient (F) measures the probability that two alleles at any locus within an individual are identical by descent from the common ancestor(s) of the two parents (Otyama et al. 2019). If the F value is zero (i.e. as in a random mating system), the genotype frequencies are expected to be at Hardy–Weinberg equilibrium. On the other hand, if the F value is 1, this indicates complete inbreeding with the frequency of heterozygotes being zero (Oteng-Frimpong et al. 2019). A negative F value indicates the presence of excess heterozygotes. This may be due to high outcrossing or mutation event at a specific locus. In this study, the F value ranged from -0.09 to 0.77, with an average of 0.39 which is a moderate value for groundnut, a self-pollinating crop. Otyama et al. (2019) reported negative inbreeding coefficients in groundnut.

4.4.4. Cluster analysis

The molecular genetic diversity study included 99 genotypes, of which 30 and 69 were Virginia bunch and Spanish bunch, respectively. The UPGMA clustering classified the genotypes into five groups based on pedigree, selection history and market type. Cluster I comprised of 94% advanced breeding lines and 6% cultivars. Cluster II, cluster III, cluster IV, and cluster V consisted of 6%, 43%, 12%, and 25% cultivars, respectively. Most of the Virginia bunch class genotypes grouped in cluster I. In addition, cluster II and cluster IV comprised 27% and 16% Virginia bunch, respectively. On the contrary, cluster III and cluster V entirely consisted of Spanish bunch groundnut genotypes. Cluster III included foliar disease-resistant genotypes. The majority (71%) of the genotypes have a common ancestor, GPBD-4 cultivar. This cultivar is resistant to late leaf spot (*Phaeoisariopsis personata)* and rust (*Puccinia arachidis*) (Gowda et al. 2002). Cluster V consisted of four drought-tolerant genotypes, of which ICGV 00350, ICGV 00351, and ICGV 99241 were derived from a cross between ICGV 87290 and 87846, while ICGV 181489 has a common ancestor, ICGV 00351. CO 7 (ICGV 00351) is a high yielding variety developed at ICRISAT for

cultivation in drought-prone areas (Vindhiyavarma et al. 2014). The clustering result showed partial clustering of accessions based on the two botanical types, Spanish bunch and Virginia bunch. Similar findings were reported by Varshney et al. (2009) and Otyama et al. (2019).

A pairwise genetic distance is used to measure genetic variation in a population (Shpak et al. 2017). The genetic distance estimates ranged from 0.4 to 0.52 for the 25% of test genotypes and 0.1 to 0.2 for 3%. The former genetic distance range indicated that the genotypes under this category are relatively distant, or with limited common parentage. The genetic distance between var. *vulgaris* and var. *fastigiata* ranged from 0.11 to 0.52, showing a wide population differentiation between the two species. In contrast, low genetic distances of 0.073 and 0.083 were reported for the two subspecies, in that order (Zheng et al. 2018). Ren et al. (2014) reported the highest genetic distance (0.4) between groundnut genotypes. This result agrees with the current findings. The lowest genetic distance among the cultivars was recorded between ICGV 93260 (Vijetha) and ICGV 93261 (Ajeya). The highest genetic distance (0.4) was observed between Vijetha and GPBG 4. As expected, a relatively wider range of genetic distance was observed in the advanced breeding lines than cultivars. The most genetically distant genotypes identified in the present study should be used as potential parents in the groundnut breeding program to enhance the genetic base of the available genetic resources and hasten groundnut improvement. In general, the results indicated the availability of considerable genetic diversity among the tested genotypes in the present study.

The genetic population structure reveals the presence of genetically distinct subgroups that result from shared ancestry within a large population (Sloan et al. 2009). The population structure analysis showed three main-subpopulations and most genotypes (68%) had a high membership coefficient to their respective subpopulations, this corroborates with the findings reported by Daudi et al. (2020). Genotypes with similar genetic backgrounds tended to cluster in the same sub-group, indicating the effectiveness of SNP markers used in this study in assigning the tested genotypes into homogenous groups (Adu et al. 2019). Allele frequency divergence measures the magnitude of differentiation between sub-populations. The highest allele frequency divergence was recorded between sub-populations 1 and 3. In contrast, the lowest was recorded between sub-populations 1 and 2, indicating sub-populations 1 and 3 being the more divergent than sub-populations 1 and 2. The lower levels of heterozygosity among the tested genotypes within the three sub-population indicate that the SNP markers were effective in constructing homogenous subpopulations (Adu et al. 2019). The expected heterozygosity values indicate that sub-population 2 (0.08) had the highest genetic diversity, followed by sub-population 1 (0.05) and sub-population 3 (0.01). Low allele frequency divergence between the two sub-populations representing the sub-species is a consequence of intercrossing between the two subspecies in the groundnut breeding program. Zheng et al. (2018) reported lower nucleotide diversity or

expected heterozygosity than found in the current study among three sub-populations with values of 0.048 (C1), 0.035 (C2), and 0.012 (C3). Hence, the test genotypes used in this study exhibited relatively wider genetic diversity for selection.

4.5. Conclusions

This study revealed the presence of considerable genetic variation in yield and yield-related components among the tested genotypes evaluated under drought-stressed and non-stressed conditions. The correlation and regression results exhibited PY, HI, HSW and SHP are positively and strongly associated with SY under the two water regimes, suggesting these traits can be used for indirect selection during the development of high yielding and drought tolerant cultivar. The negative and strong association between DF and yield and; yield-related components under drought-stressed, indicating early flowering has an advantage of drought escape during the critical growth stage. The study selected genotypes, ICGV 07222, ICGV 06040, ICGV 01260, ICGV 15083, ICGV 10143, ICGV 03042, ICGV 06039, ICGV 14001, ICGV 11380 and ICGV 13200, with high PY under drought stressed and non-stressed condition. This provides opportunity for their selection as divergent parental lines in groundnut breeding for enhanced pod yield.

Clustering based on the Bayesian method and 3D PCA grouped the genotypes into three subpopulations. UPGMA and Kinship matrix further stratified the genotypes into five groups. The UPGMA clustering grouped the studied 99 genotypes based on pedigree, selection history, and botanical types. The information generated in this study provides detailed understanding of the genetic relationships among the tested genotypes. High genetic distance among paired genotypes revealed the uniqueness of the studied genotypes and the existence of substantial genetic variability to be exploited in groundnut breeding. Overall, the study selected the following genetically divergent genotypes: ICGV 13189, ICGV 95111, ICGV 14421, and ICGV 171007 useful for develop breeding populations in groundnut improvement programs.

4.6. References

Abady, S., Shimelis, H. and Janila, P. 2019. Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding. *Journal of Crop Improvement* 33, 1-17. https://doi.org/10.1080/ 154275 28.2019. 1625836

Adu, B. G., Badu-Apraku, B., Akromah, R., Garcia-Oliveira, A.L., Awuku, F.J. and Gedil, M. 2019. Genetic diversity and population structure of early-maturing tropical maize inbred lines

using SNP markers. *PLoS ONE* 14(4): e0214810. https:// doi.org/10.1371/journal.pone.0214810

Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons. Inc. New York

Bertioli**,** D.J., Cannon**,** S.B., Froenicke, L., Huang**,** G., Farmer, A.D., Cannon, E.K.S., Liu, X., Gao, D., Clevenger, J., Dash, S., Ren, L., Moretzsohn, M.C., Shirasawa, K., Huang, W., Vidigal, B., Abernathy, B., Chu, Y., Niederhuth, C.E., Umale, P., Araújo, A.C.G., Kozik, A., Kim, K.D., Burow, M.D., Varshney, R.K., Wang, X., Zhang, X., Barkley, N., Guimarães, P.M., Isobe, S., Guo, B., Liao, B., Stalker, H.T., Schmitz, R.J., Scheffler, B.E., Leal-Bertioli, S.C.M., Xun, X., Jackson, S.A., Michelmore R. and Ozias-Akins, P. 2016. The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut. *Nature Genetics* 48, 438–446

Bradbury, P.J., Zhang, Z., Kroon, D.E., Casstevens, T.M., Ramdoss, Y. and Buckler, E.S. 2007. TASSEL: software for association mapping of complex traits in diverse samples. *Bioinformatics* 23, 2633–2635

Burton, G. W. and Devane E.H. 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal materials. *Agronomy Journal* 45, 487-488

Carvalho, M.J., Vorasoot, N., Puppala, N., Muitia, A. and Jogloy, S. 2017. Effects of terminal drought on growth, yield and yield components in Valencia peanut genotypes. *SABRAO Journal of Breeding and Genetics* 49, 270-279

Clevenger, J.P., Korani, W., Ozias-Akins, P. and Jackson, S. 2018. Haplotype-based genotyping in polyploids. *Frontiers Plant Science* 9:564. https://doi.org/10.3389/fpls.2018.00564

Central Statistical Agency (CSA). 2018. Agricultural sample survey 2017/18: Report on area and production of major crops (private peasant holdings, main season), Vol.1. CSA, Addis Ababa

Daudi, H., Shimelis, H., Mathew, I., Oteng-Frimpong, R., Ojiewo, C. and Varshney, R.K. 2020. Genetic diversity and population structure of groundnut (*Arachis hypogaea* L.) accessions using phenotypic traits and SSR markers: implications for rust resistance breeding. *Genetic Resources and Crop Evolution.* https://doi.org/10.1007/s10722-020-01007-1

Desmae, H., Janila, P., Okori, P., Pandey, M.K., Motagi, B.N., Monyo, E., Mponda, O., Okello, D., Sako, D., Echeckwu C, Oteng-Frimpong, R., Miningou, A., Ojiewo, C. and Rajeev K. Varshney, R.K. 2017. Genetics, genomics and breeding of groundnut (*Arachis hypogaea* L.). *Plant Breeding* 138, 425–444. https://doi.org/10.1111/pbr.12645

Dutra, W.F., Guerra, Y.L., Ramos, J.P.C., Fernandes, P.D., Silva, C.R.C., Bertioli, D.J., Leal-Bertioli, S.C.M and Santos, R.C. 2018. *PLoS One*. 13(6): e0198776

Earl, D.A. and vonHoldt, B.M. 2012. STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* 4:359–361

Elston, R.C. 2005. Polymorphic information content. Encyclopedia of Biostatistics in 2005 by John Wiley & Sons, Ltd. https://doi.org/10.1002/0470011815.b2a05078

Evanno, G., Regnaut, S. and Goudet, J. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14:2611–2620

Falke, A.B., Hamidou, F., Halilou, O. and Harou, A. 2019. Assessment of groundnut elite lines under drought conditions and selection of tolerance associated traits. *Advances in Agriculture* 2019, 1-10. https://doi.org/10.1155/2019/3034278

FAOSTAT. 2018. "Food and Agriculture Organization of the United Nations Database of Agricultural Production."FAO Statistical Databases, Accessed 25 December 2020.http://www.fao.org/faostat/

Gangadhara, K. and Nadaf, H.L. 2016. Inheritance of high oleic acid content in new sources of Groundnut (*Arachis hypogaea* L.). *Agricultural Science Digest* 36, 299-302. https://doi.org/ 10.18805/asd. v36i4.6472

Gonzalez, L. and Gonzalez-Vilar, M. 2001. Determination of relative water content. *In* Handbook of plant ecophysiology techniques. *Edited by* M.J. Reigosa Roger. Kluwer Academic Publishers, New York. pp. 207–212

Gowda, M.V.C., Motagi, B.N., Naidu, G.K., Diddimani, S.B. and Sheshagarir, R. 2002. GPBD 4: A Spanish bunch groundnut genotype resistant to rust and late leaf spot. *International Arachis Newsletter* 22, 29-32

Gulluoglu, L., Basal, H., Onat, B., Kurt, C. and Arioglu, H. 2016. The effect of harvesting on some agronomic and quality characteristics of peanut grown in the Mediterranean region of Turkey. *Field Crops Research* 21, 224–232. https://doi.org/10.17557/tjfc.20186

Hamidou, F., Halilou, O. and Vadez, V. 2012. Assessment of Groundnut under Combined Heat and Drought Stress. *Journal of Agronomy and Crop Science* 199:1-11. https://doi.org/10.1111/j.1439-037X.2012.00518.x

Janila, P. and Nigam S.N. 2013. Phenotyping for Groundnut (Arachis hypogaea L.) Improvement: In book Phenotyping for Plant Breeding: Phenotyping for Groundnut (Arachis hypogaea L.) Improvement (pp.129 - 167). Springer New York publisher. https://doi.org/10.1007/978-1-4614-8320-5_5

Janila, P., Variath, M.T, Pandey, M.K., Desmae, H., Motagi, B.N., Okori, P., Manohar, S.S., Rathnakumar, A.L., Radhakrishnan, T., Boshou, L.B. and Varshney, R.K. 2016. Genomic tools in groundnut breeding program: status and perspectives. *Frontiers in Plant Science* 7:289. https://doi.org/10.3389/fpls.2016.00289

Janila, P., Manohar, S., Deshmukh, D., Chaudhari, S., Papaiah, V. and Variath, M.T. 2018a. Standard operating procedures for groundnut breeding and testing. Documentation ICRISAT

JMP®, Version *15.1*. SAS Institute Inc., Cary, NC, 1989-2019

Johnson, H.W., Robinson, H.F. and Comstock, R.F. 1955. Genotypic and phenotypic correlation in Soya bean and their implication in selection. *Agronomy Journal* 47, 314-318

Jongrungklang, N., Toomsan, B., Vorasoot, N., Jogloy, S., Kesmala, T. and Patanothai, A. 2008. Identification of peanut genotypes with high water use efficiency under drought stress

conditions from peanut germplasm of diverse origins. *Asian Journal Plant Sciences* 7, 628-638

Krapovickas, A. and Gregory, W. 1994. Taxonomía del género *Arachis* (*Leguminosae*). *Bonplandia* 8:1–186

Lipka, A.E., Tian, F., Wang, Q., Peiffer, J., Li, M., Bradbury, P.J, Gore, M.A., Buckler, E.S. and Zhang, Z. 2012. GAPIT: genome association and prediction integrated tool. *Bioinformatics* 28, 2397–2399. https://doi.org/10.1093/bioinformatics/ bts444

Liu, K. and Muse, S.V. 2005. PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics* 21, 2128-2129

Mace, E.S., Buhariwalla, K.K., Buhariwalla, H.K. and Crouch, J.H. 2003. A high-throughput DNA extraction protocol for tropical molecular breeding programs. Plant Molecular Biology Reporter 21, 459-460. https://doi.org/10.1007/BF02772596

Mathew, I., Shimelis, H., Shayanowako, A.I.T., Laing, M. and Chaplot, V. 2019. Genome-wide association study of drought tolerance and biomass allocation in wheat. *PLoS ONE* 14(12): e0225383. https: //doi.org/ 10.1371/journal. pone.0225383

Moretzsohn, M.D.C., Hopkins, M.S., Mitchell, S.E., Kresovich, S., Valls, J.F.M. and Ferreira, M.E. 2004. Genetic diversity of peanut (*Arachis hypogaea* L.) and its wild relatives based on the analysis of hypervariable regions of the genome. BMC Plant Biology 4:11. https://doi.org/10.1186/1471-2229-4-11

Mukhtar, A.A., Babaji, B.A., Ibrahim, S., Mani, H., Mohammad, A.A. and Ibrahim, A. 2013. Dry matter production and harvest index of groundnut (*Arachis hypogaea L.*) varieties under irrigation. *Journal of Agricultural Science* 5, 153-162

Nadia, B., Fatima, G., Rachid, M. and Mona, T. 2019. The genetic potential of Moroccan lentil landraces pp 291-306

Nageswara Rao, R.C., Talwar, H.S. and Wright, G.C. 2001. Rapid assessment of specific leaf area and leaf chlorophyll meter. *Journal of Agronomy and Crop Science* 189, 175-182.

Nigam S.N., Chandra, S., Sridevi, R. K., Bhukta, M., Reddy, A.G.S., Rachaputi, R.N., Wright, G.C., Reddy, P.V., Deshmukh, M.P., Mathur, R.K., Basu, M.S., Vasundhara, S., Varman, V.P. and Nagda, A.K. 2005. Efficiency of physiological trait based and empirical selection approaches to drought tolerance in groundnut. A*nnals of Applied Biology* 146, 155–162

Nigam, S.N. 2014. Groundnut at a glance. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. Pp 121

Oteng-Frimpong, R., Kassim, Y.B., Danful, R., Akromah, R., Wireko-Kena, A. and Forson, S. 2019. Modeling groundnut (*Arachis hypogaea* L.) performance under drought conditions. *Journal of Crop Improvement* 33, 125-144. https://doi.org/10.1080/15427528.2018.1542363

Otyama, P.I., Wilkey, A., Kulkarni, R., Assefa, T., Chu, Y., Clevenger, J., O'Connor, D.J., Wright, G.C., Dezern, S.W., MacDonald, G.E., Anglin, N.L., Cannon, E.K.S., Ozias-Akins, P. and Cannon, S.B. 2019. Evaluation of linkage disequilibrium, population structure, and genetic diversity in the U.S. peanut mini core collection. *BMC Genomics* 20:481. https://doi.org/10.1186/s12864-019-5824-9

Pande, S., Upadhyaya, H.D., Narayana, R.J., Lakshmi, R.P. and Parthasarathy, R. 2005. Promotion of integrated disease management for ICGV 91114, a dual-purpose, early maturing groundnut variety for rainfed areas. Information BulletinNo. 68. Technical report. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India. Pp 28

Pandey, M.K., Monyo, E., Ozias-Akins, P., Liang, X., Guimarães, P., Nigam, S.N., Upadhyaya, .HD. Janila, P., Zhang, X., Guo, B., Cook, D.R., Bertioli, D.J., Michelmore R. and Varshney, R.K. 2012. Advances in *Arachis* genomics for peanut improvement. *Biotechnolology Advances* 30, 639–651. https://doi.org/10.1016/j. biotechadv.2011.11.001

Paul, P.J., Samineni, S., Sajja, S.B., Rathore, A., Das, R.R., Chaturvedi, S.K., Lavanya, G.R., Varshney, R.V. and Gaur, P.M. 2018. Capturing genetic variability and selection of traits for heat tolerance in a chickpea recombinant inbred line (RIL) population under field conditions. *Euphytica* 214:27. https://doi.org/10.1007/s10681-018-2112-8

Peakall, R. and Smouse, P.E. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. Bioinformatics 28, 2537-2539

Pereira, J.W.D., Albuquerque, M.B., Filho, P.A.M., Nogueira, R.J.M.C., Lim, L.M. and Santos, R.C. 2016. Assessment of drought tolerance of peanut cultivars based on physiological and yield traits in a semiarid environment. *Agricultural Water Management* 166, 70–76

Pritchard, J.K., Stephens, M. and Donnelly, P. 2000. Inference of population structure using multi locus genotype data. *Genetics* 155, 945–959

Ratnakumar, P. and Vadez V. 2011. Groundnut (*Arachis hypogaea*) genotypes tolerant to intermittent drought maintain a high harvest index and have small leaf canopy under stress. *Functional Plant Biology* 38, 1016–1023

Ravi, K., Vadez, V., Isobe, S., Mir, R.R., Guo, Y., Nigam, S.N., Gowda, M.V.C., Radhakrishnan, T., Bertioli, D.J., Knapp, S.J. and Varshney, R.K. 2011. Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). *Theoretical and Applied Genetics* 122, 1119–1132

Ren, X., Jiang, H., Yan, Z., Chen, Y., Zhou, X., Huang, L., Lei, Y., Huang, J., Yan, L., Qi, Y., Wei, W. and Liao, B. 2014. Genetic diversity and population structure of the major peanut (*Arachis hypogaea*L.) Cultivars grown in China by SSR markers. *PLoS ONE* 9(2): e88091. https://doi.org/10.1371/ journal. pone.0088091

Rao, R.C.N., Talwar, H.S. and Wright, G.C. 2001. Rapid assessment of specific leaf area and leaf chlorophyll meter. *Journal of Agronomy and Crop Science* 189, 175-182

SAS. 2011. SAS/IML 9.3 User's Guide. Cary, NC: SAS Institute Inc

Shpak, M., Ni, Y., Lu, J. and Müller, P. 2017. Variance in estimated pairwise genetic distance under high versus low coverage sequencing: The contribution of linkage disequilibrium. *Theoretical Population Biology*. https://doi.org/10.1016/j.tpb.2017.08.001

Singh, B.D. and Singh, A.K. 2015. Marker-Assisted Plant Breeding: Principles and Practices pp 367-400

Silva, D.F.G., Coelho, C.D., Romanek, C., Gardingo, J.R., da Silva, A.R., Graczyki, B.L., Oliveira, E.A.T. and Matiello, R.R. 2016. Genetic dissimilarity and definition of recombination clusters

among green corn half-sib progenies. *Plant Breeding* 75, 401-410. http://dx.doi.org/10.1590/1678-4499.343

Singh, A.K. and *Nigam, S.N.* 2016. *Arachis* gene pools and genetic improvement in groundnut. In: Rajpal VR, Rao SM, Raina *SN* (eds.) Gene Pool Diversity and Crop Improvement, Sustainable Development and Biodiversity. https://doi.org/10.1007/978-3-319-27096-8_2

Singh, R.K. and Chaudhary, B.D. 1977. *Biometrical methods in quantitative genetic analysis*. Kalyani publishers, New Delhi-Ludhiana, India.PP. 318

Sloan, C.D., Andrew, A.D., Duell, E.J., Williams, S.M., Karagas, M.R. and Moore, J.H. 2009. Genetic Population Structure Analysis in New Hampshire Reveals Eastern European Ancestry. *PLoS ONE* 4(9): e6928. https://doi.org/10.1371/journal. pone.0006928

Suvi, W. T., Shimelis, H., Laing, M., Mathew, I. and Shayanowako, A. I. T. 2019. Assessment of the genetic diversity and population structure of rice genotypes using SSR markers. *Acta Agriculturae Scandinavica.* Section B—Soil & Plant 70, 76–86. https://doi.org/10.1080/09064710.2019.1670859

Thermo Fisher Scientific Inc 2018. *Axiom™Analysis Suite (AxAS) v4.0 USER GUIDE.* Available at: https://downloads.thermofisher.com/Affymetrix_Softwares/Axiom_Analysis_Suite_AxAS_v4.0_User_Guide.pdf

Vadez, V. and Ratnakumar, P. 2016. High transpiration efficiency increases pod yield under intermittent drought in dry and hot atmospheric conditions but less so under wetter and cooler conditions in groundnut (*Arachis hypogaea* (L.). *Field Crops Research* 193: 16–23.

Varshney, R.K., Mahendar, T., Aruna, R., Nigam, S.N., Neelima, K., Vadez, V. and Hoisington, D.A. 2009. High level of natural variation in a groundnut (*Arachis hypogaea* L.) germplasm collection assayed by selected informative SSR markers. Plant Breeding 128:486-494

Vindhiyavarman, P., Nigam, S.N., Janila, P., Vaidhyalingan, M., Manivannan, N., Saravanan, S., Meenakumari, B., Gopalakrishnan, C. and Kennedy, J.S. 2014. A new high yielding Spanish bunch groundnut variety CO 7 (ICGV 00351) for the drought prone areas of Tamil Nadu. *Electronic Journal of Plant Breeding* 5, 192-196

Wang, H., Lei, Y., Yan, L., Wan, L., Cai, Y., Yang, Z., Lv, J., Zhang, X., Xu, C. and Liao, B. 2018. Development and validation of simple sequence repeat markers from Arachis hypogaea transcript sequences. *Crop Journal* 6, 172–180. https://doi.org/10.1016/j.cj.2017.09.007

You, Q., Yang, X., Peng, Z., Xu, L. and ang, J. 2018. Development and applications of a high throughput genotyping tool for polyploidy crops: Single Nucleotide Polymorphism (SNP) Array. *Frontiers in Plant Science* 9:104. https://doi.org/10.3389/fpls.2018.00104

Zaman, M.A., Tuhina-Khatun, M., Ullah, M.Z., Moniruzzamn, M. and Alam, K.H. 2011. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). *The Agriculturists* 9, 29-36

Zhang, B., Sun, L., Wu, Y., Xu, H., & Tu, K. (2017). Adsorption kinetics of flavonoids from peanut hull by macroporous resin. China Oils and Fats, 42, 122–126.

Zheng, Z., Sun, Z., Fang, Y., Qi, F., Liu, H., Miao, L., Du, P., Shi, L., Gao, W., Han, S., Dong, W., Tang, F., Cheng, F., Hu, H., Huang, B. and Zhang, X. 2018. Genetic diversity, population structure, and botanical variety of 320 global peanut accessions revealed through tunable genotyping-by-sequencing. *Scientific reports* 8:14500. https://doi.org/10.1038/s41598-018-32800-9

Zongo, A., Nana, A.T., Sawadogo, M., Konate, A.K., Sankara, P., Ntare, B.R. and Desmae, H. 2017. Variability and correlations among groundnut populations for early leaf spot, pod yield, and agronomic traits. *Agronomy* 7, 2:11. https://doi.org/10.3390/ agronomy7030052

Appendix 4.1. Mean values for 13 quantitative traits of 100 groundnut genotypes evaluated under drought-stressed condition in 2018/19 and 2019/20 post-rainy seasons.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
1	ICGV 16667	50.00	16.70	8.15	49.64	56.49	121.80	20.79	3.74	24.53	14.67	48.01	18.79	1.79
2	ICGV 93128	50.25	11.90	7.38	49.40	54.22	107.55	19.80	2.88	22.68	11.97	48.71	21.44	1.40
3	ICGV 95066	50.25	13.73	6.65	47.68	57.51	123.73	17.88	5.64	23.51	21.71	44.73	24.70	2.52
4	ICGV 96174	48.75	14.53	7.95	46.63	54.18	122.37	17.08	2.97	20.02	12.01	51.59	20.70	1.53
5	ICGV 97087	50.00	15.43	7.15	43.19	70.87	129.17	20.03	4.79	24.82	16.63	50.45	24.89	2.42
6	ICGV 98077	49.50	13.30	7.55	46.44	44.67	136.63	22.50	3.18	25.68	11.90	48.73	20.87	1.55
7	ICGV 01279	49.75	13.80	8.65	46.94	59.27	128.87	20.62	3.25	23.87	12.79	54.89	24.06	1.78
8	ICGV 03042	49.50	13.78	8.93	45.90	58.49	118.84	18.94	5.86	24.80	22.48	54.84	22.49	3.21
9	ICGV 06039	51.00	12.18	7.23	47.35	55.70	117.72	13.98	5.69	19.67	26.44	50.98	20.45	2.90
10	ICGV 06040	50.50	15.98	8.28	52.70	54.86	123.83	20.49	8.03	28.53	25.66	52.41	24.84	4.21
11	ICGV 07010	49.25	13.95	8.45	45.93	50.41	138.04	20.51	4.92	25.43	16.49	45.99	23.47	2.26
12	ICGV 10143	49.00	12.90	7.88	47.11	60.73	136.04	16.31	6.21	22.52	25.04	61.28	25.64	3.81
13	ICGV 11422	50.25	13.03	8.45	48.08	48.51	115.07	21.99	2.30	24.29	10.03	43.80	19.35	1.01
14	ICGV 11396	49.00	12.05	7.13	49.61	57.12	138.15	20.29	2.83	23.12	12.85	45.21	18.77	1.28
15	ICGV 11418	50.50	14.03	7.23	46.48	56.92	126.52	20.49	2.88	23.37	11.55	51.65	20.74	1.49
16	ICGV 91223	49.75	15.15	7.48	48.55	62.33	125.64	13.91	2.97	16.89	16.68	49.50	23.36	1.47
17	ICGV 94118	49.75	15.45	6.60	43.99	60.48	115.79	14.55	4.96	19.51	21.88	52.34	23.67	2.60
18	ICGV 99019	50.50	15.00	8.35	50.23	48.08	117.11	20.83	5.74	26.57	20.60	47.62	20.59	2.74
19	ICGV 00162	49.50	16.18	8.23	43.60	47.33	120.30	17.12	3.86	20.98	17.77	50.21	21.34	1.94
20	ICGV 00211	50.00	15.08	8.05	47.32	51.99	141.77	17.09	4.37	21.47	18.33	51.18	27.85	2.24
21	ICGV 00187	49.25	14.50	7.33	53.56	63.82	113.56	17.10	4.97	22.06	22.65	46.24	19.47	2.30
22	ICGV 00213	49.75	14.68	6.05	55.21	48.30	115.70	16.84	4.70	21.54	20.61	47.30	19.60	2.22
23	ICGV 06146	50.50	15.88	7.75	40.87	57.57	115.01	14.48	5.51	19.99	24.83	54.96	23.06	3.03
24	ICGV 07120	50.50	12.88	7.85	44.89	50.07	135.78	21.60	6.46	28.05	22.27	46.52	25.29	3.00
25	ICGV 10178	49.75	15.68	7.53	43.12	48.50	129.83	23.01	7.12	30.13	22.04	55.99	24.03	3.99
26	ICGV 11380	50.75	14.08	8.70	44.67	58.16	113.68	12.98	6.22	19.20	28.96	54.49	24.83	3.39
27	ICGV 14001	50.50	14.98	7.68	42.56	57.87	115.47	17.17	5.40	22.57	21.83	52.71	21.21	2.85
28	ICGV 14030	50.00	12.78	8.05	45.97	58.85	116.17	13.77	3.45	17.22	19.03	54.09	20.63	1.87
29	ICGV 86015	50.00	11.35	8.25	49.26	56.82	120.28	13.90	3.87	17.77	20.51	53.48	25.29	2.07
30	ICGV 93260	49.25	16.43	8.43	44.68	62.92	125.35	11.33	4.14	15.47	27.07	51.35	26.01	2.13
31	ICGV 93261	49.00	13.65	7.43	47.17	48.35	114.21	14.30	5.28	19.58	27.24	49.53	19.55	2.61
32	ICGV 92121	49.75	14.30	7.30	46.46	52.30	116.31	22.95	5.57	28.52	17.07	55.01	20.44	3.06
33	ICGV 99241	49.50	15.23	8.30	45.45	52.05	135.45	23.26	6.50	29.76	20.78	52.47	22.96	3.41

Appendix 4.1. Continued.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
34	ICGV 00351	50.25	16.70	6.98	43.61	54.47	129.18	19.44	4.14	23.58	16.21	53.80	21.00	2.23
35	ICGV 01260	50.50	13.45	6.70	50.17	52.65	121.62	28.56	8.57	37.13	20.74	48.68	26.04	4.17
36	ICGV 01265	49.75	13.55	7.38	50.90	58.21	121.24	18.09	5.50	23.59	19.77	50.61	25.02	2.78
37	ICGV 13200	50.25	14.88	6.45	44.30	58.16	121.13	15.19	7.04	22.22	26.74	49.59	20.78	3.49
38	ICGV 07220	50.50	12.48	9.18	45.76	54.65	121.35	13.16	2.35	15.51	13.00	46.47	22.57	1.09
39	ICGV 07222	50.00	12.25	7.85	45.13	61.16	124.53	18.61	7.19	25.80	25.21	54.49	26.51	3.92
40	ICGV 13317	50.25	11.63	7.88	46.87	58.74	119.32	17.95	4.65	22.60	20.78	55.55	24.88	2.58
41	ICGV 13254	48.75	13.23	7.75	52.38	54.34	119.00	17.60	3.87	21.47	17.49	50.14	19.79	1.94
42	ICGV 181026	50.75	12.75	7.65	49.39	47.98	130.97	16.21	3.77	19.98	16.98	50.46	20.46	1.90
43	ICGV 15073	48.75	16.33	8.75	47.85	53.43	112.82	18.07	5.05	23.12	19.86	52.34	20.73	2.64
44	ICGV 15074	50.00	14.98	8.50	49.73	53.74	116.71	15.50	5.20	20.70	22.67	49.04	20.02	2.55
45	ICGV 15083	50.25	15.93	9.60	47.15	55.14	118.43	18.03	6.74	24.77	25.66	48.91	22.83	3.30
46	ICGV 15019	49.50	13.75	7.50	46.00	45.22	124.05	16.16	5.73	21.90	23.14	51.04	23.09	2.93
47	ICGV 06420	51.50	14.28	8.05	47.75	74.07	141.75	18.51	4.50	23.01	18.69	56.58	28.06	2.54
48	ICGV 05155	50.50	13.85	8.73	48.48	45.62	126.23	20.51	4.45	24.96	18.26	46.85	18.18	2.08
49	ICGV 16688	48.75	15.23	8.75	49.25	60.98	140.61	20.87	4.80	25.67	17.36	51.51	24.67	2.47
50	ICGV 03043	50.50	14.23	8.25	44.34	59.82	125.91	19.17	4.64	23.81	18.57	54.22	24.10	2.52
51	ICGV 00350	47.75	13.13	7.35	42.03	53.10	129.92	16.89	4.60	21.49	19.37	52.59	25.50	2.42
52	ICGV 86590	50.00	14.10	5.68	46.01	67.49	126.04	17.93	4.61	22.54	17.26	53.75	24.23	2.48
53	ICGV 02266	49.25	13.53	7.55	50.30	58.12	134.38	14.61	6.13	20.74	27.01	48.77	32.53	2.99
54	ICGV 13189	49.50	13.85	5.18	43.48	58.23	129.67	12.47	5.11	17.58	26.76	57.48	27.03	2.94
55	ICGV 13207	49.50	11.25	8.58	46.65	59.73	110.68	9.74	4.98	14.72	29.87	52.43	23.30	2.61
56	ICGV 14421	49.50	11.95	6.43	43.88	62.35	118.59	14.21	6.35	20.56	28.96	54.92	24.08	3.49
57	ICGV 13219	48.75	13.08	4.70	43.65	59.10	128.94	13.62	4.26	17.88	21.35	52.76	23.76	2.25
58	GPBD 4	49.25	13.50	6.28	41.91	46.18	125.53	12.73	3.68	16.40	19.67	48.31	18.99	1.78
59	ICGV 86031	49.50	14.78	7.40	50.05	52.58	108.92	13.66	3.70	17.36	20.11	50.57	20.89	1.87
60	ICGV 16686	50.75	16.30	7.38	50.65	47.06	131.13	21.28	4.94	26.22	16.56	47.08	18.76	2.33
61	ICGV 16005	50.00	13.85	6.03	49.20	56.60	122.12	17.10	3.73	20.83	17.58	50.69	20.57	1.89
62	ICGV 171013	49.00	13.45	7.60	54.28	59.28	121.61	17.17	5.50	22.67	22.33	55.23	24.45	3.04
63	ICGV 171026	49.75	12.28	7.78	49.30	53.86	122.64	20.13	5.13	25.27	18.32	53.30	21.17	2.74
64	ICGV 171039	48.25	15.53	7.28	51.32	61.48	118.64	15.89	5.81	21.71	23.18	49.36	22.71	2.87
65	ICGV 171046	50.25	13.78	8.03	45.68	55.41	117.42	14.97	6.75	21.72	26.64	52.16	29.16	3.52
66	ICGV 181017	50.00	12.15	7.98	40.73	65.06	115.73	20.20	5.88	26.08	19.78	51.08	26.20	3.00
67	ICGV 181063	49.00	14.50	8.60	48.97	67.87	123.98	19.15	3.56	22.71	14.12	49.18	26.92	1.75

Appendix 4.1. Continued.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
68	ICGV 98412	49.25	17.98	7.95	52.31	48.01	133.98	21.08	5.56	26.64	17.53	46.65	26.22	2.59
69	ICGV 181489	50.25	15.38	7.85	42.57	57.89	136.94	22.21	3.63	25.84	12.58	44.74	23.11	1.62
70	ICGV 181490	50.25	14.00	6.65	50.26	71.68	129.11	16.51	5.42	21.93	20.91	60.85	26.99	3.30
71	ICGV 92054	51.75	14.55	8.03	48.64	58.43	122.08	19.73	3.88	23.62	16.78	51.33	22.40	1.99
72	ICGV 93162	51.00	15.83	9.10	44.86	51.48	133.84	23.72	3.96	27.68	14.48	47.34	26.55	1.88
73	ICGV 95111	52.00	13.78	9.45	46.68	45.78	123.14	21.15	5.27	23.92	21.20	50.12	21.43	2.64
74	ICGV 96165	51.50	11.50	9.83	45.93	71.47	107.41	26.72	4.06	30.78	12.55	50.95	21.28	2.07
75	ICGV 97115	51.75	13.18	8.13	51.31	57.86	129.50	18.44	4.05	22.49	16.83	48.84	22.35	1.98
76	ICGV 98184	50.25	13.25	7.33	45.73	56.56	127.76	22.37	4.61	26.98	17.24	48.53	23.43	2.24
77	ICGV 01491	51.00	16.95	7.83	47.98	48.08	124.03	19.72	3.40	23.12	15.20	51.01	20.23	1.74
78	ICGV 03287	51.50	15.50	9.30	48.00	51.81	125.78	18.41	4.20	22.61	17.21	48.07	18.73	2.02
79	ICGV 05057	51.75	11.93	10.38	53.45	55.29	118.34	18.94	3.79	22.74	17.30	48.26	24.07	1.83
80	ICGV 06175	50.00	14.35	8.18	47.10	54.32	130.16	18.66	7.51	26.17	27.76	52.78	25.24	3.96
81	ICGV 00064	51.50	13.40	6.85	42.99	54.35	133.74	23.07	5.17	28.25	16.61	51.91	21.36	2.69
82	ICGV 00246	51.00	15.70	8.00	45.17	65.42	130.07	19.36	4.58	23.94	18.37	48.45	22.21	2.22
83	ICGV 97150	51.00	14.10	9.40	48.80	58.82	130.11	20.29	2.51	22.79	10.62	45.70	25.42	1.15
84	ICGV 98385	51.50	15.63	9.95	47.40	61.53	124.64	20.11	2.23	22.33	10.18	45.73	21.62	1.02
85	ICGV 96266	51.50	13.63	9.73	51.19	66.40	125.92	24.59	3.27	27.86	11.83	48.86	22.28	1.60
86	ICGV 14224	50.25	12.65	8.98	54.17	51.29	126.27	21.35	5.02	26.37	18.64	49.26	23.00	2.47
87	ICGV 14232	51.25	14.88	8.23	49.18	51.71	127.97	23.85	5.29	29.14	17.02	52.40	21.76	2.77
88	ICGV 07262	51.00	15.38	9.35	45.63	61.03	120.27	18.59	4.25	22.84	18.84	50.42	22.73	2.14
89	ICGV 07247	51.25	11.98	7.93	47.01	56.55	120.97	16.84	3.93	20.77	16.90	49.45	23.92	1.94
90	ICGV 10371	50.25	15.40	7.93	46.82	53.04	129.02	17.90	4.41	22.31	19.28	49.01	22.32	2.16
91	ICGV 10373	52.50	13.73	8.98	47.87	45.10	117.89	21.37	6.57	27.93	21.64	60.11	17.98	3.95
92	ICGV 10379	51.50	13.73	9.03	49.20	59.72	122.93	21.01	5.08	26.08	19.46	49.60	19.52	2.52
93	ICGV 15094	52.00	17.15	8.50	48.62	65.42	133.51	19.30	2.90	22.20	12.63	47.97	20.07	1.39
94	ICGV 87846	51.75	15.73	10.05	50.86	59.50	123.57	19.27	4.71	23.98	18.70	48.82	23.63	2.30
95	ICGV 86699	50.50	13.58	8.35	46.36	52.63	117.17	20.25	4.15	24.40	16.90	45.04	25.83	1.87
96	GG 20	52.25	12.43	9.10	49.53	62.35	125.74	22.05	3.74	25.80	14.27	50.89	24.24	1.91
97	ICGV 171007	49.75	13.70	8.95	51.42	57.24	126.25	17.93	2.95	20.88	13.83	48.67	27.08	1.44
98	ICGV 171027	51.50	15.38	9.25	43.65	59.78	117.09	25.21	4.24	29.45	14.46	50.88	20.14	2.16
99	ICGV 181006	51.25	13.30	10.05	45.80	53.94	125.30	18.97	2.74	21.71	12.68	54.57	23.39	1.49
100	ICGV 181033	51.25	13.63	10.58	45.98	52.38	125.89	20.61	6.24	26.85	20.96	51.85	23.30	3.24

Appendix 4.1. Continued.

	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
CV (%)	1.99	14.61	16.19	19.56	25.98	10.31	18.20	27.17	15.61	21.35	7.59	19.15	33.70
SE	1.00	2.06	1.29	9.35	14.64	12.81	3.38	1.28	3.69	4.04	6.95	4.39	0.84
LSD (5%)	1.40	2.88	1.81	13.06	20.44	17.89	4.73	1.79	5.15	5.64	9.70	6.13	1.17

DF = days to 50% flowering, PH = plant height, PB = number of primary branches per plant, SCMR = SPAD chlorophyll meter reading, LRWC = leaf relative water content, SLA = specific leaf area ($cm^2\ g^{-1}$), HAULM = haulm weight (g $plant^{-1}$), SHP = shelling percentage, HSW = hundred seed weight(g), PY = pod yield (g $plant^{-1}$), HI = harvest index (%), TBM = total biomass production (g $plant^{-1}$) (g), SY = seed (g $plant^{-1}$).

Appendix 4.2. Mean values for 13 phenotypic traits of 100 groundnut genotypes evaluated under non-stressed condition in 2018/19 and 2019/20 post-rainy seasons.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
1	ICGV 16667	50.75	17.55	8.15	49.45	61.05	129.64	28.23	11.14	39.37	28.76	48.03	21.88	5.35
2	ICGV 93128	50.25	13.85	6.15	51.64	65.88	137.97	22.71	10.44	33.15	31.97	60.85	27.69	6.36
3	ICGV 95066	50.25	20.4	8.6	48.27	66.23	117.22	27.55	10.84	38.40	28.70	47.88	21.98	5.19
4	ICGV 96174	48.75	20.45	8.05	46.10	64.08	124.81	28.86	8.34	37.20	23.57	55.03	28.43	4.59
5	ICGV 97087	50.25	18.8	9.85	42.48	59.67	132.27	32.39	9.34	41.73	24.20	48.61	29.23	4.54
6	ICGV 98077	50.5	16.9	8.05	49.46	72.66	135.84	27.86	8.25	36.11	23.30	56.95	31.49	4.70
7	ICGV 01279	51	16.45	9.75	47.60	68.35	132.09	25.88	10.66	36.54	29.72	60.63	31.65	6.46
8	ICGV 03042	50.25	17.5	7.95	50.04	71.71	133.75	23.13	14.64	37.77	38.71	62.36	30.77	9.13
9	ICGV 06039	52	20.05	7.55	46.63	67.19	120.43	20.62	14.95	35.57	42.76	60.64	27.96	9.07
10	ICGV 06040	49.25	17.15	10.1	50.57	70.70	127.52	23.06	14.13	37.19	38.02	58.88	25.86	8.32
11	ICGV 07010	50	21.15	10.1	45.28	68.00	140.56	23.56	12.86	36.42	36.02	54.29	32.45	6.98
12	ICGV 10143	49.75	20.2	9.65	45.93	81.11	142.00	23.53	15.49	39.03	40.45	67.88	29.37	10.52
13	ICGV 11422	49.75	19.15	9.05	46.40	63.88	131.65	30.17	8.74	38.91	22.69	52.21	27.18	4.56
14	ICGV 11396	51	19.25	8.2	50.70	77.07	138.28	27.28	13.20	40.48	33.55	56.94	24.78	7.52
15	ICGV 11418	50.75	19.4	8.9	46.49	53.57	136.75	30.26	10.61	40.87	27.51	50.71	26.73	5.38
16	ICGV 91223	51	20.95	9.35	39.20	77.14	155.83	24.55	9.51	34.06	30.34	57.10	28.89	5.43
17	ICGV 94118	49.5	17.9	8.3	49.30	61.85	109.38	27.90	13.05	40.94	30.54	50.99	21.93	6.65
18	ICGV 99019	50.25	18.45	7.45	50.95	80.61	127.29	28.53	11.50	40.04	28.64	62.39	27.89	7.18
19	ICGV 00162	50.25	23	9.5	46.97	53.02	138.52	25.43	9.00	34.43	25.85	53.79	22.50	4.84
20	ICGV 00211	50	17.05	7.55	44.40	75.86	142.81	31.56	12.69	44.25	30.86	55.96	24.11	7.10
21	ICGV 00187	49.5	18.7	5.9	52.89	65.34	119.65	22.30	8.80	31.10	28.30	52.97	26.15	4.66
22	ICGV 00213	49.25	19.2	7.2	50.85	75.84	130.65	24.51	11.11	35.63	33.72	56.70	22.18	6.30
23	ICGV 06146	49.75	20.45	9.45	43.04	66.14	123.16	17.22	10.25	27.48	37.88	52.39	29.47	5.37
24	ICGV 07120	52.25	13.85	9.1	50.02	66.45	142.82	22.35	8.52	30.86	27.86	57.19	36.09	4.87
25	ICGV 10178	49.75	19.95	10.1	46.18	53.11	127.15	27.13	10.79	37.92	30.88	49.32	26.65	5.32
26	ICGV 11380	52	21.95	7.65	46.57	68.77	123.36	20.33	13.08	33.41	39.78	61.62	24.14	8.06
27	ICGV 14001	50.25	18.75	8.8	43.10	63.57	119.75	22.78	15.09	37.87	42.56	56.12	22.35	8.47
28	ICGV 14030	50.5	19.8	9.6	47.34	72.07	139.04	20.06	12.26	32.32	38.12	64.24	30.25	7.88
29	ICGV 86015	48.75	17.2	7.5	49.25	61.78	123.44	20.81	12.59	33.40	38.78	55.51	23.38	6.99
30	ICGV 93260	50	15.85	8.75	45.77	73.75	128.73	23.85	14.11	37.96	36.82	59.10	26.85	8.34
31	ICGV 93261	49.5	19.05	7.3	51.04	57.68	118.61	18.63	14.00	32.63	41.69	52.03	23.15	7.28
32	ICGV 92121	50	18.65	8.7	43.73	71.18	127.75	26.65	11.05	37.70	28.47	52.11	26.99	5.76
33	ICGV 99241	51	19.85	9.25	42.40	69.91	130.85	30.33	11.94	42.26	28.68	56.17	29.55	6.71

Appendix 4.2. Continued.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
34	ICGV 00351	50.25	20.3	6.05	42.57	73.93	151.97	21.58	10.47	32.05	33.93	56.12	29.25	5.88
35	ICGV 01260	50.75	17.65	7.5	48.30	65.36	147.81	28.07	11.68	39.75	29.65	54.45	36.10	6.36
36	ICGV 01265	50.5	16.55	8.15	54.26	64.66	116.20	22.20	9.35	31.55	30.17	64.06	34.29	5.99
37	ICGV 13200	49.5	18.9	8.6	43.80	57.95	128.37	15.77	11.50	27.27	40.87	53.46	20.51	6.15
38	ICGV 07220	51	15.65	11.4	47.13	79.73	144.16	19.55	12.37	31.92	38.30	58.17	25.75	7.20
39	ICGV 07222	50.75	14.5	10.85	43.46	75.88	130.05	18.45	15.93	34.38	47.21	60.90	29.88	9.70
40	ICGV 13317	50.5	15.2	8.55	46.66	74.91	129.26	22.97	13.38	36.35	37.14	64.25	32.71	8.59
41	ICGV 13254	50.25	19.45	7.75	52.09	69.98	128.96	29.13	14.39	43.52	31.78	53.37	22.73	7.68
42	ICGV 181026	50.5	18.95	9.35	44.48	70.96	130.00	27.89	12.34	40.23	30.82	53.09	24.94	6.55
43	ICGV 15073	50	17.2	9.9	46.88	57.38	130.70	27.40	9.94	37.34	26.77	49.82	27.05	4.95
44	ICGV 15074	50.25	22.3	9.55	48.21	64.70	132.53	26.50	13.03	39.52	32.52	55.28	27.10	7.20
45	ICGV 15083	50.75	19.55	9.2	51.10	55.26	127.24	29.24	14.69	43.93	33.79	51.79	28.09	7.61
46	ICGV 15019	49.25	19.55	8.7	49.39	80.59	132.09	28.13	10.11	38.25	27.94	60.35	27.78	6.10
47	ICGV 06420	49.75	20.15	8.85	53.56	74.95	130.72	29.14	12.50	41.64	30.56	53.03	22.68	6.63
48	ICGV 05155	51.25	16.8	8.6	50.60	73.72	136.39	19.81	10.76	30.57	34.12	65.26	24.03	7.02
49	ICGV 16688	49.25	21.8	8.6	49.65	66.72	126.86	28.48	12.44	40.92	30.99	53.83	25.28	6.70
50	ICGV 03043	50	19.2	10	48.79	81.17	133.15	23.89	12.59	36.47	34.61	55.13	30.22	6.94
51	ICGV 00350	49.25	19.35	6.55	48.16	55.98	136.44	25.93	14.68	40.61	35.91	52.65	26.04	7.73
52	ICGV 86590	50.75	19.35	8.5	48.65	66.20	124.94	28.84	9.69	38.53	25.37	55.07	27.13	5.34
53	ICGV 02266	50.5	17.25	9	47.37	62.48	132.10	24.41	12.76	37.16	35.59	49.16	27.73	6.27
54	ICGV 13189	50.25	16.5	6.55	49.12	69.79	136.07	19.49	12.33	31.82	41.08	60.91	26.80	7.51
55	ICGV 13207	50.25	12.35	6.1	45.07	58.95	131.33	12.97	10.43	23.41	44.40	54.10	19.70	5.65
56	ICGV 14421	48	14.2	6.4	44.83	80.53	132.28	21.94	12.26	34.20	38.31	66.31	26.15	8.13
57	ICGV 13219	49.5	12.95	4.7	46.53	71.32	128.95	15.82	7.64	23.46	34.00	52.81	24.43	4.03
58	GPBD 4	50	19.1	6.7	44.63	81.34	134.39	22.53	7.30	29.84	25.45	63.78	28.92	4.66
59	ICGV 86031	50	20.65	5.75	52.34	62.42	131.66	21.08	8.75	29.83	29.25	59.62	24.62	5.21
60	ICGV 16686	49.75	20.75	8	49.03	76.50	133.21	27.29	10.42	37.72	29.20	54.54	23.60	5.68
61	ICGV 16005	48.75	15	7.1	52.01	57.90	134.56	25.63	11.85	37.47	32.14	49.13	21.69	5.82
62	ICGV 171013	50.5	13.2	7.1	57.39	75.93	143.11	16.90	10.29	27.18	40.80	57.48	35.70	5.91
63	ICGV 171026	50.25	14.2	8	51.60	61.28	128.54	25.93	10.07	36.00	28.15	46.83	21.41	4.72
64	ICGV 171039	49.75	22.75	8	49.57	75.33	138.81	22.78	11.62	34.40	34.43	56.36	29.03	6.55
65	ICGV 171046	50.25	17.45	8.8	46.05	65.27	130.15	23.19	10.12	33.31	31.03	50.66	27.35	5.13
66	ICGV 181017	51	20.25	9.5	41.29	77.99	121.57	31.13	10.74	41.87	26.75	50.95	23.80	5.47
67	ICGV 181063	50.5	26.2	8.45	48.47	63.05	144.04	29.41	6.97	36.37	18.91	42.94	26.05	2.99

Appendix 4.2. Continued.

Serial number	Genotype	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
68	ICGV 98412	50.75	24.1	10.75	51.08	72.96	137.41	24.92	16.21	41.13	40.79	55.70	36.22	9.03
69	ICGV 181489	52	18.9	10.2	41.47	61.23	131.67	29.03	6.75	35.78	19.24	47.53	22.25	3.21
70	ICGV 181490	49.5	18.95	8.85	47.62	70.17	128.60	20.12	10.43	30.56	34.77	60.54	29.34	6.32
71	ICGV 92054	51	18.1	9.6	51.78	50.75	132.45	27.74	8.03	35.77	22.48	46.88	23.68	3.76
72	ICGV 93162	50	20.35	9.55	44.73	73.16	133.94	27.06	8.47	35.53	24.46	59.28	28.66	5.02
73	ICGV 95111	51.75	16.45	10.25	50.99	61.91	127.88	29.10	7.12	36.22	19.04	54.78	24.89	3.90
74	ICGV 96165	50.75	15.4	7.95	50.99	80.45	137.85	25.20	7.68	32.88	23.89	59.04	30.31	4.53
75	ICGV 97115	52.75	15.4	9.35	41.78	70.85	129.67	31.34	9.19	40.52	23.56	49.60	23.62	4.56
76	ICGV 98184	51	16.2	9.95	49.32	78.45	125.48	23.78	7.87	31.65	24.77	61.95	30.21	4.88
77	ICGV 01491	51.25	22.9	9	47.07	63.06	121.55	34.51	8.59	43.09	19.67	50.56	23.70	4.34
78	ICGV 03287	51.5	22.7	9.25	50.19	76.84	124.12	25.12	8.52	33.64	24.69	64.10	26.22	5.46
79	ICGV 05057	51	17.75	9.25	44.47	59.81	120.72	23.87	9.63	33.50	29.21	55.03	25.65	5.30
80	ICGV 06175	50.75	20.8	10.85	49.63	78.37	132.57	25.35	12.18	37.53	32.15	62.90	25.25	7.66
81	ICGV 00064	50.75	16.2	9.05	46.43	61.09	130.39	28.38	8.53	36.91	24.44	57.31	21.38	4.89
82	ICGV 00246	50.5	23.35	8.15	48.27	76.87	125.89	24.94	8.23	33.17	24.45	57.01	23.88	4.69
83	ICGV 97150	50.5	19.85	10.85	48.00	65.43	120.56	28.94	6.09	35.03	17.00	45.51	23.56	2.77
84	ICGV 98385	50.75	19.8	13.15	45.33	78.78	131.08	30.16	6.57	36.73	18.48	58.08	28.68	3.81
85	ICGV 96266	49.75	21.5	8.4	47.35	63.16	124.65	28.01	6.78	34.79	20.97	49.59	21.89	3.36
86	ICGV 14224	51	17.1	10.3	49.66	71.93	129.14	26.48	10.46	36.94	26.77	65.74	28.27	6.88
87	ICGV 14232	51.25	19.05	11.35	50.76	68.93	126.40	24.40	10.94	35.35	30.89	53.39	28.80	5.84
88	ICGV 07262	52.25	17.2	8.5	47.01	85.62	125.87	22.34	8.96	31.31	27.94	64.38	32.34	5.77
89	ICGV 07247	51.5	15.05	10.55	49.39	60.32	117.10	26.39	14.81	41.20	35.58	51.56	26.16	7.64
90	ICGV 10371	51.25	18.05	9.5	47.49	79.83	128.32	24.93	8.87	33.80	25.63	61.09	25.38	5.42
91	ICGV 10373	52	20	9.9	50.02	67.16	129.11	26.04	11.51	37.56	30.74	54.10	23.89	6.23
92	ICGV 10379	52.25	19.55	9.7	50.21	79.26	132.60	29.43	10.90	40.33	27.04	65.63	27.17	7.15
93	ICGV 15094	52.25	22.75	11.35	49.38	54.44	125.58	28.56	8.08	36.64	21.87	55.82	29.94	4.51
94	ICGV 87846	52.25	24.1	11.5	46.34	81.84	122.90	29.66	11.23	40.89	27.17	61.55	37.64	6.91
95	ICGV 86699	50	19.45	10.35	49.46	70.56	117.92	25.99	8.63	34.62	24.86	52.73	23.20	4.55
96	GG 20	51	17.15	8.6	48.23	79.98	128.37	27.24	12.96	40.19	28.17	63.34	28.44	8.21
97	ICGV 171007	50	19.9	9.75	53.33	62.59	125.56	24.95	8.64	33.58	25.02	56.24	29.62	4.86
98	ICGV 171027	53	20.2	11	44.73	80.32	127.42	26.96	7.41	34.37	21.33	63.16	30.14	4.68
99	ICGV 181006	52.25	22.55	12.4	48.07	67.79	131.27	32.78	8.53	41.31	20.36	58.45	24.03	4.98
100	ICGV 181033	51.25	19.85	10.45	50.50	83.37	139.14	28.34	11.79	40.12	29.17	65.38	31.06	7.71

Appendix 4.2. Continued.

	DF	PH	PB	SCMR	LRWC	SLA	HAULM	POD	TBM	HI	SHP	HSW	SY
CV (%)	2.47	15	23.77	7.97	11.85	11.9	20.45	26.66	17.44	19.43	5.96	11.08	30.3
SE	1.25	2.81	2.11	3.82	8.19	15.53	5.18	2.87	5.29	7.02	3.35	2.98	1.82
LSD (5%)	1.74	3.92	2.94	5.33	11.44	21.24	7.24	4.01	7.39	9.8	4.68	4.17	2.54

DF = days to 50% flowering, PH = plant height, PB = number of primary branches per plant, SCMR = SPAD chlorophyll meter reading, LRWC = leaf relative water content, SLA = specific leaf area ($cm^2\ g^{-1}$), HAULM = haulm weight (g $plant^{-1}$), SHP = shelling percentage, HSW = hundred seed weight(g), PY = pod yield (g $plant^{-1}$), HI = harvest index (%), TBM = total biomass production (g $plant^{-1}$) (g), SY = seed (g $plant^{-1}$).

Appendix 4.3. Percentage of mature pods per plant and mean pod yield per plant at 100, 110 and 120 days after sowing (DAS) for 100 groundnut genotypes evaluated in 2019 rainy season.

Serial number	Genotype	Percentage of mature pods per plant recorded at			Mean Pod yield (g plant^{-1}) recorded at			Days to maturity
		100 DAS	110 DAS	120 DAS	100 DAS	110 DAS	120 DAS	
1	ICGV 16667	39	56	71	9.6	16.4	13.2	120
2	ICGV 93128	64	55	89	13.2	16	15.6	120
3	ICGV 95066	26	79	75	12.8	14	10.4	110
4	ICGV 96174	63	49	78	14	14	17.6	120
5	ICGV 97087	69	45	64	16	1.6	14	100
6	ICGV 98077	75	55	79	9.2	12.4	8	100
7	ICGV 01279	35	44	83	12	7.6	7.6	130
8	ICGV 03042	42	56	75	19.2	18	10.4	130
9	ICGV 06039	86	50	63	7.2	13.2	12.8	130
10	ICGV 06040	42	41	84	18.8	25.2	18.4	130
11	ICGV 07010	85	60	72	16	18.4	15.6	100
12	ICGV 10143	57	37	85	14.8	3.2	14	130
13	ICGV 11422	25	65	60	8.4	16.4	12.8	130
14	ICGV 11396	39	50	83	12	8	7.2	120
15	ICGV 11418	26	53	65	6	6.8	11.6	130
16	ICGV 91223	37	58	84	8	12.8	16.4	120
17	ICGV 94118	51	51	83	12.4	12	15.2	120
18	ICGV 99019	43	77	79	9.2	6.8	14	110
19	ICGV 00162	57	56	83	8	10	10	120
20	ICGV 00211	66	83	74	6.8	9.2	13.6	120
21	ICGV 00187	68	52	70	17.2	7.2	20.4	120
22	ICGV 00213	50	82	92	12.8	10.8	12.4	110
23	ICGV 06146	49	69	47	14.8	17.2	15.6	110
24	ICGV 07120	48	77	56	16	16	16	110
25	ICGV 10178	32	50	82	7.2	21.6	15.2	120
26	ICGV 11380	69	81	86	10	8	8.4	110
27	ICGV 14001	40	53	66	10.4	9.2	15.6	130
28	ICGV 14030	40	70	88	8.8	3.2	14.8	110
29	ICGV 86015	66	56	73	6.4	7.2	10.4	120
30	ICGV 93260	79	61	70	10.8	24	17.2	100
31	ICGV 93261	65	64	83	14	20	22.8	120
32	ICGV 92121	55	71	84	6.4	7.6	9.2	110
33	ICGV 99241	56	66	89	17.2	16.8	24	120
34	ICGV 00351	38	61	71	16.8	14.8	22	120
35	ICGV 01260	51	63	43	8	11.6	17.6	130
36	ICGV 01265	59	67	80	6	11.2	11.6	120
37	ICGV 13200	88	41	83	10	15.2	20	120
38	ICGV 07220	71	53	59	8.8	10.8	17.2	130
39	ICGV 07222	52	58	73	11.2	7.6	14.4	120
40	ICGV 13317	36	50	71	12.4	22.4	18	120
41	ICGV 13254	53	69	71	12.8	11.2	21.6	120
42	ICGV 181026	51	71	86	13.6	8.4	14.4	110
43	ICGV 15073	65	61	83	14	31.6	20.8	120
44	ICGV 15074	73	75	88	15.2	16	16	100

Appendix 4.3. Continued.

Serial number	Genotypes	Percentage of mature pods recorded at			Pod yield per plant recorded at			Days to maturity
		100 DAS	110 DAS	120 DAS	100 DAS	110 DAS	120 DAS	
45	ICGV 15083	47	74	83	19.2	13.2	20.4	110
46	ICGV 15019	76	94	88	5.2	8.4	12	100
47	ICGV 06420	36	65	77	12	16.4	14	120
48	ICGV 05155	63	79	65	14.8	13.2	16.8	110
49	ICGV 16688	42	48	64	15.6	16	19.6	130
50	ICGV 03043	86	61	86	12	15.2	14.4	100
51	ICGV 00350	50	77	74	9.2	9.2	15.2	110
52	ICGV 86590	57	53	62	9.2	11.6	16	130
53	ICGV 02266	40	54	84	12	16.4	13.6	120
54	ICGV 13189	82	68	93	14.4	11.2	14.4	100
55	ICGV 13207	56	50	92	10	14	12.8	120
56	ICGV 14421	62	50	85	14.8	11.6	16	120
57	ICGV 13219	69	77	86	17.2	26.8	18	110
58	GPBD 4	47	44	66	14.4	18.8	18	130
59	ICGV 86031	70	69	75	11.2	10	11.6	100
60	ICGV 16686	43	50	80	5.20	11.2	10.4	120
61	ICGV 16005	83	61	77	14.4	10.4	12.4	100
62	ICGV 171013	74	80	89	12.8	8.8	11.6	100
63	ICGV 171026	35	44	50	9.2	12.3	14.3	130
64	ICGV 171039	75	58	72	11.2	10	16	100
65	ICGV 171046	52	63	83	4.8	11.2	9.2	120
66	ICGV 181017	40	64	81	8	6.8	13.6	120
67	ICGV 181063	27	57	70	6.4	12.4	15.2	120
68	ICGV 98412	44	62	59	20	22.8	16.4	130
69	ICGV 181489	15	35	73	9.6	14	22	120
70	ICGV 181490	81	55	69	8.4	8.4	13.2	120
71	ICGV 92054	52	60	48	7.6	10	11.6	130
72	ICGV 93162	42	77	77	6.8	10	10.4	110
73	ICGV 95111	37	67	54	3.6	14.4	11.2	130
74	ICGV 96165	44	71	60	4.4	8	11.2	110
75	ICGV 97115	50	72	91	6.4	7.2	10.4	110
76	ICGV 98184	60	49	75	8.8	11.6	20	120
77	ICGV 01491	10	51	50	2	16.8	15.2	130
78	ICGV 03287	49	71	86	9.2	9.6	24.8	120
79	ICGV 05057	38	51	72	11.2	12	19.2	120
80	ICGV 06175	59	72	81	12	17.6	16	110
81	ICGV 00064	41	54	86	8.8	8	12.4	120
82	ICGV 00246	48	68	78	9.3	12.2	15.6	120
83	ICGV 97150	34	55	50	5.2	22	9.2	130
84	ICGV 98385	25	49	95	12.8	14.6	17.8	120
85	ICGV 96266	64	69	89	5.6	16.4	17.2	120
86	ICGV 14224	59	66	58	20.8	24.8	27.3	130
87	ICGV 14232	30	48	59	19.2	25.6	32.4	130
88	ICGV 07262	41	43	77	9.2	15.6	14.4	120
89	ICGV 07247	40	63	66	9.2	17.6	11.2	120
90	ICGV 10371	70	49	82	8.4	15.6	19.2	120
91	ICGV 10373	55	62	75	7.2	8.8	17.2	120

Appendix 4.3. Continued.

Serial number	Genotypes	Percentage of mature pods recorded at			Pod yield per plant recorded at			Days to maturity
		100 DAS	110 DAS	120 DAS	100 DAS	110 DAS	120 DAS	
92	ICGV 10379	52	63	73	10	5.2	12.4	120
93	ICGV 15094	63	67	80	10.4	16	17.2	120
94	ICGV 87846	39	74	69	15.2	11.6	15.6	110
95	ICGV 86699	41	35	70	4.4	5.6	6.8	120
96	GG 20	80	44	67	7.2	11.2	16.8	120
97	ICGV 171007	47	68	61	7.6	8.4	8.8	130
98	ICGV 171027	33	46	60	6.4	8.8	11.6	130
99	ICGV 181006	46	61	63	6	7.2	10.8	130
100	ICGV 181033	78	68	59	8.4	3.2	19.6	130

Appendix 4.4. Inferred ancestry of individuals and degree of admixture among 99 groundnut genotypes.

Serial number	Genotype	Market type	Inferred ancestry of individuals			Inferred cluster
1	ICGV94118	Spanish bunch	0.194	0.806	0	CL2
2	ICGV11422	Spanish bunch	0.925	0.075	0	CL1
3	ICGV06040	Spanish bunch	0.502	0	0.498	ADMIX
4	ICGV10373	Virginia bunch	0.57	0.362	0.068	ADMIX
5	ICGV13254	Spanish bunch	0.16	0.84	0	CL2
6	ICGV99241	Spanish bunch	0.257	0.598	0.144	ADMIX
7	ICGV181489	Spanish bunch	0.245	0.346	0.409	ADMIX
8	ICGV13219	Spanish bunch	0.002	0.131	0.867	CL3
9	ICGV171013	Spanish bunch	0.001	0	0.999	CL3
10	ICGV14030	Spanish bunch	0.926	0.001	0.073	CL1
11	ICGV91223	Spanish bunch	0.073	0.833	0.094	CL2
12	ICGV16688	Spanish bunch	0.372	0.627	0	ADMIX
13	ICGV00187	Spanish bunch	0.163	0.837	0	CL2
14	ICGV06146	Spanish bunch	1	0	0	CL1
15	ICGV01265	Spanish bunch	0.001	0	0.999	CL3
16	ICGV16686	Spanish bunch	0.294	0.705	0	CL2
17	ICGV15073	Spanish bunch	0.352	0.648	0	ADMIX
18	ICGV97087	Spanish bunch	0.002	0.973	0.026	CL2
19	ICGV13200	Spanish bunch	0.964	0	0.036	CL1
20	ICGV01279	Spanish bunch	0.983	0.003	0.015	CL1
21	ICGV15074	Spanish bunch	0.344	0.656	0	ADMIX
22	ICGV181063	Spanish bunch	0.024	0.701	0.275	CL2
23	ICGV10178	Spanish bunch	0.717	0.283	0	CL1
24	ICGV11418	Spanish bunch	0.928	0.072	0	CL1
25	ICGV86031	Spanish bunch	0.002	0	0.998	CL3
26	ICGV07222	Spanish bunch	1	0	0	CL1
27	ICGV93260	Spanish bunch	0.001	0	0.999	CL3
28	ICGV98412	Spanish bunch	0.001	0	0.998	CL3
29	ICGV93261	Spanish bunch	0.001	0	0.999	CL3
30	ICGV07220	Spanish bunch	1	0	0	CL1
31	ICGV07010	Spanish bunch	0.254	0.015	0.731	CL3
32	ICGV171046	Spanish bunch	0.92	0.001	0.079	CL1
33	ICGV92121	Spanish bunch	0.012	0	0.988	CL3
34	ICGV13207	Spanish bunch	0.012	0.236	0.752	CL3
35	ICGV171026	Spanish bunch	0.721	0.001	0.278	CL1
36	ICGV93128	Spanish bunch	0.106	0	0.894	CL3
37	ICGV15019	Spanish bunch	0.209	0.006	0.785	CL3
38	ICGV00350	Spanish bunch	0.119	0.702	0.179	CL2
39	ICGV01260	Spanish bunch	0.2	0	0.799	CL3
40	ICGV13317	Spanish bunch	0.547	0	0.453	ADMIX
41	ICGV02266	Spanish bunch	0.232	0.333	0.435	ADMIX
42	ICGV07120	Spanish bunch	0.001	0.948	0.051	CL2
43	ICGV00351	Spanish bunch	0.184	0.567	0.249	ADMIX
44	ICGV181017	Spanish bunch	0.906	0	0.094	CL1
45	ICGV96174	Spanish bunch	0.001	0.995	0.004	CL2
46	ICGV10143	Spanish bunch	0.997	0.002	0.001	CL1
47	ICGV181026	Spanish bunch	0.868	0	0.132	CL1

Appendix 4.4. Continued.

Serial number	Genotypes	Market type	Inferred ancestry of individuals			Inferred cluster
48	ICGV14001	Spanish bunch	1	0	0	CL1
49	GPBD4	Spanish bunch	0.023	0.393	0.585	ADMIX
50	ICGV98077	Spanish bunch	0.667	0.257	0.076	ADMIX
51	ICGV16667	Spanish bunch	0.328	0.672	0	ADMIX
52	ICGV15083	Spanish bunch	0.432	0.568	0	ADMIX
53	ICGV00162	Spanish bunch	0.13	0.869	0	CL2
54	ICGV00211	Spanish bunch	0.597	0.401	0.002	ADMIX
55	ICGV11380	Spanish bunch	0.906	0.003	0.091	CL1
56	ICGV14421	Spanish bunch	0.059	0.25	0.692	CL3
57	ICGV16005	Spanish bunch	0.292	0.415	0.293	ADMIX
58	ICGV95066	Spanish bunch	0.031	0	0.969	CL3
59	ICGV86590	Spanish bunch	0.003	0.001	0.996	CL3
60	ICGV171039	Spanish bunch	0.348	0.553	0.099	ADMIX
61	ICGV99019	Spanish bunch	0.122	0.878	0	CL2
62	ICGV11396	Spanish bunch	1	0	0	CL1
63	ICGV181490	Spanish bunch	0.004	0	0.996	CL2
64	ICGV86015	Spanish bunch	0.001	0.4	0.599	ADMIX
65	ICGV13189	Spanish bunch	0.006	0.034	0.959	CL3
66	ICGV00213	Spanish bunch	0.091	0.909	0	CL2
67	ICGV06039	Spanish bunch	0.545	0	0.454	ADMIX
68	ICGV03043	Spanish bunch	1	0	0	CL1
69	ICGV14224	Virginia bunch	0.37	0.323	0.308	ADMIX
70	ICGV171007	Virginia bunch	0.088	0.001	0.912	CL3
71	ICGV171027	Virginia bunch	0.402	0	0.597	ADMIX
72	ICGV10379	Virginia bunch	0.48	0.52	0	ADMIX
73	ICGV181006	Virginia bunch	0.523	0.374	0.103	ADMIX
74	ICGV181033	Virginia bunch	0.893	0	0.107	CL1
75	ICGV06175	Virginia bunch	0.116	0.884	0	CL2
76	ICGV96165	Virginia bunch	0.44	0.56	0	ADMIX
77	ICGV00246	Virginia bunch	0.116	0.884	0	CL2
78	ICGV00064	Virginia bunch	0.129	0.798	0.073	CL2
79	ICGV07247	Virginia bunch	1	0	0	CL1
80	ICGV97150	Virginia bunch	0.001	0.999	0	CL2
81	ICGV87846	Virginia bunch	0.072	0.928	0	CL2
82	ICGV03287	Virginia bunch	1	0	0	CL1
83	ICGV07262	Virginia bunch	1	0	0	CL2
84	GG20	Virginia bunch	0.136	0.022	0.842	CL3
85	ICGV95111	Virginia bunch	0.392	0.306	0.302	ADMIX
86	ICGV96266	Virginia bunch	0.009	0.606	0.384	ADMIX
87	ICGV97115	Virginia bunch	0.06	0.275	0.665	ADMIX
88	ICGV10371	Virginia bunch	0.572	0.362	0.066	ADMIX
89	ICGV93162	Virginia bunch	0.001	0.072	0.927	CL3
90	ICGV98385	Virginia bunch	0.001	0.999	0	CL2
91	ICGV14232	Virginia bunch	0.36	0.332	0.309	ADMIX
92	ICGV05057	Virginia bunch	0.436	0.21	0.355	ADMIX
93	ICGV92054	Virginia bunch	0.146	0.18	0.674	ADMIX
94	ICGV15094	Virginia bunch	0.641	0.3	0.058	ADMIX
95	ICGV98184	Virginia bunch	1	0	0	CL1
96	ICGV86699	Virginia bunch	0.001	0.999	0	CL2

Appendix 4.4. Continued.						
Serial number	Genotypes	Market type	Inferred ancestry of individuals			Inferred cluster
97	ICGV01491	Virginia bunch	0.003	0	0.997	CL3
98	ICGV05155	Spanish bunch	0.83	0.17	0	CL1
99	ICGV03042	Spanish bunch	0.999	0.001	0	CL1

CL = cluster, ADMIX = admixture

Chapter-5

Combining ability analysis of groundnut (*Arachis hypogaea* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions

---

Abstract

Genetic advancement and gains in yield and related traits are dependent on selection of best combiner parents and progenies under the prevailing growing conditions. The objective of this study was to determine the combining ability effects of eight selected drought tolerant groundnut parental lines and their F_2 families under drought-stressed (DS) and non-stressed (NS) conditions to select best performing parents and families for drought tolerance breeding. The eight genotypes selected for their high yields, biomass production and drought tolerance were crossed using a half-diallel mating design and 28 progenies were generated. Parents and progenies were evaluated under DS and NS and field (NS) conditions using an alpha lattice experimental design with 2 replications. Experiments were conducted at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in India during 2020. The following agronomic data were collected: days to 50% flowering (DF), number of primary branches (PB), plant height (PH) (cm), chlorophyll meter reading (SCMR), specific leaf area (SLA) (cm^2/g), pod yield (PY) (g $plant^{-1}$), shelling percentage (SHP) (%), kernel yield (KY) (g $plant^{-1}$), total biomass (TBM) (g $plant^{-1}$) and harvest index (HI) (%). The general combining ability (GCA) effects of parents were significant ($P<0.05$) for all assessed traits under all testing conditions except for PB under DS and NS conditions in the glasshouse. The specific combining ability (SCA) effects of progenies were significant ($P<0.05$) for all traits except for PH across all testing environments and PB under field condition. Genotype ICGV 10178 was the best general combiner with positive contribution to SCMR, PY, SHP, KY, TBM and HI and reduced SLA. Crosses, ICGV 10178 X ICGV 11369, ICGV 10373 x ICGV 15083, ICGV 98412 x ICGV 15094 and ICGV 10178 X ICGV 98412, were the best specific combiners for enhanced pod yield and drought tolerance. Higher GCA: SCA rations were recoded for PY, KY and TBM across all the testing environments suggesting the predominant role of additive genes conditioning the inheritance of these traits. Therefore, the above new families are recommended for genetic advancement through single seed descent selection methods to develop improved pure line groundnut varieties with high pod yield and drought tolerance.

Keywords: *Arachis hypogaea*; drought tolerance, general combining ability effect; groundnut breeding, specific combining ability

5.1. Introduction

Groundnut, (*Arachis hypogaea* L., 2n = 4x = 40), is a nutrient-rich food legume and oilseed crop, cultivated mainly in the semi-arid tropics where recurrent drought is common. Groundnut is predominantly self-pollinating crop with about 5% cross-pollination depending on season and genotype. For example, during post rainy season higher outcrossing rate was reported compared with the rainy season and the Spanish type of groundnut shows higher outcrossing level than the Virginia type (Reddy et al. 1993). Climate change studies predicted increased rainfall variability, which is likely to affect crop production and productivity under water-limited environments (Watson et al. 2015).

Groundnut yield is affected by drought stress at different growth stages (Nageswara Rao et al. 1985). Meisner and Karnok (1992) reported 49% and 37% unshelled yield reduction in groundnut due to drought stress during flowering and early pod-filling stages, respectively. Thus, breeding groundnut genotypes with high pod yield potential along with drought-tolerant and desirable agronomic traits is an overriding consideration to sustain groundnut production and productivity. Most breeding programs in groundnut have been using yield and surrogate traits for drought tolerance such as specific leaf area, chlorophyll content, biomass production, and harvest index (Nigam et al. 2005). However, the inheritance of traits associated with drought adaptation is likely to be genetically complex and governed by polygenes. Further, drought tolerance is subject to genotype x environment interaction (Ravi et al. 2011).

Genetic advancement and selection response for yield and related traits are dependent on the combining ability of parents and families when assessed under the target production conditions. Knowledge of combining ability effects and mode of gene action responsible for the regulation of expression of different traits is a prerequisite in planning appropriate breeding strategies for biotic and abiotic stress tolerance (Kiani et al. 2007; Kokeeto et al. 2020). The diallel mating design is the most widely used method to determine the combining ability effect and the nature of gene action involved in yield and yield-influencing traits (Falconer and Mackay, 1996). Sprague and Tatum (1942) introduced the concept of general combining ability (GCA) and specific combining ability (SCA) effects. GCA of parents is associated with additive gene effects, while the SCA effect of progenies is attributed to dominance and epistasis gene actions (Rojas and Sprague, 1952). Combining ability analysis enables selection of best parents and progenies with desirable GCA and SCA effects, in that order, in plant breeding programs. The magnitude of GCA and SCA ratios for various traits are computed using Baker's ratio (Baker 1978) to deduce the type of gene action and subsequently to design appropriate breeding strategy. Significantly higher GCA effects are attributed to polygenes with minor gene effect hence pure line, recurrent or single seed descent selection methods can be effective for enhanced response to selection. Conversely, significantly

higher SCA effect reveals the predominance of non-additive gene action and in this case heterosis breeding is more rewarding in sexually reproducing crops if cost-effective and efficient hybridization techniques are available. If the estimated values of GCA and SCA effects for a trait becomes equal, this suggests an equal contribution of additive and non-additive genetic variance hence population improvement can be adopted to develop superior genotypes (Singh and Narayanan, 2017; Ngaboyisonga et al. 2019). In groundnut breeding for drought tolerance, Sanogo et al. (2020) reported a significant GCA effect on pod yield, harvest index, biomass production and shelling percentage, while a significant SCA effect was found on chlorophyll meter reading based on soil plant analysis development (SPAD) under both drought-stressed and non-stressed conditions. Oppong-Sekyere et al. (2019) reported the importance of additive gene action in inheritance of pod, seed and biomass yields.

In Ethiopia, groundnut is one of the most important food and oil crops grown under rainfed condition. In these agro-ecologies water stress due to erratic rain distribution is the major impediment to crop production. A limited number of introduced groundnut varieties were released for cultivation in the country (MoANRs, 2016). However, these varieties are late maturing and low yielding and were not bred for drought tolerance. Therefore, there is a need to develop groundnut varieties with high yielding and drought stress tolerance that are adapted for cultivation under rainfed and drought-affected agro-ecologies. In an attempt to develop high yielding and drought tolerant groundnut cultivars, information on combining ability and mode of gene action responsible for drought tolerance is indispensable. There is a dearth of information on combining ability effects and genetic analysis of groundnut to guide selection and cultivar development in Ethiopia. Consequently, 100 groundnut genotypes were phenotyped under field condition and genotyped with high density single nucleotide polymorphism (SNP) markers at ICRISAT/India to select drought tolerant and genetically superior parents for breeding. Accordingly, some complementary lines were selected based on their yield potential, biomass production, early maturity and drought tolerance. The selected lines should be bred to develop drought tolerant and locally adapted cultivars under Ethiopian condition or similar agro-ecologies. Therefore, the objective of this study was to determine the combining ability effects of eight selected drought tolerant, agronomical superior and complementary groundnut parental lines and their F_2 families under drought-stressed and non-stressed conditions to select best performing parents and families for drought tolerance breeding.

5.2. Material and methods

5.2.1. Study site, plant materials, crosses and mating design

The experiments were conducted at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru in India. ICRISAT is situated at a latitude of 17.51^0N and a longitude of 78.27^0 E with an altitude of 545 m above sea level.

Eight parents were selected for crosses. The details of groundnut parents used for crosses are presented in Table 5.1. The eight parents consisted of five Spanish bunch type (such as genotypes ICGV 15083, ICGV 10178, ICGV 98412, ICGV 96174 and ICGV 11396) and three Virginia bunch type (ICGV 06175, ICGV 10373 and ICGV 15094). Parent ICGV 98412 is high yielding genotype with medium maturity period which was released for cultivation in Ghana and Ethiopia (Abady et al. 2019). Parent ICGV 15083 has high oleic acid content and released in India (ICRISAT, 2020). All the remaining genotypes are advanced breeding lines acquired from ICRISAT/India. The selected parents showed varied maturity duration. Genotypes, ICGV 06175 and ICGV 15083, attain physiological maturity at 110 days after sowing (DAS) making them early maturing genotypes for drought tolerance breeding. Genotypes, ICGV 10373, ICGV 10178, ICGV 96174, ICGV 11396 and ICGV 15094, attain maturity at 120 DAS, while ICGV 98412 mature in 130 DAS. The genotypes were selected based on field phenotypic evaluations and SNP genotyping aiming at yield potential, biomass production, early maturity, drought tolerance and genetic diversity.

Table 5.1. Description of groundnut parents used for crosses.

No	Genotype	Market type	Breeding history	Seed shape	Seed size	Pod constriction	Maturity class	Drought tolerance Phenotype
1	ICGV 06175	Virginia bunch	ABL	Round	Small	Moderate	Early	Tolerant
2	ICVG 10373	Virginia bunch	ABL	Round	Medium	Slight	Medium	Tolerant
3	ICGV 15083	Spanish bunch	Cultivar	Elongated	Large	Moderate	Early	Tolerant
4	ICGV 10178	Spanish bunch	ABL	Flat	Large	Slight	Medium	Tolerant
5	ICGV 98412	Spanish bunch	Cultivar	Elongated	Large	Moderate	Medium	Semi-tolerant
6	ICGV 96174	Spanish bunch	ABL	Round	Large	Slight	Medium	Semi-tolerant
7	ICGV 11396	Spanish bunch	ABL	Flat	Medium	Slight	Medium	Semi-tolerant
8	ICGV 15094	Virginia bunch	ABL	Round	Medium	Moderate	Medium	Semi-tolerant

ABL = advanced breeding line

The parents were grown in poly-house under controlled temperatures and light conditions at ICRISAT during 2019. Growing media were prepared with a mixture of red soil, sandy soil and farmyard manure with a ratio of 4:3:1, respectively. The media were autoclaved at 200 C^0 for two hours in two batches to ensure soil health. Crosses were made during June to October 2019 using a half-diallel mating design without reciprocals to obtain 28 F1 families. Each parent was grown

in five plastic pots and three seeds were sown in each pot and staggered planted. Hand emasculation and pollination were carried out according to the technique developed by Nigam et al. (1990). Emasculation was carried out from buds of female parents between 13:30-16:30 hours. After emasculation, buds were marked with a thread of different color to identify the emasculated buds for next day pollination. Pollination was carried out between 06:00 and 08:00 hours. Calyx, standard, and wing petals were detached from flower buds of male parents to make ready the sticky pollen mass for pollination. The lumps of pollens were deposited on the tip of the stigma of the emasculated flowers. The success of pollinations was checked based on the emergency of pegs from the axil of the leaf just below the colored thread 4-6 days after fertilization. True F_1 hybridity was confirmed based on morphological characteristics of both parents including growth habit, pod and seed features as described by Nigam et al. (2004). The F_1 seeds of all crosses were multiplied to harvest enough seeds for glasshouse and field evaluations in F_2 generation.

5.2.2. Growing parents and the F_2 families

The genotypes were evaluated under drought-stressed (DS) and non-stressed (NS) conditions in a controlled environment (glasshouse condition) and under non-stressed field condition during 2019 and 2020. The experiments involved 28 F_2 families and eight parents. The experiments were conducted using a 4 x 9 alpha lattice design with two replications. Growing media for the glasshouse experiment were prepared as described above. Under glasshouse condition, the genotypes were grown in plastic pots and evaluated under DS and NS conditions. The pots were maintained with regular irrigation until flowering for both treatments. Stress was imposed at the flowering stage by withholding water until wilting symptoms appeared (Vaidya et al. 2016). For the NS treatment, sufficient irrigation was supplied until physiological maturity. Under field condition, seeds of each genotype were sown in single row of 4-meter-long, with 30 cm between rows and 10 cm between plants. Weather data during field trial is presented in Table 5.2. The mean annual rainfall during 2020 was 43.9mm. The field experiment was conducted with supplementary irrigation to evaluate genotypes under optimal condition. The mean minimum and mean maximum temperatures during the experimental period were 22.70 and 30.96 ^{0}C, respectively.

Table 5.2 Monthly weather data during the field trial at ICRISAT/India in 2020.

Month	Rainfall (mm)	Tmax (^{0}C)	Tmin (^{0}C)	RHmax (%)	RHmin (%)
June	6.37	33.45	24.05	87.8	63.9
July	7.37	31.35	23.05	90.61	71.25
August	9.69	28.92	22.65	91.87	79.32
September	8.38	30.77	22.59	93.43	76.83
October	12.09	30.33	21.14	93.52	73.35

Tmax = average maximum temperature, Tmin = average minimum temperature, RHmax = average maximum relative humidity, RH min = average minimum relative humidity

5.2.3. Data collected

Data were collected on days to 50% flowering (DF), chlorophyll meter reading (SCMR), Plant height (PH, expressed in cm), number of primary branches (PB), pod yield per plant (PY, expressed in g plant^{-1}), shelling percentage (SHP, expressed in %), kernel yield per plant (KY, expressed in g plant^{-1}), total biomass per plant (TBM, expressed in g plant^{-1}) and harvest index (HI) (%). Descriptions on data collection are summarized in Chapter 4, section 4.2.3.

5.2.4. Data analysis

5.2.4.1. Analysis of variance

The data collected were subjected to analysis of variance using SAS version 9.3 Software (SAS Institute Inc., 2011). Treatment means were separated using the least significant difference (LSD) test at the 5% significance level.

5.2.4.2. Combining ability analysis

Data were subjected to combining ability analysis using a half-diallel approach according to Griffing (1956) with Model I and Method II. The linear mathematical model used for the half-diallel per experiment was as follows:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\sum\sum e_{ijkl}$$

Where;

Y_{ij} = the value of a character measured on cross of i^{th} and j^{th} parents;

μ = the population mean;

g_i = the general combining ability effect of the i^{th} parent;

g_j = the general combining ability effect of the j^{th} parent;

s_{ij} = the specific combining ability effect of the cross between I^{th} and j^{th} parents such that $s_{ij} = s_{ji}$ and

e_{ijk} = the environmental effect associated with ijk^{th} observation;

b and c = number of blocks and sample plants, respectively.

The GCA and SCA effects were computed using the AGD-R (Analysis of Genetic Designs in R) software version 5.0 (Francisco et al. 2015) and SAS version 9.0 Software. The relative importance of the GCA and SCA effects was computed according to the formula proposed by Baker (1978).
GCA: SCA = $(2MS_{GCA})/ (2MS_{GCA} + MS_{SCA})$

Where MS_{GCA} is GCA mean square, MS_{SCA} is SCA mean square.

The GCA to SCA ratio close to unity indicates the importance of additive genetic effects and the ratio less than unity suggests the predominant of non-additive gene effects conditioning trait inheritance (Baker 1978).

5.3. Results

5.3.1. Analysis of variance

Analysis of variance revealed significant ($p<0.05$) difference among parents and F_2 families for all assessed traits except PB under both drought-stressed (DS) and non-stressed (NS) conditions in the glasshouse and PH under NS in the field condition (Table 5.3). Under all testing environments, the GCA effects of the parents showed significant differences for all the traits except PB under DS condition. Furthermore, significant SCA effects were noted for DF, SCMR, PY, SHP, KY, TBM and HI under DS condition and for DF, PY, SHP and KY under NS in the glasshouse. The relative importance of GCA and SCA effects ranged from 0.56 for DF to 0.94 for KY under DS condition and 0.61 for DF to 0.96 for PY. Under field condition, significant SCA effects were recorded for DF, PB, PY, SHP and KY.

5.3.2. Mean performance

The analysis of variance revealed significant ($p \leq 0.05$) genotype differences for PH, SLA, DF, SCMR, PY, SHP, KY, TBM and HI under the DS condition (Table 5.4). Under the NS condition in the glasshouse, there was significant ($p \leq 0.05$) genotype differences for PH, SCMR, SLA, HI, DF, PY, SHP, KY and TBM (Table 5.5) while under field condition, significant ($p \leq 0.05$) genotype differences were recorded for SHP, DF, PY and KY (Table 5.6).

Under the DS condition in the glasshouse, the lowest DF was recorded for ICGV 15094 (29 days) and crosses, ICGV 15083 x ICGV 11396 (29 days), ICGV 06175 x ICGV 96174 (30 days), ICGV 15083 x ICGV 98412 (30 days) and ICGV 06175 x ICGV 15083 (30 days). Whereas, under NS condition in the glasshouse, the lowest DF was recorded for the parents ICGV 15094 (30 days), ICGV 96174 (32 days) and ICGV 98412 (32 days) and the crosses ICGV 06175 x ICGV 96174 (31 days), ICGV 96174 x ICGV 15094 (32 days), ICGV 10178 x ICGV 15094 (32 days), ICGV 98412 x ICGV 96174 (32 days) and ICGV 06175 x ICGV 10178 (32 days). During field studies, early flowering genotypes were ICGV 15094 (33 days) and crosses ICGV 06175 x ICGV 96174 (33), ICGV 96174 x ICGV 15094 (34 days) and ICGV 06175 x ICGV 10178 (34 days).

During the field study the highest number of primary branches per plant were recorded for the parent ICGV 11396 (12 branches per plant) and crosses ICGV 10373 x ICGV 15096 (16), ICGV 96174 x ICGV 15094 (12), ICGV 10373 x ICGV 11396 (12), ICGV 15083 x ICGV 96174 (12) and ICGV 06175 x ICGV 98412 (12). Under the NS glasshouse condition, the highest mean value for plant height was recorded for the parent ICGV 06175 (30.50 cm) and crosses ICGV 10178 x ICGV 96174 (34.00 cm), ICGV 15083 x ICGV 11396 (31.25 cm) and ICGV 15083 x ICGV 98412 (31.25 cm).

The highest SCMR values were recorded for the parents ICGV 98412 (51.75) and ICGV 10178 (48.25) and crosses ICGV 10373 x ICGV 98412 (53.65) and ICGV 10178 x ICGV 15094 (52.2), ICGV 10178 x ICGV 98412 (51.35), ICGV 06175 x ICGV 11396 (51.3) and ICGV 10373 x ICGV 10178 (51.20) under DS condition. In the glasshouse studies under NS condition, higher SCMR values were recorded for the parents ICGV 06175 (58.1) and ICGV 10178 (57.75) and, crosses ICGV 10178 x ICGV 98412 (59.45), ICGV 15083 x ICGV 98412 (55.05), and ICGV 98412 x ICGV 11396 (55.05).

The lowest SLA values were recorded for the parents ICGV 10373 (121.18 $cm^2 g^{-1}$) and ICGV 10178 (164.36 $cm^2 g^{-1}$) and, crosses ICGV 10178 x ICGV 96174 (131.96 $cm^2 g^{-1}$), ICGV 06175 x ICGV 10178 (132.96 $cm^2 g^{-1}$) and ICGV 15083 x ICGV 10178 (145.43 $cm^2 g^{-1}$) under DS condition. Under NS condition in the glasshouse, the highest SLA values were recorded for the parent ICGV 98412 (224.41 $cm^2 g^{-1}$) and crosses ICGV 15083 x ICGV 98412 (226.28 $cm^2 g^{-1}$), ICGV 15083 x ICGV 96174 (224.3 $cm^2 g^{-1}$) and ICGV 96174 x ICGV 15094 (218.98 $cm^2 g^{-1}$).

During DS condition, the highest PY were recorded for the parents, ICGV 10178 (18.15 g plant^{-1}) and ICGV 15083 (15.7 g plant^{-1}) and crosses, ICGV 15083 x ICGV 10178 (28.65 g plant^{-1}), ICGV 10373 x ICGV 15083 (23.40 g plant^{-1}), ICGV 10178 x ICGV 98412 (22.65 g plant^{-1}) and ICGV 10178 x ICGV 11396 (21.35 g plant^{-1}). Under NS condition in the glasshouse, the highest PY were recorded for the parents ICGV 10178 (25.37 g plant^{-1}), ICGV 98412 (23.75 g plant^{-1}) and ICGV 15083 (22.9 g plant^{-1}) and crosses ICGV 10178 x ICGV 98412 (34.2 g plant^{-1}), ICGV 15083 x ICGV 10178 (31.05 g plant^{-1}) and ICGV 15083 x ICGV 98412 (31.05). Under field condition, the highest PY were recorded for parents ICGV 10178 (15.00 g plant^{-1}) and ICGV 15083 (12.80 g plant^{-1}) and crosses ICGV 15083 x ICGV 98412 (23.21 g plant^{-1}), ICGV 98412 x ICGV 11396 (23.20 g plant^{-1}) and ICGV 98412 x ICGV 96174 (23.16 g plant^{-1}).

Under DS condition in the glasshouse study, the highest SHP values were recorded for the parents ICGV 06175 (66.36%), ICGV 96174 (65.79%) and ICGV 10178 (61.10%) and, crosses ICGV 10178 x ICGV 98412 (67.32%), ICGV 10373 x 15083 (65.99%) and ICGV 178 x ICGV 11396 (65.81%) in a desirable direction. Under NS condition in the glasshouse, the highest SHP were recorded for the parents ICGV 06175 (63.97%) and ICGV 96174 (63.60%) and, crosses ICGV 15083 x ICGV 96174 (64.83%), ICGV 10373 x ICGV 96174 (64.22%) and ICGV 15083 x ICGV 98412 (64.30%). Under field condition, the highest SHP values were recorded for the parents ICGV 10373 (69.18%) and ICGV 11396 (60.73%) and, crosses ICGV 15083 x ICGV 98412 (61.70%), ICGV 98412 x ICGV 11396 (60.50%) and ICGV 15083 x ICGV 10178 (60.30%).

The highest KY values were noted for ICGV 10178 (11.05 g plant^{-1}) and ICGV 15083 (9.35 g plant^{-1}) and crosses ICGV 10373 x ICGV 15083 (15.45 g plant^{-1}), ICGV 10178 x ICGV 98412 (15.25 g plant^{-1}), ICGV 15083 x ICGV 10178 (14.15) and ICGV 10178 x ICGV 11396 (14 g plant^{-1}) under DS condition in the glasshouse study. Under NS condition in the glasshouse, the highest KY were recorded for parents ICGV 98412 (14.10 g plant^{-1}), ICGV 10178 (13.70 g plant^{-1}) and ICGV 15083 (12.60 g plant^{-1}) and crosses ICGV 10178 x ICGV 98412 (20.75 g plant^{-1}), ICGV 15083 x ICGV 98412 (20.00 g plant^{-1}) and ICGV 15083 x ICGV 10178 (18.10 g plant^{-1}). During the field study, the highest KY were recorded for the parents, ICGV 10178 (8.76 g plant^{-1}) and ICGV 15083 (7.14 g plant^{-1}) and crosses, ICGV 15083 x ICGV 98412 (14.32 g plant^{-1}), ICGV 98412 x ICGV 11396 (14.04 g plant^{-1}) and ICGV 98412 x ICGV 96174 (13.35 g plant^{-1}).

In the glasshouse study and under DS condition, the highest TBM were recorded for the parents ICGV 10178 (54.70 g plant^{-1}) and ICGV 15083 (48.05 g plant^{-1}) and crosses, ICGV 15083 x ICGV 10178 (70.05 g plant^{-1}), ICGV 10178 x ICGV 98412 (67.10 g plant^{-1}) and ICGV 15083 x ICGV 98412 (64.55 g plant^{-1}). Under NS condition in the glasshouse, the highest TBM were noted for parents, ICGV 10178 (61.70 g plant^{-1}) and ICGV 15083 (61.20 g plant^{-1}) and, crosses, ICGV 10178 x ICGV

98412 (71.3 g plant^{-1}), ICGV 15083 x ICGV 98412 (67.75 g plant^{-1}) and ICGV 10178 x ICGV 11396 (63.40 g plant^{-1}).

Under DS condition in the glasshouse, the highest HI values were recorded for the parents, ICGV 10178 (49.64%) and ICGV 15083 (48.54%) and, crosses, ICGV 15083 x ICGV 10178 (69.84%), ICGV 10373 x ICGV 15083 (58.42%) and ICGV 10178 x ICGV 11396 (54.19%). Under NS condition in the glasshouse, the highest HI values were recorded for the parents, ICGV 98412 (59.05%) and ICGV 10178 (41.07%) and, crosses, ICGV 15083 x ICGV 96174 (50.38%), ICGV 10178 x ICGV 98412 (48.95%), ICGV 98412 x ICGV 96174 (48.51%) and ICGV 98412 x ICGV 96174 (48.51%).

Table 5.3. Analysis of variance showing mean square values due to replications (REP), general combining ability (GCA) effects of the parents, specific combining ability (SCA) effects of crosses and GCA:SCA ratios for the nine phenotypic traits and chlorophyll meter reading (SCMR) evaluated in the glasshouse (drought-stressed and non-stressed conditions) and non-stressed field conditions.

Traits	Env.	REP (*df* = 1)	Genotypes (*df* = 35)	GCA (*df* = 7)	SCA (*df* = 28)	Residual (*df* = 29)	GCA:SCA
DF	DS	0.12**	4.66**	3.24**	5.02**	0.18	0.56
DF	NS	0.47*	3.56**	3.04**	3.82**	0.3	0.61
DF	NSF	0.68ns	6.65**	6.54**	6.68**	0.37	0.66
PB	DS	0.11ns	1.68ns	2.54ns	1.46ns	1.84	0.78
PB	NS	1.95*	1.55ns	2.94ns	1.30ns	1.52	0.82
PB	NSF	0.13**	9.35*	9.18*	9.39*	3.75	0.66
PH	DS	19.51*	28.11*	42.27*	25.98ns	14.88	0.76
PH	NS	38.51**	21.41*	32.05*	19.61ns	11.08	0.77
PH	NSF	16.06*	62.17ns	161.11*	37.43ns	48	0.90
SCMR	DS	37.77**	18.53**	50.40**	10.62*	4.5	0.90
SCMR	NS	2.01ns	24.01*	53.23*	14.74ns	11.35	0.88
SLA	DS	1152.60ns	2475.78*	5795.99*	1645.73ns	1044.24	0.88
SLA	NS	98.26ns	2275.92*	3664.74*	1928.72*	704.73	0.79
PY	DS	15.74**	70.00**	234.65**	33.51**	2.37	0.93
PY	NS	107.80**	79.70**	289.93**	27.14*	9.73	0.96
PY	NSF	4.92ns	48.85**	83.57**	40.17*	13.86	0.81
SHP	DS	2.23**	110.33**	187.89**	90.94**	11.39	0.81
SHP	NS	118.42*	67.94**	120.98**	54.68*	19.05	0.82
SHP	NSF	37.75**	95.32*	171.99*	76.44*	40.17	0.82
KY	DS	2.00*	27.80**	97.31**	13.05**	0.92	0.94
KY	NS	57.78*	35.13**	113.27**	15.59*	4.65	0.94
KY	NSF	0.02**	19.95**	32.34**	16.85**	3.52	0.79
TBM	DS	179.24ns	258.36**	802.65**	122.29*	45.91	0.93
TBM	NS	699.38**	231.37**	744.84**	103.01ns	58.06	0.94
HI	DS	35.17*	332.68**	916.14**	217.68**	32.98	0.89
HI	NS	1.38ns	127.17*	352.66**	76.96ns	56.84	0.9

Env., Environments; DS, drought-stressed; NS, non-stressed; NSF, non-stressed at field condition; DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SLA, specific leaf area ($cm^2\ g^{-1}$); PY, pod yield per plant (g); SHP, shelling percentage (%); KY, kernel yield per plant (g); TBM, total biomass yield per plant (g); HI, harvest index (%); ns, non-significant; * significant at 5% level of significance, ** significant at 1% level of significance.

Table 5.4. Mean values for the nine phenotypic traits and chlorophyll meter reading (SCMR) among eight groundnut parents and 28 F_2 families under drought-stressed glasshouse condition.

Entry	DF	PB	PH	SCMR	SLA	POD	SHP	KY	TBM	HI
Parents										
ICGV 06175	33	8	31.5	45.3	231.87	10.7	66.36	7.10	46.00	30.31
ICGV 10373	31	7.5	24.875	47.4	121.18	8.60	53.53	4.60	37.35	29.67
ICGV 15083	33	7.25	33	46.95	181.35	15.70	59.47	9.35	48.05	48.54
ICGV 10178	35	6.25	35.25	48.25	164.36	18.15	61.10	11.06	54.70	49.64
ICGV 98412	32	6.5	33.25	51.75	245.96	9.80	50.98	5.00	35.85	38.13
ICGV 96174	32	6.5	27	44.3	262.88	5.45	65.79	3.60	25.80	29.91
ICGV 11396	34	7.5	25.5	47.85	194.46	10.80	56.95	6.15	45.50	31.33
ICGV 15094	29	8.5	26	47.3	237.34	2.95	42.73	1.30	29.05	10.65
Mean	32.38	7.25	29.55	47.39	204.8	10.27	57.11	6.02	40.29	33.52
Crosses										
ICGV 06175 X ICGV 15094	33	6.75	34	43.55	251.84	12.65	46.31	5.85	46.95	36.93
ICGV 10373 X ICGV 15094	35	8.25	26.25	48.2	181.23	8.40	59.03	4.90	39.90	26.68
ICGV 15083 X ICGV 15094	33	8	32.5	49.7	188.96	6.80	60.29	4.10	57.80	13.33
ICGV 10178 X ICGV 15094	32	9.25	22.75	52.2	177.55	17.35	64.73	11.25	54.95	46.32
ICGV 98412 X ICGV 15094	34	7	28.75	50.8	169.71	13.85	53.85	7.40	41.90	49.31
ICGV 96174 X ICGV 15094	32	6.25	23.75	39.85	245.95	8.15	42.83	3.50	33.35	36.33
ICGV 11396 X ICGV 15094	32	8.25	31.25	46.85	164.68	9.60	51.94	5.10	48.00	24.85
ICGV 06175 X ICGV 11396	33	7.25	28.25	51.3	194.86	11.85	55.94	6.65	38.35	45.40
ICGV 10373 X ICGV 11396	32	8.25	25	49	196.11	8.85	59.33	5.25	37.35	31.51
ICGV 15083 X ICGV 11396	29	9.25	26.25	47.75	159.24	8.15	50.24	4.10	43.45	23.12
ICGV 10178 X ICGV 11396	31	7.25	25.75	48.45	156.86	21.35	65.81	14.05	60.75	54.19
ICGV 98412 X ICGV 11396	33	6.25	25.75	49.3	147.95	10.95	46.54	5.10	42.50	34.70
ICGV 96174 X ICGV 11396	32	6.5	24.25	46.75	215.22	3.50	51.62	1.80	32.00	11.99
ICGV 06175 X ICGV 96174	30	6.25	19.75	45.7	190.91	13.10	50.02	6.55	48.55	37.26
ICGV 10373 X ICGV 96174	32	7.25	24.75	42	166.18	12.40	62.41	7.70	40.10	44.35
ICGV 15083 X ICGV 96174	33	8.25	29.5	42.05	167.51	8.00	61.33	4.90	46.25	22.47
ICGV 10178 X ICGV 96174	34	7.5	24.5	47.65	131.96	20.90	63.99	13.4	62.30	50.91
ICGV 98412 X ICGV 96174	33	8.25	26.5	45.3	195.91	12.10	54.55	6.60	42.45	40.15
ICGV 06175 X ICGV 98412	31	6.5	26	47.2	201.56	11.30	49.19	5.60	43.90	34.17
ICGV 10373 X ICGV 98412	33	7.25	24	53.65	200.16	11.85	63.79	7.55	40.45	41.97
ICGV 15083 X ICGV 98412	30	6	22	49.9	176.9	20.70	43.35	8.95	64.55	47.36
ICGV 10178 X ICGV 98412	33	6.25	33	51.35	180.93	22.65	67.32	15.25	67.10	51.32
ICGV 06175 X ICGV 10178	32	8	29	44.55	132.96	20.20	61.72	12.45	56.90	55.06
ICGV 10373 X ICGV 10178	34	7.75	27.5	51.2	166.68	20.40	61.98	12.60	62.30	48.65
ICGV 15083 X ICGV 10178	32	7	27.25	45.8	145.43	28.65	49.34	14.15	70.05	69.84
ICGV 06175 X ICGV 15083	30	9	33.5	47.4	214.28	17.50	62.61	10.95	55.75	45.80
ICGV 10373 X ICGV 15083	34	7.5	25.5	48.45	146.26	23.40	65.99	15.45	63.45	58.42

Table 5.4. Continued.

Entry	DF	PB	PH	SCMR	SLA	POD	SHP	KY	TBM	HI
ICGV 06175 X ICGV 10373	32	8.5	23.75	45.55	194.41	9.15	62.39	5.70	35.55	35.38
Mean	32.29	7.49	26.82	47.55	180.79	14.06	56.73	8.10	49.18	39.92
Grand mean	32.43	7.43	27	47.51	186.12	13.22	56.81	7.64	47.20	38.49
CV (%)	1.34	18.24	14.23	4.46	18.04	11.62	5.98	12.53	15.18	14.87
LSD (5%)	0.88	2.77	7.98	4.34	68.68	3.14	6.95	1.95	14.66	11.71
F test	**	ns	ns	*	*	**	**	**	**	**

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SLA, specific leaf area ($cm^2\ g^{-1}$); POD, pod yield per plant (g); SHP, shelling percentage (%); KY, kernel yield per plant (g); TBM, total biomass yield per plant (g); HI, harvest index (%), CV (%); percentage of coefficient of variation; LSD, Least significant difference; F, Fisher's, ns, non-significant; * significant at 5% level of significance, ** significant at 1% level of significance.

Table 5.5. Mean values for the nine phenotypic traits and chlorophyll meter reading (SCMR) among eight groundnut parents and 28 F_2 families under non-stressed glasshouse condition.

Entry	DF	PB	PH	SCMR	SLA	POD	SHP	KY	TBM	HI
Parents										
ICGV 06175	33.5	8	30.5	58.1	140.27	14.75	63.67	9.35	44.8	33.44
ICGV 10373	33	6.5	24	53.4	129.57	12.2	59.83	7.45	34.45	35.73
ICGV 15083	34	7.5	28.5	51.7	194	22.9	55.01	12.60	61.20	37.43
ICGV 10178	35	5.75	28	57.75	220.38	25.35	54.07	13.70	61.70	41.07
ICGV 98412	32	6.5	27.25	54.25	224.41	23.75	59.49	14.10	41.00	59.05
ICGV 96174	32	5	29.25	52.15	148.31	14.3	63.60	9.10	54.95	26.03
ICGV 11396	35	7.5	24.75	48.2	124.97	14	43.09	6.05	46.15	30.57
ICGV 15094	30	7	21	50.4	167.15	12.5	52.19	6.55	49.85	25.52
Mean	33.06	6.72	26.66	53.24	168.63	17.47	56.37	9.86	49.26	36.10
Crosses										
ICGV 06175 X ICGV 15094	36	7.25	27.5	53.75	138.47	17.65	59.84	10.75	55.75	31.73
ICGV 10373 X ICGV 15094	35	6.75	23	52	181.7	9.6	47.99	4.60	32.75	30.44
ICGV 15083 X ICGV 15094	33.5	8.25	27	55.2	119.32	19.1	56.81	10.85	55.10	34.68
ICGV 10178 X ICGV 15094	32	7.25	28.75	55.25	151.59	23.5	59.07	13.85	63.10	37.21
ICGV 98412 X ICGV 15094	35	6.25	27	52.4	145.1	16.6	55.93	9.30	56.65	29.52
ICGV 96174 X ICGV 15094	32	6	26.75	50.3	218.98	11.85	57.82	6.90	36.05	41.62
ICGV 11396 X ICGV 15094	33	7.75	31	46.05	128.6	16.8	44.53	7.55	53.75	31.26
ICGV 06175 X ICGV 11396	34.5	7	32	54.1	197.15	17.3	50.87	8.80	53.90	32.10
ICGV 10373 X ICGV 11396	32.5	6.25	25.75	52.25	147.68	16.45	57.37	10.00	40.30	40.31
ICGV 15083 X ICGV 11396	34	9	31.25	53.25	148.54	21.9	66.54	14.60	54.50	40.77
ICGV 10178 X ICGV 11396	32.5	6.75	30.25	54.75	154.71	21.6	58.00	12.50	63.40	34.04
ICGV 98412 X ICGV 11396	33	7	30	55.05	155.35	19.7	60.91	12.00	42.50	46.35

Table 5.5. Continued.

Entry	DF	PB	PH	SCMR	SLA	POD	SHP	KY	TBM	HI
ICGV 96174 X ICGV 11396	33.5	6.25	31	53	168.89	16.9	52.02	8.85	53.90	31.42
ICGV 06175 X ICGV 96174	31	4.75	24.25	51.3	159.67	13.85	59.72	8.35	40.6	34.37
ICGV 10373 X ICGV 96174	34	6	27.25	53.35	189.43	13.25	64.26	8.50	34.65	38.19
ICGV 15083 X ICGV 96174	33	6.25	24.5	52.4	224.3	25.3	64.83	16.40	50.6	50.38
ICGV 10178 X ICGV 96174	35.5	8.25	34	55.8	169.96	25.6	63.88	16.35	61.85	41.39
ICGV 98412 X ICGV 96174	32	6.25	21.75	51.05	158.25	24.05	61.29	14.75	49.6	48.51
ICGV 06175 X ICGV 98412	32.5	7.75	19.5	53.8	183.2	14.6	50.95	7.50	37.15	38.23
ICGV 10373 X ICGV 98412	33	6.75	23.5	48.6	186.47	16.25	62.37	10.40	42.45	36.52
ICGV 15083 X ICGV 98412	32.5	6.75	31.25	55.05	226.28	31.05	64.30	20.00	67.75	45.84
ICGV 10178 X ICGV 98412	34	6.5	29	59.45	207.7	34.2	60.66	20.75	71.3	48.95
ICGV 06175 X ICGV 10178	32	6.5	30.5	54.85	117.56	22.75	56.62	12.85	51.15	44.44
ICGV 10373 X ICGV 10178	35	6.5	26.75	50.7	190.2	18.9	62.66	11.85	50.15	37.69
ICGV 15083 X ICGV 10178	34	6.25	25.75	65.05	163.05	31.05	58.41	18.10	71.15	43.57
ICGV 06175 X ICGV 15083	32.5	6.25	26.75	54.25	91.02	12.1	52.33	6.35	47.35	25.35
ICGV 10373 X ICGV 15083	35	7	24.25	55.8	177.23	9.35	49.14	4.60	33.65	26.42
ICGV 06175 X ICGV 10373	32.5	5.25	27.25	52.75	166.49	9.25	54.84	5.15	42.35	21.84
Mean	33.39	6.74	27.41	53.63	166.67	18.95	57.64	11.16	50.48	37.26
Grand mean	33.31	6.73	27.24	53.54	167.1	18.61	57.35	10.87	50.2	36.99
CV (%)	1.64	18.49	12.16	6.33	16.52	16.87	8.18	20.55	15.72	20.69
LSD (5%)	1.12	2.54	6.77	6.94	56.47	6.42	9.59	4.56	16.15	15.66
F test	**	ns	*	*	*	**	*	**	*	*

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SLA, specific leaf area ($cm^2\ g^{-1}$); POD, pod yield per plant (g); SHP, shelling percentage (%); KY, kernel yield per plant (g); TBM, total biomass yield (g); HI, harvest index (%);CV (%); percentage of coefficient of variation; LSD, Least significant difference; F, Fisher's, ns, non-significant; * significant at 5% level of significance, ** significant at 1% level of significance.

Table 5.6. Mean values for the six phenotypic traits among eight groundnut parents and 28 F_2 families under non-stressed field condition.

Entry	DF	PH	PB	PY	SHP	KY
Parents						
ICGV 06175	35.5	59	7	11.62	46.32	5.288
ICGV 10373	37	54.5	7	8.10	69.18	5.278
ICGV 15083	36	57	9	12.80	55.85	7.14
ICGV 10178	39	67	9	15.00	58.35	8.757
ICGV 98412	34	48.5	6	9.76	49.06	4.802
ICGV 96174	35	57	8	11.00	57.49	6.345
ICGV 11396	39	59	12	4.74	60.37	2.794
ICGV 15094	33	55.5	9.5	9.29	57.00	5.291
Mean	36.06	57.19	8.44	10.29	56.70	5.712
Crosses						
ICGV 06175 X ICGV 15094	40	59	8.5	14.4	44.36	6.39
ICGV 10373 X ICGV 15094	39	55	16.5	10.02	48.66	4.88
ICGV 15083 X ICGV 15094	36	51	11.5	8.78	56.19	4.96
ICGV 10178 X ICGV 15094	36.5	65	9	16.25	57.75	9.39
ICGV 98412 X ICGV 15094	39	59	8	14.68	57.62	8.47
ICGV 96174 X ICGV 15094	34	58.5	12	9.77	46.91	4.52
ICGV 11396 X ICGV 15094	35.5	56.5	10.5	8.27	47.67	3.93
ICGV 06175 X ICGV 11396	36.5	65.5	9.5	11.66	49.51	5.61
ICGV 10373 X ICGV 11396	37	50.5	11.5	5.21	50.80	2.63
ICGV 15083 X ICGV 11396	36	60	7	9.08	46.79	4.28
ICGV 10178 X ICGV 11396	35.5	75	8.5	16.40	52.28	8.58
ICGV 98412 X ICGV 11396	35.5	58	6.5	23.20	60.50	14.04
ICGV 96174 X ICGV 11396	35.5	55.5	8	8.32	54.22	4.58
ICGV 06175 X ICGV 96174	33	60	9.5	10.73	32.15	2.73
ICGV 10373 X ICGV 96174	35.5	58	7.5	15.79	53.05	8.39
ICGV 15083 X ICGV 96174	35.5	58	11.5	20.82	53.81	11.21
ICGV 10178 X ICGV 96174	39.5	65	10.5	10.48	47.13	4.98
ICGV 98412 X ICGV 96174	37	53	11	23.16	57.85	13.35
ICGV 06175 X ICGV 98412	36	55.5	11.5	13.48	45.44	6.06
ICGV 10373 X ICGV 98412	36	53	9.5	17.98	52.20	9.38
ICGV 15083 X ICGV 98412	35	61.5	5.5	23.21	61.70	14.32
ICGV 10178 X ICGV 98412	37	64	9	14.16	44.77	6.27
ICGV 06175 X ICGV 10178	34	65	8.5	14.47	50.01	7.22
ICGV 10373 X ICGV 10178	39	60	7	12.96	55.06	7.11
ICGV 15083 X ICGV 10178	35.5	51	7	18.80	60.30	11.35
ICGV 06175 X ICGV 15083	36	51	9	7.54	41.50	3.17
ICGV 10373 X ICGV 15083	39	50.5	8.5	6.48	53.93	3.38
ICGV 06175 X ICGV 10373	36	55.5	10.5	8.66	48.90	3.96
Means	36.42	58.20	9.39	13.38	51.11	6.97
Mean	36.34	57.97	9.18	12.69	52.39	6.69
CV (%)	1.69	11.49	21.03	30.35	12.39	27.74
LSD (5%)	1.25	13.62	3.95	7.88	2.04	3.79
F test	**	ns	*	*	*	**

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); PY, pod yield per plant (g); SHP, shelling percentage (%); KY, kernel yield per plant (g); ; CV (%); percentage of coefficient of variation; LSD, Least significant difference; F, Fisher's, ns, non-significant; * significant at 5% level of significance, ** significant at 1% level of significance.

5.3.3. General combining ability effect of groundnut parents

The parental line ICGV 06175 exhibited significant negative GCA effect for DF under DS condition in the glasshouse and NS field conditions in a desirable direction (Table 5.7). ICGV 10373 exhibited significant ($p \leq 0.05$) positive GCA effect for SHP and negative GCA for SLA under DS condition. ICGV 15083 exhibited significant negative GCA effect for DF under DS condition and positive GCA effects for PY, KY and TBM under both DS and NS conditions in the glasshouse. ICGV 10178 showed significant positive GCA effects for PY and KY in all environments and, positive GCA effect for SCMR and negative GCA effect for SLA under DS condition. In addition, ICGV 10178 exhibited significant positive GCA effect for DF under DS condition in the glasshouse and NS field condition. ICGV 98412 exhibited significant negative GCA effect for DF and positive GCA effects for PY and KY under NS condition in the glasshouse and NS field condition. In addition, ICGV 98412 exhibited significant positive GCA effects for HI under both DS and NS conditions in the glasshouse. ICGV 96174 showed significant negative GCA effect for DF and positive GCA effect for SHP under DS condition in the glasshouse. ICGV 15095 exhibited significant negative GCA effect for DF under DS and NS conditions in the glasshouse. Due to desirable GCA effects for PY, KY and HI the parental line, s ICGV 10178, ICGV 15083 and ICGV 98412, were selected for future groundnut breeding programs.

Table 5.7. General combining ability effects for the nine phenotypic traits and chlorophyll meter reading (SCMR) of eight parental genotypes of groundnut evaluated in the glasshouse (drought-stressed and non-stressed conditions) and non-stressed field conditions.

Traits	Env.	Parents							
		ICGV 06175	ICGV 10373	ICGV 15083	ICGV 10178	ICGV 98412	ICGV 96174	ICGV 11396	ICGV 15094
DF	DS	-0.39*	0.41*	-0.44*	0.71ns	0.11ns	-0.14ns	0.01ns	-0.29*
DF	NS	-0.19ns	0.31*	0.26ns	0.51*	-0.39*	-0.49*	0.31*	-0.34*
DF	NSF	-0.46*	0.84**	-0.21ns	0.79**	-0.36*	-0.71*	0.24ns	-0.11ns
PB	DS	0.13ns	0.28ns	0.26ns	-0.14ns	-0.64ns	-0.37ns	0.10ns	0.38ns
PB	NS	0.01ns	-0.31ns	0.41ns	-0.11ns	-0.04ns	-0.69ns	0.44ns	0.29ns
PB	NSF	-0.16ns	0.24ns	-0.46ns	-0.51ns	-0.96*	0.34ns	0.29ns	1.24*
PH	DS	1.04ns	-2.03**	1.57ns	1.34ns	0.57ns	-1.98*	-0.93ns	0.44ns
PH	NS	0.36ns	-1.94*	0.26ns	1.58ns	-0.87ns	0.28ns	1.56ns	-1.22ns
PH	NSF	0.78ns	-3.03ns	-2.48ns	5.73*	-2.08ns	0.03ns	1.73ns	-0.65ns
SCMR	DS	0.91ns	-0.96ns	1.25ns	2.95*	0.20ns	-1.04ns	-1.70*	-1.61ns
SCMR	NS	-1.18*	0.52ns	-0.27ns	1.01ns	2.34*	-2.97**	0.75ns	-0.19ns
SLA	DS	11.21ns	-34.04*	-7.20ns	-4.01ns	3.46ns	17.77*	-5.13ns	17.95*
SLA	NS	-17.0*	-19.3	12.3ns	13.5*	11.0ns	8.2ns	-9.9ns	1.2ns
POD	DS	-0.18ns	-0.73ns	2.56**	6.88**	0.4ns	-2.99**	-2.31**	-3.63**
POD	NS	-3.06*	-5.01**	2.81*	6.07**	3.64*	-0.82ns	-0.89ns	-2.75*
POD	NSF	-1.01ns	-2.10*	0.60ns	1.92*	3.51*	0.68ns	-2.26*	-1.35ns
SHP	DS	0.96ns	3.06*	0.08ns	4.58**	-3.08*	0.7ns	-1.6ns	-37.52
SHP	NS	-0.37ns	0.21ns	0.61ns	1.12ns	1.92ns	3.48*	-3.98*	-2.99*
SHP	NSF	-6.67*	2.98ns	1.47ns	1.28ns	0.70ns	-1.11ns	1.14ns	0.2ns
KY	DS	-0.08ns	-0.04ns	1.25**	4.65**	-0.23ns	-1.71**	-1.44**	-2.41**
KY	NS	-1.94*	-2.78*	1.83*	3.58**	2.51*	0.05ns	-1.14*	-2.09*
KY	NSF	-1.45*	-0.99*	0.67ns	1.22*	2.13*	0.22ns	-1.10*	-0.71ns
TBM	DS	-0.69ns	-3.1ns	7.26*	11.90**	-1.03ns	-6.82*	-3.14ns	-4.39*
TBM	NS	-3.40ns	-10.67*	5.06*	10.36**	-0.25ns	-1.47ns	0.27ns	0.10ns
HI	DS	0.41ns	-0.02ns	3.09*	12.91**	2.88*	-4.32*	-5.81*	-9.14**
HI	NS	-3.81*	-3.01ns	0.89ns	3.64ns	7.90*	0.49ns	-1.56ns	-4.55*

Env., environments; DS, drought-stressed; NS, non-stressed; NSF, non-stressed at field condition; DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SLA, specific leaf area ($cm^2\ g^{-1}$); Pod, pod yield per plant (g); SHP, shelling percentage (%); KY, kernel yield per plant (g); TBM, total biomass yield per plant(g); HI, harvest index (%); GCA values of parents in a row followed by ns are non-significant; * significant at 5% level of significance, ** significant at 1% level of significance.

5.3.4. Specific combining ability effect of crosses

During the glasshouse study under DS condition, higher and significantly negative SCA effects in a desirable direction were detected for DF by the families, ICGV 15083 x ICGV 11396 (-3.01), ICGV 10178 x ICGV 11396 (-1.66) and ICGV 06175 x ICGV 15083 (-1.61) (Table 5.8). Under NS condition in the glasshouse, ICGV 10178 x ICGV 96174 (4.89) and ICGV 15083 x ICGV 98412 (4.62) exhibited significant positive SCA effects for PH which is desirable for breeding groundnut genotypes for increased plant height (Table 5.9). Crosses ICGV 10373 x ICGV 15094 and ICGV 06175 x ICGV 98412 showed significantly positive SCA effects for PB under field condition at 5.84 and 3.44, in that order (Table 5.10). These are desirable families for enhanced biomass yield in groundnut.

Families, ICGV 06175 x ICGV 11396 (4.22), ICGV 10178 x ICGV 15094(3.87) and ICGV 10373 x ICGV 98412 (3.28), displayed significant positive SCA effect for SCMR under DS condition which is

desirable for breeding groundnut genotypes with enhanced photosynthetic capacity and productivity in drought stress environments. Under NS condition in glasshouse, ICGV 15083 x ICGV 98412 exhibited significant positive SCA effect (7.31 $cm^2 g^{-1}$) for SCMR. Under DS condition, significant negative SCA effect for SLA was recorded for ICGV 06175 x ICGV 96174 (-54.54 $cm^2 g^{-1}$), whereas significant positive SCA for SLA were recorded for ICGV 15083 x ICGV 96174 (68.26 $cm^2 g^{-1}$), ICGV 15083 x ICGV 98412 (44.45 $cm^2 g^{-1}$), ICGV 96174 x ICGV 15094 (42.48 $cm^2 g^{-1}$) and ICGV 10178 x ICGV 98412 (39.57 $cm^2 g^{-1}$) under NS condition in the glasshouse. Families with significant and negative SCA effects for SLA under DS condition and positive SCA effects for the same trait under NS condition are ideal candidates for breeding groundnut genotypes with enhanced water use efficiency and photosynthetic capacity in that order.

Under DS condition, crosses ICGV 10373 x ICGV 15083 (8.35 g $plant^{-1}$), ICGV 15083 x ICGV 10178 (5.99 g $plant^{-1}$), ICGV 15083 x ICGV 98412 (4.52 g $plant^{-1}$), ICGV 98412 x ICGV 15094 (3.86 g $plant^{-1}$), CGV 10178 x ICGV 96174 (3.79 g $plant^{-1}$) and ICGV 10178 x ICGV 11396 (3.56g $plant^{-1}$), exhibited significant positive SCA effects for PY. Under NS condition in glasshouse, crosses ICGV 15083 x ICGV 98412 (5.98 g $plant^{-1}$), ICGV 10178 x 98412 (5.87 g $plant^{-1}$), ICGV 06175 x ICGV 15094 (4.83 g $plant^{-1}$) and ICGV 15083 x ICGV 96174 (4.69 g $plant^{-1}$), displayed significant positive SCA effects for PY. Under field condition, crosses, ICGV 98412 x ICGV 11396 (9.26 g $plant^{-1}$), ICGV 15083 x ICGV 96174 (6.84 g $plant^{-1}$), ICGV 98412 x ICGV 96174 (6.27 g $plant^{-1}$) and ICGV 15083 x ICGV 98412 (6.40 g $plant^{-1}$), displayed significant positive SCA effects for PY. Hence the above selected families are ideal candidates to develop groundnut lines with enhanced pod yield.

Under DS condition, desirable and significant positive SCA effects for SHP were recorded for ICGV 10178 x ICGV 98412 (9.01%), ICGV 15083 x ICGV 15094 (8.08%), ICGV 10178 x ICGV 15094 (8.03%) ICGV x ICGV 98412 (6.99%) and ICGV 10373 x ICGV 15083 (6.04%). Under NS condition in the glasshouse, ICGV 15083 x ICGV 11396 and ICGV 06175 x ICGV 15094 exhibited significant positive SCA effects for SHP at 12.54% and 5.84%, in that order. Under DS condition, crosses such as ICGV 10373 x ICGV 10178, ICGV 10178 x ICGV 15094, ICGV 10178 x ICGV 96174, ICGV 10178 x ICGV 11396 and ICGV 06175 x ICGV 10178 exhibited significant positive SCA effects for KY with values of 6.60, 3.30, 3.19, 2.82 and 2.14 g $plant^{-1}$, respectively. Under NS condition in the glasshouse, ICGV 15083 x ICGV 98412, ICGV 06175 x ICGV 15094, ICGV 10178 x ICGV 98412, ICGV 15083 x ICGV 96174 and ICGV 10373 x ICGV 11396 exhibited significant positive SCA effects for KY with values of 4.8, 3.91, 3.79, 3.66 and 3.06 g $plant^{-1}$, respectively. Under field condition families ICGV 98412 x ICGV 11396, ICGV 15083 x ICGV 98412, ICGV 98412 x ICGV 96174, ICGV 15083 x ICGV 96174 and ICGV 15083 x ICGV 10178 expressed significant positive SCA effects for KY at 6.32, 4.83, 4.31, 3.63 and 2.76 g $plant^{-1}$, in that order. This suggests that the aforementioned selected families can be used to improve groundnut yield under drought-stressed and non-stressed environments.

Crosses ICGV 10373 x ICGV 10178, ICGV 15083 x ICGV 96174 and ICGV 10178 x ICGV 11396 exhibited significant positive SCA effects for TBM at 12.09, 11.12 and 10.03 g plant^{-1}, respectively under DS condition. Whereas ICGV 15083 x ICGV 98412 (12.73 g plant^{-1}) and ICGV 10178 x ICGV 98412 (10.98 g plant^{-1}) displayed significant positive SCA effects for TBM under NS condition in the glasshouse. Under DS condition, ICGV 98412 x ICGV 15094 (17.08%), ICGV 10373 x ICGV 15083 (16.85%), ICGV 15083 x ICGV 10178 (15.33%), ICGV 06175 x ICGV 11396 (12.29%), ICGV 96174 x ICGV 15094 (11.29) and ICGV 10373 x ICGV 96174 (10.19%) exhibited significant positive SCA effects for HI in a desirable direction. Significant positive SCA effect for HI was recorded for ICGV 15083 x ICGV 96174 (12.00%) under NS condition in the glasshouse. Therefore, the selected crosses such as ICGV 10373 x ICGV 10178, ICGV 15083 x ICGV 96174 and ICGV 10178 x ICGV 11396 are ideal candidates to improve biomass production and ICGV 98412 x ICGV 15094, ICGV 10373 x ICGV 15083, ICGV 15083 x ICGV 10178, ICGV 06175 x ICGV 11396, ICGV 96174 x ICGV 15094 and ICGV 10373 x ICGV 96174 to enhance harvest index and yield gains in groundnut under drought stress environments.

Table 5.8. Specific combining ability effects for the nine phenotypic traits and chlorophyll meter reading (SCMR) of 28F_2 groundnut families under drought-stressed condition in the glasshouse.

	Traits									
Crosses	DF	PB	PH	SCMR	SLA	PY	SHP	KY	TBM	HI
ICGV 06175 X ICGV 15094	1.24**	-1.20ns	5.09ns	-2.60ns	2.65ns	3.24*	-6.77*	0.53ns	-5.03ns	7.16ns
ICGV 10373 X ICGV 15094	2.44**	0.15ns	0.42ns	0.35ns	19.12ns	-0.46ns	3.84ns	-0.91ns	-3.61ns	-2.66ns
ICGV 15083 X ICGV 15094	1.29**	-0.08ns	3.07ns	2.64ns	-14.55ns	-5.35**	8.09*	-3.35**	-7.87ns	-152.96
ICGV 10178 X ICGV 15094	-0.86*	1.58ns	-6.46*	3.87*	9.91ns	0.88ns	8.03*	3.20**	4.79ns	4.06ns
ICGV 98412 X ICGV 15094	1.74**	-0.18ns	0.32ns	1.14ns	-36.51ns	3.86*	4.80*	-0.87ns	-0.54ns	17.08**
ICGV 96174 X ICGV 15094	-0.01ns	-1.2	-2.13ns	-4.50*	16.45ns	1.55ns	-10.00**	-2.69**	-5.24ns	11.29*
ICGV 11396 X ICGV 15094	-0.16ns	0.33	4.32ns	-1.22ns	18.60ns	2.32*	1.42ns	1.39*	4.58ns	1.30ns
ICGV 06175 X ICGV 11396	1.44**	-0.43ns	0.72ns	4.22*	-24.20ns	1.13ns	-0.23ns	0.70ns	8.86ns	12.29*
ICGV 10373 X ICGV 11396	-0.86*	0.43ns	0.54ns	0.22ns	-33.71ns	-1.32ns	1.05ns	1.81*	2.82ns	-1.16ns
ICGV 15083 X ICGV 11396	-3.01**	1.45ns	-1.81ns	-0.24ns	-29.19ns	-5.32**	-5.05*	-2.28*	-1.39ns	-12.66*
ICGV 10178 X ICGV 11396	-1.66**	-0.15ns	-2.08ns	-0.82ns	-24.43ns	3.56*	6.02*	2.82**	10.03*	8.59*
ICGV 98412 X ICGV 11396	0.44ns	-0.65ns	-1.31ns	-1.30ns	-11.44ns	-0.36ns	-5.60*	0.90ns	3.09ns	-0.86ns
ICGV 96174 X ICGV 11396	-0.31ns	-0.68ns	-0.26ns	1.46ns	41.21*	-35.28	-4.29ns	-0.62ns	-7.76*	-16.38**
ICGV 06175 X ICGV 96174	-1.91ns	-0.95ns	-6.73*	2.34ns	-54.54*	3.06*	-8.45*	-1.73*	-1.59ns	2.67ns
ICGV 10373 X ICGV 96174	-0.71*	-0.10ns	1.34ns	-3.06*	14.58ns	2.91*	1.83ns	0.18ns	-2.62ns	10.19*
ICGV 15083 X ICGV 96174	1.14**	0.93ns	2.49ns	-2.22ns	-5.48ns	-4.79**	3.74ns	0.29ns	11.12*	-14.80**
ICGV 10178 X ICGV 96174	0.99*	0.58ns	-2.28ns	2.10ns	9.63ns	3.79*	1.91ns	3.19**	9.03*	3.82ns
ICGV 98412 X ICGV 96174	1.09**	1.83*	0.49ns	-1.58ns	52.91*	1.47ns	0.11ns	-2.18**	-9.30*	3.10ns
ICGV 06175 X ICGV 98412	-0.66*	-0.43ns	-3.03ns	-1.47ns	-13.75ns	-2.14*	-5.50*	0.24ns	-1.51ns	-7.61*
ICGV 10373 X ICGV 98412	0.04ns	0.18ns	-1.96ns	3.28*	18.61ns	-1.04ns	6.99*	0.35ns	6.31ns	0.61ns
ICGV 15083 X ICGV 98412	-2.11**	-1.05ns	-7.56*	0.32ns	-12.92ns	4.52**	-10.46**	0.60ns	3.69ns	2.89ns
ICGV 10178 X ICGV 98412	-0.26ns	-0.40ns	3.67ns	0.49ns	3.14ns	2.15*	9.01**	-5.88**	-16.29**	-2.96ns
ICGV 06175 X ICGV 10178	-0.76*	0.58ns	-0.81ns	-2.79*	24.15ns	0.28ns	-0.62ns	2.14*	1.98ns	3.24ns
ICGV 10373 X ICGV 10178	0.94*	0.18ns	0.77ns	2.16ns	26.65ns	1.03ns	-2.47ns	6.60**	12.09*	-2.73ns
ICGV 15083 X ICGV 10178	-0.71*	-0.55ns	-3.08ns	-2.45ns	25.39ns	5.99**	-12.13**	-0.80ns	-13.67*	15.33**
ICGV 06175 X ICGV 15083	-1.61**	1.18ns	3.47ns	1.33ns	1.08ns	1.90ns	4.77*	-1.82*	-7.87ns	3.79ns
ICGV 10373 X ICGV 15083	2.09**	-0.48ns	-1.46ns	0.68ns	-30.34ns	8.35**	6.04*	-2.96**	-3.65ns	16.85*
ICGV 06175 X ICGV 10373	-0.46ns	0.65ns	-2.68ns	-1.31ns	22.32ns	-3.15*	1.55ns	-0.38ns	0.17ns	-3.51ns

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SCMR, chlorophyll meter reading; SLA, specific leaf area ($cm^2\ g^{-1}$); PY, pod yield per plant (g); SHP, shelling percentage (%); KY = kernel yield per plant (g); TBM, total biomass yield per plant (g); HI, harvest index (%); SCA values of traits in a column followed by ns are ns, non-significant; * significant at p ≤0.05% and ** significant at p ≤0.01 among crosses..

Table 5.9. Specific combining ability effects for the nine phenotypic traits and chlorophyll meter reading (SCMR) of 28F_2 groundnut families under non-stressed glasshouse condition.

	Traits									
Crosses	DF	PB	PH	SCMR	SLA	POD	SHP	KY	TBM	HI
ICGV 06175 X ICGV 15094	3.21**	0.21ns	1.12ns	1.35ns	-12.83ns	4.83*	5.84*	3.91*	8.85ns	3.09ns
ICGV 10373 X ICGV 15094	1.71**	0.04ns	-1.08ns	1.37ns	1.09ns	-1.26ns	-6.59*	-1.39ns	-6.89ns	1.00ns
ICGV 15083 X ICGV 15094	0.26ns	0.81ns	0.72ns	0.16ns	-29.69ns	0.42ns	1.82ns	0.25ns	-0.27ns	1.34ns
ICGV 10178 X ICGV 15094	-1.49**	0.34ns	1.14ns	-0.04ns	-6.77ns	1.55ns	3.58ns	1.49ns	2.43ns	1.11ns
ICGV 98412 X ICGV 15094	2.41**	-0.74ns	1.84ns	3.01ns	-34.13ns	-2.91ns	-0.36ns	-1.98ns	6.59ns	-10.83*
ICGV 96174 X ICGV 15094	-0.49ns	-0.34ns	0.44ns	2.20ns	42.48*	-3.21ns	-0.03ns	-1.92ns	-12.78*	8.68ns
ICGV 11396 X ICGV 15094	-0.29ns	0.29ns	3.42ns	-1.94ns	-30.18ns	1.82ns	-5.86*	-0.08ns	3.18ns	0.36ns
ICGV 06175 X ICGV 11396	1.06*	-0.19ns	2.84ns	-2.12ns	33.49ns	2.63ns	-2.14ns	1.01ns	6.83ns	0.46ns
ICGV 10373 X ICGV 11396	-1.44**	-0.61ns	-1.11ns	1.81ns	-45.28*	3.73ns	3.79ns	3.06*	0.49ns	7.89ns
ICGV 15083 X ICGV 11396	0.11ns	1.41ns	2.19ns	-1.36ns	-12.83ns	1.36ns	12.54**	3.05*	-1.04ns	4.44ns
ICGV 10178 X ICGV 11396	-1.64**	-0.31ns	-0.13ns	0.35ns	-16.01ns	-2.20ns	3.50ns	-0.81ns	2.56ns	-5.04ns
ICGV 98412 X ICGV 11396	-0.24ns	-0.14ns	2.07ns	-1.66ns	-36.25*	-1.67ns	5.62ns	-0.23ns	-7.73ns	3.01ns
ICGV 96174 X ICGV 11396	0.36ns	-0.24ns	1.92ns	0.68ns	-19.97ns	-0.01ns	-4.84ns	-0.92ns	4.90ns	-4.51ns
ICGV 06175 X ICGV 96174	-1.64**	-1.31ns	-3.63ns	-0.86ns	1.33ns	-0.90ns	-0.75ns	-0.63ns	-4.73ns	0.68ns
ICGV 10373 X ICGV 96174	0.86*	0.26ns	1.67ns	-4.18ns	1.78ns	0.46ns	3.21ns	0.37ns	-3.42ns	3.71ns
ICGV 15083 X ICGV 96174	-0.09ns	-0.21ns	-3.28ns	0.05ns	68.26*	4.69*	3.37ns	3.66*	-3.20ns	12.00*
ICGV 10178 X ICGV 96174	2.16**	2.31*	4.89*	2.76ns	4.57ns	1.72ns	1.93ns	1.85ns	2.75ns	0.25ns
ICGV 98412 X ICGV 96174	-0.44ns	0.24ns	-4.91*	0.30ns	-28.02ns	2.61ns	-1.46ns	1.33ns	1.11ns	3.12ns
ICGV 06175 X ICGV 98412	-0.24ns	1.04ns	-7.23*	-2.55ns	22.13ns	-4.60*	-7.95*	-3.94*	-9.41ns	-2.86ns
ICGV 10373 X ICGV 98412	-0.24ns	0.36ns	-0.93ns	-4.83*	-3.91ns	-1.00ns	2.89ns	-0.19ns	3.16ns	-5.37ns
ICGV 15083 X ICGV 98412	-0.69ns	-0.36ns	4.62*	7.31*	44.45*	5.98*	4.41ns	4.80*	12.73*	0.05ns
ICGV 10178 X ICGV 98412	0.56ns	-0.09ns	1.04ns	-1.69ns	39.57*	5.87*	0.27ns	3.79*	10.98*	0.40ns
ICGV 06175 X ICGV 10178	-1.64**	-0.14ns	1.32ns	-1.46ns	-22.63ns	1.11ns	-1.49ns	0.34ns	-6.02ns	7.60ns
ICGV 10373 X ICGV 10178	0.86*	0.19ns	-0.13ns	1.97ns	20.70ns	-0.78ns	3.97ns	0.18ns	0.25ns	0.06ns
ICGV 15083 X ICGV 10178	-0.09ns	-0.79ns	-3.33ns	-4.35*	25.15ns	3.55ns	-0.69ns	1.82ns	5.52ns	2.04ns
ICGV 06175 X ICGV 15083	-0.89*	-0.91ns	-1.11ns	-0.74ns	-39.82*	-6.27*	-5.27ns	-4.41*	-4.52ns	-8.73ns
ICGV 10373 X ICGV 15083	1.11*	0.16ns	-1.31ns	1.78ns	17.08ns	-7.07*	-9.04*	-5.31*	-10.95*	-8.45ns
ICGV 06175 X ICGV 10373	-0.94*	-1.19ns	1.59ns	2.73ns	4.05ns	-1.30ns	-2.35ns	-1.00ns	6.21ns	-8.34ns

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); SCMR, chlorophyll meter reading; SLA, specific leaf area ($cm^2\ g^{-1}$); POD, pod yield per plant (g); SHP, shelling percentage (%); KY = kernel yield per plant (g); TBM, total biomass yield per plant (g); HI, harvest index (%); SCA values of traits in a column followed by ns are ns, non-significant; * significant at p $\leq$0.05% and ** significant at p $\leq$0.01 among crosses.

Table 5.10. Specific combining ability effects for the six phenotypic traits of 28F_2 groundnut families under non-stressed field condition.

	Traits					
Crosses	DF	PB	PH	POD	SHP	KY
ICGV 06175 X ICGV 15094	4.23**	-1.76ns	0.93ns	4.07ns	-1.53ns	1.86ns
ICGV 10373 X ICGV 15094	1.93**	5.84**	0.73ns	0.77ns	-6.87ns	-0.11ns
ICGV 15083 X ICGV 15094	-0.02ns	1.54ns	-3.82ns	-3.17ns	2.16ns	-1.70ns
ICGV 10178 X ICGV 15094	-0.52ns	-0.91ns	1.98ns	2.98ns	3.92ns	2.19ns
ICGV 98412 X ICGV 15094	3.13**	-1.46ns	3.78ns	-0.17ns	4.37ns	0.36ns
ICGV 96174 X ICGV 15094	-1.52*	1.24ns	1.18ns	-2.25ns	-4.54ns	-1.68ns
ICGV 11396 X ICGV 15094	-0.97*	-0.21ns	-2.52ns	-0.81ns	-6.01ns	-0.96ns
ICGV 06175 X ICGV 11396	0.38ns	0.19ns	5.03ns	2.24ns	2.69ns	1.47ns
ICGV 10373 X ICGV 11396	-0.42ns	1.79ns	-6.17ns	-3.12ns	-5.66ns	-1.97ns
ICGV 15083 X ICGV 11396	-0.37ns	-2.01ns	2.78ns	-1.96ns	-8.17ns	-1.98ns
ICGV 10178 X ICGV 11396	-1.87**	-0.46ns	9.58ns	4.04ns	-2.49ns	1.76ns
ICGV 98412 X ICGV 11396	-0.72ns	-2.01ns	0.38ns	9.26*	6.31ns	6.32**
ICGV 96174 X ICGV 11396	-0.37ns	-1.81ns	-4.22ns	-2.79ns	1.84ns	-1.24ns
ICGV 06175 X ICGV 96174	-2.17**	0.14ns	1.23ns	-1.64ns	-12.43*	-2.73*
ICGV 10373 X ICGV 96174	-0.97*	-2.26ns	3.03ns	4.51ns	-1.17ns	2.46*
ICGV 15083 X ICGV 96174	0.08ns	2.44ns	2.48ns	6.84*	1.09ns	3.63*
ICGV 10178 X ICGV 96174	3.08**	1.49ns	1.28ns	-4.82ns	-5.40ns	-3.15*
ICGV 98412 X ICGV 96174	1.73**	2.44ns	-2.92ns	6.27*	5.90ns	4.31*
ICGV 06175 X ICGV 98412	0.48ns	3.44*	-1.17ns	-1.72ns	-0.95ns	-1.31ns
ICGV 10373 X ICGV 98412	-0.82*	1.04ns	0.13ns	3.87ns	-3.84ns	1.56ns
ICGV 15083 X ICGV 98412	-0.77ns	-2.26ns	8.08ns	6.40*	7.17ns	4.82**
ICGV 10178 X ICGV 98412	0.23ns	1.29ns	2.38ns	-3.98ns	-9.57*	-3.77*
ICGV 06175 X ICGV 10178	-2.67**	-0.01ns	0.53ns	0.86ns	3.04ns	0.75ns
ICGV 10373 X ICGV 10178	1.03*	-1.91ns	-0.67ns	0.43ns	-1.55ns	0.19ns
ICGV 15083 X ICGV 10178	-1.42*	-1.21ns	-10.22*	3.57ns	5.19ns	2.76*
ICGV 06175 X ICGV 15083	0.33ns	0.44ns	-5.27ns	-4.75ns	-5.66ns	-2.74*
ICGV 10373 X ICGV 15083	2.03**	-0.46ns	-1.97ns	-4.73ns	-2.88ns	-2.99*
ICGV 06175 X ICGV 10373	-0.72ns	1.24ns	-0.22ns	-0.93ns	0.23ns	-0.29ns

DF, days to 50% flowering; PB, number of primary branches per plant; PH, plant height (cm); POD, pod yield per plant (g); SHP, shelling percentage (%); KY = kernel yield per plant (g); SCA values of traits in a column followed by ns are ns, non-significant; * significant at p $\leq$0.05% and ** significant at p $\leq$0.01 among crosses.

5.4. Discussion

5.4.1. Analysis of variance

Development of promising groundnut genotypes with high yield potential and drought tolerance would enhance production and productivity of the crop under dry-land conditions. The analysis of variance (Table 5.3) revealed significant differences among test parents and crosses for most of the assessed traits across all test environments. This indicates that parents and the new crosses exhibited considerable variability for most of the studied traits. Similar trends were reported in previous findings (Zongo et al. 2017; Chavadhari et al. 2017).

5.4.2. Mean responses of parents and crosses for agronomic parameters

In the present study, the mean PH for the test genotypes under DS was shorter than under NS condition in glasshouse and field conditions (Tables 5.5 and 5.6). These results agree with the findings of Arruda et al. (2015) who pointed out that 34% of PH reduction in groundnut is due to mid-season moisture stress.The highest mean PH were recorded for the parent ICGV 06175 (30.5 cm) and crosses ICGV 10178 x ICGV 96174 (34.00 cm), ICGV 06175 x ICGV 11396 (32.00 cm), ICGV 15083 x ICGV 11396 (31.25 cm) and ICGV 15083 x ICGV 98412 (31.25 cm) under NS glasshouse condition (Table 5.5). In groundnut, strong positive associations between HI and POD under optimum environments were reported by Zongo et al. (2017) and Kamdar et al. (2020). Taller plants have better radiation interception and TBM productivity than shorter plants (Mathew et al. 2019). Groundnut genotypes with the capability to maintain high chlorophyll content and biomass yield under drought-stressed condition could show better tolerance to drought (Oppong-Sekyere et al. 2019; Songsri et al. 2008). The mean values of TBM for crosses were higher than their parents under both DS and NS conditions in the glasshouse (Tables 5.4 and 5.5). Under DS condition, the highest TBM was recorded for the parents, ICGV 10178 (54.70 g plant^{-1}) and ICGV 15083 (48.05 g plant^{-1}) and, crosses, ICGV 15083 x ICGV 10178 (70.05 g plant^{-1}), ICGV 10178 x ICGV 98412 (67.10 g plant^{-1}) and ICGV 15083 x ICGV 98412(64.55 g plant^{-1}). These genotypes can be used in groundnut breeding programs to enhance biomass production under stress environments such as in Ethiopia. Under NS condition in the glasshouse, the highest TBM was recorded for the parents ICGV 10178 (61.70 g plant^{-1}), ICGV 15083 (61.20 g plant^{-1}) and crosses ICGV 10178 x ICGV 98412 (71.3 g plant^{-1}), ICGV 15083 x ICGV 10178 (71.15 g plant^{-1}) and ICGV 15083 x ICGV 98412 (67.75 g plant^{-1}). Genotypes with higher TBM were recommended for production under intermittent drought in groundnut (Ratnakumar et al. 2009). Higher TBM production under drought-stressed conditions associates with the root system of the genotypes

to mobilize water from the soil for stem elongation and biomass accumulation. This refers to transpiration efficiency of the genotypes.

The highest pod yields were recorded for crosses ICGV 15083 x ICGV 10178, ICGV 10373 x ICGV 15083, ICGV 10178 x ICGV 98412 and ICGV 10178 x ICGV 11396 under DS and ICGV 10178 x ICGV 98412, ICGV 15083 x ICGV 10178 and ICGV 15083 x ICGV 98412. This suggests that ICGV 10178 was the best parent for increasing POD under both moisture conditions. Identification of genotypes with high and stable yield performance under drought-stressed and non-stressed environments is pertinent to ensure production and productivity of groundnut (Shrief et al. 2020).

Drought stress during flowering and grain filling stage can drastically cause POD reduction in groundnut. This is associated with a reduction in SHP, as expressed by the decrease in weight ratio of the seeds and the pods (Ratnakumar and Vadez, 2011). This suggests that selection of genotypes with high SHP and/ or seed yield could help to sustain groundnut production in drought stress and non-stressed environments. The following crosses were selected with high SHP: ICGV 10178 x ICGV 98412, ICGV 10373 x 15083 and ICGV 178 x ICGV 11396 under DS condition in the glasshouse and, ICGV 15083 x ICGV 96174, ICGV 10373 x ICGV 96174 and ICGV 15083 x ICGV 98412 under NS condition in the glasshouse and crosses ICGV 15083 x ICGV 98412, ICGV 98412 x ICGV 11396 and ICGV 15083 x ICGV 10178, under field conditions. Sanogo et al. (2020) reported the importance of additive genetic effect on SHP in groundnut. Thus, the selected crosses could offset groundnut yield reduction which occurs due to the SHP reduction.

HI is a proportion of total biomass partitioned into grain (Suriharn et al 2005). Strong and positive associations between HI and POD in groundnut have been reported in previous findings (Sanogo et al. 2019; Oppong-Sekyere et al. 2019). HI is a useful trait to improve pod yield in groundnut. The present study identified the following crosses with high HI values: ICGV 15083 x ICGV 10178, ICGV 10373 x ICGV 15083 and ICGV 10178 x ICGV 11396 under DS condition in the glasshouse and, ICGV 15083 x ICGV 96174, ICGV 10178 x ICGV 98412, ICGV 98412 x ICGV 96174 and ICGV 98412 x ICGV 96174 under NS condition in the glasshouse. The above selected crosses with enhanced harvest index under both drought-stressed and non-stressed environments are suitable candidates for future variety development and release.

5.4.3. Mean responses of parents and crosses for physiological parameters

SCMR is used to measure leaf chlorophyll concentration. It is a useful trait to identify drought tolerant genotypes in groundnut (Sheshshayee et al. 2006). Under DS condition, the SCMR readings varied from 44.3 for parent ICGV 96174 to 51.75 for parent ICGV 15083 (Table 5.4).

Among the assessed crosses, the SCMR values ranged from 42 for ICGV 10373 x ICGV 96174 to 53.65 for ICGV 10373 x ICGV 98412 (Table 5.4). Under NS glasshouse condition, SCMR values varied from 50.4 for the parent ICGV 15094 to 57.75 for parent ICGV 10178 and from 48.6 for the parent ICGV 10373 x ICGV 98412 to 65 for ICGV 15083 X ICGV 10178 (Table 5.5). Regarding the SCMR values, a wider range was recoded for crosses than their parents under both DS and NS conditions in the glasshouse (Tables 5.4 and 5.5). This presents an opportunity to select genotypes with higher chlorophyll content which would enable to maintain high photosynthetic capacity and productivity under drought stress environments.

Groundnut genotypes that maintain higher SCMR and lower SLA values under drought stress should be more tolerant to drought, and hence maintain higher WUE under severe drought conditions (Songsri et al. 2009). Reduced SLA is facilitated by increasing leaf thickness, which results in thicker cell wall to prevent water loss by evaporation and to achieve higher water use efficiency .(Zhou et al. 2020). Under DS condition, low SLA was recorded for the parents ICGV 10373 and ICGV 10178, and crosses ICGV 10178 x ICGV 96174 and ICGV 06175 x ICGV 10178 at 121.18, 164.36, 131.96 and 132.96 cm^2 g^{-1}, respectively. Under NS glasshouse condition, the highest SLA values were recorded for the parent ICGV 98412 (224.41 cm^2 g^{-1}) and crosses ICGV 15083 x ICGV 98412 (226.28 cm^2 g^{-1}) and ICGV 15083 x ICGV 96174 (224.30 cm^2 g^{-1}). Genotypes with higher SLA values were recommended for areas where sufficient moisture is available. Zhou et al. (2020) that selection of plants with higher SLA helps to enhance photosynthetic capacity and productivity in maize. Sheshshayee et al. (2006) reported strong relation between SLA and SCMR under well-watered conditions in groundnut. This suggests that selection of genotypes with higher SLA under optimum condition could help to enhance the photosynthetic capacity and productivity in groundnut.

5.4.4. General combining ability effect of parents

Information on GCA effects of parents helps to estimate the genetic potential of breeding material for traits of interest (Amelework et al. 2015). Parental line ICGV 10178 exhibited significant positive GCA effects for SCMR, PY, SHP, KY, TBM and HI under DS condition and significant positive GCA effect for SLA under NS glasshouse condition (Table 5.7). This suggests the predominant role of additive gene effect in controlling the inheritance of these traits. Kokeeto et al. (2020) reported the importance of additive gene effect in the inheritance of SCMR and HI in groundnut. SLA, TBM production and HI have been used as surrogate traits for breeding drought tolerant genotypes in groundnut (Nigam et al. 2005; Jongrungklang et al. 2008; Janila et al. 2015; Kokeeto et al. 2020). ICGV 15083, ICGV 06175 and ICGV 15094 were best combiner

genotypes for breeding early flowering genotypes. In this study early flowering was observed in both *hypogaea* (ICGV 15094 [33 days]) and *fastigiata* (ICGV 96174 [32 days])) parents and their respective progenies (ICGV 06175 x ICGV 96174; ICGV 96174 x ICGV 15094 (34 days). This suggests the variability for early flowering in both species for selection and development of cultivars with early flowering for drought scape during the critical growth stage. Early maturity is a novel drought escape mechanism which would otherwise occur during flowering and pod filling stages. Rantakumar and Vadez (2011) reported that water stress during flowering and pod filling stages reduced pod initiation and thereby reduced HI in groundnut. ICGV 98412 exhibited significant positive GCA effect for HI under both DS and NS conditions in the glasshouse (Table 5.7). Under DS condition, significant negative GCA effect for SLA was recorded for ICGV 10373 (-34.04 $cm^2 g^{-1}$), whereas significant positive GCA effect for SLA was recorded for ICGV 10178 (13.50 $cm^2 g^{-1}$) under NS condition. This result suggests that the two genotypes can enhance water use efficiency in groundnut under drought-stressed environment with effective photosynthetic capacity of the crop under optimum condition (Upadhyaya et al. 2011).

5.4.5. Specific combining ability effects of crosses

Information on SCA effects of crosses is useful to identify best specific combiners for economic traits. Under DS condition, significant negative SCA effects for PH were recorded for ICGV 06175 x ICGV 96174 (-6.73) and ICGV 10178 x ICGV 15094 (-6.46). Under NS condition in the glasshouse, ICGV 10178 x ICGV 96174 and ICGV 15083 x ICGV 98412 exhibited significant positive SCA for PH. In an earlier report by John and Reddy (2018), positive correlations were recorded between PH and PY under non-stress condition, while Arruda et al. (2015) reported significant negative association between PH and PY under drought-stressed condition. Hence selection of crosses with short PH is probably a good strategy under drought-stressed condition to enhance productivity.

Crosses ICGV 06175 x ICGV 11396 (4.22), ICGV 10178 x ICGV 15094 (3.87) and ICGV 10373 x ICGV 98412 (3.28) showed significant positive SCA effects for SCMR under DS and CGV 15083 x ICGV 98412 (7.31) under NS condition in the glasshouse. This suggests that the parents of these crosses had complementary traits for high SCMR values and this would be useful for transgressive breeding. A strong and positive association between SCMR and water use efficiency was reported by Sheshshayee et al. (2006) and Janila et al. (2015). Arunyanark et al. (2008) suggested SCMR as a surrogate trait for breeding drought tolerance in groundnut. Selection of genotypes with high SCMR and best combiners enable to enhance drought tolerance in groundnut breeding.

Under DS condition, ICGV 06175 x ICGV 96174 exhibited significant negative SCA effects for SLA at -54.54 $cm^2 g^{-1}$ (Table 5.8). Under NS condition in the glasshouse, the crosses ICGV 15083 x ICGV 96174 (68.26 $cm^2 g^{-1}$), ICGV 15083 x ICGV 98412 (44.45 $cm^2 g^{-1}$), ICGV 96174 x ICGV 15094 (42.48 $cm^2 g^{-1}$) and ICGV 10178 x ICGV 98412 (39.57 $cm^2 g^{-1}$) showed significant positive effects for SLA. This indicates that these crosses have reduced SLA under drought-stressed condition which contributes to water use efficiency to enhance photosynthetic capacity and yield gains.

Under DS, crosses, ICGV 10373 x ICGV 15083 and ICGV 98412 x ICGV 15094, exhibited significant positive SCA effects for POD, SHP and HI. Passiour et al. (1986) reported that HI is directly related with water use efficiency under stress condition. Thus, these crosses could be selected for high pod yield and HI under drought stress environments. The present study identified ICGV 10178 x ICGV 98412 with significant SCA effects for SLA, PY, KY and TBM and, ICGV 15083 x ICGV 96174 with significant positive SCA effects for SLA, PY, KY and HI and, ICGV 15083 x ICGV 98412 with significant positive SCA effects for PH, SCMR, SLA, PY, KY and TBM. These crosses were selected for genetic advancement and to breed promising groundnut genotypes with improved yield and yield components under drought-stressed environments.

5.4.6. The ratio of GCA to SCA effects

The ratio of GCA to SCA effects ranged from 0.56 for DF to 0.94 for KY under DS condition and 0.61 for DF to 0.96 for PY under NS glasshouse condition (Table 5.3). The closer the GCA to SCA ratio to unity is, the greater would be the magnitude of additive genetic effects, while the ratio much less than unity suggests a predominant role of non-additive gene effects conditioning trait inheritance (Baker 1978). Nigam (2014) reported additive and non-additive gene actions controlling the inheritance of PH, PB, SCMR, SLA, PY, SHP, KY, TBM and HI in groundnut. In the present study the GCA: SCA ratio for all assessed traits under DS condition ranged from 0.56 to 0.94 (under NS glasshouse) and 0.61 to 0.96 (field condition). This suggests that additive gene effects are more important than non-additive gene effects in conditioning trait inheritance. The higher magnitude of additive genetic effect indicates that single seed descent selection methods would be effective in developing improved pure line groundnut varieties with high pod yield and drought tolerance.

5.5. Conclusions

The present study determined the combining ability effects of eight selected drought tolerant groundnut parental lines and 28 F_2 families under drought-stressed (DS) and non-stressed (NS) conditions. ICGV 10178 was the best general combiner with positive contribution to SCMR, PY, SHP, KY, TBM and HI. Crosses ICGV 10178 X ICGV 11369, ICGV 10373 x ICGV 15083, ICGV 98412 x ICGV 15094 and ICGV 10178 X ICGV 98412, were the best specific combiners for enhanced pod yield and drought tolerance. Higher GCA: SCA rations were recoded for PY, KY and TBM across all the testing environments suggesting the predominant role of additive genes conditioning the inheritance of these traits. Therefore, the above new families are recommended for genetic advancement through single seed descent selection methods to develop improved pure line groundnut varieties with high pod yield and drought tolerance.

5.6. References

Abady, S., Shimelis, H., Janila, P. and Mashilo, J. 2019. Groundnut (*Arachis hypogaea* L.) improvement in sub-Saharan Africa: a review. *Acta Agriculturae Scandinavica, Section B — Soil & Plant Science*, 69 (6): 528–545, Doi: https://doi.org/10.1080/15427528.2019.1625836

Amelework, B., Shimelis, H. and Laing, M. 2015. Genetic variation in sorghum as revealed by phenotypic and SSR markers: implications for combining ability and heterosis for grain yield. *Plant Genetic Resources* 15: 1-13, Doi: https://doi.org/10.1017/S1479262115000696

Arunyanark, A., Jogloy, S., Akkasaeng, C., Vorasoot, N., Kesmala, T., Rao, N.R., Wright, G,C and A. Patanothai, A. 2008. Chlorophyll stability is an indicator of drought tolerance in peanut. *Journal Agronomy and Crop Science* 194: 113-125

Arruda, I.M., Moda-Cirino, V., Buratto, J.S. and Ferreira, J.M. 2015. Growth and yield of peanut cultivars and breeding lines under water deficit. *Pesquisa Agropecuária Tropical Goiânia* 45: 146-154, Doi: https://doi.org/10.1590/1983-40632015v4529652

Baker, R.J. 1978. Issues in diallel analysis. *Crop Science* 18: 533–536

Chavadhari, R.M., Kachhadia, V.H., Vachhani, J.H. and Virani, M.B. 2017. Genetic variability studies in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding* 8:1288-1292, Doi: https://doi.org/10.5958/0975-928X.2017.00184.3

Falconer, D. and Mackay, T. 1996. *Introduction to quantitative genetics*. London, UK: Longman Group Ltd.

Francisco, R., Gregorio, A., Ángela, P., José, C. and Juan, B. 2015. "AGD-R (Analysis of Genetic Designs with R for Windows) Version 5.0", CIMMYT Research Data & Software Repository Network, V14

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences* 9: 463–493

ICRISAT (International Crops Research Institute for the Semi-Arid Tropics). 2020. New ICRISAT groundnut varieties to be available from next season. Accessed 14 December 2020. www.cgiar.org

Janila, P., Manohar, S., Rathore, A., and Nigam, S.N. 2015. Inheritance of SPAD chlorophyll meter reading and specific leaf area in four crosses of groundnut (*Arachis hypogaea* L.). *Indian Journal of Genet*ics 75:408-412, Doi: https://doi.org/10.5958/0975-6906.2015.00067.X

Jongrungklang, N., Toomsan, B., Vorasoot, N., Jogloy, S., Kesmala, T. and Patanothai, A. 2008. Identification of peanut genotypes with high water use efficiency under drought stress conditions from peanut germplasm of diverse origins. *Asian Journal of Plant Sciences* 7: 628-638

John, K. and Reddy, P.R., 2015. Combining ability and heterosis for yield and water use efficiency traits in groundnut. *Agricultural Review*s 36: 305-312, Doi: https://doi.org/10.18805/ag.v36i4.6667

Kakeeto, R., Melis, R., Biruma, M. and Sibiya, J. 2020. Gene action governing the inheritance of drought tolerance and selected agronomic traits in Ugandan groundnut (*Arachis hypogaea* L.) lines under drought environment. *Euphytica* 216: 1-21, Doi: https://doi.org/10.1007/s10681-019-2539-6

Kiani, G., Nematzadeh, G. A., Kazemitabar, S. K. and Alishah, O. 2007. Combining ability in cotton cultivars for agronomic traits. *International Journal of Agriculture and Biology* 9: 521–2

Kamdar, J.M., Jasani, M.D., Ajay, B. C., Sandip Kumar Bera, S.K. and John J. Georrge, J.J. 2020. Effect of selection response for yield related traits in early and later generations of groundnut (Arachis hypogaea L.). *Crop Breeding and Applied Biotechnology* 20(2): e317320215. Brazilian Society of Plant Breeding. Printed in Brazil. Doi: http://dx.doi.org/10.1590/1984-70332020v20n2a3

Mathew, I., Shimelis, H., Mutema, M., Clulow, A., Zengeni, R., Mbava, N. and Chaplot, V. 2019. Selection of wheat genotypes for biomass allocation to improve drought tolerance and carbon sequestration into soils. *Journal of Agronomy and Crop Science* 2019:1-16, Doi: https://doi.org/10.1111/jac.12332

Meisner, C. A., and Karnok, K.J. 1992. Peanut root response to drought stress. *Agronomy Journal* 84: 159-165, Doi: https://doi.org/10.2134/agronj1992.00021962008400020007x

Ministry of Agriculture and Natural Resources (MoANRs). 2016. “Crop Variety Register Issue No. 19. Plant Variety Release.” Protection and Seed Quality Control Directorate. MoANRs, Addis Ababa.

Mukhtar, A.A., Babaji, B.A., Ibrahim, S., Mani, H., Mohammad, A.A. and Ibrahim, A. 2013. Dry matter production and harvest index of groundnut (*Arachis hypogaea L.*) varieties under irrigation. *Journal of Agricultural Science* 5:153-162

Nageswara Rao, R.C., Singh, S., Sivakumar, M.V.K., Srivastra, K.L. and Williams, J.H. 1985. Effect of water deficit at different growth phase of peanut. I yield response. *Agronomy Journal* 77:782-786

Nageswara Rao, R.C., Talwar, H.S. and Wright, G.C. 2001. Rapid assessment of specific leaf area and leaf chlorophyll meter. *Journal of Agronomy and Crop Science* 189: 175-182

Ngaboyisonga, C., Nizeyimana, F., Gafishi, M.K., Ndayishimiye, T., Mbarushimana, J.D., Nyirabashyitsi, J., Mutanyagwa, P. and Nyombayire, A. 2019. Combining ability for grain yield and silking of maize inbred lines derived from three open pollinated varieties released for mid altitudes of RWANDA: Comparison of diallel and North Carolina Design II. *African Crop Science Journal* 27: 59-75

Nigam, S.N., Giri, D.Y. and Reddy, A.G.S. 2004. Groundnut seed production manual. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. 32 pp

Nigam, S.N., Vasudeva Rao, M. J., and Gibbons, R. W. 1990. Artificial hybridization in groundnut. Information Bulletin no. 29. Patancheru, A.P. 502 324, India: International Crops Research Institute for the Semi-Arid Tropics

Nigam, S.N., Chandra, S., Sridevi, K.R., Bhukta, A.M., Reddy, G.S., Nageswara Rao, R.C., Wright, G.C., Reddy, P.V., Deshmukh, M.P., Mathur, R.K., Basu, M.S., Vasundhara, S., Varman, P.V and Nagda, A.K. 2005. Efficiency of physiological trait-based and empirical selection approaches for drought tolerance in groundnut. *Annals of Applied Biology* 146: 433-439.

Nigam, S.N. 2014. Groundnut at a glance. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, A.P. 502 324, India. Pp 121

Oppong-Sekyere, D., Akromah, R., Ozias-Akins, P., Laary, J. K. and Gimode D. 2019. Heritability studies of drought tolerance in groundnuts using the North Carolina design II fashion and variance component method. *Journal of Plant Breeding and Crop Science* 11:234-253, Doi: https://doi.org/ 10.5897/JPBCS2018.0781

Passioura, J.B. 1977. Grain yield, harvest index, and water use of wheat. *Journal of Australian Institute of Agricultural Science* 43:3-4

Pereira, J.W.L., Albuquerque, M.B., Filho P.A.M., Nogueira, R.J.M.C., Lima, L.M. and Santos, R.C. 2016. Assessment of drought tolerance of peanut cultivars based on physiological and yield traits in a semiarid environment. *Agricultural Water Management* 166: 70-76

Ratnakumar, P., Vadez, V., Nigam, S.N. and Krishnamurthy, L. 2009. Assessment of transpiration efficiency in peanut (*Arachis hypogaea* L.) under drought using a lysimetric system. *Plant Biology* 11:124–130, Doi: https://doi.org/10.1111/j.1438-8677.2009.00260.x

Ratnakumar, P. and Vadez, V. 2011. Groundnut (*Arachis hypogaea*) genotypes tolerant to intermittent drought maintain a high harvest index and have small leaf canopy under stress. *Functional Plant Biology* 38: 1016–1023

Reddy, L. J. and Nigam, S.N. and Reddy, A.G.S. 1993. Natural outcrossing in groundnut and its implications in groundnut breeding. *Journal of Oilseeds Research* 10: 99-104

Ravi, K., Vadez, V., Isobe, S., Mir, R.R., Guo, Y., Nigam, S.N., Gowda, M.V.C., Radhakrishnan, T., Bertioli, D.J., Knapp, S.J. and Varshney, R.K. 2011. Identification of several small main-effect QTLs and a large number of epistatic QTLs for drought tolerance related traits in groundnut (*Arachis hypogaea* L.). *Theoretical and Applied Genetics* 122:1119–1132

Rojas, B.A., Sprague, G.F. 1952. A comparison of variance components in corn yield trials: III. General and specific combining ability and their interaction with locations and years. *Agronomy Journal* 44: 462-466

Sanogo, O., Tongoona, P.B., Ofori, K., Offei, S.K. and Desmae, H. 2019. Evaluation of yield and yield components of some groundnut genotypes under rainfed condition in Mali using biplot analysis. *African Journal of Agricultural Research* 14:1904-1912, Doi: https://doi.org/10.5897/AJAR2018.13776

Sanogo, O., Sissoko, S., Sangare, S., Zan I.D., Tongoona, P.B., Ofori, K., Offei, S.K and Desmae, H. 2020. Elucidation of the mechanism for drought stress through combining ability and gene action in groundnut. *Journal of Genetics, Genomics & Plant Breeding* 4: 54-67

Sheshshayee, M.S., Bindumadhava, H., Rachaputi, N.R., Prasad, T.G., Udayakumar, M., Wright, G.C. and Nigam, S.N. 2006. Leaf chlorophyll concentration relates to transpiration efficiency in peanut. *Annals of Applied Biology* 148: 7-15

Shrief, S.A., El-Mohsen, A.A., Abdel-Lattif, H.M., El Soda, M., Zein, H.S. and Mabrouk, M.M. 2020. Groundnut improvement: drought stress and water use efficiency of some groundnut genotypes grown under newly reclaimed soil. *Plant Archives* 20: 1527-1536

Singh, P. and Narayanan, S.S. 2017. Biometrical techniques in plant breeding. Kalyani Publishers, New Delhi, India

Songsri, P., Jogloy, S., Vorasoot, N., Akkasaeng, C., Patanothai, A. and Holbrook, C.C. 2008. Root distribution of drought-resistant peanut genotypes in response to drought. *Journal of Agronomy and Crop Science* 94: 92–103

Songsria, P., Jogloya, S., Holbrookb, C.C., Kesmalaa, T., Vorasoota, N., Akkasaenga and C., Patanothai, A. 2009. Association of root, specific leaf area and SPAD chlorophyll meter reading to water use efficiency of peanut under different available soil water. *Agricultural Water Management* 96:790-798

Sprague, G.F. and Tatum, L.A. 1942. General versus specific combining ability in single crosses of corn. *Journal of American Society of Agronomy* 34: 923-932

Suriharn, B., Patanothai, A. and Jogloy, S. 2005. Gene effects for specific leaf area and harvest index in peanut (*Arachis hypogaea* L.). *Asian Journal of Plant Sciences 4: 667-672,* Doi: https://doi.org/10.3923/ajps.2005.667.672

Upadhyaya, H.D., Sharma, S., Singh, S. and Singh, M. 2011. Inheritance of drought resistance related traits in two crosses of groundnut (*Arachis hypogaea* L.). *Euphytica* 177: 55-66, Doi: https://doi.org/10.1007/s10681-010-0256-2

Vadez V., Kholová, J., Hummel, G., Zhokhavets, U., Gupta, S.K. and Hash, C.T. 2015. LeasyScan: a novel concept combining 3D imaging and lysimetry for high-throughput phenotyping of traits controlling plant water budget. *Journal of Experimental Botany* 66: 5581-5593

Vaidya, S., Vanaja, M., Lakshmi, N.J., Sowmya, P. and Anitha, Y. 2016. Variability in drought stress induced responses of groundnut (*Arachis hypogaea* L.) genotypes. *Journal of Biochemical and physiology* 4: 149, Doi: https://doi.org/10.4172/2168-9652.1000149

Watson, J., Zheng, B., Chapman, S.C. and Chenu, K. 2015. Projected impact of future climate on drought patterns in complex rainfed environments. *Procedia Environmental Sciences* 29: 190 -191

Zhou, H., Zhou, G., He, Q., Zhou, L., Ji, Y. and Zhou, M. 2020. Environmental explanation of maize specific leaf area under varying water stress regimes. *Environmental and Experimental Botany 171: 103932,* Doi: https://doi.org/10.1016/j.envexpbot.2019.103932

Zongo, A., Nana, A.T., Sawadogo, M., Abdourasmane, K. K., Sankara, P., Ntare, B.R. and Desmae, H. 2017. Variability and correlations among groundnut populations for early leaf spot, pod yield, and agronomic traits. *Agronomy* 7, 52, Doi: https://doi.org/10.3390/agronomy7030052

General overview and implications of the study

Introduction and objectives of the study

Groundnut (*Arachis hypogaea* L.) is an important food and feed crop grown in the world. Groundnut production is constrained by several biotic and abiotic factors. Recurrent drought is the major yield and quality limiting factor in groundnut production globally. In Ethiopia, groundnut is commonly grown by smallholder farmers under rainfed production conditions. In the country, farmers grow unimproved groundnut varieties that are highly susceptible to drought stress, diseases and insect pests. Therefore, there is need to develop drought tolerant, locally adapted and high yielding groundnut varieties for sustainable production of the crop in the country. Breeding groundnut for drought tolerance requires relatively cheap, reproducible and high throughput screening systems. Understanding of the agro-morphological, physiological and molecular bases of drought tolerance aid in the development and release of new varieties with drought tolerance. This chapter summarizes the research objectives and highlights the major findings and implications of the study.

The objectives of this study were:

1. To assess farmers' perceived production constraints, variety choice, and preferred traits of groundnut in eastern Ethiopia to guide future groundnut variety development and release.
2. To determine drought tolerance, kernel and fodder yield and quality amongst diverse groundnut genotypes for direct production or breeding.
3. To assess the genetic diversity and population structure among 100 groundnut genotypes using agronomic traits and high density single nucleotide polymorphism (SNP) markers.
4. To determine the combining ability effects of eight selected drought tolerant groundnut parental lines and their F_2 families under drought-stressed (DS) and non-stressed (NS) conditions to select best performing parents and families for drought tolerance breeding.

Research hypothesis

V. Farmer's perception and their indigenous knowledge on drought copping mechanism have great implication for breeding groundnut varieties with better performance.

VI. There are high heritability and positively correlated drought tolerant traits that can be used for effective selection in drought tolerant variety development.

VII. There is valuable genetic diversity in the test groundnut genotypes for breeding for drought tolerance and earliness.

VIII. The selected groundnut parents and crosses exhibit good combining ability for drought tolerance, yield and yield-related traits under drought-stressed and non-stressed conditions for genetic advancement.

Major findings of the study

Farmers' perceived constraints to groundnut production, their variety choice and preferred traits in eastern Ethiopia: implications for drought-tolerance breeding

Participatory rural appraisal studies were conducted in two major groundnut-producing districts (Babile and Fedis) in eastern Ethiopia. Data were collected through a semi-structured questionnaire, transect walks, and focus group discussions. The main outcomes were as follows:

- The major constraints affecting groundnut production in the study areas included drought stress, poor soil fertility, lack of access to improved seed, pre-harvest diseases and use of low yielding varieties as reported by 99%, 88%, 67%, 59.5% and 52.5% respondent farmers, in that order.
- Inadequate access to extension services (reported by 41.5% of respondents), limited access to credit (21.5%), and limited availability of improved varieties (18.5%) were other groundnut production constraints in the study areas.
- Respondent farmers described the following preferred traits in a groundnut variety such as high shelled yield (reported by 27.67% of respondents), early maturity (16.84%), tolerance to drought stress (13.67%), market value (11.17%), good grain quality (10%), adaptability to local growing conditions (5.8%), and resistance to diseases (5.17%).
- The aforementioned production constraints and farmer-preferred traits are key drivers that need to be integrated in groundnut breeding and variety development programs in eastern Ethiopia.

Assessment of the diversity of groundnut (*Arachis hypogaea* L.) genotypes for kernel yield, and oil and haulm quantity and quality under moisture stress conditions

One hundred groundnut genotypes were field evaluated at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)/India during 2018/19 and 2019/20 under drought-stressed (DS) and non-stressed (NS) conditions using a 10 x 10 alpha lattice design with two replications. Data were collected on kernel yield (KY), oil content (OC), oil yield (OY), protein content (PC), palmitic acid content (PAC), stearic acid content (SAC), oleic acid content (OAC) and linoleic acid content (LAC), haulm yield (HY) and fodder quality parameters such as the contents of dry matter (DM), ash, nitrogen (NC), neutral detergent fiber (NDFDM), acid detergent fiber

(ADFDM), acid detergent lignin (ADLDM), *in vitro* digestibility (IVOMD) and metabolizable energy (ME). Data were subjected to parametric and non-parametric statistical analyses. The main findings of this study were:

- Combined analysis of variance revealed significant (P< 0.05) genotype differences for all assessed traits allowing genotype selection for breeding.
- Genotype × water regime interaction effects were significant for kernel yield, oil content, ash content, nitrogen content, neutral acid detergent fiber and acid detergent lignin.
- Kernel yield positively and significantly (P<0.05) correlated with oil yield (r = 0.99), linoleic acid content (r = 0.13), ash (r = 0.32), neutral acid detergent fiber (r = 0.54) under DS condition.
- Haulm yield was positively and significantly (P<0.05) correlated with oil content (r = 0.24), neutral detergent fiber (r = 0.19), acid detergent fiber (r = 0.18) and acid detergent lignin (r = 0.17) under DS condition.
- The study identified genotypes, ICGV 10178, ICGV 01260, ICGV 06175 and ICGV 10379 with high kernel and haulm yields, and CGV 181017, ICGV 01491, ICGV 15019, ICGV 181026, ICGV 16005 and ICGV 181063, with high oleic acid content.
- Further, genotypes, ICGV 7222, ICGV 10143, ICGV 6040, ICGV 03042, ICGV 06175, ICGV 01260, ICGV 99241, ICGV 96266, ICGV 171027 and ICGV 01491, were selected with relatively better drought tolerance.
- The selected genotypes are recommended for further breeding and variety release under drought stressed environments.

Assessment of the genetic diversity and population structure of groundnut germplasm collections using phenotypic traits and SNP markers: implications for drought tolerance breeding

The 99 genotypes (except genotype ICGV 06420) were profiled with 16,363 SNPs markers. The SNP data set and the phenotypic data collected above were subjected to genetic diversity and model based population structure analyses to infer genetic relationships of the test genotypes for breeding. The main findings were as follows:

- Pod yield exhibited significant ($p \leq 0.05$) correlation with seed yield, harvest index, and total biomass under both test conditions.
- In the principal component analysis, pod yield, seed yield, hundred seed weight, shelling percentage and harvest index were contributed maximum variability for yield under the two water regimes.

- Model-based population structure analysis grouped the studied genotypes into three sub-populations. Whereas cluster analysis resolved the collections into 5 clusters based on pedigree, selection history, and market type.
- Cluster III and Cluster V consisted of the Spanish bunch types, late leaf spot (*Phaeoisariopsis personata)* and rust (*Puccinia arachidis*) resistant, and drought-tolerant genotypes.
- Analysis of molecular variance revealed that 98% of the total genetic variation was attributed to among individuals, while only 2% of the total variance was due to variation among the subspecies.
- The genetic distance between the Spanish bunch and Virginia bunch types ranged from 0.11 to 0.52.
- The genotypes, ICGV 13189, ICGV 95111, ICGV 14421, and ICGV 171007, were selected for further breeding based on their wide genetic divergence.
- Data presented in this study will guide groundnut cultivar development emphasizing economic traits and adaptation to water-limited agro-ecologies including in Ethiopia.

Combining ability analysis of groundnut (*Arachis hypogaea* L.) genotypes for yield and related traits under drought-stressed and non-stressed conditions

The combining ability effects of eight selected agronomically promising and drought tolerant groundnut parental lines and their F_2 populations were evaluated under drought-stressed (DS) and non-stressed (NS) conditions under glasshouse and field conditions at ICRISAT in 2020 rainy season. Data were collected on days to 50% flowering (DF), number of primary branches (PB), plant height (PH) (cm), SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) ($cm^2\ g^{-1}$), pod yield (PY) (g $plant^{-1}$), shelling percentage (SHP) (%), kernel yield (KY) (g $plant^{-1}$), total biomass (TBM) (g $plant^{-1}$) and harvest index (HI) (%). The main outcomes were as follows:

- The general combining ability (GCA) effects of parents were significant ($P<0.05$) for all assessed traits under all testing conditions except for PB under DS and NS conditions in the glasshouse.
- The specific combining ability (SCA) effects of progenies were significant ($P<0.05$) for all traits except for PH across all testing environments and PB under field condition.
- The genotype ICGV 10178 was the best general combiner with positive contribution to SCMR, PY, SHP, KY, TBM, HI and reduced SLA.
- Crosses, ICGV 10178 X ICGV 11369, ICGV 10373 x ICGV 15083, ICGV 98412 x ICGV 15094 and ICGV 10178 X ICGV 98412, were the best specific combiners for enhanced pod yield and drought tolerance.

- Higher GCA: SCA rations were recoded for PY, KY and TBM across all the testing environments suggesting the predominant role of additive genes conditioning the inheritance of these traits.
- The above new families are recommended for genetic advancement through single seed descent selection methods to develop improved pure line groundnut varieties with high pod yield and drought tolerance.

Implications of the research findings to breeding groundnut for higher yield and drought tolerance

- Groundnut production constraints and farmer-preferred traits identified during the participatory varietal selection will be considered during the variety development of improved varieties. This would enhance the adoption rate of improved varieties, production and productivity of groundnut in eastern Ethiopia.
- There is considerable genetic variability for high yielding and drought tolerance in the test genotypes to be exploited in groundnut breeding.
- The SNP markers identified genetically divergent groundnut genotypes such as ICGV 13189, ICGV 95111, ICGV 14421, and ICGV 171007. The selected lines are useful to develop breeding population.
- Positive and strong correlations were noted between KY and PY, HI, HSW and SHP, suggesting that these traits can be used as indirect selection criteria during the development of high yielding and drought tolerant cultivar.
- The study selected genotypes, ICGV 07222, ICGV 06040, ICGV 01260, ICGV 15083, ICGV 10143, ICGV 03042, ICGV 06039, ICGV 14001, ICGV 11380 and ICGV 13200, with high PY under drought stressed and non-stressed condition. The divergent parental lines are useful in groundnut breeding for enhanced pod yield.
- Additive genes were involved influencing the inheritance of pod yield, kernel yield, total biomass and other important agronomic traits across the testing environments. Hence genetic gain could be realized through single seed descent or recurrent selection programs to develop improved groundnut varieties with high pod yield and drought tolerance.
- Genotype ICGV 10178 was the best general combiner with positive contribution to SCMR, PY, SHP, KY, TBM and HI and reduced SLA.
- New families, ICGV 10178 x ICGV 98412, ICGV 10373 x 15083 and ICGV 178 x ICGV 11396, were best specific combiners for improving shelling percentage.

- Crosses, ICGV 10178 X ICGV 11369, ICGV 10373 x ICGV 15083, ICGV 98412 x ICGV 15094 and ICGV 10178 X ICGV 98412, were the best specific combiners for enhanced pod yield and drought tolerance.
- Therefore, the above new families are recommended for genetic advancement through single seed descent selection method to develop improved pure line groundnut varieties with high pod yield and drought tolerance for cultivar release and cultivation in Ethiopia. The remaining breeding activities such as testing of groundnut genotypes across various agro-ecological zones of Ethiopia and variety verification trials will be implemented through the National Groundnut Breeding Program of Ethiopia based at Haramaya University.
- It is important to identify groundnut production constraints and farmer-preferred traits during a participatory varietal selection appraisal as was done in this study and to include then in variety development of improved varieties in breeding programs.