

Varying soil nutrition in grassland and savanna ecosystems affect plant-microbe symbiosis, nitrogen nutrition and growth of *Pisum sativum* L.

By

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SUMMARY

Sustainable agriculture is associated with soil fertility which promotes quality vegetation and higher yield potential for sustenance as either food or feed. In many developing countries with low gross domestic product (GDP) per capita, households mostly rely on agricultural produce and livestock to meet their dietary requirements. However, most of the regions are characterized by low fertility soils which negatively affect agricultural yield and overall quality of produce. The grassland and savanna ecosystems in which the majority of the population in these countries reside, are nutrient deficient and acidic. This imposes a burden on both small and large-scale farmers since they have to rely on commercial fertilizers to mitigate the effects. Furthermore, the use of these fertilizers can negatively affect the immediate environment through leaching and runoff.

Therefore, there is a need for eco-friendly, low-input high-yield farming systems that are also cost effective. This has increased research aimed at the use of biofertilizers such as leguminous plants to remediate soil nutrition in grassland and savanna ecosystems. Since biofertilizers are naturally occurring, their use has minimal threat to the environment and ecosystems. Legumes and their symbionts, whether endophytic and/or associative, might be a suitable sustainable farming system to mitigate soil quality degradation. More so, legumes are a rich source of proteins and minerals that improves the quality of feed in pastures, hence improving the quality of livestock. This project was aimed at investigating the functional adaptations of a winter legume, *Pisum sativum* L., in KwaZulu-Natal (KZN) grassland and savanna nutrient deficient ecosystem soils. The four soil collection sites were Hluhluwe, Izingolweni, Bergville, and Ashburton.


The first experiment examined soil nutrients, microbial composition and diversity and enzyme activities of KZN grassland and savanna soils. This was achieved by analyzing the soil geochemistry (nutrient concentration, pH, total cation concentrations and exchange acidity), microbial composition, arbuscular mycorrhizal (AM) fungi spore count and extracellular enzyme activities. The soils were found to vary in all aspects, ranging from nutrient concentration to the Biological Index for soil Fertility (BIF). Endophytic/associative microbes identified in the soils belonged to the families *Bacillaceae* (*Bacillus* and *Lysinibacillus*), *Nectriaceae*, *Mucoraceae*, and *Hypocreaceae*. Bergville soil had the lowest pH, dehydrogenase activity, microbial diversity, BIF, and total cations. The combined limitations led to us to postulate that this soil type was the least suitable for the growth of *P. sativum* L.

In the second experimental chapter we investigated the effects of soil nutrient availability and microbial associations on plant nutrition, growth kinetics, N-source preference and metabolite synthesis in *P. sativum* L. Soils from the four KZN regions were used as inoculum and growth medium, making up four treatments. Nodulation was only observed in Izingolweni grown plants and the root nodule inhabiting microbes were from the genera *Cupriavidus*, *Paenibacillus*, *Bacillus*, *Ralstonia*, and *Saccharibacillus*. However, plants from all four treatments relied on combined N for growth but at different extents. Bergville soil grown plants decreased growth, nutrient concentration, growth-promoting metabolites (kinetin, salicylic acid, and active cytokinins), but had high antioxidant and storage cytokinin concentrations. The current findings suggest that *P. sativum* L. is adaptable to nutrient deficient soils by associating with plant growth-promoting microbes, resource re-allocation, and using combined N.

PREFACE

The data presented in this dissertation was collected at the School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, Republic of South Africa from 2018 to 2019. Experimental work was carried out while registered at the School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, under the supervision of Dr. Anathi Magadlela.

This dissertation submitted for the degree of Master of Science in the College of Agriculture, Engineering and Science, School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, represents original work by the author and has not been submitted in any form for a degree or diploma at any other university.


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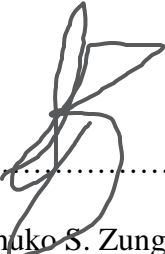
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**COLLEGE OF AGRICULTURE, ENGINEERING AND SCIENCE DECLARATION:
PUBLICATIONS**

Applied soil ecology APSOIL_2019_1308 (Under review)

Soil nutrition, microbial composition and associated soil enzyme activities in KwaZulu-Natal grasslands and savannah ecosystems soils

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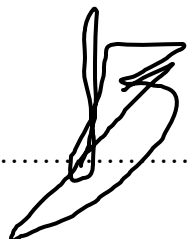
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***Pisum sativum* L. can acclimatize to nutrient deficient soils from KwaZulu- Natal
grasslands and savannah ecosystems, South Africa.**

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LIST OF ABBREVIATIONS

ABA	Abscisic acid
ACC	1-Aminocyclopropane-1-carboxylate
Al	Aluminium
AM	Arbuscular mycorrhiza
APX	Ascorbate peroxidase
ATP	Adenosine triphosphate
BIF	Biological index for soil fertility
BNF	Biological nitrogen fixation
BR	Brassinosteroids
C	Carbon
Ca	Calcium
Ca	Calcium
CFU	Colony forming unit (s)
CK	Cytokinins
cZ	<i>cis</i> -Zeatin
DHZR	Dihydrozeatin riboside
DNA	Deoxyribonucleic acid
ET	Ethylene
Fe	Iron
GA	Gibberellins
Hsp	Heat shock protein
IAA	Indole-3-acetic acid
ILDIS	International legume database
iP	Isopentenyladenine
ISR	Induced systematic resistance
JA	Jasmonate
K	Potassium
KZN	KwaZulu-Natal
Mg	Magnesium

Mn	Manganese
Mo	Molybdenum
N	Nitrogen
N ₂	Dinitrogen
NDFA	Nitrogen derived from atmosphere
NH ₃	Ammonia
NH ₄ ⁺	Ammonium
NO ₃ ⁻	Nitrate
O	Oxygen
-OG	-O-glucoside
P	Phosphorus
PCR	Polymerase chain reaction
PO ₄	Phosphate
Pro	Proline
-ROG	-Riboside O-glucoside
SA	South Africa
SNAR	Specific nitrogen assimilation rate
SNUR	Specific nitrogen utilization rate
SPUR	Specific phosphorus utilization rate
tZ	<i>trans</i> -Zeatin
Z	Zeatin
ZR	Zeatin riboside

Chapter 1

General introduction

1.1. General introduction

1.1.1. Bio-fertilizers

The term bio-fertilizer refers to the use of microorganisms to enhance soil fertility and/or promote plant growth (Mishra and Dash, 2014). Bio-fertilizers usually work through the colonization of the plant rhizosphere to provide the host plant with the necessary nutrients for growth and development (Wu *et al.*, 2005). There are currently three main groups of bio-fertilizers, which are bacteria, cyanobacteria and fungi (Wu *et al.*, 2005; Mazid and Khan, 2015). These microorganisms increase plant nutrient availability through different processes such as nitrogen fixation, secreting plant growth promoting substances like indole-acetic acid, phosphate solubilization, and the release of scavenging molecules like siderophores which chelate and transport iron (Wu *et al.*, 2005; Wani *et al.*, 2013; Mazid and Khan, 2015). Bio-fertilizers such as *Rhizobium*, *Mycorrhizal* fungi, *Azospirillum* and *Azotobacter* have been historically used to promote growth and yield potential of a variety of field crops, including *Pisum sativum* (pea), *Triticum* (wheat), *Zea mays* (maize) and *Saccharum officinarum* (sugarcane) (Awasthi *et al.*, 2011; Ei-Lattief, 2016; Celador-Lera *et al.*, 2018). The more recently used bio-fertilizers include *Paenibacillus*, which not only employ the aforementioned processes, but also promote plant growth through bio-control agent (insecticides) production and inducing systematic resistance (ISR) in the host plant (Grady *et al.*, 2016). All of the plant growth promoting microorganisms can either be free-living in soil or plant-associated in a symbiotic relationship with the host (Glick, 1995).

1.1.2. Symbiotic N₂ fixation

One of the extensively studied symbiotic N₂ fixation is between legumes and *Rhizobia*. Both the host plant and bacteria can survive independently but unlike *Azobacter*, *Rhizobia* are unable to independently fix N₂ (Prell and Poole, 2006; Ei-Lattief, 2016). In the absence of the bacteroids (nodules), plants can assimilate N from the soil but the symbiosis allows the plant to access vast N reservoir in the atmosphere (Prell and Poole, 2006). However, the symbiotic N fixation can impose a metabolic burden to the host, as it requires a significant amount of energy (i.e. ATP) and carbon (Schulze, 2004). Phosphorus is a crucial component of the energy molecule ATP, and if limited can negatively affect nodulation, protein synthesis, respiration, growth, bio-energetic processes and N nutrient acquisition and metabolism (Schulze, 2004; Sulieman and Tran, 2015). There are other nutrients that impair symbiotic N₂ fixation like molybdenum (Mo) that are required

by the nitrogenase enzyme for efficient functioning, and iron (Fe) which is a component of leghemoglobin (Allen *et al.*, 1994; Mendonça *et al.*, 1999). However, endophytic plant growth-promoting bacteria can also play a role in plant nutrient acquisition and growth.

Apart from N₂ fixation, endophytic bacteria such as *Bacillus* produce indole-3-acetic acid (IAA), siderophores, 1-aminocyclopropane-1-carboxylate (ACC) deaminase, and solubilize P and K (Glick, 2014). Different soil ecosystems have characteristic soil types, microbial population and nutrient status (Costa *et al.*, 2006). It is therefore imperative to evaluate the effects of such soil ecosystems on plant growth carbon/energy costs, protein expression profile, and N source preference and phytohormone production during symbiotic N fixation.

1.1.3. *Pisum sativum* L.

Pisum sativum L. is one of the three species under the genus *Pisum* as per the International Legume Database (ILDIS, 2018). The other two species are *P. abyssinicum* and *P. fulvum* and all three species are under the family Leguminosae (www.ildis.org). *P. sativum* L. is referred to as a winter legume as it grows optimally during the cool season (May – July), and does not grow well under elevated temperatures of the summer season (Cowie *et al.*, 1990). Furthermore, *P. sativum* L. is adapted to most soil types and is considered as a fast-growing legume that is grown across the world for various reasons, including fodder, manure and as a rotation crop (Nikolopoulou *et al.*, 2007). *P. sativum* L. is known to be nodulated by *Rhizobium leguminosarum* *bv.* *viciae* but can also establish a tripartite relationship with Arbuscular mycorrhizal fungi (Evans *et al.*, 1996; Schulze, 2004). The amount of fixed N is moderate, ranging from 166 to 286 kg/ha (Kumar and Goh, 2000). When the crops are cultivated, they act as fertilizer enriching the soil through the break down and release of proteins, carbon and other components of the plant (Piotrowska and Wilczewski, 2012). The ability of *P. sativum* L. to self-pollinate allows for easy experimentation since pure gene lines are easily obtained.

1.1.4. Phytohormones role in stress tolerance

Abiotic stresses pose a major threat to crop yield across the world (Egamberdieva *et al.*, 2017). The prevention of such stresses could assist in the alleviation of crop loss to provide sufficient food and feed for the ever-increasing population. On the other hand, global warming and climate change are gradually increasing the degree of stresses that affect agricultural land (Ahuja *et al.*,

2010). Plants are well adapted to a multitude of environments (Miura and Tada, 2014) and evaluating the adaptation events at a molecular level could be useful in sustainable agriculture. Plant phytohormones have been associated with plant growth and development, defense and to some degree, stress tolerance (Egamberdieva *et al.*, 2017).

Phytohormones that have been reported to be responsible for plant defense include salicylic acid (SA), jasmonates (JAs) and ethylene (ET), while auxins (IAAs), brassinosteroids (BRs), cytokinins and gibberellins (GAs) have been associated with plant growth and development (Egamberdieva *et al.*, 2017). Evidence suggests that abscisic acid (ABA) plays a major role in plant stress tolerance (Kohli *et al.*, 2013). Extensive work has been conducted on the role of ABA in inducing and/or mediating signaling events that lead to enhanced systematic plant stress tolerance responses. However, phytohormones can play multi-faceted roles with the possibility of crosstalk during signaling events (Kohli *et al.*, 2013; Egamberdieva *et al.*, 2017).

Indole-3-acetic acid (IAA) that promotes cell growth and differentiation (Kende and Zeevaart, 1997) is a great example of this. IAA concentration decreased in rice plants exposed to salinity stress but tolerance was achieved through increased biosynthesis of other phytohormones (Iqbal and Ashraf, 2013). Possible crosstalk was demonstrated by Iqbal and Ashraf (2007) through the IAA-induced biosynthesis of salicylic acid (SA) in plants under salt stress. It is evident that phytohormones have a collective role in plant stress tolerance. For instance, ABA enhances water and nutrient uptake during stress conditions by promoting a deeper, more complex root system (Shrivastava and Kumar, 2015). However, like SA, ABA also assists in the up-regulation of the antioxidant system through nitric oxide synthesis and osmolyte accumulation (Uchida *et al.*, 2002; Zhou *et al.*, 2005).

One of the most prominent osmolytes involved in stress tolerance is proline (Pro) (Per *et al.*, 2017). Certain phytohormones (e.g. GA) not only increase Pro accumulation, but also macro and/or micronutrients (Tuna *et al.*, 2008). Apart from the aforementioned survival strategies, plants also synthesize thiol-containing compounds like glutathione (GSH) (Anjum *et al.*, 2014). GSH is a strong antioxidant that regulates metabolic events such as the chelation of toxic metals and protein protection from oxidative stress (Hossain *et al.*, 2012). Root-associated microorganisms have also been reported to confer stress tolerance to plants through the production of phytohormones (Ruiz-Lozano *et al.*, 2012).

The plant growth-promoting microorganisms alleviate plant stress through the regulation of the nutritional and hormonal homeostasis, which in turn leads to induced systemic responses (Ruiz-Lozano *et al.*, 2012; Egamberdieva *et al.*, 2017). Root-associated *Rhizobia*, *Bacillus*, *Actinobacteria* and fungal species have been reported to produce phytohormones like IAA, ABA, and CK (Egamberdieva *et al.*, 2017). The production of such phytohormones leads to increased plant growth and alteration of the root morphology. The endogenous and exogenous production of such phytohormones also plays a role in plant protein expression (Ruiz-Lozano *et al.*, 2012).

1.2. Research questions

Does varying nutrient status in grassland and savanna ecosystem soils in KwaZulu-Natal, South Africa affect the microbe symbiosis, nutrient acquisition, cytokinin and phenolic acids in *Pisum sativum* L.?

Aims and Objectives:

The study was aimed at evaluating the effects of varying nutrients in soil collected from four different geographical sites of KwaZulu-Natal grasslands and savannas on the plant-microbe symbiosis, N nutrition, phenolic acids, cytokinins and growth of *Pisum sativum* L. under greenhouse conditions.

The objectives of the study are to:

- To examine the nutrient concentrations, pH, microbial composition and enzyme activities in soils collected from different geographic areas in KwaZulu-Natal grassland and savannah ecosystems.
- To identify nodule and root colonizing symbionts during soil nutrient stress in *Pisum sativum* L.
- To evaluate how varying nutrient availability affects the N nutrition and carbon growth costs in *Pisum sativum* L.
- To identify and quantify stress-induced phytohormones and phytochemicals during varying nutrient availability in *Pisum sativum* L.

Hypothesis:

Varying nutrient availability in KwaZulu-Natal grassland and savanna soils affect plant-microbe symbiosis, nutrition, growth and biosynthesis of cytokinin and phenolic acids in *Pisum sativum* L..

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Chapter 2

Literature review

2. Introduction

2.1. Family Leguminosae (Fabaceae)

The Leguminosae or Fabaceae commonly referred to as the pea family is one of the largest land plant families of angiosperms (Hickey and King, 1988; Wojciechowski, 2003; Pennington *et al.*, 2004). The pea family is usually placed in the order Fabales (Bello *et al.*, 2009) and is of utmost importance agriculturally and economically due to its wide distribution and other attributes, such as biological nitrogen fixation (BNF) through symbiotic association with soil micro-organisms (Ellison *et al.*, 2006). Based on species number, Fabaceae which consists of ~720 genera and ~19 000 known species is ranked third after Orchidaceae and Asteraceae (Wojciechowski, 2003; Ellison *et al.*, 2006). Most taxonomic systems identify two monophyletic (*Mimosoideae* and *Papilionoideae*) and one-paraphyletic (*Caesalpionoideae*) subfamilies that constitute the Fabaceae family (Wojciechowski, 2003; Pennington *et al.*, 2004; Ellison *et al.*, 2006).

The Fabaceae family has a worldwide distribution and is commonly distributed in the tropical, temperate and dry forest regions in Africa and America (Crews, 1999; Doyle and Luckow, 2003). The use of members of the Fabaceae family has been coupled to human evolution as the family diversified about 56-66 million years ago during the first geologic epoch of the Paleogene (Poth *et al.*, 2011). Members of the Fabaceae family with agricultural and economical importance include *Pisum sativum* (pea), *Glycine max* (soybean), *Arachis hypogaea* (peanut) and *Phaseolus* (beans) (Werner, 2005; Singh *et al.*, 2007).

The ability of Fabaceae family to undertake biological nitrogen (N) fixation through mutual symbiosis with *Rhizobium* bacteria has equipped farmers and gardeners with cheaper alternatives to expensive chemical fertilizers (Anil *et al.*, 1998). This ability makes Fabaceae important in the land-based N-cycle and has led to increased use of plants such as legumes to replenish soil with low N content (crop rotation) and increase crop yield through intercropping (Balsdon *et al.*, 1997; Anil *et al.*, 1998).

2.2. Biological nitrogen (N) fixation

Biological N fixation is a process in which various N-fixing microorganisms reduce molecular dinitrogen (N₂) in the atmosphere into ammonia (NH₃) in a reaction catalyzed by an oxygen-sensitive enzyme called nitrogenase (Robson and Postgate, 1980; Werner, 2005).



The microorganisms capable of fixing molecular nitrogen are called diazotrophs (Dixon and Wheeler, 1986) and are present in both the agricultural and natural systems as either free-living or plant-associated bacteria (Figure 2.1.) (Zahran, 1999; Herridge *et al.*, 2008). These bacteria are classified under the genus *Rhizobium* or the genus *Bradyrhizobium* (Zahran, 1999; Herridge *et al.*, 2008). Plants are unable to convert N₂ into the usable form as they lack the nitrogenase enzyme (Robson and Postgate, 1980; Werner, 2005). However they have overcome this by establishing a symbiotic association with rhizobia, in return the plants provide the rhizobia with carbon as organic acids and protection by housing the rhizobia in the root nodules (Robson and Postgate, 1980; Werner, 2005).

The symbiotic association is established by the rhizobia in soils infecting the plant root hair inducing nodulation (Gage, 2004; Werner, 2005). Certain *Rhizobium* strains have been reported to infect multiple plant species (Zahran, 1999; Anil *et al.*, 1998). In the legume-rhizobia symbiosis, the bacterium is unable to fix N₂ independently (De Varennes and Goss, 2007). However, both entities can live independent of each other (De Varennes and Goss, 2007). The symbiotic association can also be tripartite by including *Arbuscular Mycorrhizal* fungi, which increase the plant root surface area to optimize nutrient (e.g. phosphorus) and water uptake (Dodd, 2000; Johansson *et al.*, 2004). Phosphorus (P) is a major nutrient element in plants, even more in legume plants as it plays a role in cellular energy metabolism, promotes root growth and nodule development (Uchida, 2000; Khan *et al.*, 2010).

To better understand the effects of essential nutrients like P on plant growth and stress tolerance, it is imperative to assess more than just the interaction between the host and a single nodulating microbial species. With more evidence suggesting that the nodule microbiome is a complex,

perhaps even coordinated community with multiple beneficial cross talks and features (Kohli *et al.*, 2013). The best approach towards sustainable agriculture is to understand the roles of the phytomicrobiome as a collective, including endophytic, free-living and nodule-associated bacteria. Research has shown that non-rhizobial bacteria are capable of not only inhabiting root nodules but can also be potential N-fixers that induce nodulation in certain plant species (Mishra *et al.*, 2009). Nevertheless, certain microbial species (e.g. *Bacillus*) promote nodulation and N availability when co-inoculated with rhizobial strains, but fail to independently induce nodulation (Rajendran *et al.*, 2008).

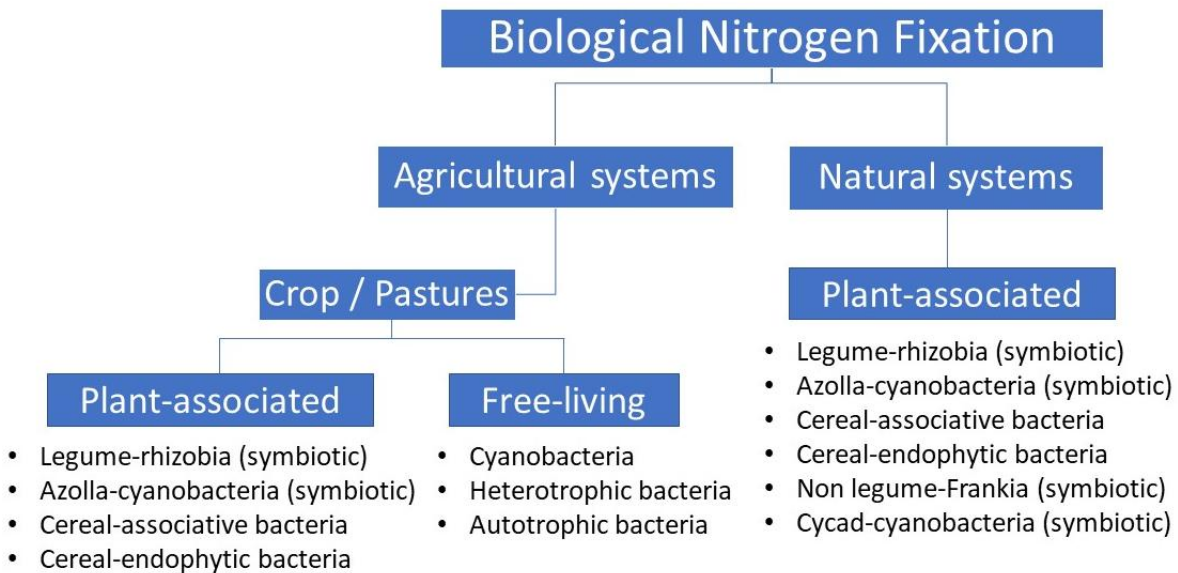


Figure 2.1.: Overview of Biological Nitrogen Fixation. Adapted from Herridge *et al.*, 2008.

2.2.1. Nodulation and types of nodules

Two main types of root nodules have been identified that are associated with nitrogen-fixing bacteria, namely the indeterminate nodules and the determinate nodules (Ferguson *et al.*, 2010). Determinate nodules are mostly found on tropical legumes such as *Glycine* and *Vigna* and are characterized by their spherical shape and loss of meristematic activity succeeding initiation, therefore making nodule growth reliant on cell expansion (Schultze and Kondorosi, 1998; D’haeseleer *et al.*, 2010). On the contrary, indeterminate nodules are found on both the tropical and temperate legumes such as *Pisum* and *Medicago* and are characterized by their cylindrical shape and persistent meristematic activity after initiation, thus nodule growth is dependent on the production of new cells (Schultze and Kondorosi, 1998; D’haeseleer *et al.*, 2010). This has led

to indeterminate nodules having zones of various stages of maturity (Figure 2.2.). Indeterminate nodules tend to produce and export amide N products while the determinate nodules produce ureide N products for plant use (Vance *et al.*, 1979; Schulze and Kondorosi, 1998).

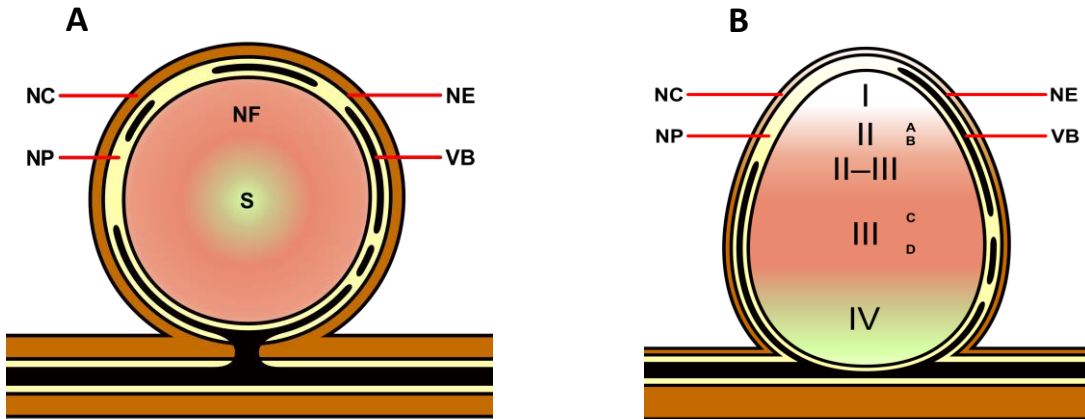


Figure 2.2.: Diagram illustrating the (A) determinate and the (B) indeterminate nodules. Both types of nodules have the **NC** – nodule cortex **NE** – nodule endodermis **VB** – vascular bundle and **NP**– nodule parenchyma. The determinate nodule has the **S** – senescence zone and the **NF** – nitrogen fixation zone. The indeterminate nodule has **I** – active meristem **II** – infection zone **II-III** – interzone (intermediate) **III** – nitrogen fixation zone **IV** – senescent zone **A** – invasion zone **B** – pre-fixing zone **C** – efficient zone **D** – inefficientzone.

Nodulation is initiated by the release of flavonoids by the legume plant roots (Subramanian *et al.*, 2007). Specific rhizobial bacteria in the surrounding inoculated soil sense these flavonoids and this results in the expression of nod genes and root hair colonization (Vasse *et al.*, 1990; Kanamori *et al.*, 2006). Upon attachment to the root hair, the rhizobial bacteria release nod factors that cause the root hair to curl in such a manner that encapsulates the rhizobial bacteria (Kanamori *et al.*, 2006). The rhizobial bacteria undergo cell division to form a micro-colony that travels down the infection thread and into the nodule cells cytoplasm, where they differentiate into nitrogen-fixing bacteroids (Kanamori *et al.*, 2006). Nodulation is dependent on external factors such as soil acidity and internal factors such as auto-regulation (Schulze and Kondorosi, 1998; Kanamori *et al.*, 2006). On average, effective N fixation and nodule development occur four weeks after seed germination. It is well accepted that symbiotic N₂ fixation imposes a metabolic burden on the host plant, as the reaction to reduce atmospheric N₂ into NH₃ is an energy-consuming reaction (Warembourg and Roumet, 1989).

2.3. Carbon (C) and energy cost during N-fixation

Lambers and De Visser (1984) approximated the cost N-fixation to be 6 mg of C per mg of N reduced while recent studies suggest that the cost is dependent on plant and/or bacterial species involved (Valentine *et al.*, 2010). During symbiotic N₂ fixation, host plant photosynthates along with 8 adenosine triphosphates (ATPs) are required to produce a single ammonium (NH₄⁺) molecule that serves as an N source to the plant (Valentine *et al.*, 2010).



During the tripartite symbiotic association, the carbon energy cost is even greater as more plant photosynthates are required by the AM and rhizobia (De Varennes and Goss, 2007). There is no evidence suggesting that N₂ fixation is detrimental to plant productivity and yield potential, and this raises the notion that C costs of N₂ fixation are not coupled to the yield potential, but this is yet to be confirmed (Vance and Heichel, 1991).

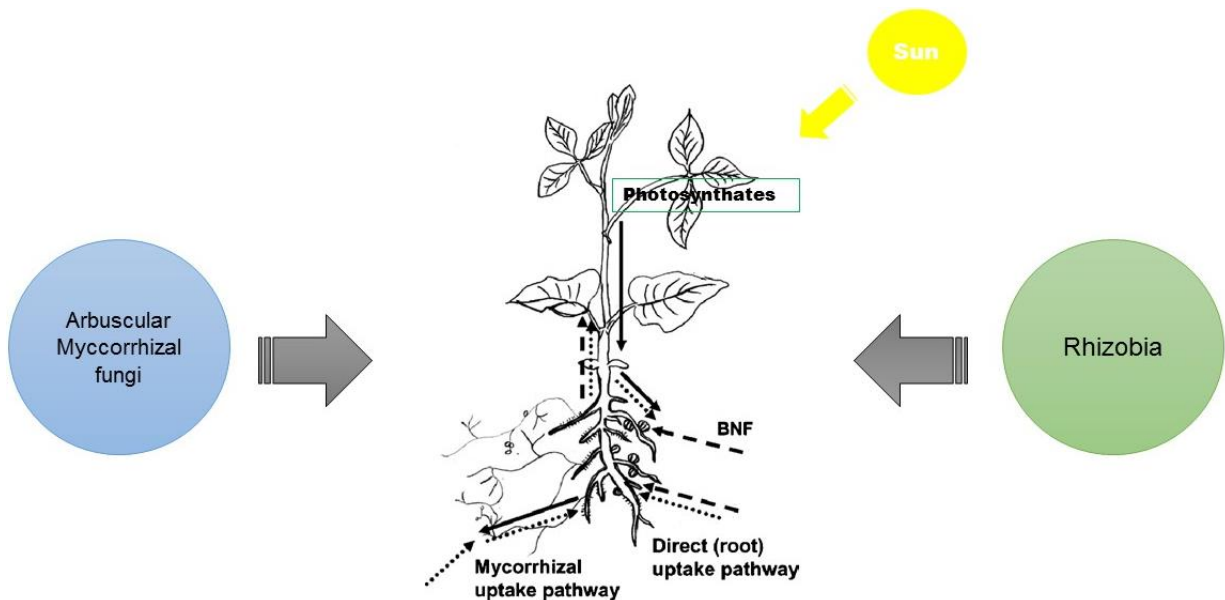


Figure 2.3.: Tripartite symbiotic association nutrient uptake pathways. Solar radiation is converted by plants into photosynthates that are transported to the *Rhizobia* and *Arbuscular Mycorrhiza*. In exchange, the microorganisms provide the plant with essential nutrients.

2.4.Environmental stresses that affect symbiotic nitrogen fixation

In most organisms (including legume plants) exposure to stress leads to either a non-specific general response or a stressor-induced response to help in the restitution or regeneration phase upon alleviation of the stressor (Lichtenthaler, 1998). The effects of physical stress such as salinity, nutrient deficiency, acidity (pH), drought and heat have been extensively studied and found to elicit plant response in terms of signal transduction, biophysical characteristics, energy metabolism, and overall growth and development (Kasuga *et al.*, 1999; Pugnaire and Luque, 2001). Extensive work in grassland and savannah ecosystems has been based on the effects of drought and salinity stress (Munns, 2002; Chaves *et al.*, 2009; Jouyban, 2012). It should be noted that plants rarely grow under optimum conditions and this has led to the notion that stress (biotic or abiotic) might play a key role in plant biological diversity (Wang *et al.*, 2006). Four distinct phases of stress response have been identified (Figure 2.4.) based on stresses that are either for plant growth (eu-stress) or against it (dis-stress) (Lichtenthaler, 1998).

When it comes to symbiotic N-fixation, most of the aforementioned stresses usually have a direct effect on the bacteria and not the host plant (O'Hara, 2001; Glick, 2012). By impairing the bacterial growth and physiology, these factors subsequently affect the host plant N acquisition (O'Hara, 2001; Glick, 2012). A notable factor is that acid soil complexes are characterized by high aluminium (Al) and manganese (Mn) that sequester P, which is an important nutrient that promotes nodulation and N fixation (O'Hara, 2001; Glick, 2012). Symbiotic N fixation is also affected by the limitation of other nutrients such as iron, calcium and molybdenum (O'Hara, 2001; Glick, 2012).

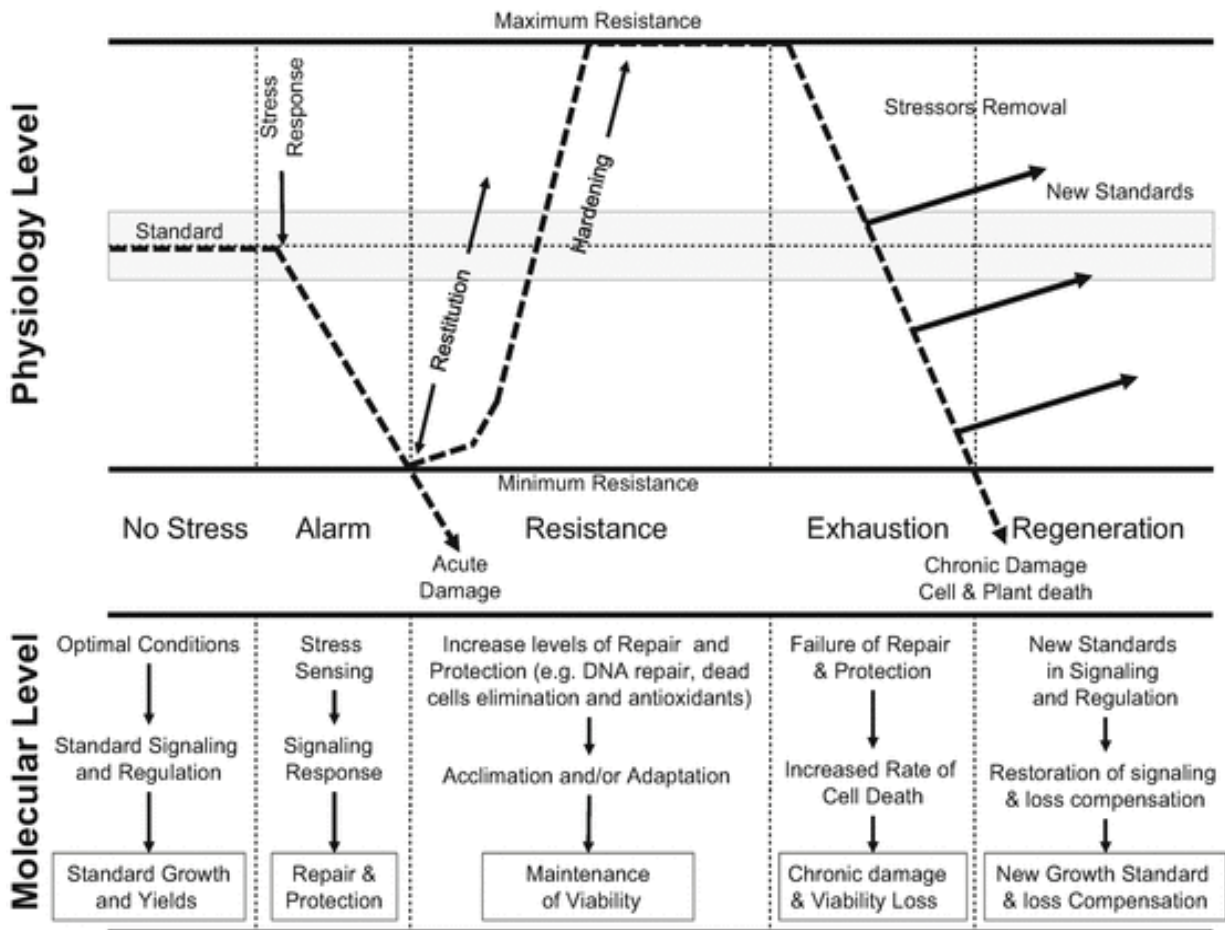


Figure 2.4.: The generic stressor-induced response in plants. The four phases of plant stress response are the Alarm, Resistance, Exhaustion and Regeneration phase. Plant stress response is initiated when a biotic/abiotic stressor is induced. The plant goes from the No Stress to the Alarm phase, which is characterized by stress sensing and response signaling. This triggers the Resistance phase in which the plant acclimatize and adapts to the stressor imposed. This is achieved by increasing levels of repair and protection to maintain cell viability. If the stressor persists, the plant enters the Exhaustion phase. In this phase, the plant experiences chronic damage and loss of viability as a result of increased rate of cell death. However, if the stressor is removed, the plant enters the Regeneration phase. During this phase, the plant achieves new standards in signaling and regulation to compensate for the loss caused by the stressor. Adapted from Lichtenthaler, 1998.

2.5. Causes and effects of soil phosphorus (P) deficiency on N₂ fixation

Symbiotic N₂ fixation has enabled legumes to be self-sufficient by acquiring N through N₂ reduction into NH₃ by *Rhizobium* and *Bradyrhizobium* bacteria that rely on host plant photosynthetic energy (Okon and Hardy, 2012). P is regarded as the main carrier molecule for photosynthesis-produced energy that is used for plant growth and reproduction (Shenoy and

Kalagudi, 2005; Blankenship *et al.*, 2011). However, P is not only present in ATP but is also a structural component of DNA and RNA which are involved in the genetic make-up and protein synthesis of all living organisms (La Roche *et al.*, 1993). P is also involved in catalysis, post-translational modification such as phosphorylation, activation/deactivation of certain proteins through phospho-transferase and kinase (La Roche *et al.*, 1993; Dyhrman, 2016).

The readily available form of P for plants is the phosphate form (PO_4), with di-hydrogen phosphate (H_2PO_4^-) being the predominant soluble P ion in soils (Sims and Pierzynski, 2005; Yadav and Verma, 2012). Sufficient P levels not only promote plant root growth but also cold tolerance, early maturity and nodulation in certain legumes (Grant *et al.*, 2001; Zaidi *et al.*, 2009). However, soil P is one of the most limiting nutrients for most forage and crop plants (Khan *et al.*, 2010). The low P availability is usually linked to aluminium (Al^{3+}) toxicity that is coupled to low soil pH (Bose *et al.*, 2013). The process in which soil P is rendered unavailable to plants is called P fixation by cations such as aluminium (Al^{3+}), iron (Fe^{+3} , Fe^{+2}), calcium (Ca^{+2}), magnesium (Mg^{+2}) and manganese (Mn^{+2}), which limits and/or reduces P mobility and solubility thus affecting P acquisition by plants (Reeve and Sumner, 1970; Reyaz, 2013).

P deficiency has a direct effect on the host plant as it stunts growth, reduces leaf area and the number of leaves thus minimizing photosynthetic ATP and other photosynthates (Khan *et al.*, 2010). This has an indirect effect on N_2 fixation as the microbial activities in the root nodules are dependent on these photosynthates to function (Denison and Kiers, 2011). Timely visual diagnosis of P deficiency in plants is hard to achieve but certain plants (e.g. maize) show purple discoloration due to anthocyanin synthesis that is triggered by low P (McCauley *et al.*, 2009). Besides flower coloration, anthocyanin have been reported to have antioxidant activity and radiation protection that reduces the rate of cell death in plants (Kano *et al.*, 2005). This makes anthocyanin production one of the many possible plant survival strategies that need to be investigated.

2.6. The use of crops as forage

Numerous varieties of field-crops such as cereals and leguminous plants have been successfully used as either forage or silage for over a decade (Hill and Leaver, 1990). The importance of such

field-crops has increased over the years, not only in the westernized countries but globally (Phipps, 1994). The increase is coupled with the field-crops potential to supply ruminant animals (such as livestock) with an adequate amount of energy-rich fodder (Hill and Leaver, 1990; Phipps, 1994). The use of field legumes (or intercropping) as forage has been favored over the use of cereals because they require minimal protein supplementation to promote milk or meat production (Phipps, 1994; Anil *et al.*, 1998). The family *Fabaceae* that includes peas has been used in crop rotations due to its various advantages that range from N-fixing ability to the reduction of soil erosion (Anil *et al.*, 1998). Legume plant genera can be divided into two groups according to seed size (Table 2.1.) (McCartney and Fraser, 2010) and used as an intercrop for forage (Table 2.2.) but the yield is dependent on external factors such as stress (Fujita *et al.*, 1992). Comparison of the survival strategies of the different genera has the potential to enable the selection of advantageous traits for sustainable agriculture.

Table 2.1.: Relative seed size of legume plant genera

Group	Genus	Seed size
One	<i>Medicago</i>	Small / Medium
One	<i>Trifolium</i>	Small / Medium
One	<i>Melilotus</i>	Small / Medium
One	<i>Lens</i>	Small / Medium
Two	<i>Lupinus</i>	Large
Two	<i>Pisum</i> *	Large
Two	<i>Phaseolus</i>	Large
Two	<i>Lathyrus</i>	Large

The table is an example of the division of legume plant genera based on seed size. *Genus of interest. Adapted from McCartney and Fraser (2010).

Table 2.2.: Intercropping research in temperate regions

Intercrop	Country	Authors	Purpose
Oats			
Faba bean	Canada	Jedel and Helm (1993)	Forage
Peas (<i>Pisum sativa</i>)	Australia	Mason and Pritchard (1987)	Forage
	North	Chapko <i>et al.</i> (1991)	Forage
Vetch (<i>Vicia sativa</i>)	America	Moreira (1989)	Forage
	Portugal	Papastylianou (1990)	Forage
	Cyprus		
Barley			
Kale	U.K.	Moorby <i>et al.</i> (1998)	Forage
Peas	N. America	Jedel and Helm (1993)	Forage
Persian clover (<i>Trifolium resupinatum</i>)	Canada	Stout <i>et al.</i> (1997)	Forage
Wheat			
White clover (<i>Trifolium repens</i>)	U.K.	Balsdon <i>et al.</i> (1997)	Forage
Peas	Canada	Walton (1975)	Forage
Soyabean (<i>Glycine max</i>)	Canada	Walton (1975)	Forage

Table shows intercropping research conducted globally in which the field crops were to be used as animal fodder. Adapted from Anil *et al.*, 1998.

2.7. Study species

Pisum sativum L. is an annual winter legume that is grown in most parts of the world, especially in farms and/or grassland ecosystems (Ceyhan and Avci, 2005). *P. sativum* L. is viewed as an essential plant for effective soil management that is coupled to soil tillage, crop rotation and the addition of green manures to form part of the terrestrial nutrient cycle (Cousin, 1997). Green manures (e.g. *P. sativum*) is broken down by soil microorganisms into nutrients that are released to enrich the soil and made readily available to succeeding plants (Cherr *et al.*, 2006). This has an overall turnover increase of soil C and N content since the proteins/amino acids in the plant are converted into nitrates (NO₃⁻) post-harvest (Midmore *et al.*, 2000). Field pea has been found

to grow best in well-drained soils with a pH range of 6.0 to 7.0, with adequate moisture due to the plant being drought intolerant (Miles and Sonde, 2003).

The pea plant has fibrous, shallow roots that are the site of nodulation, which occurs when the soil population of rhizobia is above the optimal nodulation threshold (~100/g of soil) at soil pH ≤ 6.6 (Singleton and Tavares, 1986; Rice *et al.*, 2000). The efficiency of nodulation and nodule activity is also governed by temperature (high temperature = low nodulation), *Rhizobia* viability in the soil type and duration of host plant absence (Zahran, 1999). However, the plants are more susceptible to heat and drought stress during the flowering stage which usually occurs ~50 days after sowing (Guilioni *et al.*, 1997; Morrison and Stewart, 2002). The fibrous root system also helps anchor the forage crop in a manner that minimizes soil erosion (<https://www.nda.agric.za/docs/erosion/erosion.htm>). Soil type also has an effect on the yield, with dark brown and black soils being identified as the ideal soil type to obtain better crop yield (https://www3.epa.gov/npdes/pubs/cafo_permitmanual_appendixa.pdf). There are white-flowered varieties of field pea such as Whistler pea that have less anthocyanin content than their purple-flowered counterparts but both varieties are known for vining and climbing, with vines reaching six inches (Grotewold, 2006; Moreau *et al.*, 2012; <https://www.daff.gov.za>). Field pea is known for having great grazability as a lone crop and as an intercrop e.g. with oat or vetch (<https://www.pivotandgrow.com>).

The high protein, low fat content and various applications of pea are the basis of its lucrativeness (Janzen *et al.*, 2014). Profits can be generated through retail as animal feed, human food and seeds for farming. The major production countries of field pea include Canada, China, the Soviet Union (Russia) and India (Janzen *et al.*, 2014). However, in South Africa the major production areas exclude the KwaZulu-Natal (KZN) province (Table 2.3.). KZN is a relatively mountainous province that is located on the southeastern side of South Africa (Appendix A: Figure S2). Limitation of essential soil macronutrients, like in most South African regions, has been reported in KZN grasslands and savannahs (Craine *et al.*, 2008). Therefore, the assessment of the effects of KZN soil geochemistry and microflora will determine whether forage pea maybe adapted to the nutrient-poor soils in grassland and savannah ecosystems and be used by subsistence and commercial farmers as green manure or as feed.



Figure 2.5.: *Pisum sativum* L. (A) intercropped with vetch and (B) grazed by pigs.

Table 2.3.: South African major field pea production regions

Province	District	Town	
Western Cape	Eden	George	
		Secunda	
Mpumalanga	Gert Sibande	Ermelo	
	Makaligwa	Middleburg	
	Nkangala		Delmas
			Bethlehem
Free State	Thabo Mofutsanyana	Witsieshoek	
		Harrismith	
		Ventersdorp	
		Klerksdorp	
		Rustenburg	
North West	Bojanala Platinum	Moretele	
		Koster	
		Brits	
	Dr Kenneth Kaunda	Potchefstroom	

*Information retrieved from <https://www.daff.gov.za>

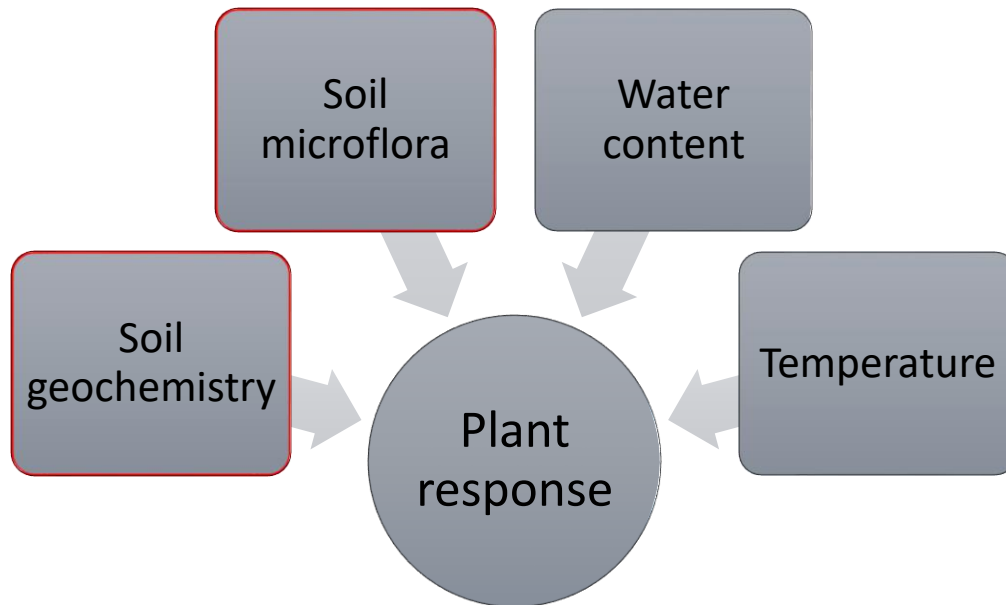


Figure 2.6.: Factors influencing plant growth and development. The current study is focused on the factors outlined in red.

2.8.References

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Chapter 3

Soil geochemistry & microflora

Soil nutrition, microbial composition and associated soil enzyme activities in KwaZulu-Natal grasslands and savannah ecosystems soils

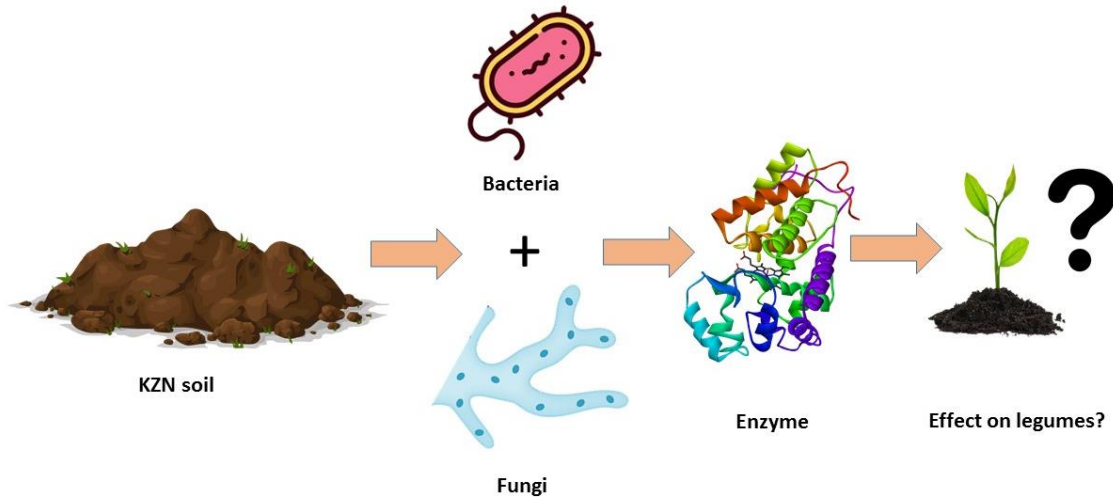
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Graphical abstract of the research conducted and presented in this write-up.

Abstract

Successful agriculture is dependent on soil quality and nutrition. Soil is the primary source of nutrients that are assimilated by plant root-systems to promote plant growth and development. The availability of these soil nutrients is regulated by factors such as pH, microbial composition and soil nutrient enzyme activities in ecosystem soils. This study aim was to determine the nutrition, microbe composition, and soil enzyme activities in four soils (from Hluhluwe, Izingolweni, Bergville, and Ashnorton) from different KwaZulu-Natal (KZN) grassland and savannah ecosystems. The four sites were found to differ significantly in all four aspects. Microorganisms identified in the soils were from the families *Bacillaceae*, *Hypocreaceae*, *Mucoraceae*, and *Nectriaceae*. Bacterial and fungal genera identified amongst these soils showed varying diversity and species richness. Bergville soils had the lowest pH, cation exchange capacity, micro, and macro nutrient concentrations. Furthermore, Bergville soil showed reduced asparaginase and lignin peroxidase activities and had the lowest dehydrogenase activities. Therefore Bergville soils had the most limiting geochemical properties which may affect the growth of grassland and savannah ecosystem vegetation and sustainable agricultural practices.

Key words: Successful agriculture, soil quality, grassland and savannah ecosystems, microbial composition.

3.1. Introduction

The poor nutrient status of soils across the African continent has posed a serious threat to plant growth and sustainable agricultural practices (Goldman, 1995; Henao and Baanante, 1999). Due to the ever-increasing population worldwide with stronger demand for agricultural products, there is a need to increase either the soil fertility of the already present agricultural land or expansion by identifying regions that are suitable for agricultural practices. African savannahs and grasslands represent putative crop areas, however, studies on geochemistry of most South African ecosystems are reported to be nutrient-poor and relatively acidic (Nandwa 2001; Mafongoya *et al.*, 2006). The decreased pH in these soils leads to decreased cation-exchange capacity, indicating the overall decrease in plant essential soil nutrients such as potassium (K^+), calcium (Ca^{2+}) and ammonium (NH_4^+) (Aprile and Lorandi, 2012). These acidic conditions also lead to the sequestration of soil nutrients like phosphorus (P), which is rendered insoluble through binding with cations (Sharma *et al.*, 2013). However, soil amelioration or even soil resetting can be achieved by the enhancement of soil-borne microorganisms, as some of them have been reported to solubilize these bound and insoluble nutrients, thus increasing their availability to plants (Latha *et al.*, 2011; Pérez-García *et al.*, 2011).

The soil microbiota consists of N_2 -fixing *Rhizobia*, *Ectomycorrhiza*, *Arbuscular Mycorrhiza*, *Pseudomonas*, *Ochrobactrum*, *Bacillus*, *Paenibacillus*, *Klebsiella*, *Lysinobacillus*, and *Actinomycetes* among others (Martínez-Hidalgo and Hirsch, 2017). All of these microorganisms are potential plant growth promoters (Martínez-Hidalgo and Hirsch, 2017). For instance, *Bacillus* has been isolated from root nodules and shown to solubilize phosphate and synthesize hydrolytic enzymes, polyamines, and lipopeptides (Maymon *et al.*, 2015). On the other hand, *Ectomycorrhiza* and *Arbuscular Mycorrhiza* increase plant below ground surface area to maximize nutrient uptake (Wardle *et al.*, 2004). While some *Pseudomonas*, *Ochrobactrum*, and *Klebsiella* species have the ability to fix nitrogen through associative symbiotic and/or endophytic relationship in combination with certain non-legume plants (Frache *et al.*, 2009). The rate of nitrogen fixation is dependent on many external factors that include competition amongst the soil microbial species, soil moisture, temperature, plant sanction for specific bacteria and pH (Nandwa 2001; Stopnisek *et al.*, 2014). The combined activity of the microbiota and the environment might be responsible for the

increased soil enzyme activity that is characteristic in most soils. Furthermore, soil quality can be determined by measuring several enzymatic activities as a surrogate of the microbial diversity in them. Soil enzymes originate from a variety of organisms and are of importance for the decomposition of many labile organic substrates, activating biogeochemical cycling. Their activity reflects the functional diversity and activity of the microorganisms involved in decomposition processes (Sinsabaugh *et al.*, 2008) at the time that they guarantee the correct soil functioning. Soil microorganisms produce extracellular enzymes that hydrolyze and transform polymeric compounds into readily available nutrients that can be assimilated by plants and microorganisms (Lucas *et al.*, 2008). These extracellular enzymes are responsible for the mineralization and cycling of terrestrial nitrogen (N), phosphate (P) and carbon (C). Furthermore, these enzymes play a role in preventing oxidative degradation caused by reactive oxygen species (Nanda *et al.*, 2010). Catalase is one of the enzymes known to be indicative of soil oxidative stress tolerance and is known to reduce hydrogen peroxide (H_2O_2) into water (H_2O) and oxygen (O_2) (Angaji *et al.*, 2012). Enzymes involved in C cycling include β -D- Cellobiohydrolase, dehydrogenase, and β -D- Glucosidase. They achieve this by releasing saccharides from glycosides and catalysis of the degradation of cellulose and cellotetraose into cellobiose that can be further transformed into glucose (Henriksson *et al.*, 1998). Apart from catalase, there are other important oxidoreductase enzymes like laccase, lignin peroxidase (LiP) and manganese peroxidase (MnP), which protect against oxidative stress (Lundell *et al.*, 2010). Their primary functions include lignin transformation and H_2O_2 reduction into H_2O . On the other hand, enzymes like asparaginase and β -D- Glucosaminidase convert asparagine into aspartic acid and ammonia (NH_3), and hydrolyze chito-oligosaccharides (Hill *et al.*, 1967; Mega *et al.*, 1972). This has an overall effect on N mineralization and increased N assimilation in plants. While phosphatases are responsible for P cycling and mineralization through the hydrolysis of phosphoric acid monoester to produce a phosphate anion (Turner *et al.*, 2002). Plants growing in grassland and savannah ecosystem soils are subjected to these collective effects of soil geochemistry and microflora composition might employ different survival strategies and show varying growth patterns.

Therefore the aim of this study was to determine soil nutrition and chemistry, soil enzyme activities and microbiota in soils collected different locations with varying altitudes in KwaZulu-Natal (KZN) province, South Africa. The specific objective was to determine the range of potential

activity of ten extracellular enzymes of South African soils and how these vary according to the soil properties and microbial diversity.

3.2. Materials and methods

3.2.1. Total soil nutrient analysis and spore count

Soil samples collected from four different locations with varying altitudes in KwaZulu-Natal (KZN) province, South Africa were sent to the KwaZulu-Natal Department of Agriculture and Rural Development's Analytical Services Unit at Cedara College of Agriculture, South Africa, for total soil nutrient and cation concentrations, cation exchange acidity and pH analysis. The four soil collection sites were: Ashburton, midland KZN (elevation 670m; 29.3855° S; 30.2642° E), Hluhluwe, northern KZN (elevation 100m; 28.058°S; 32.124° E), Bergville, mountainous KZN (elevation 1640m; 28.3414° S; 29.417° E) and Izingolweni, southern KZN (elevation 450m; 30.4332° S; 30.610° E) (supplementary figure 1). Arbuscular mycorrhizal spore count analysis was conducted according to Smith and Dickson (1991) at Rhodes University, South Africa.

3.2.1.1. Soil site description

Hluhluwe is an area situated between iSimangaliso Wetland Park and Hluhluwe-iMfolozi Park on the banks of Hluhluwe River. The climate in the area is warm and temperate, with annual average temperature and precipitation of 21.3°C and 894 mm, respectively. This site is classified as having the Zululand Lowveld (SVI23) vegetation type with *Hyparrhenia*, *Acacia* and *Dichrostachys cinerea* as indicator species (Rutherford *et al.*, 2006).

Izingolweni is an area situated inland of Port Shepstone. This area is subjected to an annual average precipitate and temperature of 450 mm and 17.0 °C respectively. This site is classified as having the Eastern Valley Bushveld (SVs6) vegetation type with *Euphorbia* and *Aloe* as indicator species (Rutherford *et al.*, 2006).

Bergville is situated in the hills of Drakensberg Mountain. This site is subjected to annual average precipitation and temperature of 684 mm and 13°C respectively. This site is classified as having the KwaZulu-Natal Highland Thornveld (Gs6) vegetation type with *Hyparrhenia hirta* and *Acacia sieberiana var woodii* as indicator species (Rutherford *et al.*, 2006).

Ashburton is situated next to the South African National road (N3), approximately 12 km east of Pietermaritzburg. This site is subjected to an average annual precipitation of 691 mm and mean annual temperatures of 18.8 °C. Moreover, the land is mostly non-rocky which makes it suitable for annual cropping and dominated by bushland vegetation pattern. This site is classified as having the Midlands Mistbelt Grassland (Gs9) vegetation type with *Themeda triandra* as an indicator species (Rutherford *et al.*, 2006).

Soil fungal spores

3.2.1.2.Extraction, purification and enumeration

Fungal spores were isolated using a modified procedure described by Gerdeman and Nicolson (1963). For each soil sample, 10g/100ml dH₂O was decanted through tri-layered sieves of 500 mm, 100 µm and 50 µm mesh sizes. The residues (spores) were later suspended in 100 mL of water in a 250 mL beaker for further purification. The residual spore fraction was re-suspended in 100 ml H₂O and purified using a modified procedure described by Daniel and Skipper (1982). The spore suspensions (10 ml/50 ml Falcon tube) were injected with 25 ml of a 70% sucrose solution (w/v) and centrifuged at 130 xg for 5 minutes. Spores collected from the interface were washed for 2 minutes on 32 µm sieves with H₂O and transferred to petri dishes for enumeration. Spores were enumerated at 40x magnification under a stereomicroscope and enumeration was based on parameters described by the international culture collection of vesicular and arbuscular mycorrhizal fungi (INVAM) (<https://invam.wvu.edu/methods/spores/enumeration-of-spores>).

3.2.1.3.Fungal DNA extraction

All the different extracted spores were grown on PDA dishes. Approximately, 10 mm of fungal mycelia were transferred from a fresh dish to a 1.5 ml sterile Eppendorf tube and its total genomic DNA was isolated using the ZR Fungal/Bacterial DNA MiniPrep™ kit (Zymo Research-USA) in accordance to the manufacturer's instructions.

3.2.1.4.DNA amplification, sequencing and identification

The extracted fungal DNA was amplified using the ITS4 (5'-T TCCTCCGCTTATTGATATGC - 3') and ITS5 (5'- GGAAGTAAAAGTCGTAACAAGG -3') primers in the PCR. The PCR mixtures consisted of 10 µl DNA, 5 µl of 10 X reaction buffer, 2 µl 25mM MgCl₂, 2.5 µl of each

primer, 0.25 µl of Taq DNA polymerase, 1 µl of 10mM dNTP and volume made up to 50 µl with MilliQ H₂O. A T100 Thermal Cycler (Biorad, USA) was used for amplification with the initial denaturation at 95 °C for 2 min, 25 cycles of denaturation at 95 °C for 30 sec, annealing at 53 °C for 45 sec and elongation at 72 °C for 8 min with a final elongation at 72 °C for 8 min. The PCR products were resolved on 1.0% (w/v) agarose gels (Seakem) and visualized after staining with ethidium bromide (0.5 µg/ml) using the Chemigenius Bio-imaging System (Syngiene, England). Positive amplicons (~600 bp) were excised and sequenced at Inqaba Biotech Pty. Ltd., South Africa and the sequences were compared against the GenBank database. Homologues were identified using the BLASTN program at the National Center for Biotechnology Information (NCBI) (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

3.2.2. Soil-borne bacteria

3.2.2.1. Isolation and enumeration

A three-fold serial dilution was conducted on 10 g of soil samples and 100 µl of each dilution was used to inoculate nutrient agar (NA) plates. The inoculated plates were incubated at 37 °C for 18 hours and distinct bacterial colonies were enumerated using the colony-forming unit method (CFU) (Goldman and Green, 2008).

3.2.2.2. Bacterial DNA extraction

Bacterial DNA was extracted using a modified boiling procedure described by Akinbowale *et al.* (2007). Bacterial colonies (≤ 5) picked off NA plates were suspended in 70 µl MilliQ H₂O, boiled in a water bath at 100 °C for 10 min and placed on ice for 5 min. The suspension was centrifuged at 13817 xg in a micro-centrifuge (Spectrafuge 16M, Labnet) for 5 minutes and the supernatant (~50 µl) was transferred to sterile Eppendorf tubes.

3.2.2.3. DNA amplification, sequencing and identification

The extracted bacterial DNA was amplified using the 63F (5'- CAGGCCTAACACATGCAAGTC -3') and 1387R (5'- GGGCGGTGTGTACAAGGC -3') primers in the PCR. The PCR mixtures consisted of 10 µl DNA, 5 µl of 10 X reaction buffer, 2 µl 25mM MgCl₂, 2.5 µl of each primer, 0.25 µl of Taq DNA polymerase, 1 µl of 10mM dNTP and volume made up to 50 µl with MilliQ H₂O. A T100 Thermal Cycler (Biorad, USA) was used for amplification with the initial denaturation at 94 °C for 2 min, 30 cycles of denaturation at 92 °C for 30 sec, annealing at 56 °C

for 45 sec and elongation at 75 °C for 45 sec. with a final elongation at 75 °C for 10 min. The PCR products were resolved on 1.0% (w/v) agarose gels (Seakem) and visualized after staining with ethidium bromide (0.5 µg/ml) using the Chemigenius Bio-imaging System (Syngiene, England). Positive amplicons (~1324 bp) were excised and sequenced at Inqaba Biotech Pty. Ltd., South Africa and the sequences were compared against the GenBank database. Homologues were identified using the BLASTN program at the National Center for Biotechnology Information (NCBI) (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

3.2.3. Measurement of microbial diversity

The biodiversity measurements were based on Total CFU/ml, Total spore/g, Percentage relative abundance, relative density, isolation frequency, Shannon-Wiener index of diversity (H), Simpson index of dominance (D), Evenness (E), $R_{margalef}$ and E_{pielou} . W

3.2.4. Soil enzyme activity

Soil β -Glucosidase and β -Cellobiohydrolase activity were determined according to Jackson *et al.* (2013). Briefly, fluorogenic 4-Methylumbelliferyl (MUB)-linked substrates were used for the colorimetric quantification. 4-MUB- β -glucopyranoside and 4-MU- β -D-cellobioside fluorogenic substrates were used to assay β -Glucosidase and β -Cellobiohydrolase, respectively. Five gram soil samples were homogenized at low speed in 50 ml milliQ H₂O for 2 hours at 4°C. The supernatants were transferred into black 96-well microplates prior to adding the respective substrates. The sample run consisted of 200 µl soil aliquot plus 50 µl substrate and incubated alongside reference standards (200 µl buffer + 50 µl standard), quench standards (200 µl soil aliquot + 50 µl standard), sample controls (200 µl soil aliquot + 50µl buffer), negative controls (200 µl buffer + 50µl substrate) and blanks (250 µl buffer). The reaction was stopped with 0.5 M NaOH after a 2 hour incubation period at 30°C. Thereafter, fluorescent absorbance was measured at 450 nm on a Glomax Multi Plus microplate reader (BioTek, USA) and the results expressed as nmol h⁻¹g⁻¹ from one unit enzyme activity of 0.001 nmol h⁻¹ g⁻¹ of the reaction mixture.

Soil Catalase (E.C. 1.11.1.6) activity was determined according to the modified method of Orta-Zavalza *et al.* (2014). The method is based on H₂O₂ decomposition were 10 ml soil suspension is mixed with 790 µl of potassium phosphate buffer (50 mM, pH 7.0) and catalysed with 100 µl of a 30 mM (v/v) H₂O₂ solution. The reaction mixture was incubated at 30°C for 3 minutes before

measuring absorbance at 240 nm on an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA) ($\epsilon=34.9 \text{ cm}^{-1} \text{ M}^{-1}$) of $0.1 \text{ nmol h}^{-1} \text{ g}^{-1}$ of the reaction mixture.

Soil dehydrogenase activity was determined according to Ezirim *et al.* (2017). Briefly, a 5g soil sample was homogenized in 10 ml of 0.2% (w/v) triphenyl tetrazolium chloride (TTC) and 10 ml of 0.1 M Tris buffer (pH=7.6) prior to incubation at 37°C for 6 hours. The reduced reaction product, triphenyl formazan (RTF) was extracted using methanol (10 ml) through centrifugation for 5 min at 4000 xg. The absorbance was measured at 485 nm using an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA) ($\epsilon=15,433 \text{ cm}^{-1} \text{ M}^{-1}$) of $0.1 \text{ nmol h}^{-1} \text{ g}^{-1}$ of the reaction mixture.

Laccase (E.C. 1.10.3.2) activity was measured according to Patel *et al.* (2009) through the oxidation of 2, 2- Azino-bis-3-ethyl-benzthiozoline-6-sulphonic acid (ABTS). Briefly, the soil suspension (100 μl) was mixed with 800 μl of 20 mM Na- Acetate buffer (pH 4.5) and 100 μl of 50 mM ABTS. The reaction was terminated with 40 μl of a 20% (v/v) trichloroacetic acid (TCA) solution after a 15 minute incubation period at 30°C. The absorbance was measured at 420 nm using an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA) ($\epsilon=34.9 \text{ cm}^{-1} \text{ M}^{-1}$) of $0.1 \text{ nmol h}^{-1} \text{ g}^{-1}$ of the reaction mixture.

Lignin peroxidase (E.C. 1.11.1.14) activity was determined using a modified method described by Agrawal and Shahi (2017). Briefly, the soil suspension (83.5 μl) was mixed with 749.5 μl of 125 mM Na-tartrate buffer (pH 3.0) and 0.16 mM azure B solution. The reaction was initiated by adding 83.5 μl of 2 mM H_2O_2 (pH 3.0) before incubating for 15 minutes at 30°C. The absorbance was measured at 651 nm using an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA) ($\epsilon=85,000 \text{ cm}^{-1} \text{ M}^{-1}$) of $0.1 \text{ nmol h}^{-1} \text{ g}^{-1}$ of the reaction mixture.

Manganese peroxidase (E.C. 1.11.1.13) activity was determined according to Patel *et al.* (2009). The method is based on the oxidation of 2, 6- dimethoxy phenol (DMP) to produce a yellow-brown coloured product. Briefly, the reaction mixture contained 83.5 μl of soil suspension, 749.5 μl of 50 mM Na-tartrate buffer (pH 4.0) and 2 mM of 2, 6-DMP. The enzymatic reaction was initiated by adding 83.5 μl of 0.4 mM H_2O_2 (pH 4.0) before incubating for 15 minutes at 30°C. The absorbance was measured at 469 nm using an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA) ($\epsilon=27,500 \text{ cm}^{-1} \text{ M}^{-1}$) of $0.1 \text{ nmol h}^{-1} \text{ g}^{-1}$ of the reaction mixture.

L-Asparaginase (E.C. 3.5.1.1) activity determined according to Shirfrin *et al.* (1974) by measuring the NH₃ released from *L*-Asparaginase hydrolysis. The soil suspension (50 µl) was mixed with 800 µl of 10 mM *L*-Asparaginase and 100 µl of 50 mM Tris buffer (pH 8.6). The mixture was incubated for 15 minutes at 37°C and the reaction was stopped by adding 50 µl of 1.5M TCA. Thereafter, the reaction mixture was centrifuged at 10000 xg for 2 minutes before transferring 20 µl of the supernatant into 4.3 ml of milliQ H₂O. The enzymatic reaction was initiated by adding 50 µl of Nessler's reagent and incubating for 15 min at 30°C. The absorbance was measured at 436 nm using an Agilent Cary 60 UV-Vis spectrophotometer (Agilent, USA). One unit of enzyme activity was expressed as an increase in absorbance of 0.1 unit min⁻¹ L⁻¹ of the reaction mix using NH₃ as standard.

Soil β-Glucosaminidase and β-phosphatase activity were determined according to Jackson *et al.* (2013) by using 4-MUB-N-acetyl-β-D-Glucosaminide and 4-MUB-Phosphate as the fluorogenic substrates, respectively.

3.2.5. Data analyses

IBM Statistics 24 was used to test for differences in soil spore counts macro, intermediate and micro nutrients, as well as pH, exchange activity, and total cation in the four study sites soil of KwaZulu-Natal (KZN), using one- way analysis of variance (ANOVA). Where the ANOVA showed significant differences between treatments, a Bonferroni's post hoc test was used to separate the means (≤ 0.05).

3.3. Results

3.3.1. Soil geochemistry

3.3.1.1. Soil colour and spore count

Ashburton soil (Figure 3.1A) had a black appearance while soils from Hluhluwe (Figure 3.1B), Bergville (Figure 3.1C) and Izingolweni (Figure 3.1D) had black/dark brown, brown and red-brown colour, respectively. Microscopic enumeration of Arbuscular mycorrhizal spores showed no significant difference ($p > 0.05$) between Izingolweni (11.6 spores/100g), Bergville (15.8 spores/100g of soil) and Ashburton (13.4 spores/100g), while Hluhluwe (5.2 spores/100g) was significantly different ($p < 0.05$) from the other sites (Figure 3.2).

3.3.1.2. Primary soil nutrients

Soil primary nutrients include phosphorus (P), nitrogen (N) and potassium (K). Hluhluwe had the highest N and K concentration but had the least P concentration, while Bergville had the highest P concentration (Figure 3.3). Ashburton and Izingolweni had the least N and K concentration, respectively (Figure 3.3).

3.3.1.3. Intermediate soil nutrients

Soil intermediate nutrients include calcium (Ca), magnesium (Mg) and sulfur (S). Hluhluwe had the highest concentration of both calcium (58.06 μmol) and magnesium (42.27 μmol), followed by Izingolweni (Ca = 31.54 μmol ; Mg = 19.48 μmol), Ashburton (Ca = 19.32 μmol ; Mg = 11.03 μmol) and Bergville (Ca = 7.77 μmol ; Mg = 3.41 μmol) (Figure 3.4).

3.3.1.4. Soil micronutrients

Soil micronutrients include zinc (Zn), manganese (Mn) and copper (Cu). Ashburton had the highest zinc (0.024 μmol) and manganese (0.24 μmol) concentration, while the other three sites showed similar Zn (0.009 μmol) concentration with Hluhluwe having the most Cu (0.29 μmol) and the least Mn (0.04 μmol), and Bergville having the least Cu (0.01 μmol) concentration (Figure 3.5).

3.3.1.5. Soil relative acidity and C: N ratios

Ashburton (pH 5.07) and Hluhluwe (pH 4.96) had the highest active acidity/pH, followed by Izingolweni (pH 4.63) and Bergville (pH 4.06) (Figure 3.6). On the other hand, Bergville had the highest exchange acidity (1.496 cmol/L) while the other three sites had similar exchange acidity \sim 0.006 cmol/L (Figure 3.6). Hluhluwe had the highest concentration of total cations (20.014 cmol/L) followed by Izingolweni (11.370 cmol/L), Ashburton (6.736 cmol/L) and Bergville (4.180 cmol/L) (Figure 3.6). Hluhluwe and Izingolweni had similar C: N ratios (15:1) while Bergville had 14:1 and Ashburton had 11:1 (Table 3.1).

3.3.2. Functional microbial diversity

Microbial diversity differed in quantity and quality from soil to soil. Hluhluwe soil had the second highest number of viable bacterial cells (2.04×10^5 CFU/ml) and had six different species that had relatively moderate diversity ($H=1.180$; $\lambda=0.622$) and evenness ($E_{\text{pielou}}=0.659$) (Table 3.2). Izingolweni soil had the least number of viable bacterial cells (1.57×10^4 CFU/ml) and had the same number of species as Hluhluwe (Table 3.2). However, Izingolweni soil was second to Hluhluwe in terms of diversity ($H=0.959$; $\lambda=0.563$) and evenness ($E_{\text{pielou}}=0.535$) (Table 3.2). Bergville soil had the second least number of viable bacterial cells (5.88×10^4 CFU/ml) and had the least number of species (Richness=5) (Table 3.2). There was also minimal diversity ($H=0.224$; $\lambda=0.096$) and evenness ($E_{\text{pielou}}=0.139$) amongst the species (Table 3.2). While Ashburton soil had the most number of viable bacterial cells (3.31×10^5 CFU/ml) and had the most number of species (Richness= 7) (Table 3.2), there was minimal diversity ($H=0.462$; $\lambda=0.222$) and evenness ($E_{\text{pielou}}=0.238$) amongst the species (Table 3.2).

The fungal (AMF) microflora, Hluhluwe soil had the most spores (2.65×10^3 spores/g) and fungal species (Richness=7) (Table 3.2). The Hluhluwe soil fungal community showed a high diversity ($H=1.594$; $\lambda=0.769$) and evenness ($E_{\text{pielou}}=0.819$) (Table 3.2). Bergville soil was second to Hluhluwe with 2.24×10^3 spores/g and three species that had moderate diversity ($H=0.884$; $\lambda=0.521$) and evenness ($E_{\text{pielou}}=0.804$) (Table 3.2). Izingolweni soil was third with 6.89×10^2 spores/g and two species that had minimal diversity ($H=0.385$; $\lambda=0.226$) and moderate evenness ($E_{\text{pielou}}=0.556$) (Table 3.2). Ashburton soil had the least fungal spores (6.76×10^2 spores/g) and two species that had minimal diversity ($H=0.471$; $\lambda=0.295$) and moderate evenness ($E_{\text{pielou}}=0.679$) (Table 3.2).

3.3.3. Endophytic microorganisms

3.3.3.1. Bacteria

A total of 21 endophytic microbial strains (bacteria and fungi) were isolated from the soil samples and identified using BLASTN. The bacterial strains belonged to the family *Bacillaceae* (Figure 3.7) while fungal strains belonged to the family Nectriaceae, Mucoraceae, and Hypocreaceae (Figure 3.8). The percentage relative abundance was determined to better understand the microbial composition of each soil site. Hluhluwe soil had a bacterial composition of 49.7% *Bacillus thuringiensis*, 35.3% *Lysinibacillus xylanilyticus*, 0.4% *Bacillus cereus*, and 4.9% of each of *Bacillus mycoides*, *Bacillus aryabhatai* and *Bacillus huizhouensis* strains. Izingolweni soil had

47.8% *B. thuringiensis*, 45.4% *L. xylanilyticus*, 4.8% *B. cereus*, 0.8% *B. methylotrophicus* and 0.6% of each of *L. boronitolerans* and *B. huizhouensis* strains. Bergville soil had 95% *L. xylanilyticus*, 4.4% *B. thuringiensis*, 0.3% *B. cereus* and 0.2% of each of *B. simplex* and *B. arbutinivorans* strains. Ashburton soil had 87.4% *L. xylanilyticus*, 10% *B. thuringiensis*, 1.5% *B. mycooides* and 0.3% of each of *B. aryabhattai*, *B. methylotrophicus* and *B. arbutinivorans* strains (Figure 3.7).

3.3.3.2. Fungi

Hluhluwe soil had a fungal composition of 32.3% *Mucor velutinosus*, 26.9% *Gibberella intermedia*, 18.3% *Fusarium sinensis*, 11.9% *Fusarium oxysporum*, 8.1% *Trichoderma spirale*, 1.2% *Trichoderma koningiopsis*, and 1.2% *Trichoderma gamsii* (Figure 3.8). Izingolweni soil had 87.1% *Amylomyces rouxii* and 12.9% *Rhizopus stolonifera*. Bergville soil had 63.5% *Fusarium conctricum*, 24.9% *Fusarium oxysporum* and 11.6% *Amylomyces rouxii* (Figure 3.8). Ashburton soil had 82% *Rhizopus stolonifera* and 18% *Fusarium conctricum* (Figure 3.8).

3.3.4. Soil enzyme activities

3.3.4.1. Carbon cycling enzymes

Nutrient cycling enzyme activities were assessed to determine factors influencing soil nutrient availability. Hluhluwe soil had the highest glucosidase, cellobiohydrolase and catalase activity. Izingolweni, Bergville and Ashburton soils had the second, third and fourth highest carbon cycling enzyme activities, respectively (Table 3.4).

3.3.4.2. Organic matter and lignin degrading enzymes

Izingolweni soil had the highest dehydrogenase, lignin peroxidase and manganese peroxidase activity, but had the lowest laccase activity (Table 3.5). Hluhluwe soil had the second highest laccase and Mn-peroxidase activity but had the second lowest dehydrogenase activity (Table 3.5). Bergville soil had the third highest laccase and Mn-peroxidase activity but had the lowest dehydrogenase activity. Lignin peroxidase activity was not detected in soils from both Hluhluwe and Bergville (Table 3.5). Ashburton soil had the second highest lignin peroxidase activity, third highest dehydrogenase and laccase activity, but had the lowest Mn-peroxidase activity (Table 3.5).

3.3.4.3. Nitrogen and phosphate cycling enzymes

Hluhluwe soil had the highest asparaginase and phosphatase activity but had the third highest glucosaminidase activity (Table 3.6). Izingolweni soil had the second highest glucosaminidase and asparaginase activity, and the third highest phosphatase activity (Table 3.6). Bergville soil had the highest glucosaminidase activity and the lowest phosphate and asparaginase activity (Table 3.5). Ashburton soil had the second, third and fourth highest phosphatase, asparaginase and glucosaminidase activity, respectively (Table 3.6).

3.4. Discussion

This study was aimed at assessing the properties of KZN soils to infer their potential effects on the growth and development of grassland and savannah ecosystem plants and to evaluate their potentiality for sustainable agriculture. There are many different factors that determine soil potential and fertility. Soil colour is one of those factors but it only provides insight on the possible composition and oxidative state of the soil (Osunade, 1992). Black/dark-brown colour of Ashburton and Hluhluwe soil could be indicative of high humus content and/or the presence of manganese (Mn) oxide (Schulze et al., 1993; Rabenhorst and Parikh, 2000). The different phases of organic matter degradation usually impart brown to black colours to soil (Tate *et al.*, 1990), while Mn-oxides have characteristic dark colours (Lindbo *et al.*, 2010). On another note, red-brown colour of Ezingolweni soil could be indicative of good drainage and the presence of iron oxides (Schwertmann, 1993). Lighter brown coloured soils like Bergville soil may be indicative of the presence of varying contents of organic matter (Konen *et al.*, 2003). However, it is difficult to draw definite conclusions from soil colour observations since it is a qualitative analysis. The use of a more quantitative method like soil nutrient testing increases confidence in conclusions drawn in most studies (Smethurst, 2000).

Soil nutrient analysis of macronutrients revealed that Hluhluwe, Ashburton and Izingolweni had the lowest P, N and K concentrations, respectively. This suggests that plants growing in Hluhluwe soils would have diminished root growth and development due to low nutrient availability, together with the reduced soil moisture due to the scarce annual precipitation. In addition, microbial identification did not reveal P solubilizing microorganisms thus reducing the amounts of this nutrient for plant growth (Williamson *et al.*, 2001). However, the low N concentration in

Ashburton soil might have minimal effects on plant growth since some plants have the potential to be self-sufficient when it comes to N acquisition (Drew *et al.*, 2012). N acquisition in these soils might happen thanks to endophytic bacteria as they are well represented in this soil (Figure 3.7). On the contrary to plants growing in Ashburton, Izingolweni grown plants are expected to have reduced growth due to low K concentration (Cakmak, 2005). Fast-growing plants including legumes such as *P. sativum* L. require high levels of K, which is essential for plant growth and development (Uchida, 2000). Potassium is required for the activation of enzymes, photosynthesis, protein synthesis and photosynthate transportation (Wang *et al.*, 2013). The latter being important to establish and maintain symbiosis with plant growth-promoting microorganisms. This means Ashburton and Izingolweni soil growing plants might have reduced growth rates and biomass accumulation as this soils have reduced concentrations of both K and N. The presence of plants in these soils indicates that the reduction of those nutrients is compensated by the presence of active soil microbial consortia aiding the plants via associative N fixation (Figure 3.7) (Latha *et al.*, 2011).

Analysis of intermediate nutrients revealed that Bergville had the lowest calcium (Ca^{2+}) and magnesium (Mg^{2+}) concentrations. Calcium plays a role in the regulation of plant cell wall rigidity and construction (Uchida, 2000). This means Bergville soil-grown plants might have stunted growth as a result of poor germination and weak stems (Bonilla *et al.*, 2004). Magnesium is present in the center of the chlorophyll porphyrin ring and is also involved in ATP production (Nelson and Ben-Shem, 2004). Plants deficient in Mg^{2+} have decreased photosynthetic rates and most likely in anabolic reactions that rely on energy from ATP hydrolysis (Candan and Tarhan, 2003). Micronutrient deficiencies have also been reported to have adverse effects on plant growth and nutrition (Uchida, 2000). For instance, zinc (Zn) deficiency mostly affects growth, hormone production and flowering (Hafeez *et al.*, 2013). While copper (Cu) and manganese (Mn) deficiencies affect protein synthesis, chlorophyll production, respiration, and leads to delayed maturity (Uchida, 2000). However, it is important to determine a plant's nutrient sufficiency range before deducing that a particular nutrient is deficient (Baldock and Schulte, 1996).

The identification of soils well suited for a particular plant's growth requires the determination of the plant's optimum growth conditions, the soil's nutritional status, and the interactions that plants

can establish with soil microorganisms. Some legumes and grasses are known to thrive in well-drained, slightly acidic soils with a pH range of 5.5 to 6.8 (McCauley *et al.*, 2009; www.agric.wa.gov.au/field-peas) and the same can be said for microorganisms (Carney and Matson, 2005). However, all the soils analysed in the present study were below this pH range. Bergville soils had the lowest pH and total cations, whilst having the highest exchange acidity. Under acidic conditions such as those in Bergville soils, base cations (like Mg^{2+} , Ca^{2+} , K^+ and Na^+) are removed from soil clay particles (Zhang *et al.*, 2007). These base cations are replaced by acidic cations such as Al^{3+} , H^+ and Mn^{2+} (Larssen and Carmichael, 2000; Zhang *et al.*, 2007). This promotes P-fixation, leaching of essential base cations and leads to an overall decrease in total exchangeable cations (Qian and Cai, 2007). The decrease in base saturation leads to elevated exchange acidity and decreased cation exchange capacity (Zhang *et al.*, 2007). Furthermore, low pH soil decreases plant uptake of K^+ , Ca^{2+} and Mg^{2+} since Mn^{2+} and H^+ outcompetes these ions for apoplast loading (Ferguson *et al.*, 2013). In addition, low pH hinders the development of profuse microbial communities (Rousk *et al.*, 2010) which results in the observed low values of richness and diversity in our soils.

Soil microflora is known to have a significant effect on soil fertility and plant growth. Numerous microorganisms have been reported to have plant growth-promoting capabilities and are essential in nutrient cycling. Members of the bacterial family *Bacillaceae*, including ones in Table 3.3 and Figure 3.7, have been reported to have such capabilities. For instance, *B. thuringiensis*, *B. cereus*, *B. aryabhatai*, *B. simplex* and *B. methylotrophicus* promote plant growth by improving nutrient availability by solubilizing P and K, regulating phytohormones, enhancing N fixation, preventing pathogens and producing abscisic acid (ABA), indole acetic acid (IAA), cytokinins and gibberellic acid (Vendan *et al.*, 2010; Pérez-García *et al.*, 2011; Kavamura *et al.*, 2013; Pérez-Fernández and Valentine, 2017), while other members like *Lysinibacillus xylanilyticus* degrade complex molecules such as hemicellulose into simpler molecules (Chantarasiri *et al.*, 2017). Furthermore, most *Bacillaceae* members are catalase, amylase and nitrate reduction positive (Logan and De Vos, 2009). Given their ubiquity in soil, their catalase activity assists in oxidative stress tolerance through the reduction of H_2O_2 into H_2O and O_2 . Another bacterial enzyme that helps improve soil nutrient availability is asparaginase (Joy, 1988). It converts asparagine into aspartic acid and ammonia (NH_3), which is used by plants as an N source.

Although we cannot directly relate the presence of soil bacteria with particular enzyme activities, we can nevertheless partly relate those activities with the soil nutritional status to depict the better scenarios for plant growth. In our study, the soil with the greatest asparaginase activity is Hluhluwe that is at the same time the one with the highest level of total N. Considering the combined dehydrogenase and catalase activities, it is possible to estimate the biological index of soil fertility (Stefanic, 1984). According to it (Table S1) Izingolweni soil is the one with the greatest fertility (59.75) that coincides with their balanced levels of all nutrients, only showing relatively reduced concentrations of K. On the other hand, Bergville soils have the lowest fertility which can be attributed to the low levels of meso and micro nutrients. Soils from Hluhluwe and Ashburton had intermediate values of fertility and similar between them. These two soils do not follow a homogeneous pattern of nutrient distribution, with the former showing P, Zn and Cu deficiencies; the later has balanced levels of macronutrients and a clear imbalance for the remaining elements.

The different soil sites in this study had the presence of fungal species that were mostly saprophytes (Figure 3.8). These species employ different strategies to improve soil fertility but some are known pathogens of certain plant species (Michielse and Rep, 2009). They serve a common role in soil organic matter and lignin degradation through extracellular enzymes (Novotný *et al.*, 2004; Jastrow *et al.*, 2007). Laccases and Mn-peroxidases are the enzymes commonly produced by fungi, while lignin peroxidase is also produced by bacteria (Theuerl and Buscot, 2010). Apart from degrading herbaceous and/or woody material, members of the fungal families present in the different soils have other beneficial abilities. For instance, *Gibberella intermedia* have the ability to promote seedling growth through the production of gibberellin (Tsavkelova *et al.*, 2008). While *Amylomyces rouxii* and *Rhizopus stolonifer* produce different kinds of glucosidases and esterases that improve carbon turnover (Ogundero 1988; Anal, 2019). Members of *Trichoderma* are able to produce ammonia, and other fungi solubilize phosphates and micronutrients and are currently commercialized as crop enhancers to replace chemical fertilizers (Ousley *et al.*, 1994; Altomare *et al.*, 1999). The phosphate-solubilizing ability is most likely a result of phosphatase activity. Their chitinase activity, which is also present in some bacteria, assists in N and C cycling in terrestrial ecosystems (Lorito *et al.*, 1993).

Based on the microbial and enzyme activity data, Bergville soil is estimated to provide plants with the least nutrition. Not only did Bergville soil have no lignin peroxidase and asparaginase activity,

but it also had low dehydrogenase activity. Dehydrogenase is an intracellular enzyme that is present in all microorganisms and can be used as a basis to determine overall microbial activity (Wolińska and Stepniowska, 2012).

3.5. Conclusions

Grassland and savanna ecosystem soil may support the establishment and growth of these ecosystem plants and sustainable agriculture practices. Given that these different soils have different diversity of microbes and various soil enzymes that can solubilize bound nutrients. However, external inputs such as liming of soils in accordance with plant sufficiency range might be required to maximize yield potential.

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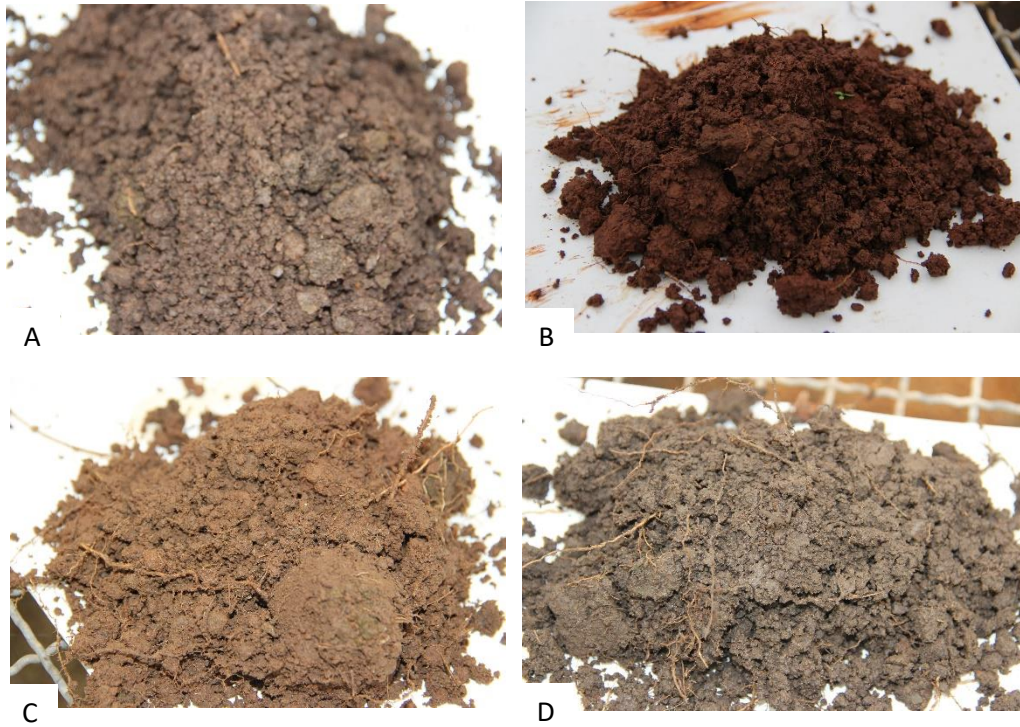


Figure 3.1: Soil colour variation between the four KZN sites. **A:** Hluhluwe (dark brown) **B:** Izingolweni (red-brown) **C:** Bergville (brown) **D:** Ashburton (black).

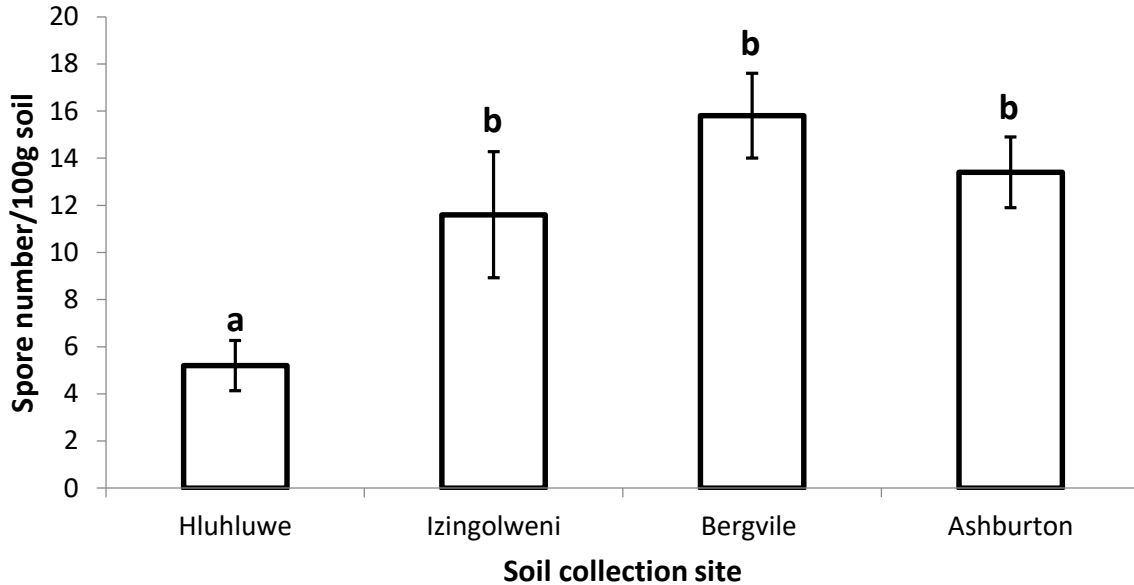


Figure 3.2: Arbuscular mycorrhizal spore count. Soil samples were processed using wet sieving and decanting technique followed by sucrose centrifugation and filtrate. Arbuscular mycorrhizal spores were observed and enumerated microscopically. Spore viability not confirmed. Results are mean ± SE, n = 5. Means with the same letter indicate that no significant differences were detected after a one-way ANOVA ($p \leq 0.05$).

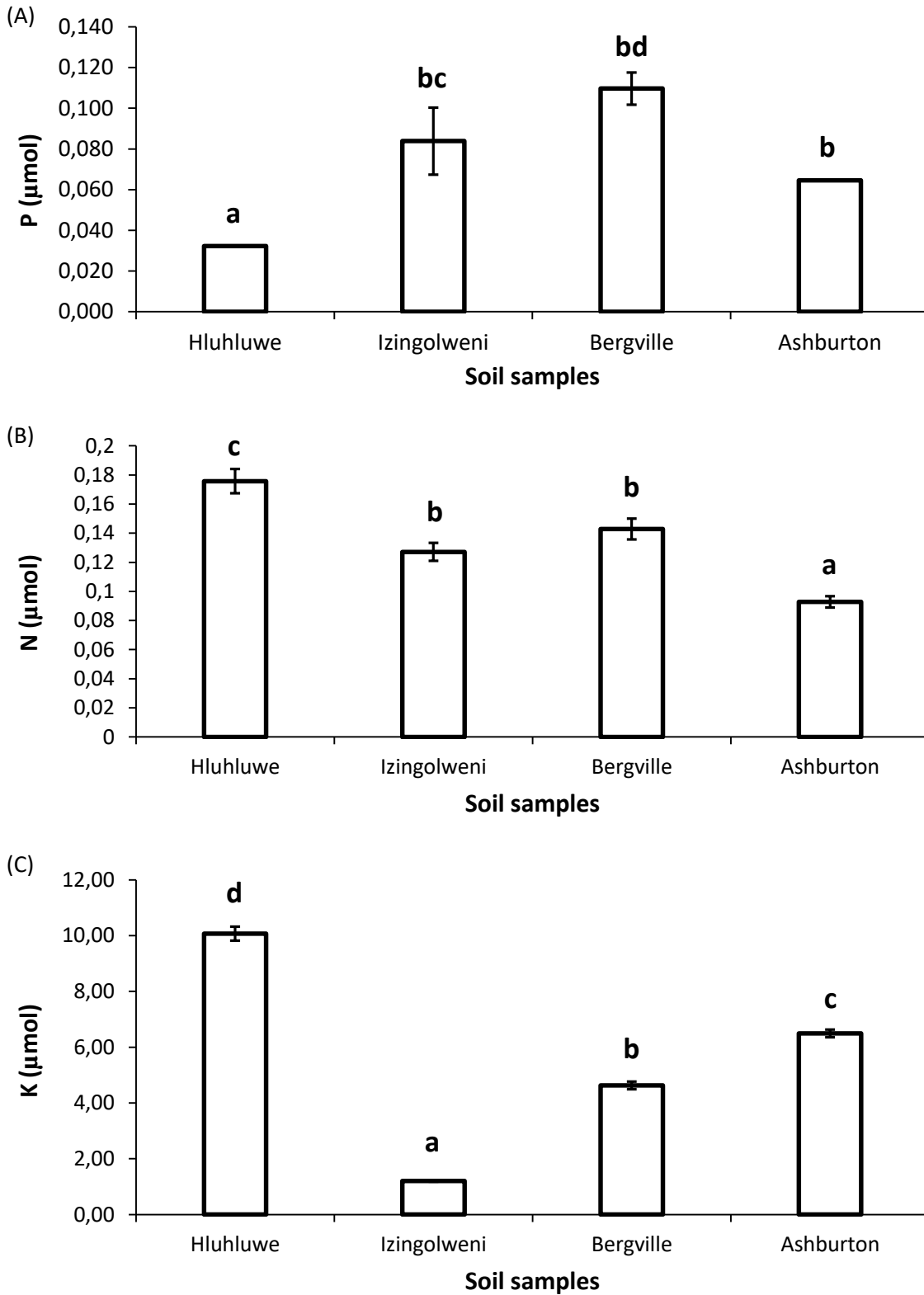


Figure 3.3: Concentration of soil primary nutrients. A: Phosphorus (P), **B:** Nitrogen (N) and **C:** Potassium (K). Results are mean \pm SE. Different letters on top of the columns indicate significant differences after one-way ANOVA ($p \leq 0.05$; $n = 5$).

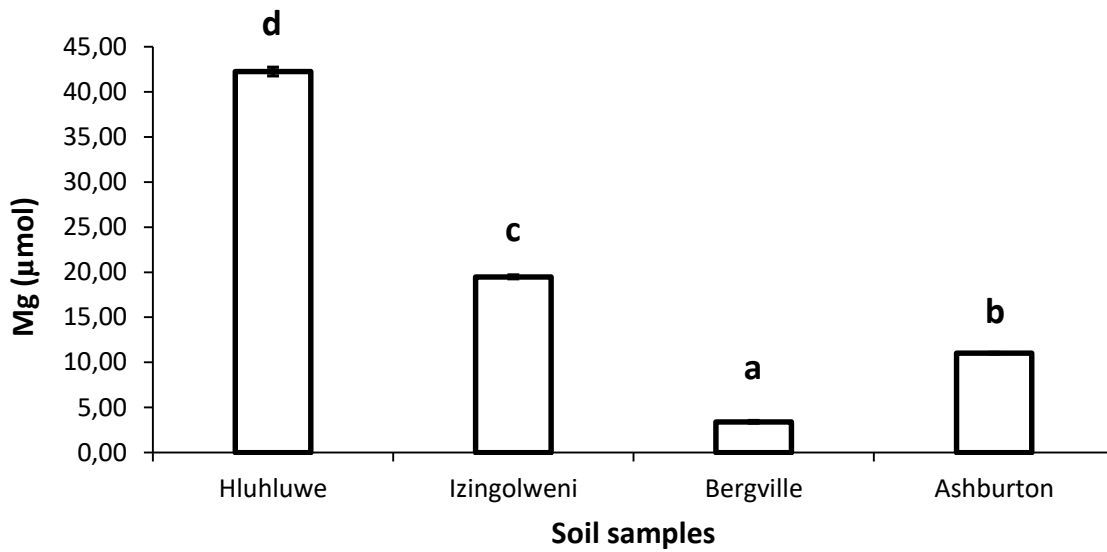
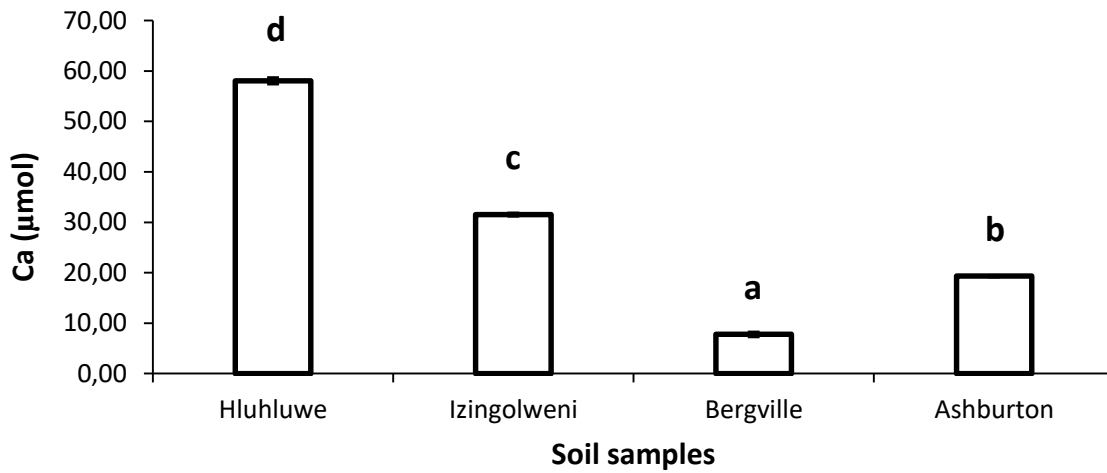


Figure 3.4: Concentration of soil intermediate nutrients. Soil samples were sent to CEDARA College of Agriculture, (South Africa) for total soil nutrient analysis. **A:** Calcium (Ca) and **B:** Magnesium (Mg). Results are mean \pm SE. Different letters on top of the columns indicate significant differences after one-way ANOVA ($p \leq 0.05$; $n = 5$).

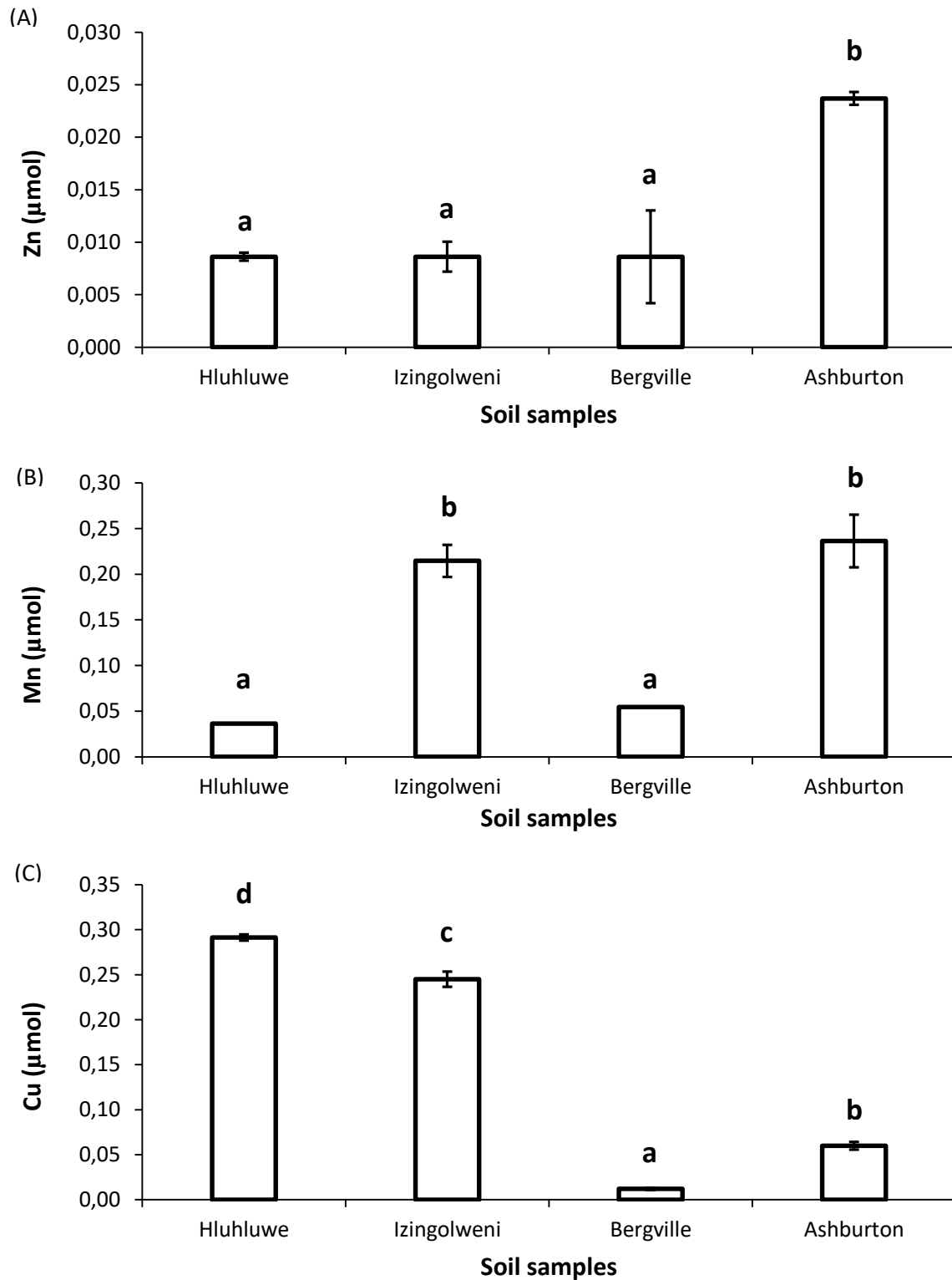


Figure 3.5: Concentration of soil micronutrients. Soil samples were sent to CEDARA College of Agriculture, (South Africa) for total soil nutrient analysis. **A:** Zinc (Zn), **B:** Manganese (Mn) and **C:** Copper (Cu). Results are mean \pm SE. Different letters on top of the columns indicate significant differences after one-way ANOVA ($p \leq 0.05$; $n = 5$).

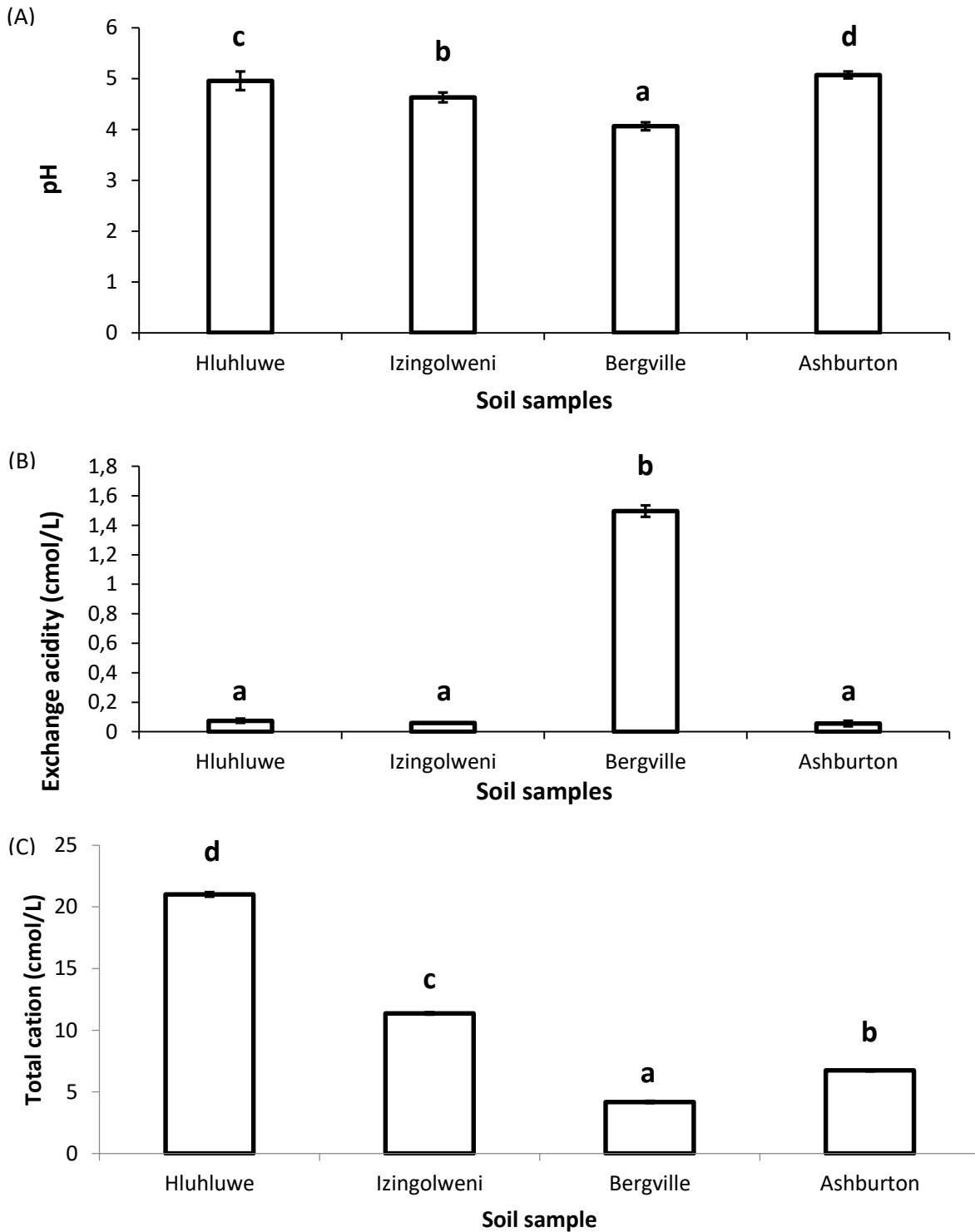


Figure 3.6: Soil relative acidity. Soil samples were sent to CEDARA College of Agriculture, (South Africa) for total soil nutrient analysis. **A:** pH, **B:** Exchange acidity and **C:** Total cation. Results are mean ± SE. Different letters on top of the columns indicate significant differences after one-way ANOVA ($p \leq 0.05$; $n = 5$).

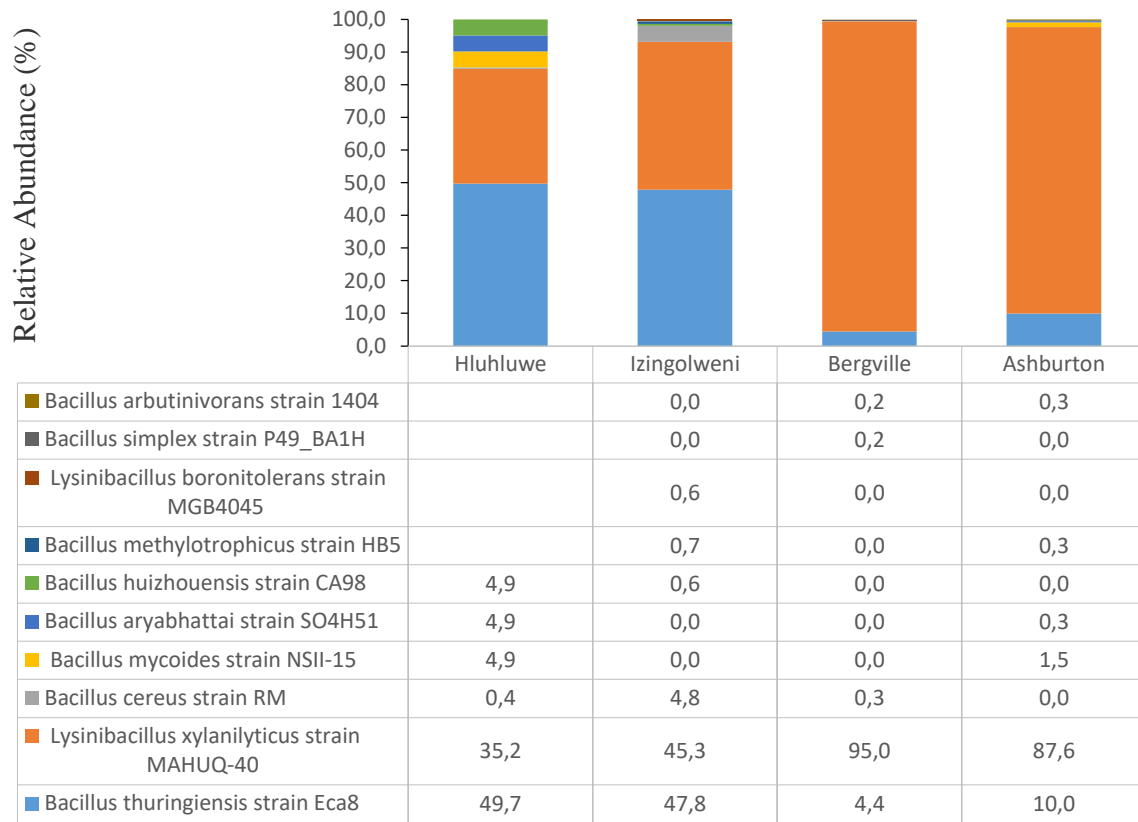


Figure 3.7: Percentage bacterial strain relative abundance.

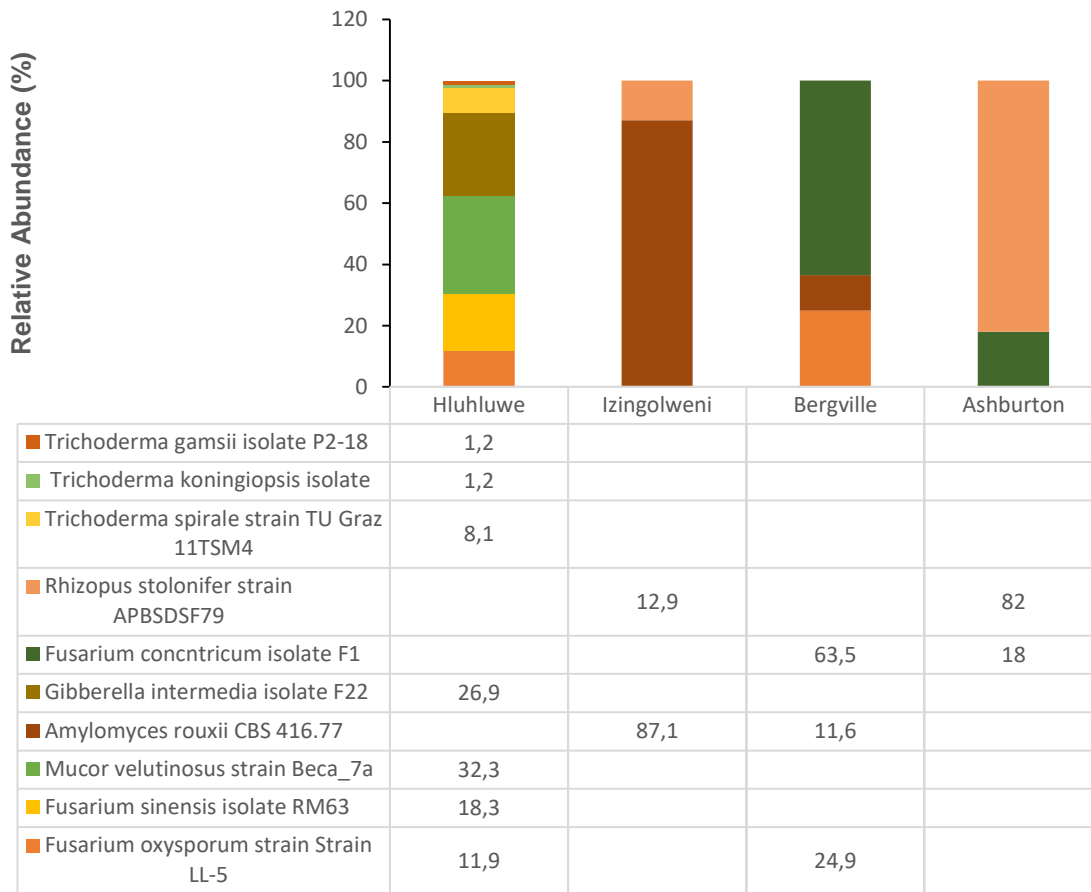


Figure 3.8: Percentage fungal strain relative abundance.

Table 3.1: Organic carbon to nitrogen ratio from soil treatments.

Soil site	Organic C (%)	N (%)	C:N ratio	Effect on soil N
Hluhluwe	3.62	0.246	15:1	Mineralization
Izingolweni	2.68	0.178	15:1	Mineralization
Bergville	2.82	0.200	14:1	Mineralization
Ashburton	1.4	0.130	11:1	Mineralization

Table 3.2: Functional Microbial diversity index of the soil samples.

Phylum	Site	Total CFU/mL	Richness	Shannon diversity index (H)	Simpson Index (λ)	R_{margalef}	E_{pielou}
Bacteria	Hluhluwe	2.04x10 ⁵	6	1.180	0.622	0.409	0.659
	Izingolweni	1.57x10 ⁴	6	0.959	0.563	0.518	0.535
	Bergville	5.88x10 ⁴	5	0.224	0.096	0.364	0.139
	Ashburton	3.31x10 ⁵	7	0.462	0.222	0.472	0.238
		Total spores/g					
Fungi (AMF)	Hluhluwe	2.65x10 ³	7	1.594	0.769	0.761	0.819
	Izingolweni	6.89x10 ²	2	0.385	0.226	0.153	0.556
	Bergville	2.24x10 ³	3	0.884	0.521	0.259	0.804
	Ashburton	6.76x10 ²	2	0.471	0.295	0.153	0.679

Table 3.3: Endophytic strains isolated from the soil samples.

Family	Strain	Accession No.	Similarity (%)
Soil bacteria			
	<i>Bacillus thuringiensis</i> strain Eca8	KY952733	99.09
	<i>Lysinibacillus xylanilyticus</i> strain MAHUQ-40	MK680116	99.19
	<i>Bacillus cereus</i> strain RM	MG230318	99.28
	<i>Bacillus mycoides</i> strain NSII-15	JN993723	98.82
<u>Bacillaceae</u>	<i>Bacillus aryabhatai</i> strain SO4H51	KP706808	98.41
	<i>Bacillus huizhouensis</i> strain CA98	MK618613	99.62
	<i>Bacillus methylotrophicus</i> strain HB5	KM659215	98.93
	<i>Lysinibacillus boronitolerans</i> strain MGB4045	MH261172	83.02
	<i>Bacillus simplex</i> strain P49_BA1H	MK883080	99.19
	<i>Bacillus arbutinivorans</i> strain 1404	JN645967	91.3
Soil fungi			
	<i>Fusarium oxysporum</i> strain Strain LL-5	MK966308	100
<u>Nectriaceae</u>	<i>Fusarium sinensis</i> isolate RM63	MG652446	99.63
	<i>Gibberella intermedia</i> isolate F22	HQ379695	99.63
	<i>Fusarium concentricum</i> isolate F1	HQ379633	98.66
	<i>Mucor velutinosus</i> strain Beca_7a	KY203942	96.7
<u>Mucoraceae</u>	<i>Amylomyces rouxii</i> CBS 416.77	Q118998	95
	<i>Rhizopus stolonifer</i> strain APBDSDF79	MG669211	99.12
	<i>Trichoderma spirale</i> strain TU Graz 11TSM4	EU871034	99.49
<u>Hypocreaceae</u>	<i>Trichoderma koningiopsis</i> isolate CTCCSJ-ASC50272	KU896317	100
	<i>Trichoderma gamsii</i> isolate P2-18	KJ439112	99.31

Table 3.4: Soil carbon cycling enzyme activities in $\text{nmolh}^{-1}\text{g}^{-1}$ of soil

Site	β -Glucosidase	β -Cellobiohydrolase	Catalase
Hlulhuwe	0.911 \pm 0.113 ^a	0.190 \pm 0.023 ^a	90.9 \pm 25.1 ^a
Izingolweni	0.546 \pm 0.095 ^b	0.178 \pm 0.006 ^a	64.3 \pm 11.9 ^a
Bergville	0.356 \pm 0.042 ^b	0.072 \pm 0.003 ^b	61.8 \pm 10.6 ^a
Ashburton	0.335 \pm 0.012 ^b	0.072 \pm 0.006 ^b	56.1 \pm 3.01 ^a
LSD (0.05)	0.231	0.036	44.7

Values in the same column with different letters as superscripts are significantly different by least significant difference ($p \leq 0.05$).

Table 3.5: Soil organic matter and lignin degrading enzyme activities in $\text{nmolh}^{-1}\text{g}^{-1}$ of soil

Site	Dehydrogenase	Laccase	Lignin Peroxidase	Manganese Peroxidase
Hlulhuwe	36,7 \pm 16,8 ^b	86,12 \pm 15,1 ^a	ND	220,9 \pm 57,2 ^{ab}
Izingolweni	123,9 \pm 41,4 ^a	28,5 \pm 29,5 ^a	105,7 \pm 49,1 ^a	338,8 \pm 121,7 ^b
Bergville	19,9 \pm 3,17 ^b	62,5 \pm 10,4 ^a	ND	185,2 \pm 18,1 ^{ab}
Ashburton	60,4 \pm 10,9 ^b	50,7 \pm 21,9 ^a	40,9 \pm 66,3 ^a	50,3 \pm 68,3 ^b
LSD (0.05)	69,12	61,6	125,5	227,7

ND: Not detected, Values in the same column with different letters as superscripts are significantly different by least significant difference ($p \leq 0.05$)

Table 3.6: Soil nitrogen and phosphate cycling enzyme activities in $\text{nmolh}^{-1}\text{g}^{-1}$ of soil

Site	β -Glucosaminidase	<i>L</i> -Asparaginase	β -Phosphatase
Hlulhuwe	0,637 \pm 0,007 ^c	574,5 \pm 12,6 ^a	1,149 \pm 0,05 ^a
Izingolweni	0,734 \pm 0,011 ^b	66,2 \pm 4,51 ^b	0,797 \pm 0,012 ^b
Bergville	0,981 \pm 0,016 ^a	ND	0,686 \pm 0,020 ^c
Ashburton	0,567 \pm 0,034 ^d	15,5 \pm 0,201 ^c	0,806 \pm 0,046 ^b
LSD (0.05)	0,059	515,7	0,103

ND: Not detected, Values in the same column with different letters as superscripts are significantly different by least significant difference ($p \leq 0.05$)

Table S1: Values of the Biological Index for Soil Fertility based on dehydrogenase and catalase activities

Site	Dehydrogenase	Catalase	BIF
Hlulhuwe	36.7	90.9	24.54
Izingolweni	123.9	64.3	59.75
Bergville	19.9	61.8	9.22
Ashburton	60.4	56.1	25.41

Biological Index of soil Fertility (Stefanic, 1984):

$$BIF = (1.5 DH k 100 CA) / 2$$

Where *DH* is dehydrogenase

CA Catalase

k proportionality Coefficient (0.01)



Figure S1.: Map of KwaZulu Natal province illustrating soil collection sites for the present study. Hluhluwe, Northern KZN ($28^{\circ}0'58''S$ $32^{\circ}12'4''$, Altitude ~ 100 m); Izingolweni, Southern KZN ($30^{\circ}43'32''S$ $30^{\circ}6'10''E$, Altitude ~ 450 m); Bergville, Mountainous KZN ($28^{\circ}34'14''S$ $29^{\circ}4'17''E$, Altitude ~ 1040 m); Ashburton, Midland KZN ($29^{\circ}38'55''S$ $30^{\circ}26'42''E$, Altitude ~ 670 m). Image retrieved from Sithole *et al.* (2019).

Chapter 4

Plant growth & nutrition

***Pisum sativum* L. can acclimatize to nutrient deficient soils from KwaZulu- Natal grasslands and savanna ecosystems, South Africa.**

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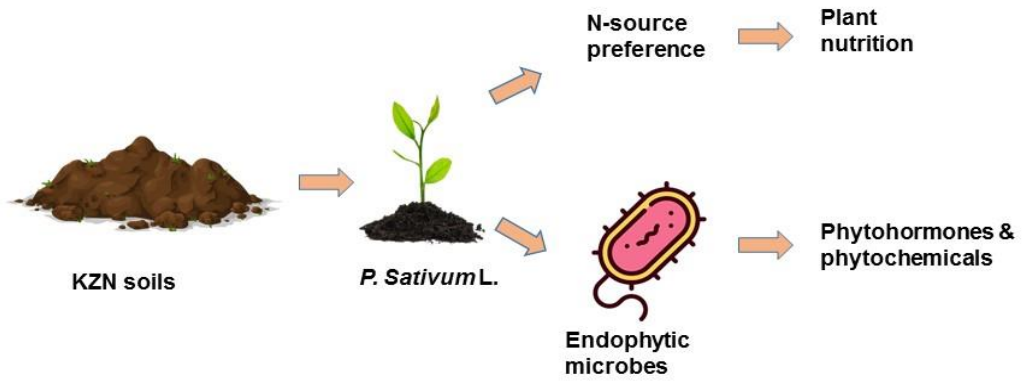
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Graphical abstract depicting the research conducted and presented in this section.

Abstract

The agricultural sector is a major contributor to many economies across the world, especially in developing countries. Unfortunately, soil quality degradation and low soil fertility presents a major threat to sustainable agriculture. Legumes have been used to improve soil fertility, however most legume research is usually focused on food and not forage legumes, especially in nutrient-deficient agri-systems. Forage legumes like *Pisum sativum* (L.) are important in these systems as they increase the nutritional value in pastures and provide relatively high amounts of protein and minerals when used as animal feed. Therefore, this study examined the effects of KwaZulu-Natal grasslands and savanna ecosystem nutrient deficient soils in plant-microbe symbiosis, plant nutrition and carbon growth costs in a forage legume, *P. sativum* (L.). Also, the phenolic acids and cytokinin concentrations in this forage legume were elucidated. Soils from four KZN geographical distinct regions covering grasslands and savanna ecosystems were used as growth substrates. These soils were nutrient deficient, acidic with varying microflora. *P. sativum* (L.) maintained its root dry weights and plant growth rates among all the soils. Low pH, total cations and high exchange acidity in Bergville soils resulted in decreased total plant dry weights. Also, Bergville soil grown plants showed decreased growth-promoting compounds (i.e. kinetin, active cytokinins, and salicylic acid) and increased cis-zeatin type and storage cytokinins. *P. sativum* (L.) grown in Izingolweni soils were more reliant on atmospheric N fixed by endophytic/associative bacteria from the genera *Cupriavidus*, *Paenibacillus*, *Cohnella* and *Bacillus*. While plants grown in Hluhluwe soils, relied on soil N. Furthermore, *P. sativum* (L.) grown in Izingolweni soil decreased shoot growth and overall plant nutrient concentration in comparison to Hluhluwe and Ashburton plants. Hluhluwe and Ashburton soil grown plants accumulated the most biomass and N nutrient concentration via N-source switching, increasing N nutrient absorption and/or decreasing N utilization rates. Therefore, plant associative microbes might modulate nutrient availability for plant uptake in grassland and savanna nutrient poor ecosystems. *P. sativum* (L.) may acclimatize to these low nutrient and acidic ecosystem soils by changing N source preferences, phenolic and cytokinin concentrations.

Keywords: *Pisum sativum* L., nutrient deficient, endophytic/associative bacteria, phenolic acids and cytokinin.

4.1. Introduction

Sustainable soil management is viewed as a fundamental aspect of sustainable agriculture for supporting the ever-increasing population and biodiversity (Nambiar *et al.*, 2001; Lal, 2008; Ohyama, 2017). However, African countries are still faced with accelerating declines in agricultural yield due to unsustainable agricultural practices and environmental factors. The environmental factors include climate change, rainfall variability, soil quality degradation, and recurrent droughts (Lema and Majule, 2009; Doso Jnr, 2014). These aforementioned environmental factors do not only have detrimental effects on soil fertility but on ecosystem functioning and vegetation structure and composition (Lema and Majule, 2009; Doso Jnr, 2014). The agricultural sector plays a pivotal role in most economies and since the soil is a non-renewable resource (Doran and Zeiss, 2000), sustainable strategies need to be developed to help mitigate the negative impact on soil quality and yield potential. To achieve this, the importance of soil must be recapitulated and more research must be aimed at the identification of plants that can withstand such environmental stress conditions. This would enable the establishment of high nutrient pastures for animal feed and also improved soil fertility through the use of legumes.

Soil is a sink of essential minerals, nutrients, and microflora that contribute to the growth of plants (Rutigliano *et al.*, 2004). Soil is also involved in the direct and/or indirect cycling of essential elements such as nitrogen (N), carbon (C) and oxygen (O) (Harper and Pendleton, 1993; Nannipieri *et al.*, 2003; Marschner, 2012). Soil fertility and functionality are based on the soil composition (i.e. clay content), relative acidity (pH), aeration (redox potential), microbial diversity, moisture content, temperature, nutrient availability and other chemical and physical characteristics (Voroney, 2007; Husson, 2013). All these soil characteristics are essential for plant growth and persistence during harsh environmental conditions (Voroney, 2007; Husson, 2013). However, microbial diversity tends to stand out due to the ability of some microorganisms to convert insoluble nutrients into plant-available form (Rengel and Marschner, 2005). These microorganisms can either be host-dependent or free-living such as legume *Rhizobia* and *Aspergillus niger*. *Rhizobia* are known to reduce atmospheric nitrogen (N₂) through nitrogenase activity, while *Aspergillus niger* can hydrolyze phytic acid through phytase activity (Rengel and Marschner, 2005). An example of a key plant nutrient that microorganisms recycle is phosphorus (P) and is usually present in low concentration ($\leq 10 \mu\text{M}$) in acid soils (Kunwar *et al.*, 2018).

South Africa (SA) is one of the developing African countries that have experienced soil quality degradation due to drought and poor remediation strategies which include replenishing soil organic matter (Williams *et al.*, 2004). Furthermore, SA soils are not classified as high fertility soils and those that are, tend to be easily degraded (Roberts *et al.*, 2003; Mandiringana *et al.*, 2005). There are three distinct rain seasonality regions in SA i.e. the Mediterranean-like region (Western to southern Cape) that is characterized by winter rainfall, the summer rainfall region (KZN and Highveld ≥ 600 mm annual rainfall) and the bimodal region (Eastern Cape). All these regions constitute the average annual rainfall of ~ 450 mm, which makes SA a semi-arid country. It is also important to note that out of the 14 soil groups in SA, 12 are distributed across KZN (Fey, 2010). This makes KZN suitable for agricultural practices but nutrient availability is usually the limiting factor in areas like KZN and Highveld that receive ≥ 600 mm annual rainfall.

This can negatively affect agricultural productivity (Onwuka *et al.*, 2016), especially if the soils are also acidic (Maisels *et al.*, 1994; Haumaier and Zech, 1995; Buresh *et al.*, 1997). Luckily, legumes have developed adaptations to withstand these soil conditions through the establishment of tripartite symbiosis between the host plant and beneficial microorganisms (Ohyama, 2017; Sanz-Saez *et al.*, 2017). The limiting nutrients are made available in these symbiotic systems through biological N-fixation (BNF) in root nodules and P scavenging hyphae of arbuscular mycorrhizal (AM) fungi (Lambers *et al.*, 2008). However, legume research is usually focused on food and not forage legumes, especially in nutrient-deficient agri-systems. While forage legumes like *Pisum sativum* (L.) are also important in sustainable agricultural systems as they increase the nutritional value in pastures and provide relatively high amounts of N in soils required for plant growth (McCallum *et al.*, 2000). Thus, the aim of this research was to investigate the effects of distinct soil types with varying nutrient concentrations and pH on plant-microbe symbiosis, biomass accumulation, N-source preference and carbon growth costs of *Pisum sativum* (L.), and to determine the effects of these distinct soil types on phenolic and cytokinin concentrations in *Pisum sativum* (L.).

4.2. Methods and materials

4.2.1. Soil collection sites

Four geographical distinct regions in KwaZulu Natal province, South Africa, covering grassland and savanna ecosystems were used for soil sampling: Hluhluwe, Northern KZN (28°0'58''S, 30°26'42''E); Izingolweni, Southern KZN (30°43'32''S, 30°6'10''E); Bergville, Mountainous KZN (28°34'14''S, 29°4'17''E); Ashburton, Midlands KZN (29°38'55''S, 30°26'42''E). Approximately 10 soil samples (0-30 cm depth and 2 m apart) were collected in the rhizosphere from each of the four sites and pooled for homogeneity.

4.2.2. Soil geochemistry and arbuscular mycorrhizal fungi analysis

Five 50 g soil samples from each respective site were sent to the KwaZulu-Natal Department of Agriculture and Rural Development's Analytical Services Unit at Cedara College of Agriculture, South Africa, for total soil nutrient and cation concentrations, cation exchange acidity and pH analysis. Arbuscular mycorrhizal spore count analysis was conducted according to Smith and Dickson (1997) at Mycoroot (Pty) Ltd, Rhodes University, South Africa in soil samples ranging from 250 to 300 g from each site. The method used for this analysis was the wet sieving and decanting technique. Thereafter, sucrose centrifugation and filtration followed and the spores were observed and enumerated using a microscope.

4.2.3. Seed germination, bacterial inoculation, and growth

P. sativum (L.) seeds obtained from AGT foods Africa, Marji Mizuri farm, KZN, were planted in soils collected from the four KZN sampling regions. The seeds were sown ~2 cm deep in 19 cm diameter pots containing soil used as natural inoculum and growth substrate. The seeds were watered daily with ~300 ml H₂O pre-germination and every second or third day post-germination. Each treatment was replicated 20 times and seedling emergence was assessed for up to 10 days from sowing. Initial and final harvests were conducted 25 and 55 days after sowing, respectively. The experiment was conducted under ambient conditions in glasshouse No. 12 at the University of KwaZulu Natal botanical gardens, Pietermaritzburg, South Africa. The daytime and night-time temperatures ranged from 30 to 35 °C and 12 to 14 °C, respectively. The daily average humidity was 75% and the irradiance was ca. 35% of full sunlight (415.6 μmol m² sec⁻¹).

4.2.4. *Plant nutrient analysis*

Five plants per treatment were separated into different organs (leaves, stem and roots) and oven-dried at 80 °C for 7 days and the dry weights (DW) recorded. The dry plant material was ground in a mortar and pestle using liquid nitrogen and analyzed for their C, P and $\delta^{15}\text{N}$ concentrations. $\delta^{15}\text{N}$ concentrations analysis was conducted using a LECO-nitrogen analyzer at the Archaeometry Department, University of Cape Town, South Africa, and C and P concentrations were analysed using the inductively coupled mass spectrometry (ICP-MS) at the Central Analytical Facilities, Stellenbosch University, South Africa.

4.2.5. *Growth calculations*

4.2.5.1. *Relative growth rate (RGR)*

Agren and Franklin (2003) method was used to calculate the relative growth rate.

$$RGR = [(\ln W_2 - \ln W_1) / t_2 - t_1]$$

Where W is the dry weights accumulated from initial to final harvest and t is the time for plant growth.

4.2.5.2. *Specific N absorption rate (SNAR)*

Plant total N content was used to calculate the specific N absorption rate according to Nielsen *et al.* (2001).

$$SNAR = (L_2 - L_1 / t_2 - t_1) * [(\log_e R_2 - \log_e R_1) / (R_2 - R_1)]$$

Where L , t and R represent total N content, duration of plant growth and root dry weight, respectively.

4.2.5.3. *Specific N/P utilization rates (SNUR/SPUR)*

Plant total N/P content was used to calculate the specific N/P utilization rate according to Nielsen *et al.* (2001).

$$SNUR = (W_2 - W_1 / t_2 - t_1) * [(\log_e L_2 - \log_e L_1) / (L_2 - L_1)]$$

$$SPUR = (W_2 - W_1 / t_2 - t_1) * [(\log_e M_2 - \log_e M_1) / (M_2 - M_1)]$$

Where W , L and M represent plant DW, total N and P content, respectively.

4.2.5.4. Percentage N derived from the atmosphere (%Ndfa)

%Ndfa was calculated according to Shearer and Kohl (1986) as $\delta = 1000 (R_{sample} / R_{standard})$, where R is the molar ratio of ^{15}N and ^{14}N of the samples and standards. Sample preparation and analysis was conducted according to Matiwane *et al.* (2019) using the same equipment, standards, and facilities.

$$\delta = 100 ((\delta^{15}\text{N}_{reference\ plant} - \delta^{15}\text{N}_{legume}) / (\delta^{15}\text{N}_{reference\ plant} - \beta))$$

Where β value represents the $\delta^{15}\text{N}$ natural abundance of the N derived from biological N_2 -fixation of *P. sativum* L., grown in a N-free culture. The β value of *P. sativum* was -2.58%.

4.2.5.5. Carbon cost (C_w)

Carbon growth cost was calculated using the formula modified by Peng *et al.* (1993).

$$C_w = (C + kN / 14 * 180 / 24) (1 / 0.89) (6000 / 180)$$

Where C_w represents the tissues' total carbon construction cost, C is the total concentration of carbon, k is the reduced state of N substrate (i.e. $\text{NH}_3 = -3$) and N is the total organic nitrogen content of the tissue (Williams *et al.*, 1987).

Given: Atomic mass of N = 14; Conversion factor from mol to g glucose = 180; No. of e^- in glucose molecule = 24; Estimate of growth efficiency = 0.89; Constant conversion factor = 6000 / 180

4.2.6. Bacterial isolation, colony PCR and identification

Because Izingolweni soil grown *P. sativum* (L.) were the only plants that formed root nodules, root nodules from these plants were rinsed with ddH₂O to remove residual soil particles. The nodules were then surface sterilized using 70% (v/v) ethanol for 30 seconds before submerging them in 3.5% (v/v) sodium hypochlorite solution for 3 minutes. Thereafter, the nodules were thoroughly rinsed (~10 times) with dH₂O and stored in vials containing silica gel. The vials were subsequently placed inside a fridge at 4°C. Endophytic bacteria were isolated by crushing the stored root nodules in 15% (v/v) glycerol and culturing the suspension on yeast mannitol agar (YMA) and incubated at 28°C under micro-aerobic conditions. Single colonies were obtained by repeated streaking and culturing at 72 h incubation periods at 28°C under micro-aerobic conditions.

Colony PCR to amplify a portion of the 16S rDNA gene was carried out using the following primers set: 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and the 1492R (5'-GGTTACCTTGTTACGACTT-3'). The PCR reaction volumes (for a total of 25 µl) was 11 µl sterile distilled water, 12.5 µl TAKARA-EmeraldAmpGT PCR Master Mix (Separations, South Africa), 1 µl colony, 0.25 µl forward primer and 0.25 µl reverse primer. The PCR conditions were: Initial denaturation at 94°C for 5 minutes; 30 cycles of denaturation at 94°C for seconds; annealing at 55°C for 30 seconds; extension at 72°C for 2 minutes; final elongation step at 72°C for 10 minutes. The resulting PCR products were resolved on a 1% (w/v) agarose gel using 1x TAE buffer and run at 100V for 40 minutes. The PCR products were then sent for sequencing at the Central Analytical Facilities at Stellenbosch University, South Africa. The resulting sequences were subjected to BLASTN searches for identification (National Center for Biotechnology Information, NCBI (<https://www.ncbi.nlm.nih.gov>)).

4.2.7. Cytokinin and phenolic acids quantification

Nine plants per treatment were pulverized in liquid nitrogen using a mortar and pestle and freeze dried. The samples were then sent for cytokinin and phenolic acids quantification at the Laboratory of Growth Regulators, Centre of the Region Haná for Biotechnological and Agricultural Research, Faculty of Science, Palacký University & Institute of Experimental Botany AS CR, Šlechtitelů, Czech Republic. Plant cytokinin concentrations were determined according to Novák *et al.* (2008) with slight modification (Novák *et al.*, 2003), while phenolic acid concentrations were determined by extracting the compounds with 80% (v/v) methanol and metal bead with 20 µl internal standard [10^{-4} mol/L; solution of salicylic acid ($3.4.5.6\text{-}^2\text{H}_4$) and 4- hydroxybenzoic acid ($2.3.5.6\text{-}^2\text{H}_4$)]. Thereafter, the mixture was homogenized for a period of 3 minutes in the oscillatory ball mill homogenizer (frequency 27 sec^{-1}) then subjected to the ultrasonicator for 15 minutes and further centrifuged for 10 min at 17 000 RPM at temperature of 4 °C. Then the supernatants were transferred into Eppendorf tubes and the pellet was re-extracted. The extracts were then combined and evaporated to dryness in an oil evaporator for a period of 6-8 hours.

The ultra-high-performance liquid chromatography-tandem mass spectrometry quantification was determined using a UHPLCTM system (Waters. Milford. MA. USA) connected simultaneously to both a PDA 2996 photodiode array detector (Waters. Milford. MA. USA) and a Micromass Quattro

microTM API benchtop triple quadrupole mass spectrometer (Waters MS Technologies, Manchester, UK), equipped with a Z-spray electrospray ionization (ESI) source operating in negative mode (Gruz et al., 2008). The extracts were injected into a reversed-phase column (BEH C₈, 1.7 µm, 2.1 × 150 mm, Waters, Milford, MA) and incubated at a temperature of 30 °C. Linear gradients and isocratic flows of the mobile phase had a sequencing of 9.5 min with solvent B (acetonitrile) balanced with solvent A (aqueous 7.5 mM HCOOH) at a flow rate of 250 µl min⁻¹. After sequencing, the column was equilibrated for 2.5 min under initial conditions with pressure from 4000 to 8000 psi during the chromatographic run. The eluent was added into a PDA detector (scanning range 210-600 nm, resolution 1.2 nm), thereafter into an electrospray source (source block temperature 100 °C, desolvation temperature 350 °C, capillary voltage 2.5 kV, cone voltage 25 V). Argon was applied as a collision gas (collision energy 16 eV) and N₂ was the desolvation gas (500 L h⁻¹). Different retention windows were used for quantification

4.2.8. Statistical analysis

IBM SPSS Statistics 25 software was used for all data analysis. Analysis of variance (ANOVA) statistical model was used to compare means and values were considered significant when $P \leq 0.05$. Where the ANOVA showed significant differences between treatments, a Bonferroni's post hoc test was used to separate the means. The least significant difference test was used to compare cytokinin concentrations.

4.3. Results

4.3.1. Geochemistry and microflora

The geochemical analysis revealed that the KZN soils differed in macronutrient concentrations, relative acidity and microflora. Bergville soil had the highest P concentration whilst having the second and third highest N and K concentration respectively (Table 4.1). Hluhluwe soil had the highest N and K concentration but had the lowest P concentration (Table 4.1). Izingolweni and Ashburton soils fell in-between the two extremes for N and P concentration (Table 4.1). However, Izingolweni soil had the lowest K concentration (Table 4.1). All the sites had acidic soils, with Bergville having the lowest pH, total cations, and the highest exchange acidity (Table 4.1). All the sites had relatively low AM fungi spore count per 100 g of soil. The average spore count ranged between 5.20 - 15.80 spores per 100 g of soil (Table 4.1). Ashburton and Hluhluwe soils had the

most bacterial colony forming units, while Izingolweni and Bergville had the first and second lowest bacterial CFU, respectively (Table 4.1).

4.3.2. Seedling emergence and growth kinetics

A comparison of seedling emergence showed that Hluhluwe and Ashburton had the highest and similar percentage seedling emergence after four (91%) and seven days (100%) of planting, followed by Izingolweni (four days = 82%; seven days = 95%) and Bergville (four days = 86%; seven days = 91%) (Table 4.2). All plants grown in these different experimental soils maintained their growth rates (Table 4.3). Hluhluwe soil grown plants had the highest total plant biomass followed by Ashburton grown plants then Izingolweni and Bergville soil grown plants (Table 4.3). Hluhluwe and Ashburton soil grown plants had the highest aboveground biomass and decreased root-shoot (Table 4.3). Izingolweni and Bergville soil grown plants had root-shoot ratio of 1.39 and 5.52 respectively (Table 4.3). Bergville plants also had the lowest above-ground biomass whilst having the highest root biomass (Table 4.3).

Plants grown in soils from all four sites relied on both soil and atmospheric N for growth. There was no significant difference in total plant N concentration in plants grown in Ashburton (2.23 ± 0.087) and Hluhluwe soils (2.14 ± 0.093) (Table 4.3). Plants grown in Izingolweni soils (1.12 ± 0.15) and Bergville (0.70 ± 0.080) had the lowest total plant N concentration, respectively (Table 4.3). Izingolweni soil grown plants relied more on N₂-fixation (~55%) than Ashburton (~43%) then Bergville (~31%) and Hluhluwe soil grown plants (~5%) (Table 4.3). Ashburton and Izingolweni soil grown plants had the highest concentration of N derived from the atmosphere (Table 4.3). Hluhluwe soil grown plants had the most soil-derived N (~95%), followed by Bergville (~69%), Ashburton (~57%), and Izingolweni (~45%) (Table 4.3). Hluhluwe and Ashburton soil grown plants assimilated the most N, while Bergville soil grown plants had the least N absorption rate (Table 4.3). However, Ashburton and Hluhluwe soil grown plants utilized the least N per day in comparison to Izingolweni and Bergville plants which had the highest specific N utilization rate (Table 4.3).

Ashburton soil grown plants had the highest total plant P concentration, while Bergville soil grown plants accumulated the least total plant P concentration (Table 4.3). Izingolweni and Hluhluwe soil grown plants had the second and third least total plant P concentration, respectively (Table 4.3).

However, there was no significant difference between the treatments when it comes to the carbon construction costs (Table 4.3) and specific P utilization rates (Table 4.3).

4.3.3. Endophytic bacteria identification

Izingolweni soil grown plants were the only plants that developed nodules and were selected for endophytic bacteria identification. Amplification and comparison of the 16S ribosomal RNA gene partial sequence revealed that the root-nodule inhabiting bacteria were from the genera *Paenibacillus*, *Cupriavidus*, *Ralstonia*, *Saccharibacillus*, *Cohnella*, and *Bacillus* (Table 4.4). The species identity ranged between 90 – 100% (Table 4.4). Isolates from *Paenibacillus* were *P. polymyxa*, *P. jamilae*, *Paenibacillus. sp.*, *P. favisporus*, and *P. endophyticus* (Table 4.4). Members of *Cupriavidus* were *C. necator*, *C. oxalaticus*, *Cupriavidus. sp.*, and *C. metallidurans* (Table 4.4). Isolates from *Bacillus* were *B. cereus*, *Bacillus sp.*, and *B. thuringiensis* (Table 4.4). Other nodule isolates were *Ralstonia sp.*, *Saccharibacillus sp.*, and *Cohnella plantaginis* (Table 4.4).

4.3.4. Phenolic acids concentration

The concentration of phenolic acids was higher in plant shoots than in the roots, with the exception of salicylic and vanillic acid (Table 4.5). The only phenolic acid concentrations that showed significant differences were the shoot concentrations of caffeic, vanillic, and sinapic acid (Table 4.5). Izingolweni soil grown plant shoots had the highest caffeic and vanillic acid concentration, while Hluhluwe soil grown plant shoots had the highest sinapic acid concentration (Table 4.5). Izingolweni and Bergville soil grown plants had an overall increase in the concentration of most phenolic acids, with the exception of salicylic acid in which Bergville soil grown plants had the least concentration (Table 4.5). Furthermore, Bergville soil grown plants had the highest 4-coumaric acid concentration (Table 4.5).

4.3.5. Cytokinin concentration

The concentration of most of the cytokinins was higher in plant roots than in the shoots (Table 4.6). Bergville soil grown plants had high concentrations of *O*-glucoside and riboside *O*-glucoside containing cytokinins, as well as the cis isomer of zeatin (cZ) and DHZR (Table 4.6). However, Bergville plants lacked tZ7G, DHZ, iP, and kinetin (Table 4.6). Hluhluwe and Ashburton plants

had higher concentrations of the active cytokinins and their ribosides (i.e. Z, iP, DHZR, kinetin) but lacked DHZ (Ashburton) and tZROG (Table 4.6). Ashburton plants also had elevated tZ7G concentration. Izingolweni plants lacked iP and had moderate to high concentrations of all the other cytokinins (Table 4.6).

4.4. Discussion

Pisum sativum L. was able to grow in soils from KZN savanna and grassland ecosystems by modulating their growth kinetics, plant nutrient assimilation and utilization rates and regulating their phenolic acid and cytokinin concentrations. Additionally, Izingolweni soil grown plants established symbiosis with multiple bacterial genera.

Plants grown in Bergville soils had decreased total plant dry weight, however their root dry weights increased significantly. This may be due to the significant decrease in pH of Bergville soils. Low soil pH decreases the base saturation, nutrient availability, total cations and increase exchange acidity in soils (Stiles, 2004). This results in limited essential nutrients and co-factors required for growth and development. For instance, under slightly acidic conditions, phosphate available for plants is sequestered into insoluble cation bound phosphate making it unavailable for plant assimilation (Giesler *et al.*, 2002). Additionally, Low pH alters the soil microflora composition, diversity, abundance and viability (Zhalnina *et al.*, 2015). This results in decreased efficiency of plant growth-promoting microorganisms (Siciliano *et al.*, 2014; Zhalnina *et al.*, 2015). However, plants have been reported to have increased root systems under stress conditions to mitigate the effects and prevent senescence (Huang and Fry, 1998; Franco *et al.*, 2011). This agrees with our observations in Bergville soil grown plants increased root dry weights, increasing root surface area increasing the probability that plant roots will contact more plant growth-promoting microorganisms and soil nutrients. This is evident in Bergville soil grown plants as they increased their reliance on soil-derived N rather than N derived from the atmosphere. The low plant nutrient concentrations and absorption rates could indicate resource management by Bergville soil grown plants. Resource management is one of many survival strategies that plants employ under unfavorable conditions (Chapin, 1991; Robert *et al.*, 2014). Regulation of metabolites like phenolic acids has also been reported to play a role in plant stress response through antioxidant activity (Jaleel *et al.*, 2009). Bergville soil grown plants showed an increased vanillic, 4-coumaric, ferulic, and hydrobenzoic acid concentration but decreased salicylic acid concentration. Increased phenolic acid concentration are usually associated with unfavorable soil conditions, weather,

radiation and limited water availability (2000). Ghasemzadeh *et al.* (2010) reported increases in antioxidant activity and phenolic acid concentrations (gallic, vanillic, ferulic, cinnamic, and salicylic acid) in *Zingiber officinale* Roscoe under high CO₂ levels. This corresponds with the findings of the present study since plant phenolic acid concentrations increased as a result of nutrient deficient soils (Ghasemzadeh *et al.*, 2010). Salicylic acid appears to be the key phenolic acid that directly affects the growth of Bergville soil grown plants since other phenolic acid are known for their antioxidant activity (Rivas-San Vicente and Plasencia, 2011; Saxena *et al.*, 2012). In addition, salicylic acid also plays a role in ion uptake and photosynthesis (Horváth *et al.*, 2007; Rivas-San Vicente and Plasencia, 2011).

Cytokinin concentrations also support the notion of resource management in Bergville soil grown plants since these plants showed increased concentrations of *Cis*-Zeatin(s) (cZ), *O*-glucosides (~OG) and riboside *O*-glucosides (~ROG). CZ concentrations are known to increase in response to resource reallocation when plant growth is decreased or stopped to prevent senescence (Gajdošová *et al.*, 2011). Furthermore, OG and ROG are viewed as storage molecules as they are shut down during unfavorable conditions and activated under favorable conditions (Mok *et al.*, 1992). However, in Bergville soils grown plants DHZ, iP, tZ7G, and kinetin were not detected. Contrary to OGs and ROGs, DHZ and iP are some of the more active compounds during plant growth phase (McGaw, 1987). While kinetin promotes cell division, hence it was non-detection, this could be indicative of decreased plant growth in these plants (Mukherjee and Kumar, 2007).

Izingolweni soils had adequate P and N amounts but decreased K concentration. K plays an essential role in plant growth and development (Prajapati and Modi, 2012). Plants with decreased K concentrations, photosynthates, nutrients and H₂O movement are negatively affected (Prajapati and Modi, 2012). Also, K acts as a co-factor in enzyme activation, therefore, limited K affects the rate of photosynthesis and production of proteins and energy (Gajdanowicz *et al.*, 2011). Koksál *et al.* (1988) reported that K deficiency resulted in increased abscisic acid (ABA) concentration, causing inhibition to shoot growth. This means Izingolweni soil grown plants would have decreased above-ground biomass or shoot length, nutrient concentrations and growth kinetics. However, the impact of K deficiency may have been reduced in these plants by establishment of symbiosis with endophytic microorganisms. Different species from the genera *Bacillus*, *Pseudomonas/Cupriavidus*, *Paenibacillus* and *Burkholderia* possess K solubilizing capabilities

which help by increasing exchangeable K in soils for plant uptake (Sheng *et al.*, 2008; Rajawat *et al.*, 2012; Syed and Patel, 2014). Sequence analysis of the 16S rRNA gene revealed that *P. sativum* (L.) formed a symbiotic relationship with multiple genera of root nodule inhabiting bacteria, some of which are efficient N₂-fixers.

Members of *Paenibacillus* like *P. polymyxa* have been previously reported to be efficient N₂-fixers (free-living and/or symbiotic) and increase plant-available P through solubilization and mineralization (Wang *et al.*, 2012; Puri *et al.*, 2016; Villadas *et al.*, 2019). Also, members of *Ralstonia* (*Ralstonia taiwanensis*) and *Cohnella* have been reported to fix N₂ in *Mimosa* roots (Chen *et al.*, 2003; Wang *et al.*, 2015). While members of *Bacillus* (including *B. cereus* and *B. thuringiensis*) promote root growth and nodulation and N₂ fixation in co-inoculation experiments (John Bullied *et al.*, 2002; Mishra *et al.*, 2009). These may have resulted in Izingolweni soil grown plants increased reliance in atmosphere derived N. Changes in phenolic acid and cytokinin concentrations could be a response to reactive oxygen species caused by the soil condition (endogenous production) or released exogenously by rhizobacteria (Ghasemzadeh *et al.*, 2010).

Compared to Hluhluwe soil grown plants, Ashburton soil grown plants had decreased plant biomass, N absorption rate, salicylic acid and active CK concentration (iP, DHZ, Z, and their ribosides). The biomass could be attributed to decreased phytohormone and phytochemical concentrations (Thiruvengadam *et al.*, 2016). The inverse might be true for Hluhluwe soil grown plants which had higher concentrations of molecules like kinetin, salicylic acid, and other active CKs. Ashburton plants were reliant on both soil N and atmosphere N during growth but the plants did not develop nodules. This suggests the possibility of Ashburton soils containing free-living N₂-fixing bacteria reducing atmosphere N for plant uptake. Both Hluhluwe and Ashburton soils showed relative soil acidity but Hluhluwe soils had lower P concentration, however Hluhluwe soil grown plants showed a significantly increased P concentration compared to Izingolweni and Bergville soil grown plants. In all the four treatments there is the possibility that P-solubilizing microorganisms, especially microbial fungi like *Aspergillus*, *Fusarium*, *Trichoderma*, AM fungi could have assisted in P acquisition (Sharma *et al.*, 2013) as fungal spore enumeration conducted in this study does not reflect viability.

The varying concentration of cytokinins and phenolic acids in different plant parts might indicate that these compounds have different roles in process regulation and as signaling molecules that

elicit localized and/or systemic responses. The presence of the cytokinin tZ7G in three of the treatments maybe an example of this. Since tZ7G is regarded as an irreversible inactivation product, its presence could induce a homeostatic response (i.e. to initiate a different phase like flowering) by influencing the transcriptome (Schäfer *et al.*, 2015; Raines *et al.*, 2016).

4.5. Conclusion

Pisum sativum (L.) was able to grow under nutrient-poor and acidic grassland and savanna soils by maintaining their growth rates and relying on both soil and atmospheric N-source. Nutrient deficient soils induced changes in phenolic acids and cytokinin concentrations to enable the persistence of *P. sativum* (L.) to grassland and savanna ecosystem soils. Therefore, *Pisum sativum* (L.) may have a potential to be used as a forage and biofertilizer in sustainable agricultural practices in these nutrient poor ecosystems.

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Declaration of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Table 4.1. KwaZulu-Natal soil geochemistry and microflora data.

Parameter	Site			
	Hluhluwe	Izingolweni	Bergville	Ashburton
Soil macronutrients (μmol)				
Phosphate (P)	0.032 ± 0.00^a	0.084 ± 0.02^{bc}	0.11 ± 0.01^{bd}	0.065 ± 0.00^b
Nitrogen (N)	0.18 ± 0.01^c	0.13 ± 0.01^b	0.14 ± 0.01^b	0.093 ± 0.00^a
Potassium (K)	10.07 ± 0.41^d	1.20 ± 0.00^a	4.63 ± 0.03^b	6.49 ± 0.05^c
Relative acidity (cmol/L)				
pH	4.96 ± 0.00^c	4.63 ± 0.00^b	4.06 ± 0.00^a	5.07 ± 0.02^d
Exchange acidity	0.074 ± 0.00^a	0.060 ± 0.00^a	1.50 ± 0.04^b	0.056 ± 0.00^a
Total cations	21.01 ± 0.18^d	11.37 ± 0.10^c	4.18 ± 0.08^a	6.74 ± 0.07^b
Microflora				
Fungal spore count (no./100 g soil)	5.20 ± 1.07^a	11.60 ± 2.68^b	15.80 ± 1.80^b	13.40 ± 1.40^b
Bacteria CFU/ml	2.04×10^5	1.57×10^4	5.88×10^4	3.31×10^5

Values are means \pm SE, n = 3. In each row, values with the same letter do not differ significantly ($p \leq 0.05$)



Figure 4.1. Forage pea (*Pisum sativum* L.) seedlings after (A) four and (B) seven days of growth in Ashburton soil.

Table 4.2. Relative seedling emergence comparison between soil sites.

Soil collection site	Seedling emergence (%)	
	Day 4	Day 7
Ashburton	91	100
Bergville	86	91
Hluhluwe	91	100
Izingolweni	82	95

Seedling emergence refers to the initial seedling visualization above soil surface. Where n = 32 per soil collection site.

Table 4.3. Growth kinetic of *Pisum sativum* L. grown in KwaZulu-Natal soils.

Parameter	Treatment			
	Hluhluwe	Izingolweni	Bergville	Ashburton
Biomass data				
Leaves (g)	0.35 ± 0.028 ^a	0.20 ± 0.047 ^b	0.06 ± 0.003 ^c	0.22 ± 0.041 ^b
Shoot (g)	0.63 ± 0.094 ^a	0.31 ± 0.066 ^{bc}	0.10 ± 0.023 ^c	0.52 ± 0.087 ^{ab}
Roots (g)	0.36 ± 0.048 ^a	0.40 ± 0.018 ^a	0.47 ± 0.088 ^a	0.43 ± 0.006 ^a
Total plant (g)	1.34 ± 0.064 ^a	0.92 ± 0.011 ^b	0.63 ± 0.080 ^c	1.16 ± 0.068 ^{ab}
Growth kinetics				
Growth rate (g/day)	0.024 ± 0.0012 ^a	0.017 ± 0.0020 ^a	0.011 ± 0.0015 ^a	0.021 ± 0.0012 ^a
Root: Shoot ratio	0.62 ± 0.15 ^a	1.39 ± 0.26 ^a	5.52 ± 2.24 ^b	0.88 ± 0.15 ^a
SNAR (mg N g ⁻¹ root DW day ⁻¹)	8.03 ± 0.36 ^d	3.80 ± 0.53 ^b	2.02 ± 0.24 ^a	7.05 ± 0.28 ^c
SNUR (mg N g ⁻¹ DW day ⁻¹)	3.75 ± 0.14 ^b	4.46 ± 0.42 ^c	4.38 ± 0.35 ^c	3.08 ± 0.10 ^a
SPUR (mg P g ⁻¹ plant DW day ⁻¹)	0.011 ± 0.00 ^a	0.011 ± 0.00 ^a	0.010 ± 0.00 ^a	0.009 ± 0.00 ^a
Carbon costs (mmol C g ⁻¹ DW)	0.0069±0.00 ^a	0.0070±0.00 ^a	0.0069±0.00 ^a	0.0066±0.00 ^a
N nutrition				
Total plant nitrogen (mmol N g ⁻¹)	2.14 ± 0.093 ^c	1.12 ± 0.15 ^b	0.70 ± 0.080 ^a	2.23 ± 0.087 ^c
Standard corrected ¹⁵ N/ ¹⁴ N	4.00 ± 0.20 ^c	1.17 ± 0.31 ^a	2.17 ± 0.43 ^b	1.33 ± 0.13 ^a
%NDFA	4.43 ± 2.86 ^a	54.49 ± 4.43 ^d	31.00 ± 3.24 ^b	43.21 ± 1.94 ^c
Atmospheric derived N (mmol N g ⁻¹)	0.073 ± 0.046 ^a	0.70 ± 0.15 ^c	0.32 ± 0.015 ^b	0.83 ± 0.059 ^c
Soil derived N (mmol N g ⁻¹)	1.52 ± 0.073 ^d	0.52 ± 0.022 ^a	0.78 ± 0.13 ^b	1.09 ± 0.041 ^c
P nutrition				
Total plant phosphate (μmol P g ⁻¹)	56.08 ± 1.28 ^c	32.53 ± 2.15 ^b	23.52 ± 1.61 ^a	80.19 ± 8.47 ^d

Values are means ± SE, n = 3. In each row, values with the same letter do not differ significantly (p ≤ 0.05)

Table 4.4. Identities of root nodule inhabiting microorganisms.

Site	Possible match	Identity (%)	Accession number
Izingolweni	<i>Paenibacillus polymyxa</i> BEb-40	95.78	AB863035.1
	<i>Paenibacillus sp.</i> Bs57	95.69	GU328694.1
	<i>Paenibacillus jamilae</i> IIF5SW-B4	95.68	KY218874.1
	<i>Cupriavidus sp.</i> Strain NGha2	91.46	MN197795.1
	<i>Cupriavidus necator</i> strain H16	91.46	CP039287.7
	<i>Cupriavidus oxalaticus</i> strain X32	91.46	CP038634.1
	<i>Cupriavidus metallidurans</i> I115	91.46	MK216985.1
	<i>Ralstonia sp.</i> AMF 1009	90.42	JQ316396.1
	<i>Saccharibacillus sp.</i> ATSA2	100	CP041217.1
	<i>Paenibacillus polymyxa</i> ZF197	100	MK961276.1
	<i>Paenibacillus favisporus</i> JF2-8	100	MK016488.1
	<i>Paenibacillus endophyticus</i> JBRI-MO-0041	100	MK302256.1
	<i>Cohnella plantaginis</i> JBRI-MO-0012	100	MK302227.1
	<i>Bacillus cereus</i> strain I7	93.01	MH892088.1
	<i>Bacillus sp.</i> KK-35	93.01	KU352795.1
	<i>Bacillus thuringiensis</i> strain BDzG	93.01	MN203618.1
	<i>Bacillus sp.</i> 69G6-C	93.01	JQ388720.1

Table 4.5. Concentration of phenolic acids ($\mu\text{g/g}$) in *Pisum sativum* L. grown in KwaZulu-Natal soils.

Compound	Part	Site			
		Hluhluwe	Izingolweni	Bergville	Ashburton
Protocatechuic acid:	Roots	0.97 \pm 0.49 ^a	0.68 \pm 0.22 ^a	1.20 \pm 0.39 ^a	0.66 \pm 0.12 ^a
	Shoot	1.85 \pm 0.22 ^a	1.88 \pm 0.029 ^a	1.79 \pm 0.22 ^a	1.53 \pm 0.10 ^a
4-hydroxybenzoic acid:	Roots	14.92 \pm 6.78 ^a	18.28 \pm 7.93 ^a	13.56 \pm 1.44 ^a	10.11 \pm 4.99 ^a
	Shoot	19.05 \pm 3.20 ^a	27.93 \pm 0.61 ^a	24.46 \pm 10.14 ^a	10.23 \pm 1.57 ^a
Caffeic acid:	Roots	0.73 \pm 0.32 ^a	0.41 \pm 0.24 ^a	0.19 \pm 0.043 ^a	0.35 \pm 0.19 ^a
	Shoot	1.14 \pm 0.065 ^a	2.01 \pm 0.23 ^b	1.01 \pm 0.21 ^a	0.49 \pm 0.089 ^a
Vanillic acid:	Roots	1.42 \pm 0.40 ^a	1.18 \pm 0.50 ^a	4.27 \pm 1.38 ^a	1.89 \pm 0.38 ^a
	Shoot	1.18 \pm 0.17 ^{ab}	4.39 \pm 0.24 ^c	2.61 \pm 0.82 ^{bc}	1.33 \pm 0.23 ^{ab}
Syringic acid:	Roots	0.61 \pm 0.46 ^a	0.28 \pm 0.11 ^a	0.27 \pm 0.056 ^a	0.34 \pm 0.041 ^a
	Shoot	0.77 \pm 0.075 ^a	1.04 \pm 0.10 ^a	1.31 \pm 0.71 ^a	0.36 \pm 0.040 ^a
4-coumaric acid:	Roots	13.57 \pm 1.18 ^a	25.56 \pm 11.82 ^a	14.23 \pm 2.17 ^a	21.89 \pm 3.54 ^a
	Shoot	87.79 \pm 15.41 ^a	85.80 \pm 2.64 ^a	105.47 \pm 38.40 ^a	43.01 \pm 4.73 ^a
Sinapic acid:	Roots	0.19 \pm 0.042 ^a	0.25 \pm 0.18 ^a	0.11 \pm 0.00 ^a	0.26 \pm 0.060 ^a
	Shoot	18.52 \pm 1.37 ^b	10.13 \pm 1.62 ^a	8.77 \pm 1.53 ^a	5.42 \pm 0.50 ^a
Ferulic acid:	Roots	6.03 \pm 3.02 ^a	13.18 \pm 11.42 ^a	3.05 \pm 0.48 ^a	7.50 \pm 1.60 ^a
	Shoot	26.69 \pm 6.13 ^a	46.66 \pm 1.45 ^a	35.15 \pm 10.81 ^a	19.43 \pm 2.70 ^a
Salicylic acid:	Roots	1.82 \pm 0.71 ^a	3.90 \pm 1.95 ^a	0.83 \pm 0.12 ^a	0.92 \pm 0.36 ^a
	Shoot	0.29 \pm 0.060 ^a	0.34 \pm 0.039 ^a	0.36 \pm 0.13 ^a	0.31 \pm 0.032 ^a

Values are means \pm SE, n = 9. Rows with the same letter do not differ significantly ($p \leq 0.05$).

Table 4.6. Concentration of cytokinins (pmol/g) in *Pisum sativum* L. grown in KwaZulu-Natal soils.

Cytokinin metabolite	Part	Site			
		Hluhluwe	Izingolweni	Bergville	Ashburton
<i>trans</i> -Zeatin (tZ)	Roots	0.85 ± 0.85 ^a	0.61 ± 0.61 ^a	< LOD	1.69 ± 0.87 ^a
	Shoot	0.47 ± 0.47 ^a	< LOD	0.37 ± 0.37 ^a	0.98 ± 0.02 ^a
<i>trans</i> -Zeatin riboside (tZR)	Roots	1.38 ± 1.38 ^a	2.90 ± 2.90 ^a	< LOD	< LOD
	Shoot	2.00 ± 0.55 ^a	2.05 ± 0.05 ^a	4.92 ± 1.09 ^b	1.21 ± 0.61 ^a
<i>trans</i> -Zeatin riboside <i>O</i> -glucoside (tZROG)	Roots	< LOD	1.80 ± 1.80 ^a	< LOD	< LOD
	Shoot	< LOD	< LOD	1.02 ± 1.02 ^a	< LOD
<i>trans</i> -Zeatin 7-glucoside (tZ7G)	Roots	2.09 ± 1.09 ^{ab}	0.96 ± 0.68 ^{ab}	< LOD	5.76 ± 3.22 ^b
	Shoot	0.78 ± 0.78 ^a	< LOD	< LOD	1.59 ± 1.59 ^a
<i>cis</i> -Zeatin (cZ)	Roots	4.48 ± 2.25 ^a	8.67 ± 5.65 ^a	3.88 ± 0.11 ^a	4.72 ± 0.74 ^a
	Shoot	9.34 ± 1.43 ^a	3.50 ± 0.40 ^a	13.08 ± 7.23 ^a	4.52 ± 1.10 ^a
<i>cis</i> -Zeatin <i>O</i> -glucoside (cZOG)	Roots	3.46 ± 1.18 ^a	1.54 ± 0.80 ^a	12.17 ± 2.24 ^b	3.09 ± 0.63 ^a
	Shoot	3.33 ± 0.40 ^b	1.97 ± 0.99 ^{ab}	5.91 ± 0.80 ^c	< LOD
<i>cis</i> -Zeatin riboside (cZR)	Roots	79.21 ± 52.56 ^a	26.61 ± 21.84 ^a	27.63 ± 8.04 ^a	107.53 ± 47.09 ^a
	Shoot	210.01 ± 22.69 ^{ab}	200.03 ± 2.50 ^{ab}	177.15 ± 15.76 ^a	269.20 ± 8.15 ^b
<i>cis</i> -Zeatin riboside <i>O</i> -glucoside (cZROG)	Roots	14.24 ± 9.43 ^a	5.29 ± 5.29 ^a	9.89 ± 4.60 ^a	17.48 ± 6.22 ^a
	Shoot	38.51 ± 9.62 ^b	7.76 ± 0.46 ^a	15.23 ± 0.60 ^a	15.62 ± 1.93 ^a
Dihydrozeatin (DHZ)	Roots	17.96 ± 3.98 ^b	< LOD	< LOD	< LOD
	Shoot	< LOD	6.82 ± 0.49 ^b	< LOD	< LOD
Dihydrozeatin <i>O</i> -glucoside (DHZOG)	Roots	< LOD	< LOD	< LOD	< LOD
	Shoot	3.81 ± 0.20 ^a	2.07 ± 0.04 ^a	5.03 ± 1.93 ^a	2.75 ± 0.29 ^a
Dihydrozeatin riboside (DHZR)	Roots	2.91 ± 0.83 ^a	3.02 ± 1.84 ^a	1.88 ± 0.49 ^a	1.93 ± 1.02 ^a
	Shoot	5.04 ± 0.38 ^a	9.05 ± 0.23 ^a	10.99 ± 2.75 ^a	5.14 ± 0.19 ^a
Isopentenyladenine (iP)	Roots	0.79 ± 0.79 ^a	< LOD	< LOD	1.91 ± 1.00 ^a
	Shoot	7.22 ± 2.33 ^b	< LOD	< LOD	3.60 ± 0.63 ^b
Isopentenyladenine riboside (iPR)	Roots	11.75 ± 6.99 ^a	10.3 ± 8.12 ^a	4.44 ± 1.17 ^a	19.06 ± 6.50 ^a
	Shoot	271.88 ± 15.59 ^c	121.08 ± 4.43 ^{ab}	115.29 ± 9.84 ^a	173.98 ± 4.23 ^b
Kinetin (K)	Roots	7.88 ± 0.76 ^c	7.26 ± 0.44 ^{bc}	< LOD	5.71 ± 0.50 ^b
	Shoot	8.51 ± 0.29 ^c	5.64 ± 2.91 ^{ab}	< LOD	6.20 ± 0.48 ^{bc}

LOD: Below detection range or zero. Values are means ± SE, n = 9. Rows with the same letter do not differ significantly (p ≤ 0.05).

Chapter 5

General discussion

5.1. General discussion

Nutrient availability and soil acidity are two of the major factors that influence plant establishment, growth, and functions in grassland and savanna ecosystems (Ledgard and Steele, 1992; Sarmiento *et al.*, 2006). Potassium (K) is the only macronutrient that is infrequently reported as limited in these ecosystems (Han and Lee, 2005). However, nitrogen (N) and phosphorus (P) limitations are frequently reported as limited and this adversely affects ecosystem vegetation structures, crop production, quality and overall nutrition (Lima *et al.*, 2000; Augusto *et al.*, 2013). The identification of leguminous plants and associated microbes as means to mitigate low soil N availability in soils has resulted in more research aimed at understanding the ecology and biochemistry used by these plants in nutrient-deficient ecosystems. However, nutrient deficiency (especially P) retards nodulation, biological N fixation (BNF), nutrient assimilation and metabolism and overall plant growth in legume plants (Plénet *et al.*, 2000). Also, P deficiency negatively affects photosynthesis and ATP production leading to decreased plant growth (Uchida, 2000). Therefore, it is pertinent that more research is conducted on remediation procedures to improve and sustain nutrient fertility and plant establishment in these ecosystems by elucidating the role and importance of soil microflora and associated extracellular enzymes in soil nutrient cycling.

Chapter 3 investigated the potential of soil-borne microbes and extracellular enzymes in soil nutrient cycling in KZN grassland and savanna ecosystem soils to suit the establishment and growth of forage leguminous plants such as *Pisum sativum* (L.). Soil microflora plays a crucial role in terrestrial nutrient cycling through complex mechanisms like organic acid production and extracellular enzymes to solubilize sequestered soil nutrients (Schloter *et al.*, 2003). In grassland and savanna nutrient-deficient ecosystem soils analyzed in the current study, we identified the presence of *Bacillus* and *Lysinibacillus* species. These bacterial species have been reported to solubilize cation-bound P, increasing soil available P for plant uptake in nutrient-poor soils (Lacava and Azevedo, 2013). Additionally, some *Bacillus* members are able to solubilize insoluble K and also fix atmospheric N (Raj, 2010; Ahmad *et al.*, 2016). Potassium-solubilizing bacteria (KSB) are important when it comes to soil fertility because of their multifaceted mechanisms that promote plant growth. These mechanisms include (but not limited to) hormone production, root colonization, micronutrient solubilization, antibiotic production, chitinase and catalase activity

(Ahmad *et al.*, 2016). Apart from *Bacillus*, other nutrient solubilizing bacteria include *Paenibacillus*, *Burkholderia*, and *Pseudomonas* (Sheng and Huang, 2002; Uroz *et al.*, 2007; Sangeeth *et al.*, 2017). However, the efficiency and method for nutrient solubilization vary between species (Ahmad *et al.*, 2016).

In addition to beneficial growth-promoting and nutrient solubilizing bacteria, fungi may also facilitate plant growth more efficiently than bacteria since they transverse better and can form complex networks in soil (Sharma *et al.*, 2013). This is evident in the findings of this study as different fungal species were identified and quantified in experimental soils. Hluhluwe soils had low P concentration but showed the highest fungal species richness and this was associated with high phosphate solubilizing enzyme activities. Therefore, these nutrient solubilizing microbes and atmospheric N reducing bacteria may play an important role in KwaZulu-Natal (KZN) grassland and savanna nutrient-poor soil cycling. These soil-borne microbes (rhizobacteria and fungi) may also regulate the release of enzymes into the soils to cycling and mineralize soil nutrients. There are numerous soil microorganisms that contribute to the turnover of organic matter into plant-available nutrients (Richardson, 2001). Organic matter is the major source of soil organic P which usually exists as high molecular weight (MW) compounds that are typically resistant to chemical hydrolysis (Rodríguez and Fraga, 1999). This means the organic P compounds must be bio-converted into ionic phosphate or low MW organic P compounds by microbial phosphatases and/or phytases (Peix *et al.*, 2001). This leads to increased P availability since the immobilized P undergoes a mineralization process, hence becoming readily available for plant absorption (Richardson and Simpson, 2011). Low soil P concentrations in KZN grassland and savanna ecosystems resulted in increased β -Phosphatase enzyme activities. Also increased activities of carbon (C) cycling, organic matter and lignin-degrading enzymes in these ecosystem soils were observed. Therefore, grassland and savanna ecosystem soil may support the establishment and growth of plants that define these ecosystems and forage legumes in sustainable agriculture practices. Given that these nutrient-poor and acidic ecosystem soils have varying diversity of microbes and soil enzyme activities that can solubilize and recycle nutrients.

In chapter 4 we investigated this assumption and the effects of KZN soils on the growth of *P. sativum* L. The results showed that *P. sativum* L. was adaptable to KZN grassland and savanna ecosystem soils by associating with beneficial soil microorganisms. *P. sativum* L. was able to

utilize both soil and atmospheric N, even in the absence of visible nodulation. The absence of nodulation can be attributed to the lack of a suitable *Rhizobial* strain or competition between the soil microbes since some can produce antimicrobial compounds (Wolpert and Albersheim, 1976; Vlassak *et al.*, 1997). *Paenibacillus polymyxa* is one of the microbes that protect the plant host from pathogenic fungi and bacteria through antibiotic production (Storm *et al.*, 1977; Jeong *et al.*, 2019). However, some microbes could be complementary to one another and enhance their action (Jeong *et al.*, 2019). For instance, a mycotoxin released by *Penicillium citrinum* induces swarming motility in *P. polymyxa* (Park *et al.*, 2008). We assume that *P. sativum* L. was nodulated by *Cupriavidus* while the other bacteria like *Paenibacillus* and *Bacillus* acted as plant growth-promoting bacteria (Martínez-Hidalgo and Hirsch, 2017). The basis of this notion is that *Cupriavidus* is from the family *Burkholderiaceae* which has multiple members that induce nodulation in leguminous plants (Coenye, 2014). While *Paenibacillus* and *Bacillus* are unable to induce nodulation in species that they were previously identified as inhabitants of their root nodules (Velázquez *et al.*, 2013; Lai *et al.*, 2015). Furthermore, the plants were able to upregulate the production of antioxidants and storage molecules while downregulating growth-promoting compounds during stress conditions. In essence, this study has highlighted the beneficial role of soil microflora on plant growth and the synergy involved in plant physiology.

5.2. Future work

As more insights are gained on plant-microbe interactions, there is reason to believe that the knowledge, if applied appropriately, could contribute to sustainable agricultural and soil management systems. The present study delineates the role of soil microflora and extracellular enzymes in terrestrial nutrient cycling, mineralization, and their possible applications in nutrient-deficient grassland and savanna ecosystems. The persistence of forage pea employing the above-mentioned strategies in these nutrient stressed ecosystems suggests its potential use in improving soil fertility in nutrient stressed ecosystems and in sustainable agricultural practices. The simplicity, execution, and results obtained from this study can be translated into environmentally friendly low-input farming. However, more research is required to minimize the ambiguity, and the findings relayed to farmers in a more accessible format. The first step would be the inoculation of *P. sativum* L. with single bacterial strains of the isolated strains using selective media and exposing them to soil nutrient stress under glasshouse and/or field conditions. The plants could

then be subjected to transcriptomic and proteomic profile studies. This knowledge would provide insight into the efficiency of single bacterial strains in solubilizing limited soil nutrients and N₂ fixation. Additionally, the transcripts and proteins regulated enabling forage pea to cope in soil nutrient-poor ecosystems. These results will draw the full picture of how *P. sativum* L. is able to cope under nutrient-poor ecosystem soils.

5.3. References

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APPENDIX A

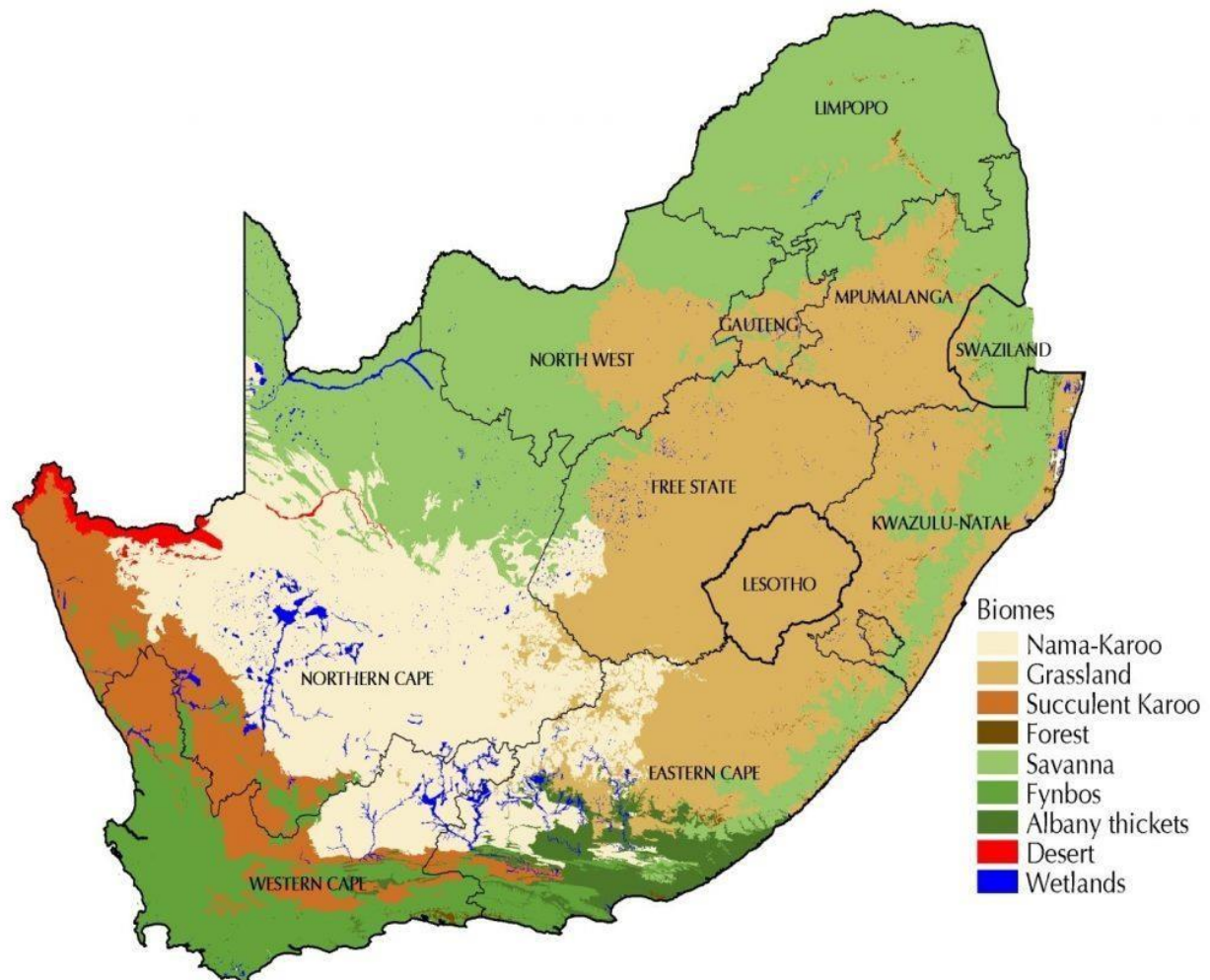


Figure S2: Biomes of South Africa. Retrieved from <https://rangerdiaries.com/diary/south-africas-biodiversity-guides-perspective/>