

**EVALUATION OF SOYBEAN [*Glycine max* (L.) Merrill] GENOTYPES  
FOR GRAIN YIELD AND ASSOCIATED AGRONOMIC TRAITS  
UNDER LOW AND HIGH PHOSPHORUS ENVIRONMENTS**

By

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## GENERAL ABSTRACT

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Phosphorus is an important element for growth, development and seed formation in soybean and other plant species. This element is less available for plants. The capacity of absorbing phosphorus in the soil varies from one genotype to another, so that, the selection of phosphorus use efficient soybean lines is crucial in order to enhance the production. The main objectives of this study were: i) to identify soybean varieties that are tolerant to phosphorus deficiency ii) to determine the agronomic characters that contribute directly and indirectly to the yield improvement by correlation and path coefficient analysis and iii) to determine genotype x environment interaction effects and stability of soybean genotypes in respect to grain yield across low and optimum phosphorous environments. Thirty advanced soybean lines were evaluated in an alpha-lattice design, with two replications during 2016/2017 cropping season under low phosphorus (0 kg/ha) and high phosphorus (100 kg/ha) levels in seven environments. Data were collected for fifteen phenotypic traits (both quantitative and qualitative) and analysed using SAS, breeding view (BV) in breeding management system (BMS), and Excel. Correlation and path coefficient analysis were done to determine the traits that contributed directly and indirectly to yield. Results for correlation and path coefficient analysis demonstrated strong and significant associations of yield with yield components. Harvest index was highly significant and positively correlated with grain yield but negatively with plant height, days to maturity and days to flowering. Path analysis revealed that under low P environment, total dry biomass, harvest index, number of pods could be used to screen soybean lines for low P, likewise in high P, harvest index, 100-seed weight, and plant height could be used in selection for high P use efficiency. Plant height, number of pods and nodule weight were identified as the traits that could be used for selection of the lines across all environments. The yield was high under high phosphorus (1551.20 kg/ha) than under low phosphorus environment (1154.30 kg/ha). The best yielding genotypes under high phosphorus were TGx2025-9E, TGx2025-6E and TGx2016-3E. Likewise, for low phosphorus the best genotypes were TGx2025-9E TGx2016-3E and TGx2023-3E. Across the two environments, genotypes TGx2025-9E and TGx2016-4E were the best. The genotypes were clustered into six groups with the maximum dissimilarity index of 0.6. In AMMI analysis, genotype TGx2025-9E, was the most stable and high yielding, suggesting the potential value of the variety as an alternative for soybean production across all environments. GGE biplot resulted in three mega-environments from the seven environments; Kabwe1, Lilongwe1, Lilongwe2 and Lusaka composed mega environment one, Gurue1 and Gurue2 formed mega environment two and Kabwe2 mega environment three. The best performing genotypes in

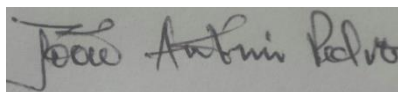
these mega-environments were SCSAFARI and TGx2019-1E (mega-environment 1), TGx2025-9E (mega-environment 2) and TGx2025-6E (mega-environment 3). These findings highlighted the need for increased GxE studies to enhance efficiencies of breeding for broad adaptability in respect to responsiveness to low phosphorus.

## DECLARATION

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I, João António Pedro, declare that:

- i) The research reported in this dissertation, except where otherwise indicated or acknowledged, is my original work;
- ii) This dissertation has not been submitted in full or in part for any degree or examination to any other university;
- iii) This dissertation does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons;
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Signed: Date: 30/11/2018

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



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Julia Sibiya (Supervisor)



Signed: Date: \_\_10\_\_/\_03\_/2018

Godfree Chigeza (Co-supervisor)

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## DEDICATION

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## ABBREVIATIONS

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AMMI	-	Additive Main Effect and Multiplicative Interaction
ANOVA	-	Analysis of variance
BIO	-	Biomass
CV	-	Coefficient of variation
DF	-	Days to 50% flowering
df	-	Degrees of freedom
DM	-	Days to 50% maturity
FD	-	Days to flowering
G	-	Genotype
GEI	-	Genotype by environment interaction
GGE	-	Genotype main effects and genotype by environment interaction
GYD	-	Grain yield
HI	-	Harvest index.
IPCA	-	Interaction principal components
LSD	-	Least significance difference
NODP	-	Nodules per plant
NODP	-	Number of Nodules nodules per plant
NODW	-	Nodule weight
PCLEAR	-	Pod clearance
PH	-	Plant height
PODP	-	Pods per plant
SEEDP	-	Number of seed per pod
SEEDW	-	Seed weight
SS	-	Sum of squares
ST-ERROR	-	Standard error



# CHAPTER 1

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## INTRODUCTION

### 1.1 Background

Soybean (*Glycine max* Merrill L.) is the fourth most important oilseed crop cultivated in the world for the high oil content and protein. The crop was first cultivated and domesticated in the eastern half of north China around 11<sup>th</sup> century BCE (Hymowitz, 1970), thus China is often referred to as the 'soybean home'. However, most of the soybean production is concentrated in the United States of America, Brazil and Argentina. Africa contributes not more than 1% of the total global output (FAOSTAT, 2015). One of the major production constraints in Africa is low phosphorus (P) due to a major part of the continent being localized in the tropics where the soils have low available P. Phosphorus plays a major role in growth, development and seed formation (Ochigbo and Bello, 2014; Xia *et al.*, 2014). Moreover, Wang *et al.* (2010) and Yan *et al.* (2009) reported that there is substantial variation among genotypes for plant phosphorus use efficiency, with some cultivars showing better performance under phosphorus deficiency than others. Breeding can thus be one of the strategies to identify these cultivars with better performance under low phosphorus.

However, selecting and recommending the best genotypes is often complicated by genotype by environment interactions (GEI). The presence of GEI underscores genotypic performance in certain environmental conditions. Genotype by environment interaction has been defined as the variation of the phenotypic response of a genotype that results in changes in ranking from one environment to another (Yamada, 1962; Yan *et al.*, 2007). The GEI is divided into adaptability and phenotypic stability. Whereas adaptability explains the ability of the genotype to respond well to environmental effects attaining its yield potential, stability implies that the genotypes are able to maintain that yield potential across various environments (Laxami *et al.*, 2017, Aina *et al.*, 2009; Becker and Leon, 1988; Ssemakula and Dixon, 2007). Consequently, developing high yielding cultivars that are adapted and stable in various growing environments is essential.

In any breeding programme, yield improvement is considered as a primary objective. However, the yield trait is recognized to be a very complex character because it is controlled by many other factors. Thus, understanding of the relationship between yield components is crucial in determining the best genotypes (Hama *et al.*, 2016; Honarnejad *et al.*, 2000; Mehta

and Asati, 2008. Correlation and path coefficient analyses are some of the tools that can be used in order to assess the relationship between the secondary traits that could be used to select for yield indirectly for outstanding genotypes (Hasan *et al.*, 2013). A careful selection of the crop and the variety most suited to certain agro-environmental conditions is of utmost importance for achieving great and efficient production (Doorenbos *et al.*, 1979).

The maximum yield of a crop is defined as the harvested yield of a well-adapted variety in a given environment, including other factors such as time available to reach maturity, water, nutrients and pests and diseases (Doorenbos *et al.*, 1979). Correlation coefficients explain the degree of association among traits but is not sufficient when the causal effects of the trait association between them are not known. Therefore, path analysis is commonly applied to determine the causal effects explaining the direct and indirect effects of independent variables on the dependent variable (Sarutayophat, 2012). In this study, the objectives were thus to determine the responsiveness of soybean genotypes to high and low phosphorus in the soil in different environments as well as to identify the phenotypic traits and secondary yield components that could be used to select outstanding genotypes under low and high phosphorus environments.

## **1.2 Problem statement**

Africa is a marginal producer of soybean due to a number of constraints (FAOSTAT, 2015). Some of these constraints causing low production include lack of improved varieties that respond to the African agro-environmental conditions, pests and diseases, drought and low nutrient availability (FAOSTAT, 2015). Phosphorus availability is a major crop production constraint as it is required in considerably large quantities (Pan *et al.*, 2008). Compared to nitrogen, phosphorus is considered an “immobile nutrient” as it has a short range of movement in the soil (Wang *et al.*, 2010). In Africa, most of the arable areas are localized in the tropics where the available phosphorus is low for the plants (Hinsinger, 2001; Ochigbo and Bello, 2014). Fertilisers are not readily available or are too expensive, and most of the production of soybean in Africa, apart from South Africa, primarily comes from small-scale resource-limited farmers who cannot afford to purchase the fertilisers and have limited capacity to manage environmental risks (Ochigbo and Bello, 2014; Pedro *et al.*, 2015).

There is, therefore, a need to provide soybean cultivars that can be produced with less amounts of phosphorus inputs. Even where farmers can afford the fertiliser, the issue is that most of the phosphorus applied to the soil is converted into an unavailable form meaning that

plants cannot utilise it (Pan *et al.*, 2008; Ramaekers *et al.*, 2010; Wang *et al.*, 2010). In this case, breeding is one of the best ways to enhance the production and productivity of this crop. However, Pan *et al.* (2008) indicated that selection of genotypes for phosphorus use efficiency is difficult and time consuming thus there is need to select for phosphorus responsiveness. Since yield is a complex trait, it is necessary to understand the association among the traits that may be useful for improved phosphorus use efficiency in genotype selection.

### **1.3 Justification**

Genetic improvement through breeding will continue to play an important role in improving yield through development of high yielding cultivars adapted to a wide range of agricultural ecosystems. Phosphorus is a major limiting nutrient for soybean growth, therefore improving phosphorus use efficiency of cultivars can result in higher yields under phosphorus deficiency. Such efficient cultivars will have added advantages including minimizing the cost of production associated with application of fertilizers as well as minimizing pollution of the environment and contributing to the maintenance of phosphorus resources globally. Promising cultivars would encourage the adoption and production of soybean by farmers and contribute to the reduction of malnutrition and mortality amongst children as well as increasing both rural and urban opportunities for earning cash. This study was aimed at providing breeders with information on characters that contribute directly and indirectly to the yield, and morphological traits that can be used to select for phosphorus use efficiency in cultivars. In addition, some desirable genotypes will be advanced to the next generation of evaluation.

### **1.4 Main objective**

The study aimed at developing new soybean cultivars that are tolerant to phosphorous deficiency and adapted to a wide range of environments in sub-Saharan Africa (SSA), from marginal to fertile soils, in order to optimize production and productivity and to meet the growing demand for the crop and its derivatives.

### **1.5 Specific objectives**

The specific objectives of the study were:

- To identify soybean lines that have high phosphorous use efficiency under variable P conditions.
- To determine agronomic characters that contribute directly and indirectly to the grain yield improvement of soybean using correlation and path coefficient analysis.

- To determine the magnitude of genotype x environment interaction and stability of soybean lines in respect to grain yield across low and optimum phosphorous environments.

## **1.6 Outline of the study**

The dissertation is organised into six chapters following a journal paper format. As a result, some repetition in the references and some overlaps in the introductory information between chapters is unavoidable. The referencing format is based on the Crop Science journal style. The outline of the dissertation is presented below:

Chapter 1: Introduction to dissertation

Chapter 2: Literature review

Chapter 3: Evaluation of soybean genotypes for yield and agronomic performances under low and high phosphorous conditions

Chapter 4: Correlation and path coefficient analysis for soybean grain yield and agronomic traits under low and high phosphorus across four environments

Chapter 5: Study of genotype x environment interaction of 30 soybean lines across seven environments under high and low phosphorus

Chapter 6: General overview

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## CHAPTER 2

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### LITERATURE REVIEW

#### 2.1 Introduction

This review focuses on providing information on the soybean crop that relates to its origin, centre of diversity, distribution, characterization and importance. In addition, the effects of phosphorus on the crop's growth are discussed. Methods used to assess traits that can be used in selection of cultivars and the genotype by environment interaction effects on soybean are highlighted. These topics are relevant to the research focus and thus provide the theoretical base for the research.

#### 2.2 Production of soybean

Soybean [*Glycine max* L. Merrill.] is one of the most important crops in the world, providing proteins for both human consumption and fodder for livestock (Darwesh *et al.*, 2013). The crop is grown largely in the United States of America, followed by Brazil and Argentina contributing 35.00%, 28.75% and 17.56% of the total world production, respectively (FAOSTAT, 2017). In China, soybean is a major oilseed crop and is grown on about eight million hectares, whereas in Africa, despite the chronic problem of malnutrition, soybean consumption is still low and its production contributes to only about 0.63% of the total global soybean production (FAOSTAT, 2017). Soybean production in Africa is affected by several constraints, which include low phosphorus availability in the majority of the soils that leads in most cases to unsatisfactory yields (Ochigbo and Bello, 2014; Sample *et al.*, 1980). In addition, grain yield is a complex trait that is controlled by many genes and has low heritability, making it difficult to select for as it is greatly influenced by the environment and other secondary traits (Sample *et al.*, 1980; Yan and Tinker, 2005). Therefore, it is important to determine secondary phenotypic traits that are highly heritable and can be used to select for grain yield indirectly (Chandel *et al.*, 2014; Cyprien and Kumar, 2011; Yan *et al.*, 2007). Additionally, yield stability of the genotypes is important in cultivar development, due to the influence of the environment on yield and therefore, should be addressed during breeding.



### 2.3 Taxonomy of soybean

Soybean (*Glycine max* Merrill L.) is a legume species that is native to eastern Asia. Soybean belongs to the *Fabaceae/Leguminosae* family, subfamily *Papilionoideae*, the tribe *Phaseoleae*, the genus *Glycine* Willd and the subgenus *Soja* (Moench). The species of soybean are grouped into two major sub genera, *Glycine* and *Soja* (moench) F. J. Hermann. Subgenus *Glycine* is perennial and comprises of about 18 species, while the annual subgenus *Soja* (Moench) consists of annual species. The subgenus *Soja* and is further subdivided into two major species; the wild species, *Glycine soja* and the cultivated soya which is *Glycine max* (Hymowitz, 2004). The *Glycine max* species is a self-pollinating diploid with 20 chromosome pairs ( $2n=40$ ) (Cober *et al.*, 1996; Gizlice *et al.*, 1996).

### 2.4 Origin, domestication and distribution of soybean

The origin of soybean has been widely discussed but most of the studies indicate that the crop was discovered and gradually domesticated over the centuries in the orient, north-east of China (Hymowitz, 1970). Cytological information, morphological as well as molecular data support that *Glycine soja* is the ancestor of *Glycine max*. *Glycine gracilis* is a weedy or semi-wild form of *Glycine max*, with some phenotypic characteristics intermediate to those of *Glycine. max* and *Glycine soja*. Thus, *Glycine gracilis* is considered intermediate in the speciation of *Glycine. max* from *Glycine soja* (Fukuda, 1933) or a hybrid between *Glycine soja* and *Glycine max* (Hymowitz, 1970). China is considered as the centre of origin of soybean, as well as the centre of diversity (Hinson and Hartwig, 1977). After its discovery in China, some landraces of soybean were introduced into Indonesia, Malaysia, Myanmar, Thailand, North India, Philippines, Japan and Vietnam (Chandel *et al.*, 2014; Hymowitz, 2004). These countries constitute secondary zones of origin. However, the form of soybean that is being cultivated today is very different from its ancestors, which were creeping plants that developed on the east coast of Asia, especially along the Yangtze River in China. Its evolution began with the appearance of plants from natural crosses between two species of wild soybeans, which were domesticated and improved by scientists of ancient China (Hinson and Hartwig, 1977).

### 2.5 Uses of soybean

Since ancient times, soybean has been considered one of the most important cultivated legumes. Now, it is classified as one of the most important cultivated oilseed crop in the world because of its high oil content and protein (Liu *et al.*, 2017). Soybean is used as food in its

simple form, more either as a vegetable or as any of soy derivatives or products. It also serves as feed for livestock and aquaculture; and is used for biofuel production. Soybean forms a greater part of oil and protein in the human diet (Pedro *et al.*, 2015; Valencia *et al.*, 1979; Willaarts *et al.*, 2014). It is a cheap and easy food to prepare, high in protein, fats, minerals and vitamins. The products of soybean such as milk, tofu, bean sprouts, soy sources and others replace meat, milk and eggs in food, due to its richness in nutrients, aids in growth, helps form the bones, muscles and teeth. In general, all these products and derivatives of soybean are increasing in all parts of the world. Because of its versatility, it can be classified as one of the biggest cash crops and contributes to the income of farmers (Liu *et al.*, 2017; Valencia *et al.*, 1979). On the other hand, its characteristics related to nodule fixation, contribute to soil improvement. It is used in intercropping systems and crop rotations (Pedro *et al.*, 2015). In addition, soybean makes excellent high nutritional quality hay when used as forage (Cassidy *et al.*, 1995; Liu *et al.*, 2017; Valencia *et al.*, 1979).

## **2.6 General characteristics of soybean**

Soybean is an erect plant that can reach a height of 1.5 metres. According to Fehr (1980), there are three types of growth habit amongst cultivars of soybean, which include determinate, semi-determinate or indeterminate. The determinate type is characterized by the cessation of vegetative activity of the terminal bud when it becomes an inflorescence at both axillary and terminal racemes (Stumborg *et al.*, 1996). For indeterminate cultivars, vegetative stages continue throughout the flowering time while semi-determinate genotypes have indeterminate stems that terminate vegetative growth abruptly after the flowering period (Stumborg *et al.*, 1996).

According to Valencia *et al.* (1979) primary leaves are unifoliate, opposite and ovate, while secondary leaves are trifoliate and alternate, and compound leaves with four or more leaflets occasionally are present. The root system is nodulated and consists of a taproot from which emerges a lateral root system (Buzzell *et al.*, 1977; Valencia *et al.*, 1979). Flowers consist of a tubular calyx of five sepals, a corolla of five petals (one banner, two wings and two keels), one pistil and nine fused stamens with a single separate posterior stamen (Buzzell *et al.*, 1977). The stamens form a ring at the base of the stigma and elongate one day before pollination, at which time the elevated anthers form a ring around the stigma (Valencia *et al.*, 1979).

The pod is straight or slightly curved, varies in length from two to seven centimetres, and consists of two halves of a single carpel, which are joined by a dorsal and ventral suture. The shape and size of the seed varies, and the shape can be oval, spherical, elongate or flattened. Soybean seed coat has a diversity of colours ranging from black, brown, blue, yellow, and mottled (Valencia *et al.*, 1979). The seed coat of the mature soybean is hard, water resistant, and protects the cotyledon and hypocotyl from damage. Normally, if the seed coat is cracked, the seed will not germinate. The scar, on the seed coat is called the hilum and the colour can be black, brown, and buff, grey and yellow (Buzzell *et al.*, 1977).

## **2.7 Reproductive biology of soybean**

Soybean is a self-pollinated crop species, which is commercially propagated by seed (Fehr, 1980). Artificial hybridisation is mostly used for cultivar development (Acquaah, 2009). The stigma is receptive to pollen approximately 24 hours before anthesis and remains receptive 48 hours after anthesis, while the anthers mature in the bud and directly pollinate the stigma of the same flower (Acquaah, 2009; da Silva *et al.*, 2017). As a result, soybeans exhibit a high percentage of self-fertilization and cross-pollination is usually less than one percent (Acquaah, 2009). Soybean plant can produce as many as 400 pods, with 2-20 pods at a single node. Each pod contains 1-5 seeds (da Silva *et al.*, 2017). Neither the seedpod, nor the seed, have morphological characteristics that would encourage animal transportation (Arpaia *et al.*, 2013; Caviness, 1966).

## **2.8 Agro-environmental requirements**

In all crops, several factors should be taken into consideration in order to maximize the yield per unit of land. Therefore, agro environmental conditions play an important role in crop growth. According to Doorenbos and Kassam (1979), the maximum yield level of a crop is primarily determined by its genetic characteristics and how well it is adapted to the environment (climate, soil and water). A combination of the genetic characteristics, soil, water and climate can provide optimum growth and greater yield, and can vary from crop to crop, and cultivar to cultivar (Doorenbos and Kassam, 1979; Liu *et al.*, 2013; Willaarts *et al.*, 2014).

Water availability is important, particularly during two soybean development periods: germination to emergence, and flowering to grain filling (Doorenbos and Kassam, 1979). During the first period, both excess water and water deficit are detrimental to obtaining good uniformity in plant population (Doorenbos and Kassam, 1979). Soybean seed needs to absorb at least 50% of its weight in water to ensure good germination. At this stage, the water content

in the soil should not exceed 85% of the maximum available total water nor be less than 50% (Doorenbos and Kassam, 1979). The need for water in soybean increases with the development of the plant, peaking during the flowering to grain-filling period (7-8 mm/day), decreasing thereafter (Doorenbos and Kassam, 1979; Willaarts *et al.*, 2014). Significant water stress during flowering and grain filling causes physiological changes in the plant, such as stomatal closure and the sheet winding resulting in premature fall of leaves and flowers and pod abortion and consequently a reduction in grain yield depending on weather conditions, the management culture and cycle time (Willaarts *et al.*, 2014). To minimize the effects of drought, sowing varieties adapted to the region and soil conditions; and sowing at proper time at lower climate risk is recommended (Liu *et al.*, 2013; Willaarts *et al.*, 2014). Sowing with adequate moisture throughout the soil profile and adopting practices that promote the storage of water in the soil are also recommended. Irrigation is effective but costly (Doorenbos and Kassam, 1979; Liu *et al.*, 2013; Willaarts *et al.*, 2014).

The favourable climate for soybean cultivation is during hot summers, with mean temperatures ranging from 20°C to 30°C (68°F to 86°F) (Doorenbos and Kassam, 1979). Thus temperatures below 20°C and over 40°C (68°F, 104°F) lead to significant reduction in growth rate (Doorenbos and Kassam, 1979). Soybean grows in a wide range of soils but optimum growth occurs in moist alluvial soils with a considerable organic content (Doorenbos and Kassam, 1979). Similar to most of legumes, soybeans can fix atmospheric nitrogen by establishing a symbiotic association with the bacterium *Bradyrhizobium japonicum* (Young *et al.*, 2001). Modern crop cultivars generally take between 80-120 days from sowing to harvesting (Kurasch *et al.*, 2017; Samanfar *et al.*, 2017).

## **2.9 Soybean nutrient requirements**

Soybean responds well to fertile soils, that is, for obtaining high yields. It needs large amounts of nitrogen, phosphorus and potassium as well as a smaller quantity of sulphur and some micronutrients. As for nitrogen, the ground portion provides 25 to 35%, and symbiotic fixation of atmospheric nitrogen provides 65 to 85% of the available nutrient. Although the three primary macronutrients are needed in large amounts, phosphorus is less extracted from the soil, either because of its dynamics in tropical soils (fixation) or because of low availability in the soil (McGrath *et al.*, 2013).

Phosphorus is a crop limiting nutrient in most of the soils, that is, it is required for growth, utilization of sugar and starch, photosynthesis, metabolic process that leads to increment of

yield (Ayub *et al.*, 2002; Marcante *et al.*, 2016). It is a nutrient required in relatively large amounts by plants. However, it is considered an “immobile nutrient” compared to N, as it has a relatively short range of movement in the soil. Efficacy of phosphorus uptake is enhanced by the availability of soil moisture. Therefore, dry soil conditions can negatively impact the uptake by the root system. Early-season phosphorus uptake will be used for crop establishment and then later will be redirected for reproduction (McGrath *et al.*, 2013).

In soybeans, the demand for phosphorus is greatest during pod and seed development where more than 60% of phosphorus ends up in the pods and seeds (Dong *et al.*, 2004). In addition, Dong *et al.* (2004) indicated that symptoms of phosphorus deficiency in soybeans include stunted plants and yellowing of the leaf margins in older leaves. The symptoms appear first on the lower leaf tips and extend down the margins toward the leaf base. Leaf edges may become brown and lower leaves often die when phosphorus deficiency is severe, especially during hot, dry, and windy conditions (Dong *et al.*, 2004). Moreover, stalks may be thin and short and maturity can be delayed. Deficiency can be confirmed with soil testing for phosphorus level (Dong *et al.*, 2004).

Plants need phosphorus for growth throughout their life cycle, especially during the early stages of growth and development. The primary role of phosphorus compounds in plants are to store and transfer energy produced by photosynthesis to be used for growth and reproduction. Adequate phosphorus levels are required to enhance shoot and root growth and promote early maturity. These effects often increase water use efficiency and yield potential. When phosphorus levels are inadequate, soybeans cannot grow, produce, or tolerate stresses, as they should. However, inadequate phosphorus levels in the soil can negatively impact the plant, especially under stressful conditions. Low phosphorus decreases the rate of shoot growth, shoot dry weight, affects total leaf area, and consequently the grain yield is reduced (Fredeen *et al.*, 1989).

## **2.10 Phosphorus use efficiency**

The efficiency of nutrient absorption (uptake/acquisition from the soil) and utilization (collectively known as phosphorous use efficiency, PUE) in plants varies within and in different crop species with some being more efficient than others are. According to Shenoy and Kalagudi (2005), understanding of the molecular and physiological basis of mineral nutrient uptake and utilization in plants is crucial in the development of cultivars with better nutrient-efficiency that can perform well under low fertilizer inputs. Wofford *et al.* (1977) divided

cultivars into two groups according to their reaction to high and low phosphorus. The first group termed “phosphorus efficient” cultivars are the ones that are higher yielding than other cultivars under low P fertilization and the second group known as “responsive cultivars” are higher yielding than other cultivars under high P supply. Parentoni *et al.* (2012) suggest selection for phosphorus responsiveness instead of phosphorus use efficiency because when selection for phosphorus use efficiency is priority in a breeding programme, breeders have to find alternative breeding strategies to meet the objective.

### **2.11 Plant mechanisms for improving P acquisition efficiency**

There are several mechanisms used by plants to escape shortages of phosphorus in the soil in both mono and dicotyledonous species (George *et al.*, 2006). According to George *et al.* (2006), dicotyledonous plants are characterized by a taproot system with a prominent primary root and basal roots ascending from the mesocotyl or hypocotyl that together compose the axes of the main root. Likewise, monocots, on the other hand, display a shoot borne root system with multiple root axes resulting in a fibrous root system consequently increasing the absorbing area, thus enhancing the P acquisition from the soil.

The other main strategy that plants use for phosphorus acquisition consists of maximal and constant soil exploration through propagation and extension of all root types, specifically on roots that are efficient metabolically and acquire available phosphorus avidly (Ho *et al.*, 2005). Vance *et al.* (2003) revealed that, when plants are grown in an environment where phosphorus is deficient, they could activate a wide range of mechanisms, which can increase phosphorus acquisition from the soil in a more efficient way. Plants tend to increase both root hair length and density to increase the phosphorus depletion (Lynch, 2007).

Phosphorus deficiency can be due to the low amounts of phosphorus in the soil or low bioavailability. An increment of root quality in crops, results in great increment of phosphorus acquisition. The root characteristics that increase the P acquisition could be improved by conventional breeding. Additionally, three strategies based on molecular breeding, the deployment of transgenic, and the use of good crop management can be used (Fageria *et al.*, 2008; Martins *et al.*, 2013). On the other hand, Miklas *et al.* (2006) indicated the disadvantages of the strategy of enhancing the phosphorus acquisition by the plants through conventional breeding indicating that it was difficult due to the involvement of phenotypic selection for root systems improvement, which is prone to environmental effects and is time-consuming.

Therefore, because the trait is quantitative, a suitable method to dissect its complex polygenic inheritance is via quantitative trait loci (QTL) analysis.

However, Ranathunge *et al.* (2003) suggested that the plant traits and mechanisms for improving P uptake efficiency should involve: i) more and longer adventitious roots; ii) more horizontally oriented basal roots; iii) more taproot laterals; iv) more dispersed higher order laterals, v) increased root hair density and length; vi) better relationship with mycorrhizae and; vii) good formation of aerenchyma, a spongy tissue with large air spaces found between the cells of the stems and leaves of plants, providing buoyancy (resistance) and allows the circulation of gases. Several attempts have been made to improve specific P acquisition processes in food crops through genetic engineering with specific bacterial, fungal or plant genes (Ramaekers *et al.*, 2010). Kaeppler *et al.* (2000), Wissuwa *et al.* (2005), Wissuwa (2005) and Zhu *et al.* (2005) reported a range of QTL identified for tolerance mechanisms to low P in various food crops. Lopez-Bucio *et al.* (2000) observed two- to-four-fold increment of the citrate efflux by roots of transgenic lines and superior growth and yield in low P alkaline soils when introduced a bacterial citrate synthase gene into tobacco (*Nicotiana tabacum* L). Nevertheless, Delhaize *et al.* (2001) could not confirm these results.

## **2.12 Correlation and path coefficient analysis**

Since yield is a complex trait, several studies have been carried out to select soybean genotypes for phosphorus use efficient through other traits. Furthermore, knowledge of the genetic relationship between traits is useful because it can help to predict the performance (Caixeta *et al.*, 2015). Correlation and path coefficients are some of the tools used to measure the relationship among traits. Generally, correlation demonstrates a degree of association between traits, but is not sufficient on its own, as it does not show the direct effect of the trait on the yield. It is, therefore, important to combine it with path analysis. Path analysis helps to identify the direct and indirect effects of the independent trait on the dependent trait (Sarutayophat, 2012). Use of both correlation and path coefficient analysis of agronomic characters is important in evaluating relationships among yield and these traits (Pacheco *et al.*, 2005).

## **2.13 Genotype by environment interaction**

A genotype x environment interaction (GEI) is a change in the relative performance of a given trait of two or more genotypes measured in two or more environments. The interactions involve changes in rank order for genotypes between environments and variations in the total and

relative magnitude of the genetic, environmental and phenotypic variances among environments (Mousavi Shalmani *et al.*, 2017). Thus, Mousavi Shalmani *et al.* (2017) advocated that the GEI analysis should be widely explored in plant breeding to guarantee valid genotype recommendation.

The genetic associations for performance of genotypes between environments are assumed to be based on both linkage and pleiotropy and in this sense are similar to genetic correlations among traits in the same genotypes and environments (Bowman, 1972). Probably correlations are not removed if only the low performance environments are not included, however, there is evidence that heritability improves according to the increment of the level of the performance of the genotype even if the change may be the result of increment in genetic variation or reduction in environmental variation or both (Bowman, 1972).

Genotype and environment interaction (GEI) has important influence on phenotypic expression, so it should be assessed and considered at the stage of the breeding programme before cultivars are recommended for release (do Prado *et al.*, 2001). However, knowing the GEI effect and yield stability is crucial for developing new cultivars with improved adaptation to the environment. Flores *et al.* (1998) advocate that the presence of significant GEI for quantitative characters like yield can severely affect the process of selection of superior genotypes.

Furthermore, identification of yield contributing traits and the GEI of yield in soybean as well as in other crops has been studied by several investigators. Ssemakula and Dixon (2007), Dixon and Nukenine (2000), Egesi *et al.* (2007), Aina *et al.* (2009) and Yan and Tinker (2005), observed significant differences among different cassava genotypes and in different environments for different root yield characters. Shaw *et al.* (2016), Chaves *et al.* (2017), Agoyi *et al.* (2017) reported that GEI contributed more to the total variation than genotypes. Kang and Gorman (1989), Kang (1997), Francis and Kannenberg (1978), studying GEI as well as yield stability in maize, observed strong involvement of the environment on total variation of grain yield. In wheat, a significant GEI effect on grain yield and yield components was observed (Kaya and Turkoz, 2016; Nowosad *et al.*, 2016; Uddin *et al.*, 2017).

According to approaches of Sabaghnia *et al.* (2008), Corrêa *et al.* (2009) and Dehghani *et al.* (2013) the GEI can be exploited through a wide array of statistical techniques (models) developed to investigate and disclose the genotype by environment interaction. Mixed linear models can be used to estimate variance components. Additive main effect and multiplicative



interaction (AMMI) analysis, can be performed to verify the stability and adaptability of genotypes and environments for those traits,

A wide array of statistical techniques has been developed to study and determine the nature GEI. These include, amongst others, Additive Main effects and Multiplicative Interaction (AMMI), which can effectively assess the stability and adaptability of genotypes (Pacheco *et al.*, 2005). Genotype plus GE interaction (GGE) biplot enables the simplistic graphical visualization of GEI (Yan *et al.*, 2000). Other methods most used in GEI according to Roostaei *et al.* (2014), are Joint Regression Analysis (JRA) and Yield–Stability index (YSi). Many researchers tend to combine two or more methods to display a GEI study. Yan *et al.* (2007), Kachala (2018), Samonte *et al.* (2005), Sibiya *et al.* (2012), Mitroviã *et al.* (2012), Balestre *et al.* (2009) applied the AMMI and GGE biplot in soybean, rice and maize to understand the behaviour of genotypes in different location, years and rank them according to their performance and stability as well as identification of the suitable environment to perform the selection of the varieties.

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## CHAPTER 3

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### EVALUATION OF SOYBEAN GENOTYPES UNDER LOW AND HIGH PHOSPHOROUS CONDITIONS IN SOUTHERN AFRICA

#### Abstract

The soils in the tropics are characterized by low availability of phosphorus (P), a macronutrient element that plays an important role in growth, development and seed formation. The objective of this study was to identify soybean lines with high phosphorus use efficiency under P limiting conditions. Twenty-five advanced soybean lines, together with an additional five local checks were evaluated during the 2016/2017 cropping season under low (random P stress) and high (100 kg ha<sup>-1</sup>) P conditions across four locations in Mozambique, Malawi and Zambia. Treatments were arranged in a 6 x 5 alpha-lattice design, with two replications. Data were collected for 15 agronomic traits including grain yield, dry biomass, days to 50% flowering, days to podding, days to physiological maturity, lodging, nodule per plant, nodule weight, plant height, plant vigour pod clearance, seed per pod and seed weight. Data were subjected to analysis of variance using SAS.9.4 statistical package. Analysis of variance showed huge variability of soybean lines for P use efficiency. There were significant ( $P \leq 0.001$ ) effects between phosphorous levels, genotypes, locations and their interactions on phenotypic expression of the traits. Under low phosphorous environment, a reduction in grain yield of 34.39% was noted. Across high P environments, TGx2025-9E, TGx2025-6E and TGx2016-3E were distinct and high yielding, while TGx2025-9E, TGx2016-3E and TGx2023-3E had better performance under low P environments. Genotypes TGx2025-9E and TGx2016-4E performed consistently better across combined P levels. Cluster analysis using Euclidian distances, resulted in six groups with a maximum dissimilarity index of 0.6. Greater distances of dissimilarity were observed between checks MWEMBESHI and the advanced lines TGx1448-2E, TGx2016-4E and TGx2025-6E with distances of 4418, 4621 and 4393, respectively.

### 3.1 Introduction

Soybean (*Glycine max* L. Merrill) is one of the important crops grown in a wide range of edaphic and climatic conditions (Pan *et al.*, 2008; Vianna *et al.*, 2013). It is grown in both tropical and temperate climates (Rao *et al.*, 2002) and is a unique crop based on its food nutritional and industrial oil qualities. It contains 40% protein, 35% carbohydrate, 20% oil and 5% of minerals (Ghani *et al.*, 2016; Song *et al.*, 2016; Van and McHale, 2017). Despite these benefits to humans, the regional contribution of soybean in the sub-Saharan Africa (SSA) region has been hindered by the poor soil quality. The soils are intrinsically poor in fertility especially for phosphorous (P) and nitrogen (N), both of which play an important role in growth, development and yield. Phosphorus deficiency is very critical in the tropics and subtropics mainly in highly weathered soils as well as calcareous/alkaline soils of Mediterranean basin (Hinsinger, 2001; Shenoy and Kalagudi, 2005). Direct availability of P plays an important role in growth, development and seed formation, thus contributing a greater part of the total biomass formation in the plant (Hill, 2012). Manjeru (2017) highlighted that P affects root development and root volume thus affecting the plant's interactive capacity with water and other nutrients. Plants that have a high P use efficiency under low P levels tend to perform better in terms of both agronomic and yield performance. Identification and selection of these cultivars will greatly improve yield productivity in low input agricultural systems that are dominant in SSA.

Phosphorus management and utilization by the crop is an important attribute for selection under low P conditions. It is available to the plant as soluble phosphates that are relatively low in the soil. Phosphorous exists also as an anion, is low water-soluble and a highly immobile nutrient that makes its uptake and availability to the plant very low (Cavalcante *et al.*, 2018; Hinsinger *et al.*, 2011; Lynch, 2011). Phosphorus is important on plant metabolic processes such as transfer of energy, photosynthesis, signal transduction, molecular biosynthesis and respiration. Sub-optimal P levels in the soil can cause yield losses from 5% up to 15% (Hinsinger, 2001; Shenoy and Kalagudi, 2005). Though application of P containing fertilizer is considered as one of the most suitable practices to enhance production under soil with phosphorus deficiency, Ramaekers *et al.* (2010) indicated that other measures, for example, genetic enhancement of plants with respect to P use efficiency can also be part of strategies to increase yield, thus should be taken into account.

Soybean has great genetic variation in response to P and P use efficiency (Pan *et al.*, 2008; Zhang *et al.*, 2008). Breeding is a numbers game – the more variability, the better suitable candidate genotypes for cultivation can be identified and selected. To discriminate soybean

genotypes for P efficiency, there must be enough genetic variability involving a larger number of germplasm (a large gene pool) that will improve selection efficiency (Powell and Barsby, 2013; Sharpley *et al.*, 1993). Research by Lynch *et al.* (2014), Owen *et al.* (2015) and Li *et al.* (2016), reported some mechanisms that plants use to enhance the acquisition of P, with some being capable of modifying soil exploration by roots to increase the absorptive area, while other plants modify the rhizosphere in order to enhance the availability of phosphorus releasing bio-molecules.

Screening involves a comparison of shoot biomass with many other growing parameters (Gill *et al.*, 2004; Ozturk *et al.*, 2005). These parameters include root system length and shoot dry mass (DoVale and Fritsche-Neto, 2013), plant height, pod yield/plant, pods/plant, green pod weight and seed weight (Iqbal *et al.*, 2003; Sarutayophat, 2012). Phosphorous use efficiency (PUE) (uptake and utilization) in wheat is a complex phenomenon that is highly interactive with the environment. Phosphorous absorption interferes with water availability, other nutrients like N and K, microbe populations (immobilization and mineralization processes), and adsorption among other processes (Pii *et al.*, 2015). This complicates its uptake and utilization by plants, and thus its use efficiency. In most plant breeding experiments, yield is the prime objective. However, yield is polygenically inherited and is affected by the environment (Aondover *et al.*, 2013; Sarutayophat, 2012). Thus selection based on secondary traits becomes imperative because yield can be modified or improved based on the genetics of other plant traits that are highly correlated with it, under P limited environments (Cavalcante *et al.*, 2018; Fabiano *et al.*, 2014; Sarutayophat, 2012).

Studies have identified potential yield and genetic gains in different crops under P limited environments (Premkumar *et al.*, 2016). These include maize (*Zea mays* L.) (Rani *et al.*, 2017), wheat (*Triticum aestivum* L.) (Desheva, 2016) and rice (*Oryza sativa* L.) (Premkumar *et al.*, 2016). In maize PUE has been identified to increase yield by 60% (Pii *et al.*, 2015). In wheat, PUE cultivars had 76% yield advantage as compared to P inefficient genotypes (Gunes *et al.*, 2006). On the other hand, Manschadi *et al.* (2014) and Marcante *et al.* (2016) recommended using low P stress and optimum (non-stress) levels as the basis for improvement of PUE. Cultivars that are high yielding under P deficiency will greatly minimize yield losses; reduce the cost of production associated with application of P fertilizers as well as minimize pollution to the environment. This study was designed to investigate the yield and agronomic performance of 25 selected soybean genotypes under limited and optimal P levels across four locations in southern Africa. The identification of high PUE genotypes will greatly improve grain yield and improve nutritional security of millions of smallholder farmers living

under nutritionally insecure communities. The development of improved soybean crop sources with high P uptake and use efficiency and well adapted to low P environments is a sustainable way of improving soybean productivity, improve household income, and a huge compliment to cereal productivity for low production agricultural economies across SSA.

## **3.2 Materials and Methods**

### **3.2.1 Genetic materials**

Thirty advanced breeding lines from IITA-Ibadan presented in Table 3.1, were used for this study. The materials were bred for tolerance to phosphorus deficiency. Five commercial varieties commonly used in the three countries where the genotypes were evaluated were incorporated in the trials as checks. The checks KAFUE, SC SAMBA, MWEMBESHI, SC SAFARI and MRIDIDINA, widely grown in Southern Africa, were also provided by IITA.

### **3.2.2 Experimental sites**

The experiment was conducted across four locations in southern Africa including Gurue at Mutequelece IIAM Research Station (Mozambique); Chitedze Agricultural Research Station, Lilongwe (Malawi); Kabwe Research Station (Zambia) and IITA-Sarah Research Station, Lusaka (Zambia). Two trials at each location were established, one under high P and another under low P (random P stress), except at IITA-Sarah research station where genotypes were evaluated under low P environment only. In total, there were three trials established under high P environment and four trials under low P resulting in seven environments (where an environment = combination of location by P level). Further location details of latitudes, rainfall patterns, dominant temperatures, and soil characteristics are presented in Table 3.2.

Table 3.1 List of 30 genotypes from IITA- Nigeria evaluated across four locations in Mozambique, Zambia and Malawi during the 2016/17 cropping season

CODE	GENOTYPE	TYPE
G1	TGx2025-9E	line
G2	TGx2025-6E	line
G3	TGx2016-3E	line
G4	TGx2016-4E	line
G5	TGx2025-8E	line
G6	TGx2017-6E	line
G7	TGx2017-5E	line
G8	TGx2025-10E	line
G9	TGx2019-1E	line
G10	TGx2025-13E	line
G11	TGx2025-11E	line
G12	TGx2023-3E	line
G13	TGx2027-2E	line
G14	TGx2016-2E	line
G15	TGx2022-4E	line
G16	TGx2020-1E	line
G17	TGx2015-1E	line
G18	TGx2027-7E	line
G19	TGx2026-2E	line
G20	TGx2025-14E	line
G21	TGx2027-1E	line
G22	TGx2026-1E	line
G23	TGx1448-2E	line
G24	TGx1989-19F	line
G25	TGx1987-14F	line
G26	KAFUE	check
G27	MWEMBESHI	check
G28	SC SAMBA	check
G29	SC SAFARI	check
G30	MRIDINA	check

Table 3.2 Summary of locations description

Location	Experiment	Latitude (E)	Longitude (S)	Altitude (masl)	T°C		Rainfall (mm)	Soil type	Relative humidity (%)
	Treatment				Max	Max	Annual average		
Mutequelece	Low P	15°33'941'S	36°72'228E	790	17	34	1857.0	Reed soils, Texture sand-clay, loamy sandy, loamy soils, shallow, deep and well drained	71.3
Mutequelece	High P	15°33'941'S	36°72'228E	790	17	34	1857.0		71.3
Chitedze	Low P	13° 85' S	33° 38' E	1050	16	35	923.7	Ferruginous leptosols (Alfisol), Medium-textured sand clay loan)	69.0
Chitedze	High P	13°85' S	33° 38' E	1050	16	35	923.7		69.0
Kabwe	Low P	14°27'44''S	28°25'51''E	1,182	16	24.4	907.7	Lixisols, Associations	63.8
Kabwe	High P	14°27'44''S	28°25'51''E	1,182	16	24.4	907.7		63.8
Lusaka	Low P	15°18'00.1'' S	28°18'29.0''E	1,279	15	24.5	1078.1	Leptosols and Acrisols	61.5

masl = metres above sea level

### 3.2.3 Experimental design and agronomic management

Twenty-five medium maturity soybean elite lines obtained from the IITA breeding programme in Nigeria and five local checks (Table 3.1) were grown under low and high P treatment levels using a 6 x 5 alpha lattice design with two replications. The high P indicated the recommended optimum P levels ( $100 \text{ kg ha}^{-1}$ ) required for optimal crop growth and development, while low P (random P stress) environment represented no additional P fertilization. Low P stress (random P stress) indicated low potential areas where majority of farmers crop their soybean varieties across SSA. Planting was done between 6<sup>th</sup>-15<sup>th</sup> January at all sites. Inter-row spacing was 0.6 m, while intra-row spacing was 0.1 m, and 2-3 seeds per hill were planted at 3-5 cm depth. Each plot consisted of four rows of 5 m long, where the two middle rows constituted the net plot. Thinning was done one week after emergence leaving one plant per hill to maintain uniformity on the plant density per plot. Plants were grown in the field under rain-fed conditions throughout the season (no additional water supplied). Weeding was done manually to control the weeds. There were no pest incidences during the trial duration hence no pesticides were applied.

### 3.2.4 Data collection

Data was collected for the traits described below:

- **Plant height (PH);** this was done by the use of a measuring ruler to measure plants from the ground level to the top of the stem and the mean calculated and recorded for each treatment.
- **Pod clearance (PCLEAR);** using measuring ruler, each of the five plants were measured from the ground level till the first branch, then the mean was recorded for each treatment.
- **Plant vigour (PLV);** the appearance of the plants, vigour and aspect, all plants were given a score using a scale ranging from 1-5, where: one was more vigorous and five poor plant. The mean for each plot was recorded.
- **Lodging (LODG);** using a scale of 1-5, all treatments were classified according to their resistance to lodging, where, one, means the plants are resistant to lodging and five are more susceptible.
- **Days to 50% flowering (DF):** the number of days from planting to the time that 50% of the plants from the two middle rows of each plot flowering was recorded. This was done by visual examination.



- **Days to podding (DP):** the number of days from planting to the time that 50% of the plants from the two middle rows of each plot started having pods was recorded. This was done by visual examination.
- **Days to physiological maturity (DM);** recorded as the number of days from planting to the time that about 50% of pods had turned brown and 75% of leaves had shed, was recorded.
- **Grain yield (GYD);** measured at maturity by harvesting all plants from the two central rows of each plot. All seeds from the two middle rows were threshed from the pods and measured the net plot yield. This was done using balance scale. The yield per hectare was calculated using the Equation 3-1.
- **Seed weight (NODW)**  
After harvesting and trashing, randomly 100 seed were sampled in each line put in labelled envelopes then weighed using a sensitive balance scale, and the mean recorded.

Equation 3-1 Determination of grain yield (kg ha<sup>-1</sup>)

$$Yield(kg/ha) = \left( \frac{(100 - \%Grain\ moisture\ content)}{(100 - 13)} \right) \times \left( \frac{(Net\ plot\ yield)}{Net\ plot\ area} \times 10000 \right)$$

### 3.2.5 Data analysis

The quantitative data were subjected to analysis of variance to test for significant differences among lines using the GLM procedure of SAS statistical package version 9.4. The means (LSMEANS) were separated using the Tukey option at 5% probability level. GenStat 18<sup>th</sup> edition (Payne *et al.*, 2015) was used for cluster analysis, using unweighted pair group method with arithmetic means across all traits and a dendrogram was constructed. Clustering the genotypes using un-weighted pair group and K-means method gives a predetermined number of groups.

A linear model below was used for analysing variance components

$$Y_{ijkl} = \mu + T_i + \rho_j + \alpha_{jk} + S_{ijk} + \varepsilon_{ijkl}$$

Where:

$Y_{ijk}$  denotes the value of the observed trait for the  $i^{\text{th}}$  treatment obtained in the  $k^{\text{th}}$  block within the  $j^{\text{th}}$  replicate,  $\mu$  is the grand mean,  $\tau_i$  is the effect of the  $i^{\text{th}}$  treatment,  $\rho_j$  is the effect of the  $j^{\text{th}}$  replicate,  $\alpha_{jk}$  is the effect of the  $k^{\text{th}}$  incomplete block within the  $j^{\text{th}}$  replicate,  $S_{ijk}$  is the location

effect and  $\varepsilon_{ijk}$  is a random error. The statistical analysis for the Alpha design was performed using the following order: Treatment + Rep + Rep/Block (Random).

### **3.3 Results**

#### **3.3.1 Analysis of variance for grain yield and yield components**

The results for combined analysis of variance (ANOVA) across both low and high P environments are presented in Table 3.3. The trials (as described in the materials and methods section), involved four low P and three high P experiments. For combined analysis, there were highly significant GEI ( $P < 0.001$ ) for all the measured traits except lodging and plant vigor. Highly significant variations were also observed for genotypes and locations. The coefficient of variation was below 17% except for plant vigour (36.3%) and lodging (34.5%). Environmental mean squares were higher than for genotypes and GEI mean squares.

Under low P environments (Table 3.3), the ANOVA showed highly significant ( $P < 0.001$ ) GEI interactions for all the measured traits. The genotypic and GEI were also highly significant. The results had the same trend across high P levels (Table 3.3).

Table 3.3 Mean squares for days to flowering, days to maturity, days to podding, grain yield, lodging, plant height, plant vigour pod clearance and seed weight

S. variation	d.f.	DF	DM	DP	GYD	LODG	PCLEAR	PHT	PLV	SEEDW
<b>Across combined (low and high P) environments</b>										
REP	1	42.5*	39.2 <sup>ns</sup>	22.8 <sup>ns</sup>	16737.0 <sup>ns</sup>	0 <sup>ns</sup>	0.03 <sup>ns</sup>	4.8 <sup>ns</sup>	0.02 <sup>ns</sup>	0.1 <sup>ns</sup>
BLK	10	13.5 <sup>ns</sup>	18.6 <sup>ns</sup>	10.9 <sup>ns</sup>	23258.0 <sup>ns</sup>	0.1 <sup>ns</sup>	1.5 <sup>ns</sup>	30.7 <sup>ns</sup>	0.7 <sup>ns</sup>	1.5 <sup>ns</sup>
GEN	29	70.3***	263.6***	86.0***	364180.0***	0.2 <sup>ns</sup>	8.79***	258.4***	0.9 <sup>ns</sup>	11.6***
Loc	6	4885.4***	37429.6***	4245.9***	16571452.0***	3.2***	1056.0***	25540.4***	33.0***	371.6***
G x E	87	72.1***	202.6***	63.8***	322646.0***	0.2 <sup>ns</sup>	10.9***	206.6***	0.6 <sup>ns</sup>	12.2***
Residual	109	9.3	17.3	8.312	33194.0	0.2	1.9	24.8	0.6	2.1
<b>Total</b>	<b>239</b>	<b>101.1</b>	<b>584.4</b>	<b>91.3</b>	<b>385830.0</b>	<b>0.3</b>	<b>19.2</b>	<b>439.8</b>	<b>1.0</b>	<b>11.5</b>
<b>Low phosphorus environment</b>										
REP	1	42.5*	39.2 <sup>ns</sup>	22.8 <sup>ns</sup>	16737.0	0.0 <sup>ns</sup>	0.03 <sup>ns</sup>	4.8 <sup>ns</sup>	0.02 <sup>ns</sup>	0.1 <sup>ns</sup>
BLK	10	13.5 <sup>ns</sup>	18.6 <sup>ns</sup>	10.9 <sup>ns</sup>	23258.0	0.3 <sup>ns</sup>	1.5 <sup>ns</sup>	30.7 <sup>ns</sup>	0.7 <sup>ns</sup>	1.5 <sup>ns</sup>
GEN	29	70.4***	263.6***	86.0***	364180.0***	0.2 <sup>ns</sup>	8.79***	258.4***	0.9	11.5***
Loc	3	4885.4***	37429.6***	4245.9***	16571452.0***	3.2***	1056.0***	25540.4***	33.0***	371.6***
G x E	87	72.1***	202.6***	63.8***	322646.0***	0.2 <sup>ns</sup>	10.9***	206.6***	0.6 <sup>ns</sup>	12.3***
Residual	109	9.3	17.3	8.3	33194.0	0.2	1.9	24.8	0.6	2.1
<b>Total</b>	<b>239</b>	<b>101.1</b>	<b>584.4</b>	<b>91.3</b>	<b>385830.0</b>	<b>0.3</b>	<b>19.2</b>	<b>439.8</b>	<b>1.02</b>	<b>11.5</b>
<b>High phosphorus environment</b>										
REP	1	0.6 <sup>ns</sup>	81.3 <sup>ns</sup>	6.42 <sup>ns</sup>	118.0 <sup>ns</sup>	0.67 <sup>ns</sup>	0.003**	0.9 <sup>ns</sup>	0.02 <sup>ns</sup>	1.7 <sup>ns</sup>
BLK	10	14.7**	144.2***	33.18**	234899.0***	0.27 <sup>ns</sup>	13.42***	119.5	1.0978	183.7***
GEN	29	35.7***	253.0***	58.50***	580017.0***	0.2 <sup>ns</sup>	11.8***	317.6	0.7554	567.3***
Loc	2	3319.1***	32357.4***	1592.17***	14188076.0***	4.6**	864.4***	26100.0	38.5***	843.6***
G x E	58	41.2***	229.8***	65.42***	344935.0***	0.2 <sup>ns</sup>	12.4***	145.6 <sup>ns</sup>	0.6	834.9***
Residual	79	5.0	19.9	12.53	56162.0	0.21	1.294	17.42	0.8	117.1
<b>Total</b>	<b>179</b>	<b>59.2</b>	<b>494.5</b>	<b>55.9</b>	<b>402172.0</b>	<b>0.2</b>	<b>16.9</b>	<b>404.64</b>	<b>1.1296</b>	<b>2548.263</b>

d.f.= Degrees of freedom; loc=Location; BLK= Block; REP=Replication; GEN=Genotype; DF= Days to 50% Flowering; DM=Days to 50% maturity; GYD=Grain yield; LODG=Lodging; PHT=Plant height; PLV=Plant vigour; PCLEAR=Pod Clearance; SEEDW=Seed weight;; <sup>ns</sup>=None significant; \*significant (P<0.05); \*\*= significant (P<0.01); \*\*\*=significant (P=0.001)

### 3.3.2 Grain yield and agronomic performance across seven combined environments

Table 3.4 shows the mean grain yield and agronomic performance of 25 selected soybean lines and 5 checks across seven high and low P stress environments. Genotypes G2, G1 and G3 had the highest mean yields of 1727, 1726 and 1635.8 kg ha<sup>-1</sup> respectively, with an overall mean of 1324.4 kg ha<sup>-1</sup>. The highest yielding lines were 15.3% better yielding than the highest check variety G29 (SCSAFARI) and 23.3% better than the overall mean. The lowest yielding genotypes included G5 (947.7 kg ha<sup>-1</sup>), G11 (1031 kg ha<sup>-1</sup>), G20 (1051 kg ha<sup>-1</sup>) and G22 (1054.7 kg ha<sup>-1</sup>) which performed 6.5% lower than the local check varieties G30 (MRIDINA) and G26 (Kafue). These soybean lines were significantly different as shown in superscripted letters in Table 3.4.

In general, days to flowering varied from 32.9 to 45.3 days with the earliest genotype being G14 (32.9 days) followed by G12 with 34 days and G24 with 35.2 days. The genotypes that took longer to flower were G6 with 45.3 days and 41 days for genotypes G15 and G22. With respect to pod formation, genotypes G14 with 41.6 days, G12 (43.4 days) and the check G30 (44.1 days) were earliest with an overall mean of 75.09 days. The later maturing genotypes observed in this experiment included G6 (111.3), G7 (102.9) and G15 (98.7 days).

G6 had the highest 100 seed weight (18.7 g), followed by G1 (18.3 g), and then G5 (18.0 g), with a mean of 16.2 g. Genotypes G13 and G26 had the lowest seed weight, both with 13.9 g, and G8, G9 and G14 all with 13.0 g. Highly significant differences were observed amongst the genotypes for total biomass.

G7 had the highest harvest index, followed by G1, G17, G12 and G21 with 0.50, 0.47, 0.44, 0.39 and 0.39, respectively, though they were lower than the highest genotypes. The checks performed well in terms of harvest index. G26, G29, G30, G28 and G27 had 0.42, 0.38, 0.32, 0.32 and 0.26 percentage harvest index, respectively. Genotype G15 had the least harvest index of 0.08.

Table 3.4 Mean performance of 30 soybean genotypes for various traits across environments

GEN	DF	DP	DM	PHT (cm)	PLV	GYD (ha <sup>-1</sup> )	SEEDW (g)	LODG
G1	39.9 <sup>bc</sup>	48.8 <sup>dbc</sup>	94.1 <sup>c-f</sup>	59.7 <sup>c-h</sup>	2.2	1726.0 <sup>a</sup>	18.3 <sup>ab</sup>	1.3
G2	38.7 <sup>b-e</sup>	47.4 <sup>d-e</sup>	91.5 <sup>d-h</sup>	62.5 <sup>a-e</sup>	1.9	1727.0 <sup>a</sup>	17.2 <sup>a-d</sup>	1.1
G3	37.9 <sup>b-f</sup>	46.9 <sup>d-e</sup>	90.6 <sup>e-i</sup>	65.4 <sup>a-d</sup>	2.5	1635.8 <sup>ab</sup>	17.1 <sup>a-e</sup>	1.4
G4	39.1 <sup>bcde</sup>	49.2 <sup>dbc</sup>	91.4 <sup>d-i</sup>	66.1 <sup>abc</sup>	2.4	1549.7 <sup>a-d</sup>	16.3 <sup>b-h</sup>	1.1
G5	37.0 <sup>b-g</sup>	48.1 <sup>d-e</sup>	95.2 <sup>cde</sup>	61.9 <sup>a-e</sup>	1.9	947.6 <sup>7i</sup>	18.0 <sup>bc</sup>	1.2
G6	45.3 <sup>a</sup>	55.4 <sup>a</sup>	111.3 <sup>a</sup>	59.9 <sup>c-h</sup>	2.4	1202.3 <sup>d-i</sup>	18.7 <sup>a</sup>	1.2
G7	38.0 <sup>b-f</sup>	46.3 <sup>d-g</sup>	102.9 <sup>b</sup>	53.7 <sup>f-m</sup>	2.9	1372.5 <sup>a-h</sup>	17.4 <sup>abc</sup>	1.1
G8	38.9 <sup>b-e</sup>	42.6 <sup>fg</sup>	85.7 <sup>hij</sup>	53.3 <sup>g-m</sup>	1.9	1498.5 <sup>a-f</sup>	14.7 <sup>ghi</sup>	1.5
G9	39.7 <sup>bcd</sup>	50.9 <sup>abc</sup>	87.2 <sup>g-i</sup>	58.4 <sup>d-h</sup>	2.4	1452.5 <sup>a-f</sup>	14.7 <sup>ghi</sup>	1.4
G10	38.7 <sup>b-e</sup>	46.4 <sup>d-g</sup>	94.6 <sup>cde</sup>	58.6 <sup>c-h</sup>	2.1	1242.8 <sup>c-i</sup>	15.9 <sup>c-i</sup>	1.2
G11	36.5 <sup>c-g</sup>	46.7 <sup>d-g</sup>	97.1 <sup>bcd</sup>	58.6 <sup>c-h</sup>	2.2	1051.0 <sup>hi</sup>	16.6 <sup>a-h</sup>	1.0
G12	34.1 <sup>fg</sup>	43.4 <sup>feg</sup>	87.7 <sup>f-j</sup>	50.2 <sup>i-m</sup>	2.2	1453.6 <sup>a-f</sup>	14.3 <sup>hi</sup>	1.2
G13	37.0 <sup>b-fg</sup>	46.9 <sup>d-e</sup>	87.6 <sup>f-j</sup>	60.4 <sup>b-g</sup>	2.0	1369.3 <sup>a-h</sup>	13.9 <sup>i</sup>	1.2
G14	32.9 <sup>g</sup>	41.6 <sup>g</sup>	86.0 <sup>hij</sup>	53.9 <sup>f-m</sup>	2.3	1166.0 <sup>e-i</sup>	14.7 <sup>ghi</sup>	1.2
G15	40.4 <sup>c</sup>	48.7 <sup>dbc</sup>	98.7 <sup>cb</sup>	68.8 <sup>a</sup>	2.4	1154.8 <sup>e-i</sup>	14.8 <sup>e-i</sup>	1.2
G16	40.4 <sup>bc</sup>	47.7 <sup>d-e</sup>	94.7 <sup>cde</sup>	48.1 <sup>m</sup>	2.3	1078.4 <sup>ghi</sup>	16.5 <sup>a-h</sup>	1.2
G17	35 <sup>efg</sup>	42.6 <sup>fg</sup>	85.0 <sup>ij</sup>	48.3 <sup>km</sup>	2.0	1593.0 <sup>abc</sup>	16.7 <sup>a-g</sup>	1.4
G18	38.2 <sup>b-f</sup>	48.6 <sup>d-e</sup>	94.1 <sup>c-f</sup>	56.6 <sup>e-j</sup>	2.3	1586.5 <sup>abc</sup>	16.6 <sup>a-h</sup>	1.2
G19	37.5 <sup>b-g</sup>	46.8 <sup>d-g</sup>	93.5 <sup>c-g</sup>	61.2 <sup>a-f</sup>	2.1	1329.4 <sup>b-h</sup>	16.6 <sup>a-h</sup>	1.5
G20	39.0 <sup>b-e</sup>	48.4 <sup>d-e</sup>	92.8 <sup>c-g</sup>	52.4 <sup>h-m</sup>	1.8	1054.7 <sup>hi</sup>	16.0 <sup>b-i</sup>	0.9
G21	38.1 <sup>b-f</sup>	48.3 <sup>d-e</sup>	89.9 <sup>e-i</sup>	57.7 <sup>e-i</sup>	1.7	1502.3 <sup>a-e</sup>	16.2 <sup>b-i</sup>	1.4
G22	41.1 <sup>abc</sup>	53.0 <sup>ab</sup>	95.5 <sup>cde</sup>	67.7 <sup>ab</sup>	2.1	1031.6 <sup>hi</sup>	17.5 <sup>abc</sup>	1.3
G23	41.2 <sup>ab</sup>	48.9 <sup>dbc</sup>	92.9 <sup>c-g</sup>	60.4 <sup>b-g</sup>	2.3	1162.2 <sup>e-i</sup>	14.8 <sup>f-i</sup>	1.2
G24	35.2 <sup>d-g</sup>	44.7 <sup>d-g</sup>	90.8 <sup>d-i</sup>	55.9 <sup>e-k</sup>	1.7	1470.8 <sup>a-e</sup>	16.3 <sup>a-h</sup>	1.4
G25	40.4 <sup>bc</sup>	53.2 <sup>ab</sup>	95.7 <sup>cde</sup>	55.0 <sup>e-k</sup>	1.8	1127.6 <sup>f-i</sup>	15.7 <sup>c-i</sup>	1.1
G26	35.2 <sup>efg</sup>	46.3 <sup>d-g</sup>	82.0 <sup>j</sup>	53.2 <sup>g-m</sup>	2.3	1428.5 <sup>a-g</sup>	13.9 <sup>i</sup>	1.4
G27	37.5 <sup>b-g</sup>	47.7 <sup>d-e</sup>	93.6 <sup>c-f</sup>	49.63 <sup>jk</sup>	1.9	1103.3 <sup>f-i</sup>	14.9 <sup>d-i</sup>	1.1
G28	35.2 <sup>d-g</sup>	45.2 <sup>d-g</sup>	85.1 <sup>hij</sup>	49.8 <sup>jk</sup>	2.0	1146.7 <sup>f-i</sup>	17.1 <sup>a-f</sup>	1.4
G29	35.0 <sup>efg</sup>	45.9 <sup>d-g</sup>	85.5 <sup>hij</sup>	46.8 <sup>m</sup>	2.2	1463.7 <sup>a-f</sup>	17.8 <sup>abc</sup>	1.2
G30	34.5 <sup>efg</sup>	44.1 <sup>d-g</sup>	85.1 <sup>hij</sup>	50.7 <sup>i-m</sup>	2.3	1103.3 <sup>f-i</sup>	16.4 <sup>a-h</sup>	1.2
Mean	37.9	50.6	91.9	56.8	1.3	1324.4	16.2	1.1
CV (%)	7.2	3.4	4.1	7.91	43.8	16.3	8.5	20.9
ST.E	0.5	0.1	0.7	0.8	0.1	39.9	0.3	0.6

GEN=Genotypes; ST-ERROR=Standard error; CV=Coefficient of variation; PHT=Plant height in centimetres; DF = Days to 50% Flowering; DP=Days to podding DM=Days to 50% maturity; SEEDW=Seed weight in grams; GYD=Grain yield (kg ha<sup>-1</sup>); LODG=Lodging, PLV = Plant vigour  
Means followed by same superscript letter were not significantly different (P=0.05)

### 3.3.3 Grain yield and agronomic performance across low P environments

On grain yield, significant differences were observed for genotype, location, phosphorous level as well as for genotype by location and by phosphorus level (Tables 3.5 and 3.7). Under low phosphorus, genotypes G1 (1420 kg ha<sup>-1</sup>), G12 (1417.2 kg ha<sup>-1</sup>) and G3 (1411.8 kg ha<sup>-1</sup>) recorded high yields while G5 (773.6 kg ha<sup>-1</sup>), G14 (818.1 kg ha<sup>-1</sup>), G20 (840.1 kg ha<sup>-1</sup>), G22 (871.9 kg ha<sup>-1</sup>) and G16 (893.5 kg ha<sup>-1</sup>) had low yields.

In case of plant height, three tallest genotypes observed were G15 (63.9 cm), followed by G4 (61.1 cm) and G3 (58.3 cm). G28 and G29, both with 45.5 cm, followed by G12 with 45.0 cm and G25 with 45.1 cm height were the shortest genotypes observed under low environment. In terms of days to 50% flowering, G6 obtained 47.2 days, that is, maximum days to reach 50% flowering, followed by G23 (44.5 days) and G22 (43.6 days), and the minimum days to 50% flowering were observed for G14 (33.7 days), G12 (35.5 days) and G30 (35.7 days). G4, G8 and G17 were the earliest genotypes to reach 50% podding with 41.1, 42.8 and 42.9 days, while G6, G25 and G22 were the latest to have pods. The number of days to mature varied from 86.0 days for G26 to 111.8 days for G6. Therefore, the mean among the genotypes under environment with low P was 94.25 days. Furthermore, G9, G6 and G18 had the highest number of pods per plant with 118.5, 98.8 and 95.9 pods, respectively, and genotypes with fewer number of pods were G7 (45.4), G1 (49.5) and G14 (49.9).

Under low phosphorus conditions, the mean seed weight was 16.52 g and the highest weight was 17.9 g observed for genotype G6, followed by G5 (17.7 g) and G2 with 17.3 g. Genotypes G15, G8, G12 and G3 had low seed weight under low phosphorus with 13.3 g, 14.2 g, 14.6 g and 14.6 g, respectively. Statistically, all 30 genotypes under the study had similar response to low phosphorus environment across all locations on parameters of plant vigour and lodging (they were not significantly different). The grand mean for lodging was 1.1. The mean for plant vigour was 2.2. High vigour was obtained for genotype G17 with 1.1 and less vigour was achieved by G7 with 2.9.

Table 3.5 Performance of the soybean genotypes for various traits under low phosphorus environments

GEN	DF	DP	DM	GYD (ha <sup>-1</sup> )	PHT (cm)	PLV	LODG	SEEDW (g)
G1	41.4 <sup>a-d</sup>	51.1 <sup>abc</sup>	100.0 <sup>cbd</sup>	1420.2 <sup>a</sup>	51.1 <sup>c-g</sup>	2.9	1.3	17.2 <sup>abc</sup>
G2	40.5 <sup>cde</sup>	49.8 <sup>b-e</sup>	94.2 <sup>c-i</sup>	1387.0 <sup>a</sup>	55.6 <sup>a-g</sup>	2.0	1.1	17.3 <sup>abc</sup>
G3	37.7 <sup>b-e</sup>	48.6 <sup>b-f</sup>	932.0 <sup>c-i</sup>	1411.8 <sup>a</sup>	58.3 <sup>a-d</sup>	2.5	1.3	14.6 <sup>a-d</sup>
G4	39.7 <sup>b-e</sup>	48.3 <sup>b-f</sup>	94.9 <sup>c-h</sup>	1334.1 <sup>ab</sup>	61.1 <sup>abc</sup>	2.8	1.0	15.6 <sup>a-d</sup>
G5	37.9 <sup>a</sup>	47.1 <sup>b-g</sup>	100.3 <sup>cb</sup>	773.6 <sup>f</sup>	53.9 <sup>a-g</sup>	2.1	1.1	17.7 <sup>a</sup>
G6	47.2 <sup>b-e</sup>	56.8 <sup>a</sup>	111.8 <sup>a</sup>	970.4 <sup>a-f</sup>	56.0 <sup>a-f</sup>	2.6	1.3	17.9 <sup>a</sup>
G7	39.1 <sup>a-d</sup>	46.6 <sup>b-g</sup>	103.6 <sup>ab</sup>	1016.5 <sup>a-f</sup>	51.8 <sup>c-g</sup>	2.9	1.2	17.3 <sup>abc</sup>
G8	42.1 <sup>a-d</sup>	42.8 <sup>fg</sup>	86.4 <sup>hi</sup>	1406.6 <sup>a</sup>	45.6 <sup>efg</sup>	1.6	1.5	14.2 <sup>cd</sup>
G9	40.6 <sup>b-e</sup>	50.5 <sup>a-d</sup>	88.6 <sup>f-i</sup>	1317.9 <sup>abc</sup>	48.5 <sup>d-g</sup>	2.5	1.3	15.0 <sup>a-d</sup>
G10	39.5 <sup>de</sup>	47.9 <sup>c-f</sup>	97.2 <sup>b-f</sup>	1125 <sup>a-f</sup>	54.9 <sup>a-g</sup>	2.5	1.3	15.1 <sup>a-d</sup>
G11	36.2 <sup>de</sup>	45.6 <sup>c-g</sup>	94.3 <sup>c-i</sup>	1120.2 <sup>a-f</sup>	54.0 <sup>a-g</sup>	1.9	1.1	15.9 <sup>a-d</sup>
G12	35.5 <sup>b-e</sup>	44.3 <sup>d-g</sup>	90.8 <sup>e-i</sup>	1417.2 <sup>a</sup>	45.0 <sup>fg</sup>	2.0	1.4	14.6 <sup>a-d</sup>
G13	38.0 <sup>e</sup>	47.4 <sup>b-f</sup>	89.3 <sup>f-i</sup>	1328.4 <sup>ab</sup>	52.5 <sup>b-g</sup>	2.3	1.3	14.3 <sup>bcd</sup>
G14	33.7 <sup>a-d</sup>	41.1 <sup>g</sup>	88.0 <sup>ghi</sup>	818.1 <sup>ef</sup>	46.9 <sup>de-g</sup>	2.2	1.1	15.3 <sup>a-d</sup>
G15	41.8 <sup>a-e</sup>	50.3 <sup>bcd</sup>	100.7 <sup>cb</sup>	1151.3 <sup>a-f</sup>	63.9 <sup>a</sup>	2.7	1.4	13.5 <sup>d</sup>
G16	40.5 <sup>de</sup>	49.6 <sup>b-e</sup>	95.8 <sup>b-g</sup>	893.5 <sup>b-f</sup>	45.4 <sup>efg</sup>	2.6	1.1	15.8 <sup>a-d</sup>
G17	36.0 <sup>b-e</sup>	42.9 <sup>fg</sup>	87.8 <sup>ghi</sup>	1371.8 <sup>a</sup>	46.4 <sup>efg</sup>	2.6	1.5	16.8 <sup>a-d</sup>
G18	39.1 <sup>b-e</sup>	49.0 <sup>b-f</sup>	96.5 <sup>b-f</sup>	1333.1 <sup>ab</sup>	54.9 <sup>a-g</sup>	2.8	1.2	16.4 <sup>a-d</sup>
G19	38.1 <sup>b-e</sup>	46.7 <sup>b-g</sup>	94.8 <sup>c-h</sup>	1268.1 <sup>a-d</sup>	57.9 <sup>a-d</sup>	2.6	1.6	16.8 <sup>abc</sup>
G20	39.7 <sup>b-e</sup>	47.4 <sup>b-g</sup>	98.9 <sup>b-e</sup>	840.1 <sup>def</sup>	47.4 <sup>d-g</sup>	2.1	0.9	16.2 <sup>a-d</sup>
G21	40.3 <sup>abc</sup>	48.2 <sup>c-f</sup>	92.5 <sup>c-i</sup>	1202.0 <sup>a-f</sup>	55.9 <sup>a-f</sup>	1.8	1.4	16.3 <sup>a-d</sup>
G22	43.6 <sup>ab</sup>	52.7 <sup>ab</sup>	98.6 <sup>b-e</sup>	871.9 <sup>cdef</sup>	63.2 <sup>ab</sup>	2.4	1.4	16.6 <sup>a-d</sup>
G23	44.5 <sup>de</sup>	50.3 <sup>bcd</sup>	94.9 <sup>c-h</sup>	1079.4 <sup>a-f</sup>	56.2 <sup>a-e</sup>	2.2	1.3	14.7 <sup>a-d</sup>
G24	35.8 <sup>a-d</sup>	43.8 <sup>efg</sup>	91.9 <sup>d-i</sup>	1245 <sup>a-e</sup>	54.6 <sup>a-g</sup>	1.8	1.4	16.6 <sup>a-d</sup>
G25	41.9 <sup>de</sup>	53.0 <sup>ab</sup>	97.8 <sup>b-e</sup>	1032.6 <sup>a-f</sup>	45.1 <sup>efg</sup>	1.8	1.0	16.5 <sup>a-d</sup>
G26	36.3 <sup>b-e</sup>	45.6 <sup>c-g</sup>	86.0 <sup>i</sup>	1172.3 <sup>a-f</sup>	47.4 <sup>d-g</sup>	2.6	1.7	14.6 <sup>a-d</sup>
G27	39.5 <sup>cde</sup>	46.8 <sup>b-g</sup>	96.7 <sup>b-f</sup>	1065.7 <sup>a-f</sup>	45.5 <sup>efg</sup>	2.1	1.0	14.4 <sup>bcd</sup>
G28	37.5 <sup>cde</sup>	46.6 <sup>b-g</sup>	88.7 <sup>g-i</sup>	1037.1 <sup>a-f</sup>	44.5 <sup>g</sup>	2.1	1.3	17.6 <sup>ab</sup>
G29	37 <sup>de</sup>	46.1 <sup>c-g</sup>	87.1 <sup>hi</sup>	1232.2 <sup>a-e</sup>	44.5 <sup>g</sup>	2.4	1.3	17.3 <sup>abc</sup>
G30	35.7 <sup>b-e</sup>	44.6 <sup>d-g</sup>	86.4 <sup>hi</sup>	985.2 <sup>a-f</sup>	47.1 <sup>d-g</sup>	2.5	1.1	15.7 <sup>a-d</sup>
Mean	39.2	47.7	94.3	1154.3	51.8	2.3	1.3	15.9
CV (5%)	7.8	5.9	3.9	16.9	9.4	31.2	36.9	9.01
ST.E	0.6	0.5	0.7	36.0	0.9	0.1	0.1	2.3

GEN=Genotypes; ST-ERROR=Standard error; CV=Coefficient of variation; DF = Days to 50% Flowering; DP=Days to podding DM=Days to 50% maturity; GYD=Grain yield (kg ha<sup>-1</sup>); LODG=Lodging; PHT=Plant height in centimetres; PLV = Plant vigour; SEEDW=Seed weight in grams. Means followed by same superscript letter were not significantly different (P=0.05)



### 3.3.4 Grain yield and agronomic performance across high P environments

According to the analysis of variance presented in Table 3.3, results demonstrated highly significant differences for all parameters amongst the genotypes, across locations including among treatments. In terms of grain yield, high yielding genotypes were G2 (2182.1 kg ha<sup>-1</sup>), G1 (2133.6 kg ha<sup>-1</sup>) and G3 (1934.4 kg ha<sup>-1</sup>), while genotypes with low yield included G11 (958.7 kg ha<sup>-1</sup>), G15 (1151.3 kg ha<sup>-1</sup>) and G5 (1179.8 kg ha<sup>-1</sup>) (Table 3.6 and 3.7).

For plant height the three tallest genotypes were G15 (75.3 cm), G3 (74.9) and G22 (73.7 cm), whereas shortest plants were observed for G29 (49.8 cm), followed by G17 (50.9 cm) and G16 (51.6 cm). Number of days to flowering under high phosphorus environment were maximum for genotypes G6 (42.9 days), G16 (40.2 days) and G25 (38.5) while the least number of days was observed for G14 (31.8 days), G12, G28 and G29 (32.2 days). The mean days to maturity observed was 88.81 days, however genotypes G6, G7 and G11, matured much later with about 110.6, 102.0 and 100.8 days, respectively. The earliest maturing genotypes under high phosphorus environment were G29 (83.3 days) followed by genotype G12 and G30 (83.5 days). Regarding days to 50% pod formation, the top genotype with less days to reach 50% pods was G17, G14, G12 G8 and G9 all with about 42 days and the rest of the genotypes completed 50% podding after 50 days.

The highest mean observed for 100 seed weight was 20.6 g achieved with genotype G3, followed by genotype G1 and G6 both with 19.8 g and G5 (18.3 g). However, the lowest seed weight of 13g was observed for genotype G26 under high phosphorus environment, followed by G12 with 13.8 g and G14 with 13.9 g. The grand mean for lodging under high P environment was 1.21. Moreover, the high vigour genotypes identified were G17 (1.1), G19 (1.3) and G19 (1.4), while less vigour was observed for G7 (2.8), G12 (2.7) and G11 (2.6).

Table 3.6 Performance of the soybean genotypes for various traits under high phosphorus environments

GEN	PHT (cm)	GYD (ha <sup>-1</sup> )	DF	DP	DM	PLV	LODG	SEEDW (g)
G1	71.1 <sup>a-d</sup>	2133.6 <sup>ab</sup>	38 <sup>a-f</sup>	45.7 <sup>a-d</sup>	86.1 <sup>d-h</sup>	1.4	1.4	19.8 <sup>ab</sup>
G2	71.6 <sup>abc</sup>	2182.1 <sup>a</sup>	36.3 <sup>b-f</sup>	44.2 <sup>bcd</sup>	88 <sup>d-g</sup>	1.7	1.1	17.1 <sup>b-f</sup>
G3	74.9 <sup>a</sup>	1934.4 <sup>abc</sup>	38.3 <sup>a-e</sup>	44.7 <sup>a-d</sup>	87.5 <sup>d-g</sup>	2.5	1.4	20.6 <sup>a</sup>
G4	72.8 <sup>abc</sup>	1837.2 <sup>a-e</sup>	38.4 <sup>a-d</sup>	50.4 <sup>a-d</sup>	86.6 <sup>d-h</sup>	1.8	1.1	17.3 <sup>a-e</sup>
G5	72.5 <sup>abc</sup>	1179.8 <sup>gef</sup>	35.8 <sup>b-f</sup>	49.5 <sup>a-d</sup>	88.3 <sup>d-g</sup>	1.7	1.2	18.3 <sup>a-d</sup>
G6	65 <sup>a-h</sup>	1511.6 <sup>b-g</sup>	42.9 <sup>a</sup>	53.5 <sup>a</sup>	110.6 <sup>a</sup>	2.2	1.1	19.8 <sup>abc</sup>
G7	56.2 <sup>f-j</sup>	1847.3 <sup>a-e</sup>	36.4 <sup>b-f</sup>	45.9 <sup>a-d</sup>	102 <sup>ab</sup>	2.9	1	17.6 <sup>a-e</sup>
G8	63.6 <sup>b-h</sup>	1621 <sup>a-f</sup>	34.7 <sup>b-f</sup>	42.4 <sup>cd</sup>	84.6 <sup>e-h</sup>	2.2	1.4	15.4 <sup>d-h</sup>
G9	71.7 <sup>abc</sup>	1632 <sup>a-f</sup>	38.4 <sup>abc</sup>	51.5 <sup>abc</sup>	85.3 <sup>e-h</sup>	2.4	1.5	14.2 <sup>e-h</sup>
G10	63.6 <sup>b-h</sup>	1399.8 <sup>c-g</sup>	37.6 <sup>a-f</sup>	44.5 <sup>a-d</sup>	91.1 <sup>d-f</sup>	1.6	1.2	17 <sup>b-f</sup>
G11	64.8 <sup>a-h</sup>	958.7 <sup>g</sup>	37 <sup>a-f</sup>	48.1 <sup>a-d</sup>	100.8 <sup>abc</sup>	2.5	1	17.5 <sup>a-e</sup>
G12	57.2 <sup>f-j</sup>	1502.1 <sup>b-g</sup>	32.2 <sup>ef</sup>	42.3 <sup>cd</sup>	83.5 <sup>e-h</sup>	2.6	0.9	13.8 <sup>f-hg</sup>
G13	71.1 <sup>a-d</sup>	1423.9 <sup>c-g</sup>	35.7 <sup>b-f</sup>	46.2 <sup>a-d</sup>	85.4 <sup>e-h</sup>	1.5	1.1	13.3 <sup>hg</sup>
G14	63.2 <sup>c-h</sup>	1629.8 <sup>a-f</sup>	31.8 <sup>f</sup>	42.2 <sup>d</sup>	83.6 <sup>e-h</sup>	2.5	1.4	13.9 <sup>f-hg</sup>
G15	75.3 <sup>a</sup>	1159.4 <sup>gf</sup>	38.5 <sup>abc</sup>	46.5 <sup>a-d</sup>	95.9 <sup>dbc</sup>	2	0.9	16.5 <sup>b-f</sup>
G16	51.6 <sup>ijk</sup>	1325 <sup>c-g</sup>	40.2 <sup>ab</sup>	45.1 <sup>a-d</sup>	93.2 <sup>c-e</sup>	1.9	1.5	17.4 <sup>a-e</sup>
G17	50.9 <sup>jk</sup>	1887.9 <sup>a-d</sup>	33.6 <sup>c-f</sup>	42.2 <sup>d</sup>	81.3 <sup>fgh</sup>	1.1	1.2	16.6 <sup>b-f</sup>
G18	58.8 <sup>e-j</sup>	1924.3 <sup>abc</sup>	36.9 <sup>a-f</sup>	48 <sup>a-d</sup>	90.8 <sup>c-f</sup>	1.5	1.2	16.7 <sup>b-f</sup>
G19	65.5 <sup>a-f</sup>	1411 <sup>c-g</sup>	36.8 <sup>a-f</sup>	46.9 <sup>a-d</sup>	91.8 <sup>b-e</sup>	1.3	1.5	16.2 <sup>d-h</sup>
G20	59.2 <sup>e-j</sup>	1340.8 <sup>c-g</sup>	38.2 <sup>a-e</sup>	49.7 <sup>a-d</sup>	84.6 <sup>e-h</sup>	1.5	1	15.6 <sup>d-h</sup>
G21	60.1 <sup>e-f</sup>	1902.7 <sup>a-d</sup>	35.1 <sup>b-f</sup>	48.3 <sup>a-d</sup>	86.2 <sup>d-h</sup>	1.5	1.4	16.2 <sup>d-h</sup>
G22	73.7 <sup>ab</sup>	1244.5 <sup>d-g</sup>	37.9 <sup>a-f</sup>	53.3 <sup>ab</sup>	91.3 <sup>d-f</sup>	1.8	1.1	18.7 <sup>a-d</sup>
G23	65.9 <sup>a-f</sup>	1272.5 <sup>c-g</sup>	36.8 <sup>a-f</sup>	47.1 <sup>a-d</sup>	90.2 <sup>d-g</sup>	2.5	1	14.9 <sup>e-h</sup>
G24	57.7 <sup>e-j</sup>	1771.9 <sup>a-f</sup>	34.4 <sup>b-f</sup>	45.9 <sup>a-d</sup>	89.2 <sup>d-g</sup>	1.5	1.3	15.9 <sup>d-h</sup>
G25	68.3 <sup>a-e</sup>	1254.3 <sup>d-g</sup>	38.5 <sup>abc</sup>	53.5 <sup>a</sup>	92.9 <sup>c-e</sup>	1.7	1.1	14.6 <sup>e-h</sup>
G26	60.9 <sup>e-i</sup>	1770.1 <sup>a-f</sup>	33.3 <sup>c-f</sup>	47.2 <sup>a-d</sup>	77 <sup>h</sup>	1.9	1	13 <sup>h</sup>
G27	55.1 <sup>h-k</sup>	1153.4 <sup>gf</sup>	34.9 <sup>b-f</sup>	48.8 <sup>a-d</sup>	89.5 <sup>d-f</sup>	1.5	1.1	15.6 <sup>d-h</sup>
G28	56.9 <sup>f-k</sup>	1292.7 <sup>c-g</sup>	32.2 <sup>def</sup>	43.5 <sup>cd</sup>	80.1 <sup>hg</sup>	1.9	1.6	16.3 <sup>c-h</sup>
G29	49.8 <sup>k</sup>	1772.2 <sup>a-f</sup>	32.2 <sup>f</sup>	45.7 <sup>a-d</sup>	83.5 <sup>e-h</sup>	1.8	1.1	18.4 <sup>a-d</sup>
G30	55.5 <sup>g-k</sup>	1260.6 <sup>g-f</sup>	32.8 <sup>c-f</sup>	43.4 <sup>cd</sup>	83.3 <sup>e-h</sup>	2	1.3	17.2 <sup>c-f</sup>
Mean	63.5	1551	36.2	46.9	88.8	1.9	3.7	16.5
CV(5%)	6.2	15.9	6.3	7.4	4.4	44.4	1.2	7.8
ST.E	0.7	45	0.4	0.6	0.7	0.2	0.07	0.2

GEN=Genotypes; ST-ERROR=Standard error; CV=Coefficient of variation; PHT=Plant height in centimetres; DF = Days to 50% Flowering; DP=Days to podding DM=Days to 50% maturity; SEEDW=Seed weight in grams; GYD=Grain yield (kg ha<sup>-1</sup>); LODG=Lodging; PLV = Plant vigour. Means followed by same letter in superscript do not significantly differ (P=0.05)

### **3.3.5 Yield reduction/gain and agronomic performance associated with P treatments**

Genotypic performance was compared between the low P and high P environments to assess yield gains or reductions due to P treatment levels (Table 3.7). Several genotypes showed positive grain yield performance upon the addition of P. The genotypes included G14 (118%), G20 (93%), G7 and G5 (90%), G16 (69%) and G18 (60%) among others. Some genotypes namely G11, G15, G12, G25 and G19 had drastic reduction in grain yield with -59%, -31% and -11% reductions, respectively. The yield of genotypes G3, G17, G19, G22, and G25 did not significantly change with the additional phosphorus.

The highest percentage increment for plant height was 45% observed for genotype G8, followed by that of genotype G9 with 31% and then genotypes G11 and G14, both with 20% increment, and least increment in height were observed for genotypes G12 with 2%, and G3 with 4%. In high phosphorus environment, the genotypes showed different performances, with most of the genotypes having less days to flowering compared to low phosphorus level treatment. Genotype G8 had the highest reduction of days to 50% flowering from 42.1 under low phosphorus to 34.7 days under high phosphorus environment, followed by G2, which reduced from 40.5 to 36.3 days, and genotype G18 with a reduction from 39.1 to 36.9 days.

The number of days to physiological maturity decreased when the phosphorus was added in the soil. Genotype G1 had the highest reduction in maturity days of 40% followed by genotypes G16, G2 and G29 with 12% reduction. Maximum percentage increment in pods per plant were observed for genotype G14 (69%). Other genotypes had appreciable increments in pods under high phosphorus and these included G21 (59%), G10 (50%), G19 (47%), G22 (43%), G5 (41%) and G1 (31%).

Table 3.7 Percentage reduction/gain in yield and yield parameters under low (LP) and high (HP) phosphorus treatments in 30 soybean genotypes

GEN	GYD (kg ha <sup>-1</sup> )			PHT (cm)			DF (days)			DP(days)			DM (days)			PLV (score 1-5)			LODG (score 1-5)			SEEDW (g)		
	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red	LP	HP	% Red
G1	2457.2	3180.6	29.4	80.6	98.0	21.6	50.4	50.0	-0.8	61.3	57.9	-5.6	114.3	68.6	-39.9	2.3	1.7	-24.5	1.6	1.0	-38.5	24.5	27.2	11.0
G2	2431.8	2765.2	13.7	101.6	96.9	-4.6	45.6	35.2	-22.8	54.3	43.4	-20.0	86.4	76.4	-11.6	1.0	1.1	17.4	1.0	1.0	2.1	18.8	18.3	-2.6
G3	1958.5	2020.5	3.2	96.0	100.3	4.5	48.5	46.4	-4.3	57.3	52.9	-7.6	88.7	93.4	5.2	1.4	0.9	-36.2	1.6	1.0	-39.2	15.5	27.2	75.3
G4	1905.2	2579.7	35.4	111.8	95.4	-14.6	47.0	46.4	-1.4	58.0	53.1	-8.4	88.4	92.6	4.7	2.3	1.2	-46.3	0.9	1.0	14.3	17.3	19.0	9.7
G5	869.7	1515.6	74.3	80.0	95.7	19.7	38.7	37.9	-2.0	48.1	46.8	-2.6	93.1	90.0	-3.4	2.0	1.0	-50.5	0.9	1.0	11.6	26.3	25.2	-4.1
G6	1044.2	1692.5	62.1	109.2	98.6	-9.8	37.2	39.2	5.4	48.4	48.5	0.2	83.2	78.3	-6.0	1.5	1.5	4.2	1.1	1.0	-11.1	27.4	28.7	4.6
G7	1017.9	1931.5	89.7	75.1	84.0	11.9	34.2	43.0	25.8	45.7	51.2	12.0	113.6	108.4	-4.6	1.5	1.0	-37.0	1.3	1.0	-20.0	21.7	24.3	12.1
G8	2098.2	2435.4	16.1	64.7	94.0	45.3	61.0	34.0	-44.2	42.5	42.8	0.7	75.4	75.2	-0.2	0.9	1.6	81.4	1.0	1.0	-2.0	13.8	16.2	17.2
G9	1303.0	1766.2	35.5	77.0	100.6	30.7	42.1	43.9	4.4	52.2	54.8	4.9	86.5	79.7	-7.9	0.7	1.5	108.8	1.0	1.0	2.1	15.4	14.4	-6.3
G10	1274.1	1535.7	20.5	81.6	86.8	6.3	47.5	46.3	-2.6	57.0	54.9	-3.5	90.8	98.8	8.8	1.5	1.0	-32.9	1.1	1.0	-9.4	16.1	17.2	7.1
G11	1969.6	816.9	-58.5	80.0	95.8	19.7	44.0	42.3	-3.8	53.3	50.5	-5.1	84.0	109.9	30.7	0.7	1.1	55.9	1.1	1.0	-9.4	23.2	23.9	3.0
G12	1335.8	1185.2	-11.3	71.1	72.4	1.9	30.6	29.6	-3.3	40.7	40.3	-1.0	73.9	77.6	5.1	1.1	1.4	28.3	1.0	1.0	0.0	10.2	11.7	14.0
G13	1733.6	2235.4	28.9	83.1	97.5	17.4	37.9	38.3	1.2	45.6	47.7	4.6	83.2	79.8	-4.1	1.7	0.9	-49.4	1.1	1.0	-9.4	13.5	15.3	13.1
G14	997.1	2175.0	118.1	66.2	79.3	19.8	32.3	31.4	-2.8	41.8	41.1	-1.7	76.8	76.8	0.1	1.0	0.9	-8.5	1.0	1.0	0.0	14.5	15.8	8.9
G15	579.4	397.5	-31.4	109.9	103.2	-6.1	48.0	48.8	1.6	60.2	57.3	-4.8	114.6	106.3	-7.3	1.8	1.1	-36.9	1.4	1.0	-26.2	12.8	18.7	46.4
G16	750.2	1268.2	69.1	72.1	68.7	-4.7	45.4	48.3	6.3	56.4	39.8	-29.4	110.2	78.6	-28.6	1.0	1.0	-4.0	0.8	1.0	33.3	15.8	18.4	16.3
G17	2247.8	2439.1	8.5	63.9	66.4	4.0	29.0	33.4	14.8	38.3	40.1	4.7	71.8	76.6	6.8	1.6	0.9	-45.5	1.0	1.0	0.0	20.2	19.4	-4.1
G18	1644.4	2625.3	59.7	94.7	89.4	-5.6	49.1	42.1	-14.1	59.6	50.9	-14.6	88.6	92.5	4.5	1.4	1.0	-26.9	0.8	1.0	33.3	25.2	19.9	-20.9
G19	1382.6	1365.5	-1.2	82.5	84.9	3.0	43.6	38.6	-11.5	51.3	47.6	-7.3	87.5	79.2	-9.5	2.5	1.0	-61.2	1.0	1.0	-2.0	17.3	16.6	-4.0
G20	740.4	1427.7	92.8	78.8	85.0	7.9	47.7	48.5	1.7	58.6	53.5	-8.7	91.3	85.5	-6.4	0.8	1.0	30.6	0.9	1.0	11.6	19.3	17.8	-7.4
G21	2270.6	2501.0	10.1	78.8	76.9	-2.5	39.0	36.8	-5.6	47.1	46.4	-1.4	80.9	81.3	0.5	0.8	0.9	22.2	1.2	1.0	-18.6	17.9	16.4	-8.7
G22	1130.8	1171.8	3.6	92.9	103.7	11.5	47.5	46.3	-2.4	57.0	53.4	-6.3	94.4	98.0	3.8	1.3	1.1	-11.7	1.0	1.0	-2.0	19.5	24.3	24.6
G23	1381.2	1748.3	26.6	98.6	97.2	-1.4	45.3	38.9	-14.1	54.9	49.5	-9.9	88.6	81.9	-7.6	1.0	1.0	-6.0	1.4	1.0	-27.3	14.3	14.3	-0.1
G24	2251.3	2710.4	20.4	87.8	74.2	-15.5	37.6	35.2	-6.5	46.0	45.1	-2.0	82.4	79.6	-3.3	1.3	0.8	-39.7	0.8	1.0	29.7	18.6	19.7	6.1
G25	1285.5	1185.1	-7.8	78.6	90.9	15.7	50.7	46.4	-8.5	60.9	56.0	-8.0	95.0	95.7	0.8	0.6	1.1	96.3	1.0	1.0	2.1	17.4	15.1	-12.9
G26	2072.5	2145.5	3.5	78.9	89.2	13.2	39.7	30.9	-22.0	47.1	38.5	-18.3	70.9	77.6	9.6	1.1	0.9	-17.0	0.9	1.0	14.3	14.7	13.5	-8.2
G27	436.1	764.6	75.3	52.7	61.5	16.7	36.3	33.3	-8.2	43.9	43.0	-1.9	80.7	79.4	-1.7	1.5	0.9	-40.8	1.0	1.0	0.0	16.3	16.6	2.2
G28	1066.2	1104.8	3.6	55.6	85.7	54.2	33.8	31.9	-5.7	44.0	38.6	-12.4	77.2	77.3	0.1	1.3	0.9	-30.6	1.3	1.0	-20.0	19.1	16.7	-12.8
G29	601.5	1312.0	118.1	65.7	59.3	-9.7	35.1	30.6	-12.8	44.4	41.6	-6.4	77.4	75.9	-2.0	0.9	1.1	23.3	0.9	1.0	11.6	15.7	19.7	25.6
G30	1033.5	1373.3	32.9	66.3	71.0	7.1	31.3	31.0	-0.9	42.2	39.7	-6.0	75.8	76.3	0.6	1.8	1.0	-41.7	1.1	1.0	-11.1	17.3	19.5	12.5

GEN=Genotypes; GYD=Grain yield; PHT=Plant height; DF = Days to 50% Flowering; DM=Days to 50% maturity; SEEDW=Seed weight; LODG=Lodging; PLV= Plant vigour;

DP = Days to podding; LP=Low phosphorus; HP= High Phosphorus; % Red =Percentage reduction

### 3.3.6 Cluster analysis

Cluster analysis was performed to understand the morphological similarity between twenty-five lines and five checks under two phosphorus environments. Figure 3.1 shows a dendrogram for the twenty-five soybean lines and five local checks used in the experiment. The results showed that the level of genetic variation was high among the soybean genotypes, hence, four groups were detected in the study, each group with a different number of genotypes (Figure 3.1). The first cluster (Cluster 4) had 43.33% of the genotypes, followed by 30% in cluster 3 and 16.67% in cluster 2. The smallest cluster had 10% of the genotypes. The Euclidean distance of dissimilarity observed ranged between 0.2 and 1.6 (Table 3.10). The maximum distance of dissimilarity was observed between genotype G27 and G4, followed by G27 and G23, and G27 with G2 with genetic distances of 4621, 4418 and 4393, respectively. The minimum distance was observed between genotypes G22 and G5, G19 and G13, and G19 with G10 of about 91, 101 and 112, consecutively.

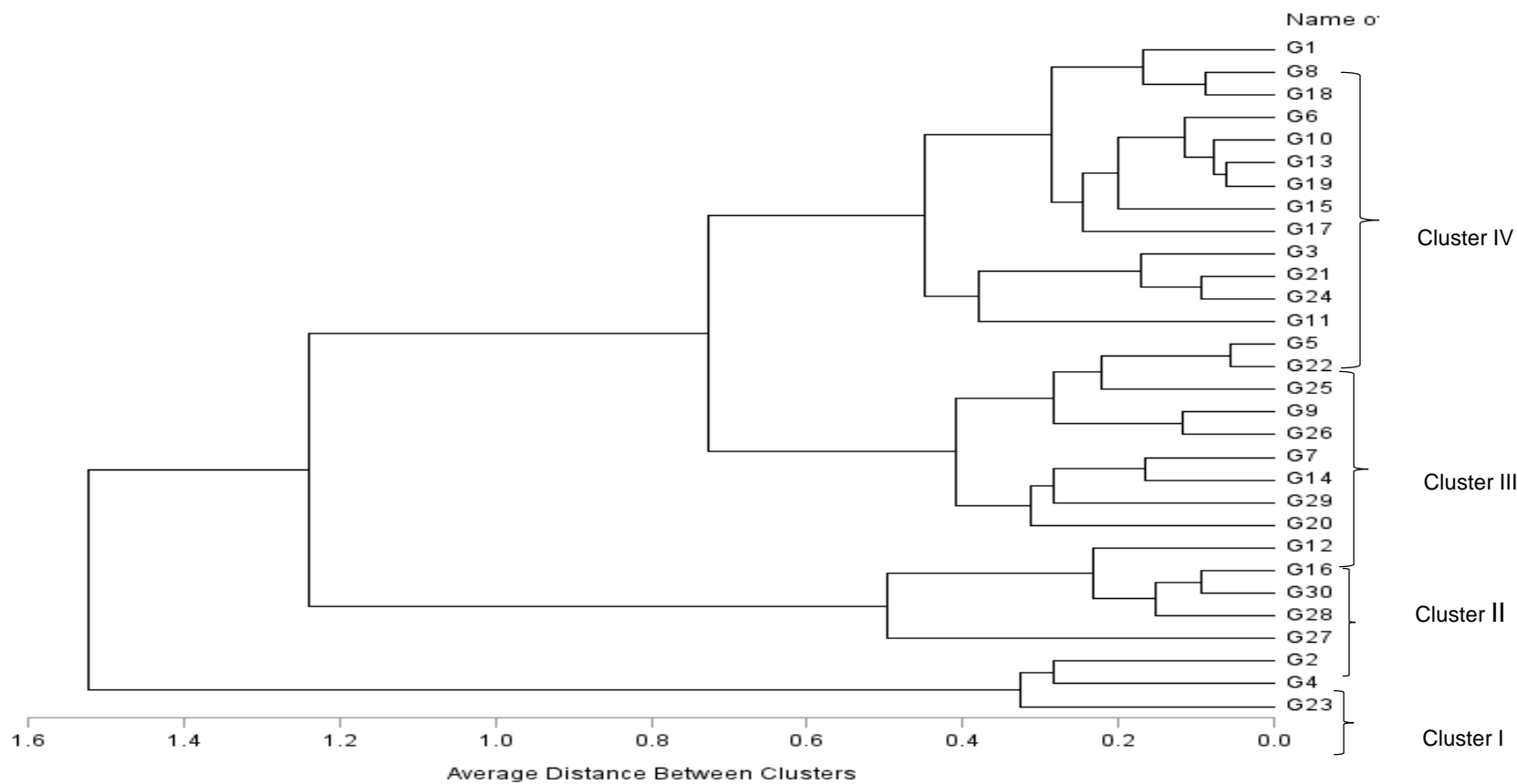


Figure 3.1 Cluster analysis for 30 soybean genotypes

Table 3.8 Matrix of dissimilarity of 30 genotypes

	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28	G29	
<b>G2</b>	1527																													
<b>G3</b>	481	1061																												
<b>G4</b>	1774	462	1305																											
<b>G5</b>	1143	2467	1471	2669																										
<b>G6</b>	542	1726	736	1925	753																									
<b>G7</b>	1167	2627	1593	2878	508	996																								
<b>G8</b>	307	1347	312	1582	1160	435	1297																							
<b>G9</b>	720	2120	1106	2390	588	586	521	817																						
<b>G10</b>	565	1836	831	2058	643	163	849	521	428																					
<b>G11</b>	892	1336	712	1573	1252	655	1524	609	1059	733																				
<b>G12</b>	2004	3502	2458	3751	1258	1875	895	2173	1401	1735	2413																			
<b>G13</b>	452	1812	778	2041	708	222	840	471	402	135	795	1722																		
<b>G14</b>	1195	2632	1595	2846	325	932	269	1290	607	806	1493	974	822																	
<b>G15</b>	597	1552	635	1759	922	228	1184	375	740	341	433	2072	399	1131																
<b>G16</b>	2074	3529	2496	3764	1141	1845	914	2195	1423	1710	2348	384	1727	924	2030															
<b>G17</b>	306	1805	748	2041	858	424	871	481	458	375	955	1715	241	889	579	1772														
<b>G18</b>	233	1407	371	1666	1140	461	1230	141	737	508	674	2099	438	1247	438	2136	415													
<b>G19</b>	464	1746	732	1979	746	173	908	423	449	112	697	1797	101	889	312	1789	313	399												
<b>G20</b>	1562	2945	1944	3194	603	1285	454	1639	866	1142	1731	792	1177	481	1446	637	1267	1583	1222											
<b>G21</b>	714	880	251	1123	1594	849	1766	478	1270	959	622	2646	937	1755	691	2660	954	559	872	2085										
<b>G22</b>	1066	2418	1409	2624	91	701	460	1098	512	585	1227	1252	638	294	882	1162	777	1073	684	625	1542									
<b>G23</b>	1684	582	1212	485	2420	1708	2685	1432	2200	1842	1253	3575	1855	2638	1514	3543	1910	1528	1779	2950	978	2388								
<b>G24</b>	711	936	305	1213	1537	810	1707	459	1203	907	514	2594	893	1707	635	2599	930	527	819	2011	150	1487	1030							
<b>G25</b>	811	2099	1108	2325	386	418	642	799	349	281	911	1518	363	583	575	1459	560	773	379	874	1229	336	2086	1164						
<b>G26</b>	819	2268	1233	2521	495	670	361	939	189	518	1204	1245	491	439	853	1270	526	870	560	749	1407	412	2336	1351	384					
<b>G27</b>	2904	4393	3347	4621	2014	2713	1769	3052	2284	2582	3236	926	2589	1782	2907	889	2607	2989	2658	1521	3524	2035	4418	3471	2339	2126				
<b>G28</b>	2286	3770	2724	3995	1398	2087	1151	2427	1668	1957	2620	392	1963	1156	2282	307	1986	2368	2033	932	2899	1414	3793	2847	1718	1506	627			
<b>G29</b>	1475	2982	1928	3215	819	1353	427	1644	914	1221	1927	547	1198	498	1560	673	1183	1576	1279	584	2121	788	3050	2078	1032	741	1432	825		
<b>G30</b>	2144	3616	2574	3842	1231	1928	1000	2275	1516	1797	2453	360	1808	998	2120	152	1842	2218	1876	765	2744	1249	3632	2690	1554	1355	788	173	706	

### 3.4 Discussion

Soils in southern Africa are low in P and this greatly affects the yield potential of most crops in the region. Breeding for high P uptake and utilization efficiency (P use efficiency) especially under limited P conditions has been established to improve crop yields (Richardson *et al.*, 2011; Tesfaye, 2012). Soybean is an economically important crop because of its nutritional quality and industrial uses. Improving soybean productivity for the smallholder farmers in low input agricultural systems raises household level incomes, reduces production costs (where fertilizers are used to ameliorate P) and improves health and nutrition status of millions of people living below US\$2/day.

In this study, 25 elite lines from the IITA breeding programme were evaluated, together with five local checks to identify the PUE across random P stress and non-P stress environments. The environments were selected based on the representativeness of the environment to farmers' fields. This was to reduce the discrepancy, which often leads to huge research outputs on experimental plots, far much beyond yields observed in farmers' fields. Hence, the low P environments were denoted as random P stress. The results indicated great variability in terms of responsiveness of the genotypes to P availability. Tesfaye (2012) also identified huge variability among selected soybean varieties for PUE in Ethiopia.

All the genotypes with the exception of genotypes G7, G11 and G24 experienced a reduction in days to physiological maturity under high P. Delay in maturity under low P might be due to the insufficient essential elements needed for development of the plant (Onasanya *et al.*, 2009). Phosphorus is a macro-element that is very important in the soil, which acts during the development and plant maturity involved in enzymatic reactions thus influencing different physiological processes. According to Silva and Uchida (2000), P is needed in large amounts during the early stages of cell division, thus a lack of this nutrient can delay maturity.

Furthermore, application of P contributed significantly to plant height in all genotypes evaluated in this study resulting in differential responses. Bharati *et al.* (1986), observed similar results which included a decrease in plant height as well as delay in growth under low P environments. Norman (1978) studied the effect of P and potassium nutrition on growth and yield of soybean in relay strip intercropping system, and reported a significant increment in plant height with increased P application of up to 17 kg ha<sup>-1</sup>. In the same study, Kumar *et al.* (2008), Shahid *et al.* (2009) and Norman (1978) all reported significant improvement in plant height of soybean as a result of P fertilization. The reduction in plant height observed under



environment with high P might be because a high dose of this nutrient tends to promote nutrient interaction and may thus affect the availability of other nutrients, which are essential for plant growth (Turuko and Mohammed, 2014). In general, all genotypes under this study demonstrated to be resistant to lodging, however overall mean for lodging was 1.1.

The study identified better grain yield responses to elevated P levels. Ochigbo and Bello (2014) obtained similar results of increased yield and yield components when they topped up P in the soil. In addition, Darwesh *et al.* (2013) and Hasan *et al.* (2013) reported that the application of P fertilizers to the soil improves the growth of the roots, thus enhancing the positive plant interaction with P in the soil. Turuko and Mohammed (2014) observed significant increment for most of the traits evaluated when they applied 25 to 75 kg ha<sup>-1</sup> P but rates of P above this level resulted in a reduction in performance for most of the yield component traits. Veeresh (2003) and Kakar *et al.* (2002) concluded that the reduction in performance of the genotypes might be due to the excess P that can lead to interruption of the availability of other essential nutrients for growth. For hundred seed weight and harvest index, the interaction among the genotypes and the P level across locations also showed significant differences. The present results also revealed that the 25 genotypes evaluated were resistant to lodging under high P environment.

Genotypes evaluated under this study, clustered into four major groups with more individuals in cluster IV and less than 60% of the individuals divided in the other three groups. These results indicate less variability and more resemblance among the genotypes under study. In fact, the low variability verified between the genotypes can be attributed to the fact that, the soybean in nature is known as a crop with a narrow genetic base in their gene pool (Villela *et al.* 2014). The soybean crop is a self-fertilizing crop and has narrow genetic diversity. The identified clustered genotypes can be crossed to enhance heterosis. Even if heterosis in soybean is reported to be low (often below 15%), it can be useful to improve yield productivity under P limiting environments. According to previous studies, cluster analysis and principal component analysis were mostly used to assess genetic diversity for breeding purposes and are very useful in parental selection (Drinić *et al.*, 2008; Jain *et al.*, 2017). Moreover, they are not used only to assess genetic diversity and parental selection, but are also crucial for efficient management and conservation of germplasm resources (Jain *et al.*, 2017).

### 3.5 Conclusion

The study identified huge variability within the studied gene pool for several traits under both low P and high P environments. Considerable distances of dissimilarity were found between the checks and the elite lines. The variability and different clustering, though low, can be useful when crossed based on their heterotic grouping. The genotypes performed differently across P treatment levels. Significant differences were observed for traits like grain yield, plant height, seed weight, days to flowering and days to maturity. Genotypes G7, G5, G2, G1, G18 and G20 had high response to P, while genotypes G3, G10, G16, G19 and G25 responded negatively to P and the rest of the genotypes had their performance unaffected by P levels. Under low P environment, the grain yield average was 1154.30 kg ha<sup>-1</sup>, and increased to 1551.20 kg ha<sup>-1</sup> under high P. In high P environment, the best genotypes in terms of yield performance were G1, G2, G3, 18 and G21 while under low P environment; they were G1, G3 G12 and G8. Across the two environments, G1 and G4 were the best.

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## CHAPTER 4

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# PATH COEFFICIENT ANALYSIS FOR SOYBEAN YIELD AND AGRONOMIC TRAITS UNDER PHOSPHOROUS STRESS CONDITIONS

### Abstract

Phosphorus (P) is one of the essential elements whose deficiency limits soybean production in the tropics. Unavailability of P to the plants can lead to partial or total loss of yield. The main objective of this investigation was to determine traits that contribute directly and indirectly to yield under low and high phosphorus conditions through correlation and path coefficient analysis. Thirty advanced soybean lines were evaluated under low and high P during the 2016/2017 cropping season at Gurue (Mozambique), Lilongwe (Malawi), and Lusaka and Kabwe (Zambia). Soil samples were taken before planting and the results showed moderate deficiency of P in the soils. An alpha-lattice design was 6\*5 with two replications was used for the study. Data were analysed using SAS to run ANOVA and obtain LSMEAN of all traits that were used to perform a correlation using SPSS 25<sup>th</sup> and GenStat. Path coefficient analysis was performed using correlation coefficient in Microsoft Excel employing the MINVERS and MMULT functions. Results showed strong and significant association of grain yield with yield components. Harvest index was highly significant and positively correlated with grain yield, but negatively correlated to plant height, days do maturity and days to 50% flowering. Path analysis revealed that under low P environment, total dry biomass, harvest index, number of pods are priority traits for selection. Nodules per plant, nodule weight and plant height had significant indirect effects on grain yield via biomass, while number of seeds per pod and days to maturity had significant indirect effects on grain yield via plant vigour and days to flowering across all P levels and thus can be used as secondary traits for yield improvement in soybean.

## 4.1 Introduction

Soybean (*Glycine max* L.  $2n=2x=20$ ) is an economically important nutritional crop in southern Africa. It constitutes an important source of protein and oil for human nutrition and meal for poultry industry (Malik *et al.*, 2011; Varnica *et al.*, 2018). It is cultivated in calcareous soils in arid and semi-arid areas (Darwesh *et al.*, 2013). However, in tropical soils, one of the major constraints for crop production is low available phosphorus (P), an essential element required for crop growth. Therefore, it is important to develop genotypes adapted to these ecosystems, investigate and explain the mechanisms of adaptation of crops under low P conditions (Eberhardt *et al.*, 2017). Use of varieties with high P efficiency increases utilization of P contained in the soil, increases fertilizer use efficiency, and consequently decreases the requirements for inorganic fertilizer input.

Genetic improvement through breeding will continue to play a leading role in the production of cultivars adapted to a wide range of agricultural ecosystems. In any breeding programme, yield improvement is considered as a prime objective, and at the same time, this trait is recognized to be a very complex character because it is controlled in nature by many other factors (Chandel *et al.*, 2014; Iqbal *et al.*, 2003). Thus, understanding the relationship between yield and yield components becomes crucial for judging genotypes (Arshad *et al.*, 2006). Agronomic traits, yield and yield component parameters are key indicators of soil fertility status in most agro ecosystems (Kakar *et al.*, 2002), so that can be used to measure the P content in the soil.

In many areas where soybean is cultivated, phosphorus (P) availability is a major problem and as a result, yields are decreasing. Selection for high yielding soybean genotypes under low P identifies genotypes with high phosphorus use efficiency (PUE). Soybean yield, just like any other crop, is highly interactive with the crop genetics and environments (Rauf *et al.*, 2004), and as a quantitative trait, its improvement will greatly require the use of secondary traits. Selection of P efficient genotypes is difficult, costly and time consuming for breeders because the process involves uprooting the entire plant and measuring the root length, architecture and root weight. Therefore, in this case, to minimize the problems encountered during the process of selection of genotypes for P use efficiency, it is essential to understand the relationship among different agronomic traits in order to identify the traits that can be indirectly selected for PUE as well as for better yield.

The relationship between two characters can be inferred through correlation and path coefficient analysis. The correlations that breeders are mostly interested in, according to Valencia-Ramírez and Ligarreto-Moreno (2012) are genetic, phenotypic and environmental. In plant breeding experiments, information on the association of traits is useful for assessing progress of plant improvement by making the selection of both parents and progeny easier and efficient. Most studies have demonstrated that the correlation between two characters is more important for direct selection of genotypes (Valencia-Ramírez and Ligarreto-Moreno, 2012). Mhike *et al.* (2012) identified potential traits (anthesis-silking interval and the number of ears per plant) linked to yield in maize. Such important traits can also be identified in soybean under low P environments and can help improve yields for southern Africa. However, the results are not fully indicative of how traits are associated with each other as it highlights direct effects alone. There is also need to determine and quantify both direct and indirect effects (path coefficient analysis) of these traits upon the targeted trait (Ali *et al.*, 2009; Sodavadiya *et al.*, 2009; Srinivas *et al.*, 2017). Path coefficient analysis is a statistical technique used in plant breeding programmes to determine the interaction among parameters (traits) of interest and other parameters useful as selection criteria in crop improvement. It computes the relationship between the traits and indicates which trait is important and what effect it has on the other specific trait (Cyprien and Kumar, 2012). This study, therefore, was conducted to identify potential secondary traits that can be used to improve grain yield under variable (low and high P treatments) in southern Africa.

## **4.2 Materials and Methods**

### **4.2.1 Genetic materials and experimental sites**

Twenty-five elite soybean material from IITA, together with five local check varieties were used in the study and the genotypes are described in Chapter 3, section 3.3.1. The experiment was conducted across four locations in southern Africa including Gurue (Mozambique) at Mutequelece IIAM Research Station; Lilongwe (Malawi) at Chitedze Agricultural Research Station; Kabwe Research Station (Zambia) and; Lusaka (Zambia) at IITA-Sarah Research Station as described in Chapter 3 section 3.3.2. In total, there were three trials established under high P environment and four trials under low P resulting in seven environments.

### **4.2.2 Experimental design and agronomic management**

The experiment was laid in a 6 x 5 alpha lattice design with two replications as described in Chapter 3 section 3.3.3. Management of trials was also done based on the descriptions in the same section in Chapter 3.

### **4.2.3 Data collection**

Summary of data collection has been presented in Chapter 3, Subsection 3.1.3.1 under materials and methods. Apart from traits described in Chapter 3, the following additional traits were collected;

- **Nodule number (NODP)**

Thirty days after planting, five sampled plants were carefully dug out from the ground, roots extracted and all nodules counted. Nodules were detached from the roots and placed in an envelope. The means were calculated and recorded for each treatment.

- **Nodule dry weight (NODW)**

Nodules harvested from five sampled plants were put in labelled envelopes, dried under normal environmental conditions for seven days, then weighed using a sensitive balance scale, and the mean recorded.

- **Pod clearance (PCLEAR)**

Using a measuring ruler, each of the five plants where measured from the ground level to the first branch, and the mean was recorded for each treatment.

- **Lodging (LODG)**

Using a scale of 1-5, all treatments were classified according to their resistance to lodging, where, one means the plants are resistant to lodging and five are more susceptible.

- **Number of pods per plant (NOPP)**

The number of pods on each of five plants was counted and means recorded accordingly.

- **iomass (BIO)**

The five sampled plants were placed in a bag, dried under normal environmental conditions, weighed and the mean recorded. Estimation of biomass per hectare was done using the following formula (Equation 4-1).

Equation 4-1: Determination of dry biomass (kg/ha)

$$\begin{aligned} & \text{Biomass yield(kg/ha)} \\ &= \frac{(\text{Net plot biomass yield})}{\text{Net plot area}} \times 10000 \end{aligned}$$

- **Grain yield (GYD)**

This was done at maturity by harvesting all plants from the two central rows of each plot. All seeds from the two middle rows were threshed from the pods and measured as the net plot yield. The yield per hectare was calculated using the Equation 3-1.

Equation 4-2: Determination of grain yield (kg ha<sup>-1</sup>)

$$\text{Yield(kg/ha)} = \left( \frac{(100 - \% \text{Grain moisture content})}{(100 - 13)} \right) \times \left( \frac{(\text{Net plot yield})}{\text{Net plot area}} \times 10000 \right)$$

### **Harvest Index (HI)**

The harvest index was calculated using the grain yield and biomass per hectare of each treatment (Equation 4-3).

Equation 4-3: Determination of harvest index

$$\text{Harvest index} = \frac{\text{Yield(kg/ha)}}{\text{Biomass yield(kg/ha)}} \times 100\%$$

#### 4.2.4 Data analysis

SAS software package (SAS Institute, 2005) and SPSS 25<sup>th</sup> edition (Weinberg and Abramowitz, 2002) were used to analyse data from all seven environments. The mean under low phosphorus and mean for high phosphorus environment were used in analysis of correlation. SAS software package (SAS Institute, 2009) was used to run ANOVA and obtain LSMEAN of all traits involved in this study according to Littell *et al.* (2002). Karl Pearson's coefficient of correlation  $r_{xy}$  was used to determine the linear relationship between two variables, using SPSS 25<sup>th</sup> edition (Weinberg and Abramowitz, 2002). Path coefficient analysis was performed using correlation data in Microsoft Excel by employing the MINVERS and MMULT functions. The correlation coefficient between two traits x and y ( $r_{xy}$ ) is based on the variance and covariance of the variables and ranges between -1 and +1. It is given by the following formula:

$$r_{xy} = \frac{Cov(xy)}{\sqrt{V(x)V(y)}}$$

Where,

For testing the significance of correlation coefficient, a *t*-test was used. A *t*-value (*t* cal) was calculated as follows.

$$t \text{ cal} = \frac{r}{\sqrt{1-r^2}} * \sqrt{n-2}$$

The calculated *t*-value (*t* cal) was compared with tabulated *t*-value at (n-2) degree of freedom according to Snedecor and Cochran (1967).

## 4.3 Results

### 4.3.1 Correlation coefficients under low P environments

The correlation coefficients of yield and agronomic characters for low phosphorus environment are presented in Table 4.1. There was positive correlation among the genotypes for BIO ( $r = 0.6350^{**}$ ), lodging ( $r = 0.4410^*$ ) and HI ( $r = 0.4050^*$ ) with grain yield. There was also positive and significant correlations among agronomic traits. Plant height was highly significant and positively correlated with PCLEAR and DM, both with  $r = 0.4660^{**}$ , DP ( $r = 0.4320^*$ ) and DF ( $r = 0.3750^*$ ). It was, however, negative and significantly correlated with SEEP ( $r = -0.390^*$ ). For PCLEAR, it was positively correlated with DP ( $r = 0.4270^*$ ). There were also high and positive correlations between DF and both DP ( $r = 0.8350^{**}$ ) and DM ( $r = 0.6390^{**}$ ). Days to podding was highly significant and positively correlated with DM ( $r = 0.7010^{**}$ ), PODP ( $r = 0.4460^*$ ) while it was negatively correlated with HI ( $r = -0.406^*$ ). Days to maturity was negatively and significantly correlated with HI ( $r = 0.4920^{**}$ ). Lodging was significantly correlated with HI ( $r = 0.5770^{**}$ ). Number of nodules per plant (NODP) was positive and significantly correlated with NODW.

Table 4.1 Correlation coefficients among 14 agronomic traits from 30 soybean lines evaluated under low P environments

	GYD	PH	DF	DP	DM	PLV	LODG	PCLEAR	NODP	NODW	PODP	SEEP	SEEW	BIO
PHT	0.0750													
DF	-0.0950	0.3780*												
DP	-0.1220	0.4320*	0.8350**											
DM	-0.3480	0.4660**	0.6390**	0.7010**										
PLV	0.0890	0.2810	0.0920	0.2680	0.2910									
LODG	0.4410*	0.1360	-0.0400	-0.1620	-0.3110	0.0780								
PCLEAR	-0.0180	0.4660**	0.2230	0.4270*	0.3020	0.0960	-0.2230							
NODP	0.1650	0.2500	0.0770	0.0790	-0.0130	-0.2530	-0.0220	0.1110						
NODW	0.1350	0.2820	0.0440	0.1090	0.0950	-0.2640	-0.0350	0.1590	0.9300**					
PODP	0.3550	0.2840	0.3260	0.4460*	0.0350	0.1010	0.1050	0.3440	0.1050	0.1460				
SEEP	0.2060	-0.3900*	-0.3170	-0.3190	-0.360	-0.330	0.0880	-0.0770	0.1900	0.2000	0.1030			
SEEW	-0.2400	-0.0280	0.0670	0.2210	0.3410	0.0870	-0.1660	0.0300	-0.1840	-0.0640	-0.1000	-0.2020		
BIO	0.6350**	0.3460	0.0510	0.0980	-0.1000	-0.0180	0.1060	0.3180	0.5080**	0.5020**	0.3150	0.0660	-0.0040	
HI	0.4050*	-0.2030	-0.2970	-0.4060*	-0.4920**	-0.2140	0.5770**	-0.1620	-0.1370	-0.1100	-0.1200	0.0510	0.1110	0.0760

\*\*P < 0.01; \*P < 0.05; PH=Plant height; DF Days to 50% Flowering; DP=Days to podding; DM=Days to 50% maturity; NODP=number of nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant Vigour; LODG=Lodging; PODP=Podes per plant; SEEP=Seed per pod; SEEW=Seed weight; GYD=Grain yield; BIO=Biomass; HI=Harvest index.



### 4.3.2 Correlation coefficients across high P environments

Table 4.2 shows results of correlation coefficients under high phosphorus environment. Grain yield was highly significant and positively correlated with HI ( $r = 0.7230^{**}$ ). The grain yield was also positively correlated but not significant to SEEDP, LODG, SEEW, PODP, and PCLEAR. Traits negatively correlated to grain yield but not significant were DP, DM, PLV, NODW, DF, NODP, and PH. Plant height was positive and significantly correlated with BIO ( $r = 0.5950^{**}$ ), DF ( $r = 0.4760^*$ ) and DP ( $r = 0.3960^*$ ). Although plant height was positively correlated with the other traits (DP, DM, SEEDW, NODW, PCLEAR), these were not significant. Harvest index was significant and negatively correlated with PH ( $r = -0.3680^*$ ), DF ( $r = -0.3950^*$ ), DP ( $r = -0.483^{**}$ ) and DM ( $r = -0.5430^{**}$ ). Seed weight was also significant and positively correlated with DF and DM, with  $r = 0.4320^{**}$  and  $r = 0.4300^{**}$  respectively. Days to flowering was positively correlated with DP ( $r = 0.6990^{**}$ ), DM ( $0.6320^{**}$ ) and BIO ( $r = 0.4040^*$ ), and negatively correlated to HI ( $r = -0.3950^*$ ). Days to podding was positively correlated with DM ( $r = 0.4530^*$ ) and negatively correlated with SEEP ( $r = -0.3190^*$ ) and HI ( $r = -0.4830^{**}$ ). Nodules per plant was positively correlated with NODW ( $r = 0.7810^{**}$ ).

Table 4.2 Correlation coefficients among 14 agronomic traits from 30 soybean lines evaluated under high P environments

	GYD	PH	DF	DP	DM	PLV	LODG	PCLEAR	NODP	NODW	PODP	SEEP	SEEW	BIO
PHT	-0.0140													
DF	-0.0940	0.4760**												
DP	-0.2610	0.3960*	0.6320**											
DM	-0.2540	0.1720	0.6990**	0.4530*										
PLV	-0.1350	0.0940	0.0030	-0.1120	0.2720									
LODG	0.1850	-0.0380	-0.0750	-0.2180	-0.2950	-0.0690								
PCLEAR	0.0690	0.1950	0.1980	-0.0770	-0.0800	-0.1600	0.0060							
NODP	-0.0350	0.2070	0.2970	0.2520	0.1370	0.1250	-0.0370	0.3410						
NODW	-0.1280	0.1420	0.3420	0.3290	0.2420	0.1180	-0.0930	0.1680	0.7810**					
PODP	0.1690	0.0680	0.1380	0.3600	0.0710	-0.1660	-0.0510	-0.2940	0.0030	0.0710				
SEEP	0.2440	0.0170	-0.2770	-0.3930*	-0.3040	0.0080	0.2670	-0.2170	-0.2440	-0.2040	-0.0750			
SEEW	0.1740	0.1520	0.4320*	0.1350	0.4300*	-0.0300	0.1140	0.2860	-0.0380	-0.2010	-0.0770	-0.1490		
BIO	0.1070	0.5950**	0.4040*	0.2610	0.3190	0.0250	-0.0290	-0.2220	0.1410	0.2050	0.2710	0.185000	0.1140	
HI	0.7230**	-0.3680*	-0.3950*	-0.4830**	-0.5430**	-0.1970	0.2890	0.1090	-0.0160	-0.1420	-0.0370	0.2880	-0.1190	-0.2810

\*\*P < 0.01; \*P < 0.05; PH=Plant height; DF Days to 50% Flowering; DP=days to podding; DM=Days to 50% maturity; NODP=Nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant vigour; LODG=Lodging; PODP=pods per plant; SEEP=Seed per pod; SEEW=Seed weight; GYD=Grain yield; BIO=Biomass; HI=Harvest Index

### 4.3.3 Correlation coefficient analysis across the combined environments

Table 4.3 shows correlation coefficients for combined low and high P environments. There was strong correlation between grain yield and HI ( $r = 0.6810^{**}$ ), BIO ( $r = 0.4710^{**}$ ) and lodging ( $r = 0.3730^*$ ). DM ( $r = 0.6550^{**}$ ) was negatively correlated with HI ( $r = -0.4890^{**}$ ). BIO ( $r = 0.6610^{**}$ ), DF ( $r = 0.4960^{**}$ ), DM ( $r = 0.3960$ ) and DP ( $r = 0.4930^{**}$ ) were significant and positively correlated to plant height. PCLEAR was significant and positively correlated to plant height with  $r = 0.4170^*$ . Likewise, HI was negatively correlated to plant height with  $r = -0.3930^*$ . Days to flowering was significant and positively correlated with DP ( $r = 0.839^{**}$ ), and DM ( $r = 0.7230^{**}$ ), and significant and negatively correlated with HI ( $r = 0.4030$ ). Number of nodules per plant showed significant and positive correlation with NODW ( $r = 0.8770^{**}$ ). Nodule weight (NODW) was positively correlated with BIO ( $r = 0.3780^*$ ). Days to maturity (DM) was positively correlated with SEEW ( $r = 0.4690^{**}$ ) and negatively correlated with HI ( $r = -0.5620^{**}$ ) and LODG ( $r = -0.4690^{**}$ ). Lodging (LODG) was significant and positively correlated with HI ( $r = 0.4910^{**}$ ). Number of pods per plant (PODP) was positively correlated with BIO ( $r = 0.3800^*$ ).

Table 4.3 Correlation coefficients among 14 agronomic trait from 30 soybean lines estimated across combined environments

	GYD	PH	DF	DP	DM	PLV	LODG	PCLEAR	NODP	NODW	PODP	SEEW	BIO
PHT	0.0640												
DF	-0.1130	0.4960**											
DP	-0.2110	0.4930**	0.8390**										
DM	-0.2900	0.3960*	0.7230**	0.6550**									
PLV	0.0680	0.1560	0.1510	0.0840	0.2830								
LODG	0.3730*	-0.0290	-0.1630	-0.2520	-0.3980*	-0.0730							
PCLEAR	0.0090	0.4170*	0.1600	0.2350	0.1980	0.0730	-0.3450						
NODP	-0.0900	0.2690	0.2350	0.1540	0.1820	-0.0370	-0.3210	0.2160					
NODW	-0.0900	0.2340	0.1930	0.1900	0.2280	-0.1540	-0.2490	0.1690	0.0080				
PODP	0.2410	0.2720	0.3580	0.4580*	0.1050	-0.0170	-0.0090	-0.0090	0.1270	0.8770**			
SEEW	0.0600	0.1280	0.2690	0.3130	0.4690**	0.0930	-0.0380	0.1580	-0.0950	-0.1300	-0.0850		
BIO	0.4710**	0.6610**	0.3440	0.2020	0.1540	-0.0300	0.0500	0.1060	0.3800*	0.3780*	0.3580	0.0720	
HI	0.6810**	-0.3930*	-0.4030*	-0.4890**	-0.5620**	-0.2180	0.4910**	-0.1260	-0.1520	-0.2310	-0.2140	-0.0010	0.0550

\*\*P < 0.01; \*P < 0.05; PH=Plant height; DF=Days to 50% Flowering; DP=Days to podding; DM=Days to 50% maturity; NODP=Nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant vigour; LODG=Lodging; PODP=pods per plant; SEEW=seed weight; GYD=Grain yield; BIO=Biomass; HI=Harvest Index.

#### **4.3.4 Path coefficient analysis**

##### **4.3.4.1 Path coefficients across low P environments**

Across low P conditions, path coefficient analysis revealed that dry biomass (BIO) had highest positive contribution to grain yield (GYD) with 0.7360. NODP, NODW, PODP and PCLEAR had positive and high indirect contribution to GYD via BIO with 0.3740, 0.3690, 0.2320, and 0.2340 respectively. Harvest index is the second trait that had high contribution to GYD with 0.4920. However, the trait that had the most contribution indirectly to GYD via HI was LODG with 0.2840 while DM, DP, DF and PLV had the most contribution negatively with -0.2420, -0.2000, and -0.1460, respectively. Number of pods per plant (0.2740), days to maturity (0.2910), nodule per plant (0.1500), seed per pod (0.1500), plant vigour (0.1640), and days to podding (0.0930) had positive direct effects on grain yield (Table 4.4). Days to 50% flowering, nodule weight, plant height, pod clearance (first pod height), and seed weight had negative direct effects on grain yield -0.1920, -0.3330, -0.0760, -0.2720 and -0.3420, respectively. Considering the effects of secondary traits on primary traits, it was verified that plant height in spite of having direct negative effect to the yield, had greater indirect contribution positively through biomass. Pod clearance, number of nodules and nodule weight had more contribution that was positive but indirect on yield via biomass (Table 4.4).

Table 4.4 Estimates of direct, indirect phenotypic (P) effects of 14 agronomic traits under low phosphorus environments

	PHT	PCLEAR	SEEW	DF	DP	DM	PLV	LODG	NODP	NODW	PODP	SEEP	BIO	HI	GYD
PHT	<b>-0.0760</b>	-0.1270	0.0100	-0.0720	0.0400	0.1360	0.0460	0.0009	0.0370	-0.0940	0.0780	-0.0580	0.2550	-0.1000	<b>0.0750</b>
PCLEAR	-0.0350	<b>-0.2720</b>	-0.0100	-0.0430	0.0400	0.0880	0.0160	-0.0015	0.0170	-0.0530	0.0940	-0.0120	0.2340	-0.0800	<b>-0.0180</b>
SEEW	0.0020	-0.0080	<b>-0.3420</b>	-0.0130	0.0210	0.0990	0.0140	-0.0011	-0.0280	0.0210	-0.0270	-0.0300	-0.0030	0.0550	<b>-0.2400</b>
DF	-0.0290	-0.0610	-0.0230	<b>-0.1920</b>	0.0780	0.1860	0.0150	-0.0003	0.0120	-0.0150	0.0890	-0.0480	0.0380	-0.1460	<b>-0.0950</b>
DP	-0.0330	-0.1160	-0.0760	-0.1600	<b>0.0930</b>	0.2040	0.0440	-0.0011	0.0120	-0.0360	0.1220	-0.0480	0.0720	-0.2000	<b>-0.1220</b>
DM	-0.0350	-0.0820	-0.1170	-0.1220	0.0650	<b>0.2910</b>	0.0480	-0.0021	-0.0020	-0.0320	0.0100	-0.0540	-0.0740	-0.2420	<b>-0.3480</b>
PLV	-0.0210	-0.0260	-0.0300	-0.0180	0.0250	0.0850	<b>0.1640</b>	0.0005	-0.0380	0.0880	0.0280	-0.0490	-0.0130	-0.1050	<b>0.0890</b>
LODG	-0.0100	0.0610	0.0570	0.0080	-0.0150	-0.0910	0.0130	<b>0.0068</b>	-0.0030	0.0120	0.0290	0.0130	0.0780	0.2840	<b>0.4410</b>
NODP	-0.0190	-0.0300	0.0630	-0.0150	0.0070	-0.0040	-0.0410	-0.0002	<b>0.1500</b>	-0.3090	0.0290	0.0280	0.3740	-0.0670	<b>0.1650</b>
NODW	-0.0210	-0.0430	0.0220	-0.0080	0.0100	0.0280	-0.0430	-0.0002	0.1390	<b>-0.3330</b>	0.0400	0.0300	0.3690	-0.0540	<b>0.1350</b>
PODP	-0.0220	-0.0940	0.0340	-0.0620	0.0420	0.0100	0.0170	0.0007	0.0160	-0.0490	<b>0.2740</b>	0.0150	0.2320	-0.0590	<b>0.3550</b>
SEEP	0.0300	0.0210	0.0690	0.0610	-0.0300	-0.1050	-0.0540	0.0006	0.0280	-0.0670	0.0280	<b>0.1500</b>	0.0490	0.0250	<b>0.2060</b>
BIO	-0.0260	-0.0870	0.0010	-0.0100	0.0090	-0.0290	-0.0030	0.0007	0.0760	-0.1670	0.0860	0.0100	<b>0.7360</b>	0.0370	<b>0.6350</b>
HI	0.0150	0.0440	-0.0380	0.0570	-0.0380	-0.1430	-0.0350	0.0039	-0.0210	0.0370	-0.0330	0.0080	0.0560	<b>0.4920</b>	<b>0.4050</b>

PH=Plant height; DF=Days to 50% Flowering; DP=Days to podding; DM=Days to 50% maturity; NODP=number of nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant vigour; LODG=Lodging; PODP=Pods per plant; SEEP=Seed per pod; SEEW=Seed weight; GYD=Grain yield; BIO=Biomass. HI=Harvest Index. The values in bold in the perpendicular direction in the table are the direct paths, that shows the direct contribution to grain yield.

#### **4.3.4.2 Path coefficients across high P environments**

Results of path coefficient analysis of 15 agronomics characteristic of soybean across high phosphorus environments showed that harvest index had higher positive and direct effects over the main variable yield with coefficient of contribution of (0.9040). In the same way, seed weight (0.3020), plant height (0.2130), plant vigour (0.0388), days to flowering (0.0043), nodule weight (0.1170, pods per plant (0.1730) and biomass (0.1650) presented positive coefficients of path analysis. However, negative direct effects were observed on traits pod clearance (-0.0521), days to podding (-0.0820), lodging (-0.0928), number of nodules per plant (-0.1433). The number of seeds per pod had higher magnitude effects as secondary traits over yield. Plant height had indirect effects via biomass and similarly, days to flowering and days to maturity had indirect effects via seed weight, meaning that, these traits can also be used in plant breeding for indirect selection for grain yield improvement (Table 4.5).

Table 4.5 Estimates of direct, indirect phenotypic (P) effects of 14 agronomic traits under high phosphorus environment across the locations

	PHT	PCLEAR	SEEW	DF	DP	DM	PLV	LODG	NODP	NODW	PODP	SEEP	BIO	HI	GYD
<b>PHT</b>	<b>0.2130</b>	-0.0102	0.0460	0.0020	-0.0320	-0.0030	0.0036	0.0035	-0.0297	0.0170	0.0120	-0.0005	0.0980	-0.3330	<b>-0.0140</b>
<b>PCLEAR</b>	0.0420	<b>-0.0521</b>	0.0860	0.0008	0.0060	0.0020	-0.0027	-0.0006	-0.0489	0.0200	-0.0510	0.0059	-0.0370	0.0990	<b>0.0690</b>
<b>SEEW</b>	0.0320	-0.0149	<b>0.3020</b>	0.0018	-0.0110	-0.0080	-0.0012	-0.0106	0.0054	-0.0230	-0.0130	0.0041	0.0190	-0.1080	<b>0.1740</b>
<b>DF</b>	0.1020	-0.0103	0.1300	<b>0.0043</b>	-0.0520	-0.0140	0.0001	0.0070	-0.0426	0.0400	0.0240	0.0076	0.0670	-0.3570	<b>-0.0940</b>
<b>DP</b>	0.0840	0.0040	0.0410	0.0027	<b>-0.0820</b>	-0.0090	-0.0043	0.0202	-0.0361	0.0380	0.0620	0.0107	0.0430	-0.4370	<b>-0.2610</b>
<b>DM</b>	0.0370	0.0042	0.1300	0.0030	-0.0370	<b>-0.0190</b>	0.0105	0.0274	-0.0196	0.0280	0.0120	0.0083	0.0530	-0.4910	<b>-0.2540</b>
<b>PLV</b>	0.0200	0.0036	-0.0090	0.0000	0.0090	-0.0050	<b>0.0388</b>	0.0149	-0.0179	0.0140	-0.0290	-0.0002	0.0040	-0.1780	<b>-0.1350</b>
<b>LODG</b>	-0.0080	-0.0003	0.0340	-0.0003	0.0180	0.0060	-0.0062	<b>-0.0928</b>	0.0053	-0.0110	-0.0090	-0.0073	-0.0050	0.2610	<b>0.1850</b>
<b>NODP</b>	0.0440	-0.0178	-0.0110	0.0013	-0.0210	-0.0030	0.0048	0.0034	<b>-0.1433</b>	0.0910	0.0010	0.0067	0.0230	-0.0140	<b>-0.0350</b>
<b>NODW</b>	0.0300	-0.0087	-0.0610	0.0015	-0.0270	-0.0050	0.0046	0.0086	-0.1119	<b>0.1170</b>	0.0120	0.0056	0.0340	-0.1280	<b>-0.1280</b>
<b>PODP</b>	0.0150	0.0153	-0.0230	0.0006	-0.0290	-0.0010	-0.0064	0.0047	-0.0004	0.0080	<b>0.1730</b>	0.0020	0.0450	-0.0330	<b>0.1690</b>
<b>SEEP</b>	0.0040	0.0113	-0.0450	-0.0012	0.0320	0.0060	0.0003	-0.0248	0.0350	-0.0240	-0.0130	<b>-0.0273</b>	0.0300	0.2600	<b>0.2440</b>
<b>BIO</b>	0.1270	0.0116	0.0340	0.0017	-0.0210	-0.0060	0.0010	0.0027	-0.0202	0.0240	0.0470	-0.0051	<b>0.1650</b>	-0.2540	<b>0.1070</b>
<b>HI</b>	-0.0780	-0.0057	-0.0360	-0.0017	0.0390	0.0110	-0.0076	-0.0268	0.0023	-0.0170	-0.0060	-0.0079	-0.0460	<b>0.9040</b>	<b>0.7230</b>

PH=Plant height; DF Days to 50% Flowering; DP=Days to podding; DM=Days to 50% maturity; NODP=number of nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant vigour; LODG=Lodging; PODP=Pods per plant; SEEP=Seed per pod; SEEW=Seed weight; GYD=Grain yield; BIO=Biomass. HI=Harvest Index. The values in bold in the perpendicular direction in the table are the direct paths, that shows the direct contribution to grain yield



#### **4.3.4.3 Path coefficients across combined (high and low P) environments**

High positive direct effects were observed for harvest index on grain yield with a coefficient of 0.7180. BIO had a high indirect positive contribution to GYD via harvest index with 0.3500 while DM, DP, DP and PH had high negative contribution to GYD via harvest index. Biomass had a high positive contribution of 0.3180 and the traits PH, PODP, NODW, NODP and DF had indirect positive contributions to GYD via BIO. High direct and positive effects were also observed on plant vigour (0.2340) and pods per plant (0.2760). Seed weight, pod clearance, plant height and nodule weight contributed positively but with less magnitude of 0.0689, 0.0485, 0.0790 and 0.0330, respectively. Lodging (-0.0082), number of nodules per plant (-0.0770), days to flowering (-0.0120) and days to maturity (-0.0140), had negative direct contribution to grain yield, but influenced the grain yield indirectly in a positive manner via biomass (Table 4.6).

Table 4.6 Estimates of direct, indirect phenotypic (P) effects of 14 agronomic traits over two phosphorus environments (high and low) across the combined environments

	NODP	NODW	PLV	PHT	DF	DP	DM	PCLEAR	PODP	SEEW	LODG	BIO	HI	GYD
<b>NODP</b>	<b>-0.0770</b>	0.0290	-0.0090	0.0210	-0.0030	-0.0180	-0.0020	0.0105	0.0020	-0.0059	0.0026	0.1140	-0.1540	<b>-0.0900</b>
<b>NODW</b>	-0.0680	<b>0.0330</b>	-0.0360	0.0180	-0.0020	-0.0230	-0.0030	0.0082	0.0350	-0.0090	0.0020	0.1200	-0.1660	<b>-0.0900</b>
<b>PLV</b>	0.0030	-0.0050	<b>0.2340</b>	0.0120	-0.0020	-0.0100	-0.0040	0.0035	-0.0050	0.0064	0.0006	-0.0100	-0.1560	<b>0.0680</b>
<b>PHT</b>	-0.0210	0.0080	0.0360	<b>0.0790</b>	-0.0060	-0.0590	-0.0050	0.0202	0.0750	0.0088	0.0002	0.2100	-0.2820	<b>0.0640</b>
<b>DF</b>	-0.0180	0.0060	0.0350	0.0390	<b>-0.0120</b>	-0.1000	-0.0100	0.0078	0.0990	0.0185	0.0013	0.1090	-0.2890	<b>-0.1130</b>
<b>DP</b>	-0.0120	0.0060	0.0200	0.0390	-0.0100	<b>-0.1190</b>	-0.0090	0.0114	0.1260	0.0216	0.0021	0.0640	-0.3510	<b>-0.2110</b>
<b>DM</b>	-0.0140	0.0070	0.0660	0.0310	-0.0090	-0.0780	<b>-0.0140</b>	0.0096	0.0290	0.0323	0.0032	0.0490	-0.4030	<b>-0.2900</b>
<b>PCLEAR</b>	-0.0170	0.0060	0.0170	0.0330	-0.0020	-0.0280	-0.0030	<b>0.0485</b>	-0.0020	0.0109	0.0028	0.0340	-0.0900	<b>0.0090</b>
<b>PODP</b>	-0.0010	0.0040	-0.0040	0.0210	-0.0040	-0.0550	-0.0010	-0.0004	<b>0.2760</b>	-0.0065	0.0001	0.1210	-0.1090	<b>0.2410</b>
<b>SEEW</b>	0.0070	-0.0040	0.0220	0.0100	-0.0030	-0.0370	-0.0060	0.0077	-0.0260	<b>0.0689</b>	0.0003	0.0230	-0.0010	<b>0.0600</b>
<b>LODG</b>	0.0250	-0.0080	-0.0170	-0.0020	0.0020	0.0300	0.0050	-0.0167	-0.0020	-0.0026	<b>-0.0082</b>	0.0160	0.3520	<b>0.3730</b>
<b>BIO</b>	-0.0280	0.0120	-0.0070	0.0520	-0.0040	-0.0240	-0.0020	0.0051	0.1050	0.0050	-0.0004	<b>0.3180</b>	0.0390	<b>0.4710</b>
<b>HI</b>	0.0170	-0.0080	-0.0510	-0.0310	0.0050	0.0580	0.0080	-0.0061	-0.0420	-0.0001	-0.0040	0.0170	<b>0.7180</b>	<b>0.6810</b>

PH=Plant height; DF Days to 50% Flowering; DP=Days to podding; DM=Days to 50% maturity; NODP=number of nodules per plant; NODW=Nodule weight; PCLEAR=Pod Clearance; PLV=Plant vigour; LODG=Lodging; PODP=Pods per plant; SEEW=Seed weight; GYD=Grain yield; BIO=Biomass. HI=Harvest Index. The values in bold in the perpendicular direction in the table are the direct paths, that shows the direct contribution to grain yield

## 4.4 Discussion

### 4.4.1 Correlation coefficient analysis

Fifteen agronomic traits were used in this study to determine the associations amongst them. Highly significant correlations among most of the traits were observed. Under low P environment, highly significant and positive correlations between grain yield with harvest index, biomass, lodging, plant vigour, number of pods per plant, plant height, pod clearance, and seed weight were observed. This strong relationship was confirmed under high phosphorus environment and in the interaction between the two P environments. This, behaviour of the morphological traits indicating the direction of yield, thus indicates that the environment in which the soybean is planted has no effect. Similar positive associations were also observed by Chandel *et al.* (2014), Oz *et al.* (2009), Malik *et al.* (2011), Machikowa and Laosuwan (2011), Sarutayophat (2012) and Tadesse *et al.* (2009).

Chandel *et al.* (2014) and Aondover *et al.* (2013) observed highly significant correlations between grain yield with number of pods per plant and plant height. Valencia-Ramírez and Ligarreto-Moreno (2012) also found positive and significant correlations between grain yield and pods number per plant, plant height, nodules number per plant, and nodule dry weight, which is similar to results obtained in this study. Srinivas *et al.* (2017) in their study of correlation and path analysis in cowpea genotypes, observed significant and positive correlations between yield and number of seeds per pod, number of pods per plant, 100 seed weight and plant height. Fabiano *et al.*, 2014 recorded the highest direct contribution of harvest index to grain yield, in spite of the fact that most of the breeders tend to disregard the harvest index parameter as a composition of path analysis. According to Fabiano *et al.* (2014), the harvest index should be considered as one of the major parameters to be included in path coefficient analysis study.

Negatively correlated parameters to yield across all phosphorus environments and locations were days to flowering, days to podding, and days to maturity. Chandel *et al.* (2014) reported similar results. Cyprien and Kumar (2011) and Srinivas *et al.* (2017) also found negative correlations between yield and days to 50% of flowering in rice and cowpea, respectively. Negative correlations were also observed between seed weight with yield under low phosphorus environment were also reported by Nandan and Singh (2010). The negative and significant correlation obtained between days to flowering, days to podding, days to maturity with yield indicates that the early matured plants are low yielding. Therefore, knowledge of

genetic correlations can provide a close measure of association between characters that is useful in the overall improvement of a crop through selection, as the success of any breeding programme depends on the efficiency of selection (Arshad *et al.*, 2006).

#### **4.4.2 Path coefficient analysis**

Path coefficient analysis was used to understand the direct and indirect effects of a dependent variable, grain yield (GYD), and other fifteen independent yield components. Results of grain yield showed that traits like total biomass, per plant biomass, harvest index, number of pods per plant, plant vigour had the highest positive direct effect towards grain yield across high and low phosphorus environment in all sites. This suggests that, a slight increment in one of the above traits may directly contribute to increase in grain yield. Chandel *et al.* (2014) and Hama *et al.* (2016) also reported highest and positive direct effects on grain yield from biological yield per plant followed by harvest index, days to 50% flowering, and days to maturity. Valencia-Ramírez and Ligarreto-Moreno (2012) reported number of pods with direct effects in respect of grain yield. Machado *et al.* (2017) reported that pod yield had an indirect positive effect on grain yield.

Moreover, days to flowering, podding and maturity had a negative effect on grain yield and they are also major traits contributing negatively and indirectly through harvest index in combined results of path indicating that selection of high yielding genotypes should not use these traits. This was in agreement with the findings of Kuswanto and Zen (2013), who observed negative and direct effects of days to flowering to grain yield. In the combined results of path, plant height, pods per plant, nodule weight and number of nodules positively contributed to the yield through biomass. Therefore, using these traits in plant breeding for phosphorus use efficiency will make the selection process more effective. Iqbal *et al.* (2003), Ariyo (1995) and El-Badawy and Mehasen (2012) observed indirect contribution of plant height, and pods per plant to the seed yield.

Some of the traits which included plant height, seed weight, days to podding, days to maturity, days to flowering, nodules per plant and nodule weight showed more sensitivity to phosphorus. These traits should be used specifically in each environment according to the P content in the soil, because they demonstrated contrasts on direct effects to the yield under low and high phosphorus. Days to maturity and podding, were positive direct effect while days to flowering showed negative direct effect to yield under high phosphorus, in contrast with the result observed under low P.

Under low phosphorus environment, the traits with negative direct effects to yield were plant height, 100-seed weight, and nodule weight. Studies by Fabiano *et al.* (2014) and Oz *et al.* (2009) corroborated negative direct contribution of 100-seed weight to the yield. Likewise, Chandel *et al.* (2014) studying genotypic correlation and path coefficient analysis in soybean genotypes of yield and yield components found negative and direct effect of 100-seed weight to the yield. However, the same traits; nodule weight, 100-seed weight and plant height under high P environment contributed positively and directly to yield. Valencia-Ramírez and Ligarreto-Moreno (2012), Fabiano *et al.* (2014) and Chandel *et al.* (2014) reported similar results of positive and direct effects of nodule weight, 100-seed weight and plant height. The path coefficient results for yield components with yield, provides information that helps breeders to exercise the selection pressure for genetic improvement in soybean grain yield.

## 4.5 Conclusion

The study revealed strong and significant correlations between yield and yield components under high and low P across all locations. Harvest index was positively and significantly correlated to the grain yield but negatively and significantly correlated to plant height, days to maturity, days to flowering. Under low P, total dry biomass, harvest index, number of pods per plant are the parameters that should be used to screen soybean lines for low P use efficiency. Harvest index, 100-seed weight, and plant height are the traits, which could be used on selection for high P use efficiency. Combined path revealed harvest index, biomass, number of pods per plant and plant vigour could be used to screen low and high P use efficient soybean lines. Moreover, important traits that could be used for selection of lines across all environments according to the results are plant height, number of pods and nodule weight. In high phosphorus environment, days to maturity, days to podding, nodules per plant, pod clearance and seed per pod had negative direct effect on yield and this was opposite of what was observed under low P environment. However, for each environment, traits that have positive direct and indirect effect on yield should be considered.

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## CHAPTER 5

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### STABILITY ANALYSIS OF SELECTED SOYBEAN LINES UNDER PHOSPHORUS STRESS CONDITIONS IN SOUTHERN AFRICA

#### Abstract

This study aimed at analysing the yield stability and genotype x environment interaction (GEI) of 30 soybean genotypes grown under low and high phosphorous (P) levels in three locations; Gurue (Mozambique), Lilongwe (Malawi) and Kabwe (Zambia), resulting in seven environments (location x P level combination). The genotypes were evaluated under rain-fed field conditions during the cropping season of 2016-2017 using a 6 x 5 alpha lattice design with two replications. The additive main effect and multiplicative interaction (AMMI) and the genotype and genotype x environment (GGE) biplot analyses were used to identify superior, stable genotypes. The AMMI analysis of variance indicated that, of the total treatment sum squares (SS), the environment explained 55.00%, GEI 32.89%, and genotypes 12.11% of the variation. Of the five interaction principal component axes (IPCA) that were significant, IPCA1 and IPCA2 contributed 72.92% of the GEI SS. AMMI biplot demonstrated that environment Gurue1, Gurue2 and Lusaka1 were highly interactive with the genotypes. Gurue1 and Gurue2 had higher grain yields average than in Lusaka1, which had yields below average. Kabwe1, Kabwe2, Lilongwe1 and Lilongwe2 had IPCA1 values closer to zero indicating stable environments. However, Lilongwe1 and Lilongwe2 had grain yields above the average, suggesting there were high yielding, in addition to being stable environments. The GGE biplot explained 73.88% of the GEI with PC1 accounting for 54.80% and PC2 19.09% of the variation. Genotypes G2 (TGx2025-6E), G17 (TGx2015-1E), G18 (TGx2027-7E) were closest to the ideal genotype as shown by the GGE biplot. Both AMMI and GGE biplot, revealed genotype TGx2025-9E (G1) as the most stable and high yielding, suggesting its potential as a variety across the environments. Furthermore, genotypes G1 (TGx2025-9E), G2 (TGx2025-6E), G3 (TGx2016-3E), G17 (TGx2015-1E), G18 (TGx2027-7E), G4 (TGx2016-4E), G8 (TGx2025-10E) and G9 (TGx2019-1E), were also selected as high yielding and stable across the seven environment. Thus, both AMMI and GGE biplot procedures were effective in describing the genotype by environment interaction.

## 5.1 Introduction

Soybean is an important legume crop that grows in tropical, subtropical and temperate climates. The recognition of its importance is related to it being a source of high quality, inexpensive protein and oil. The protein content of soybean grain ranges from 40 to 42% (Navabpour *et al.*, 2017). Compared to other legumes, soybean has 20% oil content (Wang *et al.*, 2015) while groundnut is within a range of 18 to 22% (Yusuf *et al.*, 2014). Soybean production is constrained by both biotic and abiotic stresses. The constraints include poor soil fertility, drought and heat challenges. Diseases and pests are also a common challenge in Africa. Soils in sub-Saharan Africa (SSA) are highly variable in terms of nutrient status and this complicates selection and production of soybean. Phosphorus is one of the most important nutrients that limits soybean cultivation in the tropics, as its availability to the plants is very low.

Since soybean is grown in different climatic conditions with varying weather and soil characteristics, varieties tend to perform inconsistently resulting in genotype x environment interaction (GEI) (Kang, 1997). The GEI often reduces breeders' efficiency in identifying stable and adaptable genotypes across the locations. Breeding for broad and specific adaptability is thus one of the objectives for most breeding programmes aimed at enhancing yield productivity of soybean. Genotype by environment interaction studies assist in the identification of genotypes with consistent genotypic performance with respect to environmental changes such as temperature, soil moisture content, soil type, soil fertility from one location to another and year to year.

Different tools have been used to explore GEI and identify high performing genotypes with respect to both similar or multiple environments (Peluzio *et al.*, 2005; Vianna *et al.*, 2013). These include the use of principal component biplot analysis, the additive main effects and multiplicative interaction (AMMI) and the genotype by genotype and environment (GGE) biplot analyses. These methods have evolved as the best and commonly used breeding tools to select genotypes for both adaptability and stability (Zobel *et al.*, 1988). The AMMI analysis combines a univariate method for the additive effects of genotypes and environments, associated to a multivariate analysis for the multiplicative effect of GEI. Moreover de Oliveira *et al.* (2003), reported that this method is suitable and being used in GEI studies of soybean. The GGE biplot analysis is another important tool commonly used in plant breeding to perform GEI analysis, whereby GGE biplot data is visualized graphically (Zali *et al.*, 2016). The GGE biplot is effectively used for mega-environment analysis, where specific genotypes can be recommended to specific mega-environments (Yan *et al.*, 2000; Yan and Kang, 2002; Yan

and Rajcan, 2002; Yan and Tinker, 2006). The present study was aimed at discriminating among genotypes in respect of grain yield mean performance and stability across four locations and two phosphorus environments using AMMI and GGE biplot analysis.

## 5.2 Materials and Methods

### 5.2.1 Genetic material, experimental sites, design, agronomic management and data collection

Thirty advanced breeding lines from IITA-Ibadan were evaluated and these are presented and described in sub-section 3.1.1 and Table 3.1 under materials and methods in Chapter 3. The experimental locations were the same as those described in sub-section 3.2.1 under materials and methods in Chapter 3. Summary of experimental design used and data collection are presented in the same chapter under subsection 3.1.3.

### 5.2.2 Data analysis

The analysis to generate the ANOVA, ranking of the genotypes per environment and across the environments, ranking of the environments and identification of “which- won-where” biplots was done using GenStat version 18<sup>th</sup>, employing the AMMI and GGE biplot models (Yan and Kang, 2002).

The model used for the AMMI analysis is shown in equation 5.1 (AMMI) and for GGE biplot analysis in equation 5.2.

Equation 5-1 AMMI statistical model (Gauch and Zobel, 1996)

$$Y_{ip} = \mu + G_i + E_p + \sum_{k=0}^n \lambda_k \gamma_{ik} \alpha_{pk} + \rho_{ip} + \varepsilon_{ip}$$

Where:  $\lambda_k$  = the kth singular value of GE (linear);  $\lambda_k(g \times 1)$  and  $\alpha' k(1 \times a)$  = singular values connected with  $\lambda_k$ ;  $\gamma_{ik}$  = elements allied to the ith genotype of vector  $\lambda_k(g \times 1)$ ;  $\alpha_{pk}$  = elements allied to the pth environment of vector  $\alpha' k(1 \times a)$ ;  $\rho_{ip}$  = the additional residue and;  $\varepsilon_{ip}$  = ijth error allied with the model.

The GGE biplot was constructed from the environment centred yield data following the method described by Yan *et al.* (2001) and Yan *et al.* (2007) using the model presented in equation 5-2 based on singular value decomposition (SVD) of the first two PC's (Yan, 2002).

Equation 5-2 shows the GGE biplot statistical model (Cornelius *et al.*, 1996).

$$Y_{ij} - \mu = \sum_{k=0}^n \lambda_k \gamma_{ik} \alpha_{pk} + \varepsilon_i$$

Where:  $Y_{ij}$  = mean of genotype (i) in environment (j);  $\mu_j$  = mean value in environment (j);  $i = 1, \dots, g$ ;  $j = 1, \dots, e$ , g and e being the numbers of cultivars and environments, respectively and; t=number of principal components (used or retained in the model, with  $t \leq \min(e, g - 1)$ ).

## 5.3 Results

### 5.3.1 AMMI analysis for grain yield stability

Table 5.1 shows AMMI analysis of variance for grain yield. Soybean grain yield was significantly ( $p < 0.001$ ) affected by environments, genotypes and GEI. Genotypes explained 12.11% of the total variation (total treatment sum of squares), environments (55.00%) and the GEI accounted 32.89% of the total variation. Results showed five significant Interaction Principal Component Axes (IPCA1 to IPCA5) which accounted for 97.03% of the total GEI variation (Table 5.2). The first three IPCAs accounted for 83.97% of the total GEI variation. IPCA1 to IPCA5 explained 57.19%, 15.72%, 11.05%, 7.32% and 5.75% of the total GEI variation, respectively.

Table 5.1 AMMI analysis of variance for grain yield of 30 genotypes tested in seven environments

Source	DF	SS	Mean Square	Total Variation explained	% Contribution to GEI	Cumulative %Contribution to GEI
Treatments	209	171449144	820331.0			
Genotypes	29	20764983	716034.0***	12.1		
Environments	6	94297843	15716307.0***	55.0		
Interaction (GEI)	174	56386318	324059.0***	32.9		
Block	7	225779	32254.0ns			
IPCA 1	34	32248353	948481.0***		57.2	57.2
IPCA 2	32	8865897	277059.0***		15.7	73.0
IPCA 3	30	6230221	207674.0***		11.1	84.0
IPCA 4	28	4125547	147341.0***		7.3	91.3
IPCA 5	26	3241008	124654.0***		5.8	97.0
Residuals	24	1675292	69804.0		3.0	100.0
Error	203	8734459	43027.0			
Total	419	180409382	430571.0			

DF=Degrees of Freedom SS=Sum of squares; GEI=genotype by environment interaction; IPCA=Interaction principal component axis;; ns=non significant; \*\*\*=Highly significant (P=<0.0001)

### **5.3.2 Grain yield mean and scores for the first two IPCAs of thirty soybean genotypes grown under seven environments**

The genotypes performed differently across the seven environments. Ranking the genotypes according to yield stability, the top six performers were G1, G10, G11, G12, G13 and G14 with 1750.0 kg ha<sup>-1</sup>, 1251.0 kg ha<sup>-1</sup>, 1051.0 kg ha<sup>-1</sup>, 1449.0 kg ha<sup>-1</sup>, 1364.0 kg ha<sup>-1</sup> and 1195.0 kg ha<sup>-1</sup>, respectively (Table 5.2). The poor performers for yield stability were G9 (1482.0 kg ha<sup>-1</sup>), G8 (1525 kg ha<sup>-1</sup>), G7 (1335.0 kg ha<sup>-1</sup>), G6 (1211.0 kg ha<sup>-1</sup>) and G5 (958.0 kg ha<sup>-1</sup>) (Table 5.2). Genotype TGx2025-9E (G1) had the highest mean yield performance and was the most stable genotype. Genotypes G12, G13 also showed good above average mean yield performance and good stability. Genotypes G10 and G11 had below average mean yield performance but showed greater stability in comparison to some genotypes that had above-average mean yield performance for the set of all environments (Table 5.2).

The largest negative IPCA2 showing the least stability was observed in G4 (-19.84) and G20 (-14.87) while G19 and G18 had the highest positive IPCA2, 14.001 and 13.84, respectively. The largest positive IPCA1 values were observed for G15 (28.83), G29 (21.39), G28 (19.12), G27 (10.41) and G12 (20.43), though the largest negative IPCA1 were observed in G24 (-19.5), G1 (-16.99), G21 (-15.72) and G2 with IPCA2 equal to -15.64 (Table 5.2).



Table 5.2 Mean grain yield and scores for the first two IPCA (IPCA1 and IPCA2) of 30 soybean genotypes grown in seven environments

Genotype Code	Genotype	Genotype_Rank	Grain yield (kg ha <sup>-1</sup> )	IPCAG[1]	IPCAG[2]
G1	TGx2025-9E	1	1750.0	-17.0	1.6
G10	TGx2025-13E	2	1251.0	2.4	-0.9
G11	TGx2025-11E	3	1044.0	2.1	-17.8
G12	TGx2023-3E	4	1449.0	10.4	3.4
G13	TGx2027-2E	5	1364.0	-7.4	-3.9
G14	TGx2016-2E	6	1195.0	-5.0	2.7
G15	TGx2022-4E	7	1131.0	28.9	-0.6
G16	TGx2020-1E	8	1109.0	5.7	2.2
G17	TGx2015-1E	9	1598.0	-12.5	5.1
G18	TGx2027-7E	10	1569.0	-6.4	13.8
G19	TGx2026-2E	11	1343.0	6.7	14.0
G2	TGx2025-6E	12	1722.0	-15.6	12.1
G20	TGx2025-14E	13	1006.0	3.9	-14.9
G21	TGx2027-1E	14	1465.0	-15.7	-1.5
G22	TGx2026-1E	15	1051.0	5.6	-2.2
G23	TGx1448-2E	16	1141.0	-0.6	-0.9
G24	TGx1989-19F	17	1435.0	-19.5	-4.5
G25	TGx1987-14F	18	1118.0	1.3	-2.5
G26	KAFUE	19	1468.0	-12.9	7.0
G27	MWEMBESHI	20	1103.0	19.1	10.7
G28	SCSAMBA	21	1150.0	10.4	-11.5
G29	SCSAFARI	22	1466.0	21.4	2.8
G3	TGx2016-3E	23	1648.0	-3.3	2.6
G30	MRIDINA	24	1116.0	4.8	-5.6
G4	TGx2016-4E	25	1530.0	-9.2	-19.8
G5	TGx2025-8E	26	958.0	1.5	0.3
G6	TGx2017-6E	27	1211.0	2.4	1.7
G7	TGx2017-5E	28	1335.0	5.1	-7.2
G8	TGx2025-10E	29	1525.0	-14.0	2.1
G9	TGx2019-1E	30	1482.0	7.6	11.6

### 5.3.3 Environment means ranked for grain yield (kg ha<sup>-1</sup>) and the IPCA1 and IPCA2 scores

Among environments, the mean grain yield ranged from 1033.0 kg ha<sup>-1</sup> in Lusaka1 to 1882.0 kg ha<sup>-1</sup> in Lilongwe2 (Table 5.3). Lusaka1 had the highest IPCA1 contributing to the total variation with 27.3 and moderate larger negative IPCA2 of about -10.6. Gurue1 and Gurue2 obtained largest negative values of IPCA1 of around -34.1 and -39.6 and these two environments had the lowest absolute values for IPCA2, -7.6 and 3.9. Kabwe1 and Kabwe2 had the lowest mean yields for the genotypes and IPCA1 of 11.0 and 11.1, respectively. However, the IPCA2 for Kabwe1 and Kabwe2 were negative, -13.5 and -22.2, respectively (Table 5.3).

Table 5.3 Environment means for grain yield (t ha<sup>-1</sup>) and IPCA scores

Env_Code	Environment	Environment Rank	Grain yield (kg ha <sup>-1</sup> )	PCAE[1]	IPCAE[2]
GU1	Gurue1	1	1442.0	-34.1	-7.6
GU2	Gurue2	2	1779.0	-39.6	3.9
KB1	Kabwe1	3	472.0	11.9	-13.54
KB2	Kabwe2	4	993.0	11.0	-22.2
LI1	Lilongwe1	5	1670.0	11.6	23.7
LI2	Lilongwe2	6	1882.0	12.01	26.2
LK1	Lusaka1	7	1033.0	27.3	-10.6

#### 5.3.4 Performance in Individual environments

The 30 soybean genotypes were tested under low phosphorus at three locations and high P at four locations giving seven environments (location by P level combination). Table 5.4, shows the mean performance of the genotypes in respect of grain yield in each of the seven environments as well as the ranking in each environment.

The best performing genotypes in Gurue under low P (Gurue1) were G2 (2452.0 kg ha<sup>-1</sup>), G1 (2432.0 kg ha<sup>-1</sup>), and G17 (2236.0 kg ha<sup>-1</sup>), and the least performing genotypes were G15 (527.0 kg ha<sup>-1</sup>), G16 (787.0 kg ha<sup>-1</sup>) and G20 (789 kg ha<sup>-1</sup>). Under high P (Gurue2), genotypes G1 (2994 kg ha<sup>-1</sup>), G24 (2672.0 kg ha<sup>-1</sup>) and G2 (2600 kg ha<sup>-1</sup>) had high grain yield while the lowest yielding genotypes were G15 (344.0 kg ha<sup>-1</sup>), G11 (723.0 kg ha<sup>-1</sup>) and G22 (1135.0 kg ha<sup>-1</sup>) (Table 5.4).

In Kabwe (Zambia), under low P environment (Kabwe1), the yield ranged from 116.9 (G3) to 739.9 (G5) kg ha<sup>-1</sup>. The best genotypes were G3, followed by G7 and G4 and the low yielding genotypes were G15, G16 and G20. Under high P at the same site (Kabwe2), the yield range was from 682.2 to 1426 kg ha<sup>-1</sup>. The maximum grain yield was observed in genotypes G7, followed by G4, and G3. Minimum grain yield was observed in genotypes G5, G9 and G23 (Table 5.4).

In Lilongwe, under low P (Lilongwe1) environment the grain yield for the genotypes ranged from 1426.0 to 682.2 kg ha<sup>-1</sup>. High yielding genotypes were G12 followed by genotypes G18 and G8, and the least performing genotypes were G20, followed by G11 and G4. The range observed in Lilongwe but under high P environment (Lilongwe2) was 2713 to 1097 kg ha<sup>-1</sup>. The best genotypes were G2, G1 and G3, and the least performing genotypes were G11, G13 and G20. In Lusaka, the genotypes were evaluated only under high P (Lusaka1) environment, and the genotype performance ranged from 575 to 2067 kg ha<sup>-1</sup>. The best genotype in terms of yield was G15, followed by G19 and G4. The lowest yielding genotypes were G2, followed by G21 and G24 (Table 5.4).

Table 5.4 Mean grain yield (kg ha<sup>-1</sup>) of 30 genotypes ranked from highest to lowest yielding per environment

Environment: 1		Environment:2		Environment: 3		Environment: 4		Environment: 5		Environment: 6		Environment: 7	
GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN
G2	2452.0	G1	2994.0	G29	831.6	G7	1426.0	G12	2258.0	G2	2713.0	G15	2067.0
G1	2432.0	G24	2672.0	G3	739.9	G4	1395.2	G18	2224.0	G29	2396.0	G9	1756.0
G17	2236.0	G2	2600.0	G7	725.5	G28	1368.2	G8	2199.0	G1	2387.0	G29	1736.0
G21	2211.0	G8	2550.0	G28	724.6	G29	1342.7	G27	2188.0	G3	2371.0	G4	1515.0
G24	2200.0	G18	2510.0	G4	701.5	G3	1285.9	G9	2155.0	G19	2332.0	G12	1401.0
G26	2142.0	G17	2480.0	G12	699.6	G20	1232.6	G19	2142.0	G9	2332.0	G1	1321.0
G8	2135.0	G4	2459.0	G2	593.7	G2	1119.2	G13	2134.0	G18	2284.0	G11	1199.0
G4	2014.0	G21	2411.0	G13	593.4	G12	1084.2	G29	2049.0	G26	2238.0	G3	1141.0
G11	1995.0	G26	2305.0	G27	531.8	G21	1076.1	G2	1998.0	G17	2131.0	G19	1118.0
G3	1909.0	G14	2199.0	G20	515.6	G1	1071.9	G3	1921.0	G15	2110.0	G7	1088.0
G13	1708.0	G3	2169.0	G21	508.3	G24	1023.4	G17	1921.0	G27	2018.0	G18	1079.0
G18	1642.0	G13	2137.0	G8	493.4	G10	1006.6	G26	1680.0	G12	1998.0	G23	1020.0
G9	1378.0	G7	1854.0	G10	475.3	G30	1003.7	G10	1623.0	G7	1961.0	G17	1016.0
G23	1369.0	G9	1721.0	G1	472.8	G6	974.6	G15	1609.0	G6	1934.0	G30	988.0
G12	1334.0	G6	1701.0	G17	468.7	G13	950.4	G21	1593.0	G14	1896.0	G10	979.0

Environment1= Gurue (Low/phosphorus); Environment2=Gurue (High/phosphorus); Environment3=Kabwe (Low phosphorus); Environment4=Kabwe (High/phosphorus); Environment5=Lilongwe (Low phosphorus); Environment6=Lilongwe (High phosphorus); Environment7=Lusaka (Low phosphorus).

Table 5.4 continued

Environment: 1		Environment:2		Environment: 3		Environment: 4		Environment: 5		Environment: 6		Environment: 7	
GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN	GEN	MEAN
G25	1323.0	G10	1660.0	G24	452.5	G17	933.7	G1	1570.0	G21	1868	G8	961.0
G19	1323.0	G23	1595.0	G18	432.4	G22	911.6	G16	1559.0	G22	1828.0	G28	940.0
G10	1214.0	G16	1529.0	G6	414.1	G25	907.4	G6	1530.0	G10	1798.0	G13	884.0
G22	1108.0	G5	1482.0	G30	411	G27	906.6	G23	1526.0	G16	1782.0	G16	873.0
G14	1060.0	G20	1466.0	G15	384.6	G14	889.3	G25	1522.0	G5	1630.0	G27	863.0
G6	1059.0	G30	1443.0	G25	384.3	G16	877.7	G24	1495.0	G30	1625.0	G6	862.0
G30	1015.0	G19	1421.0	G16	353.7	G15	875.7	G28	1391.0	G24	1605.0	G22	802.0
G28	960.0	G12	1369.0	G19	348.2	G11	849.6	G14	1347.0	G25	1602.0	G20	770.0
G7	945.0	G25	1360.0	G9	342.0	G26	845.3	G7	1345.0	G28	1582.0	G26	739.0
G5	892.0	G29	1218.0	G26	328.2	G8	833.5	G30	1329.0	G23	1559.0	G25	726.0
G20	789.0	G22	1135.0	G22	310.9	G18	809.6	G22	1259.0	G8	1503.0	G5	698.0
G16	787.0	G28	1083.0	G11	298.7	G19	712.3	G5	1208.0	G4	1432.0	G14	682.0
G29	686.0	G27	785.0	G14	290.2	G23	697.2	G4	1197.0	G20	1297.0	G24	600.0
G15	527.0	G11	723.0	G23	221.6	G9	692.5	G11	1147.0	G13	1140.0	G21	588.0
G27	425.0	G15	344.0	G5	116.9	G5	682.2	G20	970.0	G11	1097.0	G2	575.0
<b>Mean</b>	<b>1442.0</b>		<b>1779.0</b>		<b>472.0</b>		<b>993.0</b>		<b>1670.0</b>		<b>1882.0</b>		<b>1033.0</b>

Environment1= Gurue (Low/phosphorus); Environment2=Gurue (High/phosphorus); Environment3=Kabwe (Low phosphorus); Environment4=Kabwe (High/phosphorus); Environment5=Lilongwe (Low phosphorus); Environment6=Lilongwe (High phosphorus); Environment7=Lusaka (Low phosphorus).

### 5.3.5 Selection of four and ranking of four best genotypes in seven environment based on stability and representativeness

Tables 5.5 presents four best genotypes selected by AMMI per environment and IPCA1 of the environment ranked by the performance. Genotypes G1 and G2 were among the top four best genotypes in Gurue2, Gurue1 and Lilongwe2. Genotype G7 was in the top four in Kabwe1 and Kabwe2, while G4 appeared in the top four in Lusaka1 and Kabwe2. The check (G29) responded well in Lusaka1, Lilongwe2, Kabwe1 and Kabwe2, though the other checks; G28 performed well only in Kabwe1 and Kabwe2 and, G27 only in Lilongwe1. Gurue1 and Gurue2 did not have any checks amongst the best four genotypes.

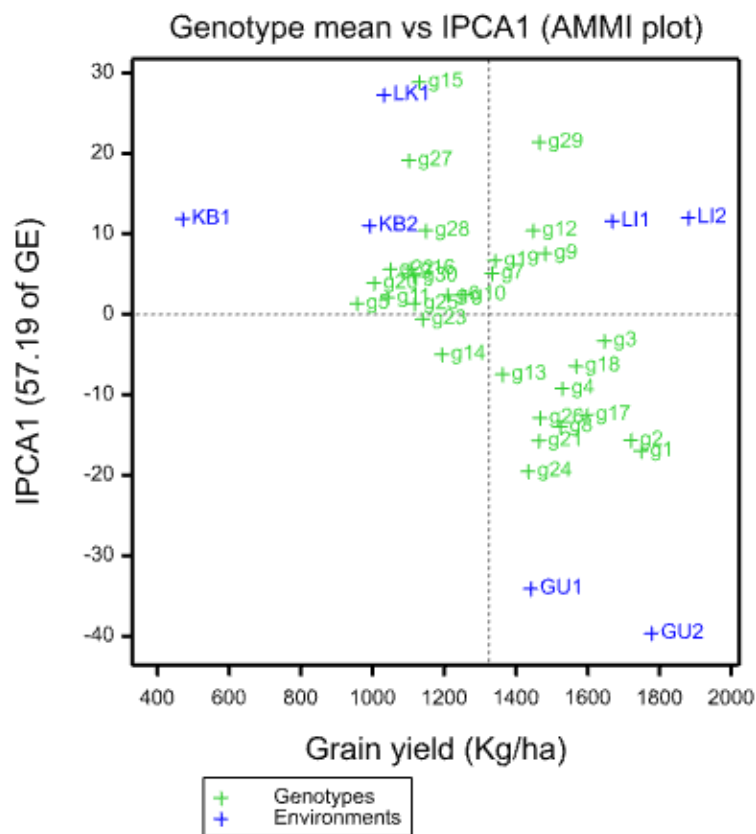
Table 5.5 First four AMMI selections per environment

N	Env_Code	Environment	Mean	Score (IPCA1)	1	2	3	4
7	(LK1)	Lusaka1	1033.0	27.3	G15	G9	G29	G4
6	(LI2)	Lilongwe2	1882.0	12.0	G2	G29	G1	G3
3	(KB1)	Kabwe1	472.0	11.9	G29	G3	G7	G28
5	(LI1)	Lilongwe1	1670.0	11.6	G12	G18	G8	G27
4	KB2	Kabwe2	993.0	11.0	G7	G4	G28	G29
1	(GU1)	Gurue1	1442.0	-34.1	G2	G1	G17	G21
2	(GU2)	Gurue2	1779.0	-39.6	G1	G24	G2	G8

### 5.3.6 AMMI biplot for genotypes and environment classification

The AMMI1 (IPCA1 vs genotypic mean yields) biplot is presented in Figure 5.1 and shows how genotypes interacted across the seven environments. It indicates genotypes that have yields above or below the mean grain yield and those with large IPCA1 scores or scores closer to zero, between 0 and -10 or +10. Most of the genotypes had little interaction with the environment as they clustered close to zero with both positive and negative IPCA1 scores. Genotypes G1, G2, G24, and G21 had high negative IPCA1 scores while G15, G27 and G29

had high positive IPCA1 scores; hence, these genotypes were more interactive across the seven environments. Genotypes G3, G18, G13 and G4 combined both high yield and stability. Likewise, an environment with high scores, either negative or positive, shows the existence of high interaction across the genotypes and vice-versa. Gurue1, Gurue2 and Lusaka1 were further away from the biplot origin, with high IPCA1 scores, meaning that these environments were highly interactive with the genotypes, unlike Kabwe1, Kabwe2, Lilongwe1 and Lilongwe2 that had IPCA values between 0 and +10. Grain yields in Gurue1 and Gurue2 were above average and in Lusaka1 the grain yields were below average. Environment Kabwe1, Kabwe2 had IPCA1 values closer to zero with grain yield below the average, in contrast to Lilongwe1 and Lilongwe2, which had low IPCA1 values, closer to zero, but grain yields above the average.

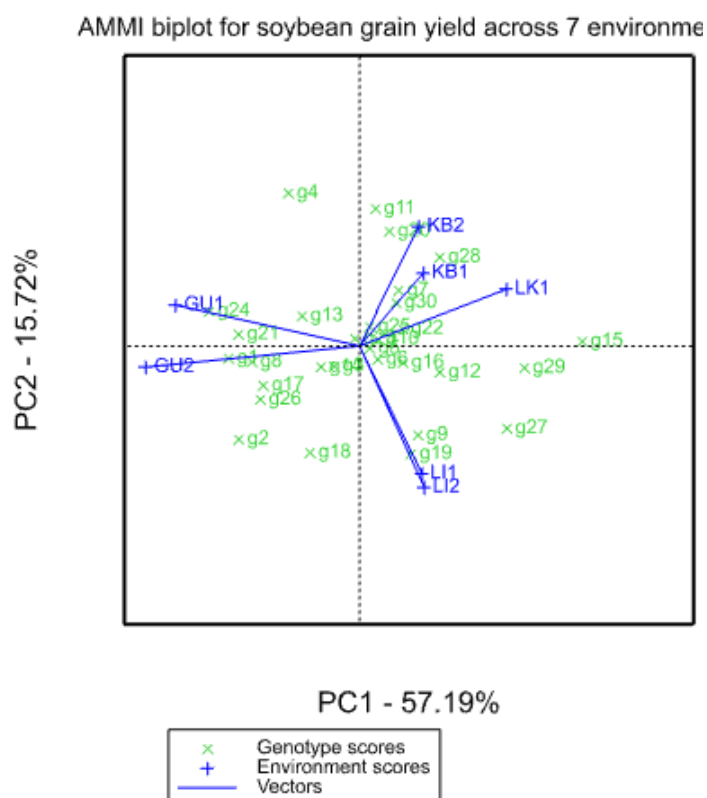


G=Genotype; L1=Lusaka low P; KB1= Kabwe low P; KB2=Kabwe High P; L1=Lilongwe low P; L2=Lilongwe high P; GU1=Gurue Low P; GU2=Gurue high P, PC1=Principal component one; PC2=Principal component two

Figure 5-1 Grain vs IPCA 1 AMMI biplot for the 30 advanced soybean lines evaluated across seven environments

### 5.3.7 AMMI biplot for IPCA1 vs IPCA2

According to the vectors drawn from the centre of biplot shows that environment Kabwe1, Kabwe2 and Lusaka1 had similar responses, as the angle between their vectors was small. Lilongwe1 and Lilongwe2 also had similar responses between them and the same was observed between Gurue1 and Gurue2. All the environmental vectors were relatively longer showing greater contribution to the GEI. However, Kabwe1 had the shortest vector. Genotype G7 was the most stable as it was located on the biplot origin. Moreover, genotypes and environment score values close to zero in the axes of IPCA1 and IPCA2 demonstrate the stability of the genotype and the environment. Genotypes that contributed less to the GEI were G7, G16, G9 and G6, while for the environments, Kabwe1, Kabwe2 and Lusaka1 were closer to the origin of the biplot.



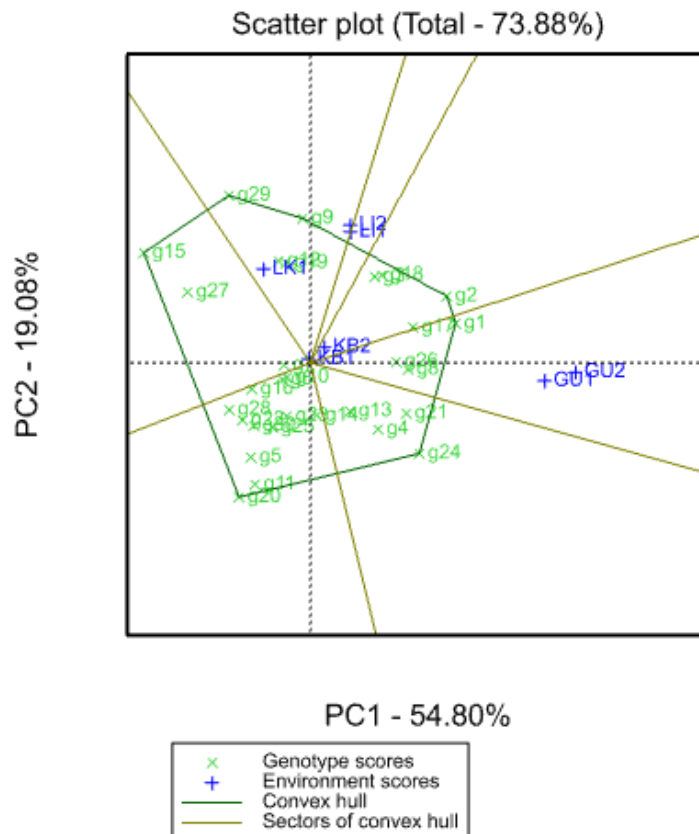
G=Genotype; L1=Lusaka low P; KB1= Kabwe low P; KB2=Kabwe High P; L11=Lilongwe low P; L12=Lilongwe high P; GU1=Gurue Low P; GU2=Gurue high P, PC1=Principal component one; PC2=Principal component two

Figure 5-2 AMMI2 analysis for grain (kg ha<sup>-1</sup>) yield of 30 advanced soybean lines obtained in seven environments



### 5.3.8 “Which-won-where” GGE biplot analysis

Figure 5.3 presents a polygon view of the GGE biplot. This biplot shows the best performing genotypes for each environment or which genotype “won-where”. Genotypes G15, G11, G29, G9, G2, G1, G24, and G20 appeared on the vertex of the polygon. The genotypes on the vertices performed either the best or poorly in one or more of the test environments. Seven rays were obtained which divided the biplot into seven sectors and the environments fell in three of these sectors. Environments were grouped as follows Lilongwe1, Lilongwe2 and Lusaka1 with G9 and G29 as the winning genotype; Kabwe1 the highest genotype was G15; environment Kabwe2 the highest genotype was G2; whereas in environments Gurue1 and Gurue2 with G1 as the vertex genotype representing the highest yielding genotype. Genotypes G1, G2, were the best performing while the other vertex genotypes (G15, G20 and G24) were poor in the test environments.

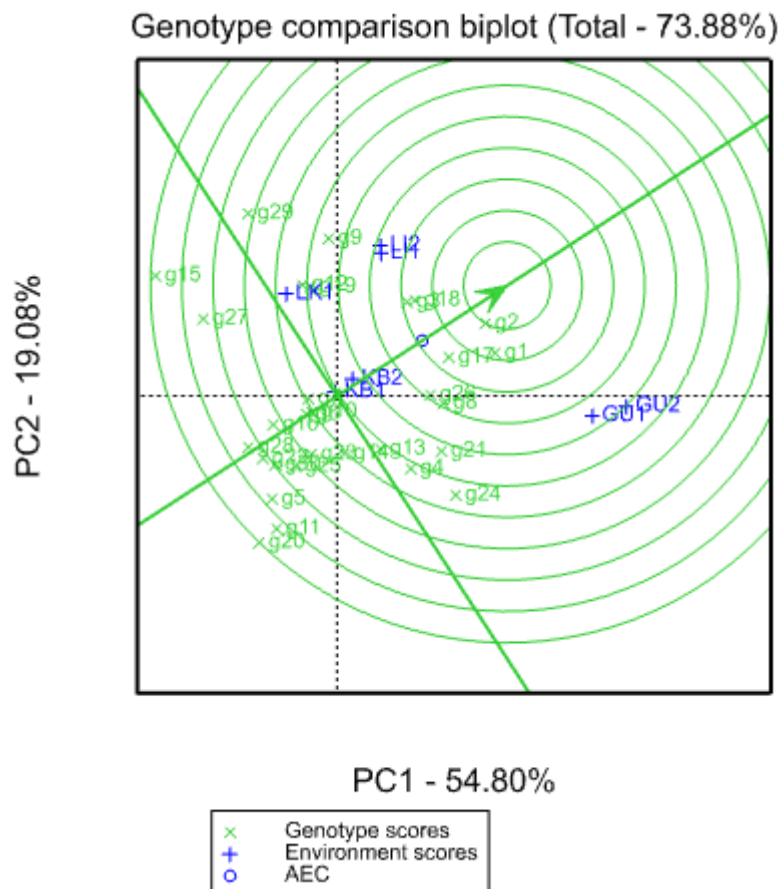


G=Genotype; L1=Lusaka low P; KB1= Kabwe low P; KB2=Kabwe High P; L1=Lilongwe low P; L12=Lilongwe high P; GU1=Gurue Low P; GU2=Gurue high P, PC1=Principal component one; PC2=Principal component two

Figure 5-3 Scatter GGE biplot displaying “which-won-where” for 30 advanced soybean lines across the seven environments

### 5.3.9 Yield performance and stability comparison of genotypes

The results of the GGE biplot comparison of the genotypes to the ideal genotype across the environments based on mean stability are shown in Figure 5.4. The GGE biplot explained 73.88% of the GEI with PC1 accounting for 54.80% and PC2 19.09% of the variation. Genotypes that were close to the arrow indicating the point of ideal genotype were considered as high yielding and more stable. Genotype G2 was closest to the ideal genotype followed by G1, G17 and G18 while genotypes G20, G11 and G15 were the farthest from the point of the ideal genotype and in the outer concentric rings.

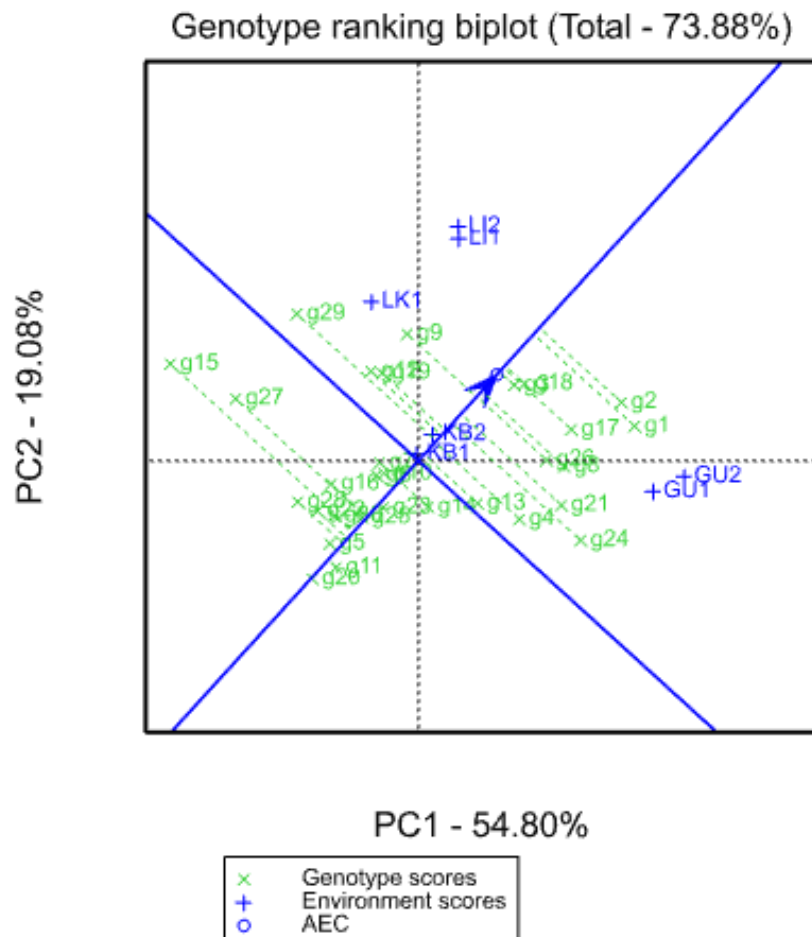


G=Genotype; L1=Lusaka low P; KB1= Kabwe low P; KB2=Kabwe High P; L11=Lilongwe low P; L12=Lilongwe high P; GU1=Gurue Low P; GU2=Gurue high P, PC1=Principal component one; PC2=Principal component two

Figure 5-4 GGE biplot comparison of genotypes relative to the centre of the concentric circle for grain yield across seven environments

### 5.3.10 Ranking genotypes based on grain yield (kg ha<sup>-1</sup>) and stability

Figure 5.5 shows the mean versus stability of the genotypes. The top eight (8) genotypes with high performance in grain yield were G1, G2, G17, G24, G21, G26, G8 and G18, whereas the most stable and high yielding genotypes were G3, G18 and G13 .



G=Genotype; L1=Lusaka low P; KB1= Kabwe low P; KB2=Kabwe High P; LI1=Lilongwe low P; LI2=Lilongwe high P; GU1=Gurue Low P; GU2=Gurue high P; PC1=Principal component one; PC2=Principal component two

Figure 5-5 Biplot genotype ranking based on grain yield (kg ha<sup>-1</sup>) across seven environments

## 5.4 Discussion

Combined results for grain yield data under high and low P environments showed significant GEI. The differences of the genotypes on responsiveness can be attributed to the low and high P across the four locations. These results are in agreement with Cornelius *et al.*, 19906, who reported that factors like the crop, diversity among the germplasm used and the range of environmental conditions can affect the degree of variation. Other studies including Tyagi and Khan (2010), Cucolotto *et al.* (2007) and Popovic (2013), have also reported greater magnitude of variation among genotypes and high significant GEI. This significant GEI for grain yield confirms the need to determine the stability and adaptability of genotypes because the environment (edaphoclimatic conditions) has a significant influence on these factors.

The results showed that more than 50% of the genotypes had above average grain yields across the seven environments. Addition of phosphorus in the soil resulted in increased grain yield of soybean in most genotypes. Tsvetkova and Georgiev (2003) reported similar results where the supply of P in nutrient solution caused significant changes in P metabolism in soybean. In addition, Darwesh *et al.* (2013) studying the effect of phosphorus fertilizers on growth and physiological P use efficiency of three soybean cultivars, indicated that the application of different rates of P in the soil affected cultivar performance significantly. The performance of the soybean cultivars for most of the traits, including the biological yield increased considerably.

AMMI analysis confirmed the existence of significant differences in grain yield in the different environments. Although five interaction principal components (IPCA) were obtained with a total contribution of 97.3%, the first two principal components accounted for most (72.92%) of the variation due to GEI with IPCA1 contributing 57.19% and IPCA2 contributing 15.72%. Similar results were obtained by Cucolotto *et al.* (2007) in three sets of genotypes, early, medium and later maturity, where they observed a total contribution of the first two IPCA of 67%, 42% and 74%, respectively. Gurmu *et al.* (2009), observed highly significant ( $P < 0.01$ ) environment variance, genotype variance and GEI variance in first two interaction principal component of AMMI model, contributing 66.15% of the interaction. Bhartiya *et al.* (2017) reported that IPCA1 and IPCA2 contributed 47.55% of the total GEI variation in AMMI analysis.

Different responses of the genotypes due to environment variation was observed. Some genotypes showed sensitiveness to environment while others high stability. Moreover, among the two groups, genotypes that are unstable but high yielding were observed as well as those that were unstable and low yielding, while others had high yield and showed high stability. Genotype (G1) was the most stable and high yielding. Other genotypes with high stability and

greater yield across the seven environment were G2, G3, G17, G18, G4, G8 and G9. Breeders are mostly interested in the last group of genotypes, which are high yielding and more stable. With AMMI analysis, it was possible to identify genotypes that were high yielding in specific environments: Genotype G24 in Gurue2; Gurue1 G21; Kabwe2 genotypes G7, G28 and G29; Kabwe1 G29, G7 and G27 performed well, while in Lusaka they were G15, G9 and G29. The high yielding and less stable genotypes are recommended for specific environments. Similar observations were made by Junior *et al.* (2017), Oliveira *et al.* (2015) and Kumar *et al.* (2014).

In AMMI biplot method, Kabwe1 and Kabwe2 had the shortest vectors, thus contributed less to the GEI. Gurue1, Gurue2, Lilongwe1, Lilongwe2 and Lusaka were slightly higher performing environments (Yan *et al.*, 2009). Nevertheless, Kabwe1 and Kabwe2 were the poorest environments and demonstrated low variability than Lilongwe1, Lilongwe2 and Lusaka, which were slightly higher performing environments. Genotypes with highest negative IPCA1 values are adapted to environments with the highest negative IPCA1. Similarly, the genotypes with high, positive IPCA1 values are adapted to the environments with high and positive IPCA1.

High absolute values of IPCA2 indicate that the genotype is less stable, while for environment it shows that the genotypes are specifically adapted in that environment. However, according to Alam *et al.* (2017), genotypes with IPCA1 scores near zero, had little interaction across environments, while the genotypes with large IPCA1 scores, either positive or negative were highly interactive. AMMI1 analysis showed that genotypes G3, G4, G13, G14, G23, G5, G6, G7, G9, G10, G11, G16, G19 and G20 were stable. The IPCA values were close to zero either in the positive direction as well as in opposite direction. Genotypes G1, G2, G24 and G21 had high negative IPCA1 scores while G15, G27 and G29 had high positive IPCA1 scores; hence, these genotypes were more interactive across the seven environment. Genotypes G3, G18, G13 and G4 combined both high yield and stability.

Stable genotypes have the potential to respond positively to agronomic inputs or better environmental conditions (Becker and Leon, 1988). The GGE biplot explained 73.88% of the GEI with PC1 accounting for 54.80% and PC2 19.09% of the variation. From the polygon view of the GGE biplot, seven sectors were formed and the environments felled into three sectors indicating grouping of the environments. The polygon view also visualised the winning genotype in each sector or group of environments. For Lilongwe1, Lilongwe2 and Lusaka1, G9 and G29 were on the vertex of the polygon, representing the best performing genotype on those environments; Kabwe1 identified G15 as the best genotype; in Kabwe2 G2 was the best and; Gurue1 and Gurue2 classified G1 as the high yielding genotype. The polygon view of the GGE biplot thus indicated the best performing genotypes in an environment or group of

environments (Kaya *et al.*, 2006). Yan and Kang, 2003 advocated that GGE biplot produce best polygons to view or visualize the GEI shape. 'Which-won-where' pattern in the polygon is useful for estimation possible presence different mega-environments in the target environment (Yan and Rajcan, 2002; Yan and Tinker, 2006). Similar results were also reported by Yan and Kang (2002), who observed highly significant association among the rankings of genotypes based on mean performance and stability in the SREG biplot and genotype ranking based on the YSi statistic.

Ideal genotypes were identified using the GGE biplot. The genotypes G2, G1, G17 and G18 were superior in terms of grain yield and stability as they were closest to the ideal genotype located in the centre of the innermost concentric circle, while the less stable and low yielding genotypes G20, G11 and G15 were located far from the ideal genotype. Features of ideal genotype or cultivar are commonly high average performance over a wide range of environments as well as stability (Eberhart and Russell, 1966). Jandong *et al.* (2011) reported that the highest stable genotypes in their study were close to the ideal genotype. Junior *et al.* (2017), indicated that an ideal genotype as well as an ideal environment, is only a theoretical concept used as a reference of the choice of sites for multi-environment trials.

Various researchers including Junior *et al.* (2017), Atnaf *et al.* (2013), Oliveira *et al.* (2015) and many others, combined methods AMMI and GGE biplot analyses in order to explore the GEI. Hence according to Ochigbo *et al.* (2016) it is important to combine two or more analytical tools to obtain reliable information regarding yield and stability and get better recommendation of genotypes to farmers. Junior *et al.* (2017) highlighted the differences among methods used for the specific GEI in most environments suggesting the use of AMMI and GGE biplot to complement each other. The biplots could be accomplished by either GGE or AMMI method. Nevertheless, Karimizadeh *et al.* (2013) indicated that the AMMI method could be misleading in identifying 'which-won-where', because it removes genotype as a main effect, whereas GGE biplot is more explanatory and enables pair-wise comparison, so using both methods can provide a good picture of the GEI.

## **5.5 Conclusion**

The best genotype across all seven environments was G1; it demonstrated high stability as well as high grain yield;

The four genotypes selected through AMMI analysis per environment according to their performance were: G1, G24, G2, and G8 in Gurue2, G2, G1, G17 and G21 in Gurue1, G7,

G4, G28-check and G29-check in Kabwe2, G29-check, G3, G7 and G27-check in Kabwe1 and G15, G9, G29-check and G4, in Lusaka;

GGE biplot identified the best genotypes as G9 Kabwe1, Lilongwe1, Lilongwe2 and Lusaka, G1 in Gurue1 and Gurue2, G2 in Kabwe2.

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## CHAPTER 6

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### GENERAL OVERVIEW

#### 6.1 Introduction

Soybean is an important source of protein, oil and micronutrients for human and animal consumption. It is mostly cultivated in the tropics, subtropical and temperate areas, often where the soils are poor in phosphorus, which is turning to be a major constraint to soybean growth and production. The study focused mainly on: selection of genotypes for phosphorus use efficiency; description of the association between grain yield with other agronomic characters and their contribution (direct and indirect) to the grain, and quantification of genotype x environment interaction effects and stability of soybean genotypes with respect to grain yield across low and optimum phosphorous environments. This chapter presents the general conclusion and recommendations from the study.

#### 6.2 General conclusion

Among 30 genotypes evaluated under low and high phosphorus, there was substantial variability in their response to phosphorus. The genotypes were divided into three classes according to their reaction to phosphorus: 1) Genotypes TGx2017-5E, TGx2025-8E, TGx2017-6E, TGx2020-1E, TGx2027-7E and TGx2025-14E respond well to phosphorus application 2) genotypes TGx2025-11E, TGx2023-3E TGx2022-4E TGx2026-2E TGx1987-14F responded negatively to phosphorus and; 3) for the rest of the genotypes, the yield performance remained constant under high and low phosphorus.

Across the high and low phosphorus environments, genotypes TGx2025-9E and TGx2016-4E were the best performing with mean grain yield for low phosphorus of 1154.30 kg/ha and 1551.20 kg/ha under high phosphorus, showing an increment of about 34.39%. The genotypes were clustered into six groups with the maximum dissimilarity index of 0.6. However, the degree of dissimilarity was very small suggesting narrow genetic diversity. Therefore, these elite lines are not suitable for inter-crossing as there is narrow diversity. Greater distances of dissimilarity were observed between the checks and the elite lines.

There were strong and significant associations between yield and yield components. Harvest index was highly significant and positively correlated with the grain yield but negatively with plant height, days to maturity, days to flowering. Under low phosphorus environment, total dry

biomass, harvest index, number of pods are the traits that should be used to screen soybean lines for low P use efficiency, likewise in high phosphorus, harvest index, 100-seed weight, and plant height are the traits recommended for selection of high P use efficiency. Harvest index, biomass, number of pods can be used to screen for both low and high phosphorus use efficient soybean lines across environments.

Path coefficient analysis assisted in finding direct and indirect trait contributions to grain yield that can be used for selection of superior lines. Nodules per plant, nodule weight and plant height contributed indirectly to yield. Number of seed per pod and days to maturity contributed indirectly and negatively to yield under high phosphorus environments. The traits that can be used for selection of lines across all environments according the results are plant height, number of pods and nodule weight. The results suggest that phosphorus influences the genetic capacity of the genotypes to deal with both low and high phosphorus in the soil. Selection based on the above traits increases the chances of selecting best genotypes for yield improvement.

From the genotype x environment (G x E) studies, the best genotype across all seven environments was G1; it, demonstrated high stability as well as high grain yield; The four genotypes selected through AMMI analysis per environment according to their performance were: G1, G24, G2, and G8 in Gurue2, G2, G1, G17 and G21 in Gurue1, G7, G4, G28-check and G29-check in Kabwe2, G29-check, G3, G7 and G27-check in Kabwe1 and G15, G9, G29-check and G4, in Lusaka. GGE biplot identified the best genotypes as G9 in Kabwe1, Lilongwe1, Lilongwe2 and Lusaka, G1 in Gurue1 and Gurue2, G2 in Kabwe2. These results highlight that GEI studies can enhance efficiencies of breeding for broad adaptability in respect to responsiveness to low and high phosphorus. AMMI and GGE biplot procedures were effective tools in describing the genotype by environment interactions (GEI). Moreover, using both tools forms a good combination for visualization and interpretation of the complex GEI.

### **6.3 Recommendations**

Genotypes TGx2017-5E, TGx2025-8E, TGx2017-6E, TGx2020-1E, TGx2027-7E and TGx2025-14E that were responsive to phosphorus application can be produced under high phosphorus as additional phosphorus results in increment of soybean grain yield. However, there is no need to invest in phosphorus fertilization when genotypes TGx2025-11E, TGx2023-3E TGx2022-4E TGx2026-2E TGx1987-14F are grown. The yield of these genotypes

remained unchanged under low and high phosphorus. Genotypes TGx2025-9E and TGx2016-4E were the best performing in both low and high phosphorus environments.

Lines are recommended for inter-crossing if they are distantly related. The elite lines used in this study had narrow genetic diversity, therefore are not recommended for inter-crossing.

Biomass, harvest index, pods per plant, plant height contributed positively and directly to the grain yield, therefore, are recommended for indirect selection of genotypes for grain yield improvement for low phosphorus use efficiency, likewise harvest index, 100-seed weight, and plant height are recommended for indirect selection of grain yield for high phosphorus use efficiency.

Based on the GEI results, soybean genotypes can be selected in one site among the four environments that composed one mega-environment, that is Kabwe1, Lilongwe1, Lilongwe2 and Lusaka; one of environment is enough to do selection between Gurue1 and Gurue2.

However, the study was conducted only in one season, therefore it is recommended that it be repeated for another two years, to see if there is repeatability in terms of the genotype performance under the different environments.