

**THE EFFECTS OF SOIL MICROBIAL DIVERSITY ON PLANT PRODUCTIVITY IN
THE GRASSLAND BIOME OF SOUTH AFRICA**

by

Pfarelo Netangula (Student no: 62065130)

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Supervisor: Dr LT Mankga

Co-Supervisor: Dr L Khomo

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DEDICATION

I dedicate this dissertation to my Parents, Mr. Netangula M.S and Mrs. Netangula M.L who encouraged me to not give up when I wanted to give up.

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ABSTRACT

Grazers occupies more than 40 to 50% of earth terrestrial surface and alters soil function, soil microbes' composition, quantity and quality resources that are produced by plants. The Grassland Biome in South Africa is an important ecosystem for rangeland production. If grazing occurs continuously altering soil function, the soil role will deteriorate, and soil may lose all valuable soil microorganisms and reduce plant productivity. The soil microbes play a significant role in regulating plant productivity as they enhance nutrient uptake, decompose soil organic matter, improve soil fertility, and protect plants from soil pathogens. We selected three Nature Reserves: Abe Bailey (ANR), Suikerbosrand (SNR) and, Roodeplaat Dam (RNR) in Gauteng Province and evaluated the effects of soil microbial diversity on plant productivity in the grassland biome. Shannon- Weiner index was used to determine the plant diversity and Jaccard dissimilarity index was used to determine species composition across all three reserves. Shannon diversity index and Jaccard dissimilarity index showed a constant form in how grazing impacts plant diversity and community structure across all three reserves. Shannon-Weiner index was highest at SNR, followed by ANR, and lowest in RNR. High H' in SNR shows that it has the greatest plant diversity than ANR and RNR. The Jaccard dissimilarity index showed that the species composition varies sturdily across all three reserves. SNR had the most unique species composition. However, ANR and RNR results showed that they share same species composition, though slightly different. QIIME2 was used to evaluate the effects of soil microbes on plant productivity. QIIME2 converts raw data to statistical results. The soil microbes between grazed and ungrazed sample plots were also identified and analyzed using QIIME 2. Results showed that indeed soil microbes play a vital role in promoting plant productivity. Actinobacteria were the most dominant phyla of bacteria in ANR and Acididobacteriota was dominant in SNR. The pre-dominant bacteria in RNR was Pseudomonadota and there was no differences in the bacteria composition between grazed and ungrazed plots. The dominant fungi was Ascomycota in all three reserves and there was no differences in fungal composition between grazed and ungrazed plots. Furthermore, plant productivity in the grazed and ungrazed plots varied throughout summer, winter and spring across ANR,SNR and RNR. In ANR and RNR, there was no statistical differences between the grazed and ungrazed conditions throughout all late spring (October 2021), summer (2021) and winter (July 2022). In

SNR, there was no statistical significance between the grazed and ungrazed conditions in late spring (October 2021) and summer (December 2021). However, there was a statistical significance between the grazed and ungrazed conditions in winter (July 2022). The winter rainfall and grazing played a role in regulating plant productivity. The Poaceae and Astraceae were the most dominant families across all three Nature Reserves. Further research on the effects of soil microbes should be done to understand why soil microbes in ungrazed and grazed plant productivity are the same during late spring (October 2021), summer (December 2021), and winter (July 2022). Also, to determine why there is no differences in bacterial and fungal composition between grazed and ungrazed plots during late spring (October 2021), summer (December 2021), and winter (July 2022). Why plant productivity is low in ungrazed plots when the rainfall is high and why plant productivity is high when the rainfall is low is a question that can be researched.

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ACRONYMS AND ABBREVIATIONS

A- Grazed plot

AMF- Arbuscular mycorrhizal fungi

ANOVA- Analysis of Variance

ANR- Abe Bailey Nature Reserve

Apr- Adenyly sulfate reductase

APR- April

AUG- August

B- Ungrazed plot

Cm – Centimetres

CSC- Acicular Consensus Sequences

DEC- December

df- Degree of freedom

DNA- Deoxyribonucleic acid

Dsr- Dissimilatory sulfite reductase

EMF- Ectomycorrhizal fungi

ERM- Ericoid mycorrhizal fungi

F- F- statistic

F-Critical- Threshold (a specific value from F- distribution)

FEB- February

ha- Hectares

IAA- Indole-3-acetic acid

ITS- Nuclear ribosomal internal transcribed spacer

JAN- January

JUL- July

JUN- June

Km- Kilometres

LAU- Large animal units

L_{SLA} – Large specific leaf area

m- Meters

MAR – March

mm- Millimetres

MWP- Modified-Whittaker plot

NGS- Next Generation Sequencing

NOV- November

OCT- October

PCA- principal Component Analysis

PCR- Polymerase Chain

pH – Potential of hydrogen

P-value- Probability Value

QC 16S- 16S ribosomal RNA Quality Control

QC fugal ITS- Quality Control fungal (Internal Transcribed Spacer)

QIIME- Quantitative Insights into Microbial Ecology

RNR- Roodeplaat Dam Nature Reserve

rRNA- Ribosomal ribonucleic acid

Sat- Sulfate adenylyltransferase

SAWS- South African Weather Services

SEP- September

Se- standard error

SNR- Suikerbosrand Nature Reserve

SOM- Soil organic matter

SS- Sum of Squares

t ha⁻¹ – tonnes per hectare

CHAPTER 1: INTRODUCTION

1. 1 Background of the study

Approximately 40% of earth's terrestrial surface is occupied by grazing lands (Reynolds, 2005). The Grassland Biome in South Africa is a crucial area for rangeland production and hosts a wide variety of plant species (O'Connor and Bredenkamp, 1997). This biome supports important ecosystem services such as crop, settlement, and livestock agriculture (O'Connor and Kuyler, 2009). However, it offers various land use such as agriculture, urban development, mining and industrial activities with 23% of cultivation, 60% permanently changed and only 2% is protected and the remaining part is used for livestock grazing (Fairbanks et al., 2000). However, the biome is under a lot of pressure due to increased human population which results in high demand for meat products, housing, climate change- induced drought, water and soil pollution caused by industrial activities, and natural fire regimes that can cause loss of grassland ecosystems to a woody vegetation. Biodiversity is threatened by human population demands which have serious implications on the environment (Reyers and Tosh, 2003).

Grasslands in South Africa can be classified into sweetveld and sourveld, based on moisture availability and palatability to livestock (Low and Rebelo, 1996). Sweetveld refers to dry grasslands that occur at lower altitudes and remain palatable and nutritious throughout the year (Tainton, 1999). Sourveld denotes moist grasslands generally found at higher altitudes, which are palatable only in spring and summer (Tainton, 1999; Mucina et al., 2006). Sweetveld grasses have lower fibre content while those in sourveld have higher fibre content (Low and Rebelo, 1996).

Usually, the Grassland Biome contributes to the production of meat and fiber in South Africa as it supports high densities of grazing animals. It is important for the production of maize crop and wheat, while sorghum and sunflowers are farmed on a small scale in the biome. However, the Grassland Biome in South Africa is at risk, as it faces significant threats such as habitat loss and degradation caused by mining, overgrazing, agricultural expansion, introduction of invasive species, and urban

development and has minimal protection measures in place (Rouget et al., 2004; Neke and Du Plessis, 2004).

Grasslands that are well managed by frost, fire and grazing which prevent the establishment of trees (Low and Rebelo, 1996). But that depends on the activity of grazing animals (Delgado-Baquerizo et al., 2016). Overgrazing and poor management of livestock farms have led to the degradation of grassland (Milton et al., 1994, with intense grazing often occurring near water points (Moreno et al., 2014). The severe degradation around water points is caused by a large number of livestock that frequently return to drink. Their intense grazing, waste production, and trampling of vegetation contribute significantly to this deterioration (Andrew, 1998)

Large grazing animals can enhance grassland plant diversity through various mechanisms (Olf and Ritchie, 1998). However, their trampling may also compact the soil, reducing its water retention capacity and limiting oxygen availability to plant roots (Steffens et al., 2008). Nutrient cycling is influenced by herbivores indirectly by fluctuations of plant species structure, richness and the way plants are organized and how their different parts work together to perform essential functions, however grazing effects on nutrient cycling depend on primary productivity (Peco et al., 2007).

Herbivores can directly increase plant diversity by consuming the dominant plant species and indirectly through effects on plant competition. The herbivores control plant diversity through mechanisms that influence local plant colonization and extinction dynamics (Olf and Ritchie, 1998). Grazing can change how soil functions by affecting the types and variety of microbes found in it (Eldridge et al., 2017), though the effects are indirect and may depend on the type of microorganism present (Epelde et al., 2017). There are two strategies that plants deal with grazing which are tolerance and avoidance. Grazing-tolerant plants use plant functional traits such as large specific area (L_{SLA}) to allow the rapid regrowth after defoliation. However, grazing-avoidant plants limit their palatability with plant functional traits such as tough leaves with small specific leaf area (S_{SLA}) and short stature (Peco et al., 2017).

Furthermore, grazing can influence soil organisms in indirect ways by altering the amount and types of resources that plants generate (Van der Heijden et al., 2008). Additionally, herbivores encourage plants to grow back stronger, which puts organic

matter back into the soil and helps support the growth of microbes (Wardle et al., 2004).

Microbial diversity refers to the genetic variety. Genetic variety includes a range of microorganisms which includes bacteria, fungi, archaea, protists and viruses that are present in a certain habitat. They are distinguished based on their characteristics of cellular metabolism, geomorphology, functioning, genomic structure and appearance (Dunlap, 2001). They can also be and there are different procedures which may be used to regulate microbial diversity such as direct counts, traditional plates, new molecular-based techniques and fatty acids analysis (Nannipieri et al, 2003). Soil microbes make up a large portion of the genetic diversity on earth (Whitman et al., 1998) and play a vital role in ecosystem processes (Sprent, 2001). They influence processes such as nitrogen cycling (Tiedje, 1988), carbon cycling (Hogberget et al., 2001), and formation of soil (Rilling and Mummery, 2006). Soil microbes maintain many ecosystem functions, like the process of primary production and soil nutrient supply (Jing et al., 2015). The microbes also support ecosystem processes including litter decomposition and organic matter mineralization, which transfer matter and energy among above and below-ground communities (Delgado-Baquerizo et al., 2016). In addition, arbuscular mycorrhizal fungi aid grassland plants to become tolerant to grazing (Epelde et al., 2017). Various types of soil microbes regulate plant productivity in various ways, these include bacteria, fungi, protozoa, and pathogens. These soil microbes form a symbiotic relationship with plants. Microbial diversity is affected by variations in environmental factors like carbon levels, soil pH, types of vegetation (Delgado-Baquerizo et al., 2016).

Plant diversity enhances the variety of soil microbes by providing a range of resources, creating different physical environments, and offering various conditions. Additionally, diverse plants serve as hosts for both beneficial and harmful microbes (Hooper et al., 2000). Soil is essential and inimitable, it regulates the plant productivity of the terrestrial ecosystems and maintains the biogeochemical cycles (Nannipieri et al., 2003). In the soil, approximately 80-90% of the processes are driven by reactions that microbes help facilitate (Iqbal et al., 2025). In temperate grassland soils, the amount of microbial biomass is quite significant. Specifically, the biomass of bacteria ranges from 1 to 2 tons per hectare, while fungal biomass is higher, ranging from 2 to 5 tons per hectare (Zhao et al., 2024).

1.2 Aim and Objectives

1.2.1 Aim of the study

To evaluate the effects of soil microbial diversity on plant productivity in the Grassland Biome of South Africa

1.2.2 Objectives of the study

- ❖ To determine the relationship between soil microbes and plant productivity
- ❖ To assess the effects of grazing on soil microbial diversity
- ❖ To investigate how plant productivity is influenced by plant functional traits
- ❖ To analyse the link between plant functional traits and grazing

1.3 Problem statement

Soil microbes are crucial to how terrestrial ecosystems work and they are the key factors influencing both plant diversity and productivity (Van der Heijden et al., 2008). However, the impact of soil microorganisms on productivity in the grassland ecosystems are poorly understood. Furthermore, grazing affects the functioning of soil because studies have shown that grazing has been found to change the way soil functions by affecting the variety and makeup of soil microorganisms (Eldridge et al., 2017). Though the effects are indirect and may depend on the type of microorganism's present (Epelde et al., 2017). If grazing occurs continuously altering soil function, the soil function will deteriorate, and soil may lose all valuable soil microorganisms and reduce plant productivity. It's challenging to gauge how much microbial pathogens affect plant productivity in natural ecosystems. This is because when one plant species loses biomass due to pathogens, other species in the community, especially in diverse groups, often grow more to make up for that loss (Van der Heijden et al., 2008).

Many studies have explored how different types of soil microbes interact with one another and plant productivity. Over the years many studies such as Chapin (1980); Grime et al (1987); Kuzyakov et al (2000); Read and Perez-Moreno (2003); van der Heijden et al (2008); Wang et al (2025); Wang et al (2024); Romero et al (2023) have been conducted on soil microbial communities and plant productivity. However, there have been limited studies conducted on how soil microbial diversity impact plant productivity in Grassland biome of South Africa.

Several studies indicate that there is a beneficial connection between the diversity of soil microbes and the plant productivity of plants (Wardle, 2006; Van der Heijden et al., 2008; Nkuekam et al., 2018). van der Heijden et al., (2008) have shown the positive effects of plant productivity and negative effects of soil microbial diversity on plant productivity. The positive effects shown by van der Heijden showed that microbes indirectly influences productivity through the free living microbes that changes the rate of nutrient supply and resource division as well as directly influencing plant productivity by forming symbiotic relationships which can stimulates plant productivity by supplying limiting nutrients to plants. However, the direct negative effects involved reducing plant productivity and the indirect effects included competition between microbes and plants for nutrients available in the soil affecting the plant nutrient availability and growth. Plants and microbes are dependent on each other. Therefore, soil microbes provide plants with nutrients by breaking down organic matter and on the other hand, plants provide soil microbes with carbon substrate through litter and root exudates, thus all enhancing plant productivity (Nkuekam et al., 2018; Hossain and Shu-ichi, 2019).

Regardless of these studies that have been previously conducted on soil microbial diversity and plant productivity, there isn't enough solid evidence to support the idea that the diversity of soil microbes directly impacts plant productivity in the Grassland biome of South Africa and their fundamental relationship remain elusive. Furthermore, to better or clearly understand the impacts of soil microbial diversity on plant productivity and plant diversity, several questions still need to be answered. Hence, this study is aimed at investigating the effects of soil microbial diversity on plant productivity in Grassland Biome of South Africa.

1.4 Justification of the study

Soil microbes are well-known for their important roles in the cycling of nutrients and elements within ecosystems, however, the fundamental relationships between plant productivity are still poorly understood (Van der Heijden et al., 2008). So far, only few studies have examined such relationships and although theory predicts predominantly positive associations, research has shown variable relationships. In grasslands, it has been shown that plant productivity is impacted by grazing (Dingaen et al., 2016) and there are suggestions that grazing can potentially alter soil function by altering soil function and microbial community composition. However, there is limited understanding of how microbial communities react to grazing and what specific functions may change when environments experience overgrazing (Eldridge et al., 2017). What is clear is that grassland microbial communities are tightly linked to plant community dynamics and therefore, there is a need to research their role further to improve our current understanding of grassland systems. This study will contribute the body of knowledge that already exist about the grassland systems.

1.5 Structure of the dissertation.

This dissertation has been divided into six chapters as follows:

Chapter 1- Background/introduction and overview to the study. The chapter outlines the purpose of the study, aim and objectives, problem statement and justification of the study.

Chapter 2- Provides an overview of the existing literature how the variety of microorganisms in the soil impacts plant growth and health in grassland ecosystems. The scholarly articles relevant to this topic have been provided.

Chapter 3- Outlines the description of the study sites namely Abe Bailey Nature reserve, Suikerbosrand Nature reserve, and Roodeplaat Dam Nature reserve. It provides the study areas geographic location, topography, vegetation, and climate. It also provides the methodology and data processing.

Chapter 4- Outlines the results of all the fieldwork and laboratory work done in the form of figures, tables, and graphs.

Chapter 5- Details the analyses and discussion of the results from the fieldwork and laboratory work.

Chapter 6- Provides conclusion on the results obtained and results discussion as well as recommendations.

Chapter 7- Provides references.

CHAPTER 2: LITERATURE REVIEW

2.1 Soil microbes and plant productivity

Soil microbes play an important role in the functioning of terrestrial ecosystems and are considered important drivers of plant productivity (Van der Heijden et al., 2008). According to Van der Heijden et al., (2008), about 20.000 plant species rely on soil microbes for their growth and survival. Symbiotic soil microbes are important regulators of plant community dynamics because they supply different limiting resources and enhance the growth and competitive ability of their host plants (Van der Heijden et al., 2008). Research by Kuzyakov et al., (2000), has shown that the tiny organisms in the soil that live near plant roots use substances released by the plants, known as rhizodeposits, as a source of carbon. This process helps these microbes break down soil organic matter (SOM) to obtain nitrogen, which can then be absorbed by the plants (Kuzyakov et al., 2000). In general, the beneficial effects of soil microbes on plant community dynamics increase with higher diversity of microbes (Johnson et al., 2003).

Soil microbes affect plant productivity through mechanisms that may be classified as direct effects and indirect effects on plants. A direct effect is a mechanism whereby organisms that live in association with plant roots can either establish beneficial relationships or cause diseases in the plants. An indirect effect is a mechanism whereby free-living microbes can alter the speed at which nutrients are supplied and how resources are distributed (Van der Heijden et al., 2008). Some of the important regulators of plant productivity are nitrogen-fixing bacteria because nitrogen is one of the main elements that limits plant productivity, the other element is phosphorus (Chapin, 1980). Plants are unable to fix atmospheric nitrogen but are assisted by nitrogen-fixing bacteria, which transform nitrogen gas into a form (ammonium) that can be utilised by plants (Van der Heijden et al., 2008). On the other hand, plant productivity can also be directly reduced by microbes and this reduction has huge effects on the ecosystem processes. The negative impacts are mostly associated with soil microbial pathogens (Van der Heijden et al., 2008). Soil microbes may further indirectly reduce plant growth by directly competing with plants for nutrients, especially

in nutrient limited soils. Plant productivity is reduced when the microbial pathogens attack the plants (Van der Heijden et al., 2008).

Soil microbes and plants form a close symbiotic associations and plant productivity can be stimulated by supply of limiting nutrients to plants (Van der Heijden et al., 2008). Some of the soil microbes include the mycorrhizal fungi, and nitrogen-fixing bacteria contribute to approximately 5-20% of the total nitrogen and 75% of phosphorus that plants obtain annually in grasslands and savannahs (Van der Heijden et al., 2008). Mycorrhizal fungi enhance the nutrient availability by supplying plants with nutrients that the roots can't reach. The key types of fungi include arbuscular mycorrhizal (AM), ecto-mycorrhizal fungi (EM) and ericoid mycorrhizal fungi (ERM) (Van der Heijden et al., 2008). AM fungi are rich in grassland and associates with shrubs, herbs, tropical trees, and grasses (Read and Perez-Moreno, 2003).

According to Grime et al. (1987), AM fungi change how nutrients are shared among different grassland species that grow together, but they don't impact the overall productivity of the plants. AM fungi increase plant productivity by enhancing phosphorus uptake mechanism (Jakobsen et al., 1992). Also, the AM fungi play various roles in ecosystems through nitrogen-fixing bacterial and fungal decomposers, and the lack of a particular group can significantly impact how productive plants are (Van der Heijden et al., 2008).

2.2 Plant productivity and functional diversity

Functional diversity can be defined as the extent to which species differ in their functional traits in a community (Tilman, 2001; Petchey and Gaston, 2002) and has commonly been measured as the number of functional groups in a community (Petchey and Gaston, 2002). Functional groups on the other hand have been defined by Tilman, (2001) as species that have similar traits, which are likely to affect ecosystem functioning in a comparable manner. Functional diversity is very important in ecology because it enhances the diversity component, ecosystems dynamics, stability, nutrient balance, productivity, and other ecosystem functioning's (Tilman, 2001). Plant productivity is one of the main ecosystem processes that are affected by functional diversity. Plant diversity loss reduces the soil microbial diversity mainly because of the decreased diversity of carbon/energy resources. The plant productivity

and community structure are reduced by the plant diversity loss. The amount of carbon/energy resources provided to soil microbial communities can be determined by plant productivity (Hutchinson, 1959).

The below-ground microbial diversity is reduced by the loss of the above-ground plant diversity (Zhang et al., 2017). In pastures, the increased plant diversity led to greater primary productivity (Tilman, 2001). The interpretation of functional diversity of vegetation is vital in separating the correlation among the ecosystem processes and community composition (Lavorel et al., 2008). Functional diversity exact estimation depends on the ecologically significant traits of choice. The number and type of traits is important when measuring functional diversity (Laureto et al., 2015). Microbial diversity is negatively associated with nutrient availability in nutrient poor ecosystems. Microbial diversity has a huge effect on ecosystems in the nutrient poor ecosystem and the impact of different types of microorganisms on how well plants grow may increase depending on the functional group (Van der Heijden et al., 2008).

A study conducted by Helgason et al., (1998), has shown that the variety of microorganisms in soil ecosystems decreases due to more intensive land use and higher levels of nutrients. In ecosystems with abundant nutrients, microbial communities tend to have more overlapping functions compared to those in ecosystems with fewer nutrients (Van der Heijden et al., 2008). The microbes need certain adaptations to collect resources in poor nutrient ecosystems (Van der Heijden et al., 2008). There is an enormous impact on plant productivity when adding various functional groups (Hooper et al., 2002). According to Tilman et al., (1997), the effects of species or functional diversity are expected to increase with the magnitude of the differences among species or functional groups, and functional diversity significantly influences plant productivity.

2.3 Grazing and functional traits

Petchey and Gaston, (2006) defined functional traits as the organismal characteristics that influence fitness and functioning of ecosystems. Some studies indicated that 30% to 40% of all the land on Earth is covered by grassland and it offers millions of individuals access to fuel, fertilizer, meat, milk, transportation, and security (Reynolds, 2005, Wirsenius et al., 2010). Grazing is a significant regulator of ecosystem

transformation, however inappropriate grazing causes extensive transformation in soil and vegetation (Schlesinger and Pilamanis, 1998). Schlesinger and Pilamanis (1998)'s study showed that the reduction in perennial grass is caused by grazing, and these reductions could result in the replacement of smaller plants with larger shrubs, causing the distribution of soil nutrients to shift from a random pattern to one that corresponds more closely with the size of shrubs, and this may have impact on plant productivity. Grazing has various impacts on functional traits, community structure and the functioning of grasslands (Cingolani et al., 2005, Zheng et al., 2015). The characteristics of plants that influence their ability to engage with beneficial symbiotic partners are crucial for increasing carbon input into the soil. This is because these partnerships can boost plant growth by helping them obtain essential resources that might be in short supply (De Deyn, 2008).

Grazing of sheep and cattle are the most extensive regional land use on native pastures (Landsberg et al., 1999). Plants are damaged through herbivory and trampling as direct impacts, while indirect impacts include changes in species composition and soil (McIntyre et al., 1999). There are changes in soil and other environmental conditions as indirect impacts of grazing and these affect plant competition and resource availability (Landsberg et al., 1999; McIntyre et al., 1999). Under heavy grazing pressure, the forage value of rangeland ecosystems is reduced because of the decrease of some species and their replacement by non-palatable species (Milton et al., 1994; Augustine and McNaughton, 1998; Cingolani et al., 2005). This negative effect of herbivores however cannot be generalized because in some rangelands wild and domestic herbivore grazing increases palatable species (Cingolani et al., 2005). The response of plants to grazing can be classified as either avoidance or tolerance and there are specific functional traits that are associated with each response strategy. Defense traits against herbivory include leaf toughness, presence of secondary compounds and thorns/prickles, and sclerophyllous leaves that have high amount of carbon-based structural and chemical defense' (McIntyre et al., 1999). Species that are tolerant to grazing have certain functional traits which are associated with high capability to capture nutrients and other resources, and consequently high growth rates (Cingolani et al., 2005). These plants are characterised by traits such as high specific leaf area (SLA) and low leaf toughness (Cingolani et al, 2005), and are short (Diaz et al., 2001).

It has been suggested that how sensitive plant communities are to grazing is influenced by how often and how effectively plants develop adaptations to either escape from or withstand being eaten by herbivores (McIntyre et al., 1999; Diaz et al., 2001). Based on their hypothesis, the impact of grazing will be reduced in the systems where these characteristics are uncommon or not well-formed (Adler et al., 2004). The drought-deciduous leaves, small stature and basal meristems have proven to be beneficial for preventing or recovering from being eaten by herbivores (Coughenour, 1985). Plant height is the most frequently used plant functional trait in assessing the grassland management (Klimesova et al., 2008). Grazing can enhance species that have a high specific leaf area (L_{SLA}), and it may be positively associated to decomposition rate (Ganier et al., 2004), however nutrient availability in the soil may be affected (Peco et al., 2017). Grazing changes the floristic composition of plants communities through different mechanisms (Olf and Ritchie, 1998). Saatkamp et al. (2010) revealed that there is no linear response by functional traits to grazing.

2.4 Plant height

Plant height is a crucial part of plant species in environmental approach (Moles et al., 2009), and it is one of the most crucial factors of plant form and function (Diaz et al., 2016). Plant height is important factor for plants capability to compete for sunlight (Moles et al., 2009). Plant height affects the above-ground competition for sunlight which influence the plant productivity. Tall plants are able to capture more sunlight than short plants which leads to high plant productivity (Ottaviani et al., 2025). The plant height and above-ground biomass/plant productivity are directly linked to each other. According to a study by (Liao et al., 2024), plant height directly regulates plant productivity in response to Nitrogen addition and indirectly controls plant diversity over light competition (DeMalach et al., 2016). More various heights can lead to high plant productivity. Plant height impacts the crucial environmental variables such as carbon sequestration ability (Moles et al., 2009). The changes in the aboveground biomass across functional groups is associated with plant height (Zhang et al., 2025).

CHAPTER 3: RESEARCH DESIGN AND METHODOLOGY

3.1 Study area

The study locations were selected in the Grassland Biome within the Highveld region of Gauteng Province, which is one of the physiographic regions of Southern Africa. Gauteng Province is in the interior plateau of South Africa and Gauteng is the most densely populated and smallest Province in South Africa. In the Highveld region, grasses, thorn trees, and small pockets of forest in the river valleys are usually the predominant vegetation.

The study locations selected were Abe Bailey Nature reserve (26°19'51.56"S, 27°20'54.18"E) in Carletonville, Suikerbosrand Nature reserve (26°29'01.66"S, 28°13'45, 38"E) in Heidelberg and Roodeplaat Dam Nature reserve (25°39'00"S, 28°21'44"E) in Tshwane (Figure 3.1). Figure 3.1 shows all the three reserves study sites. All the sites had comparable landscapes in terms of vegetation, slope, and rockiness. These Nature Reserves are protected and managed by Gauteng Department of Agriculture and Rural Development. The most common animal activity in all three nature reserves was grazing. To confirm grazing, vicinity animals were seen in all the three reserves and animal activity was footpaths, furrows and animals' stools/dung.

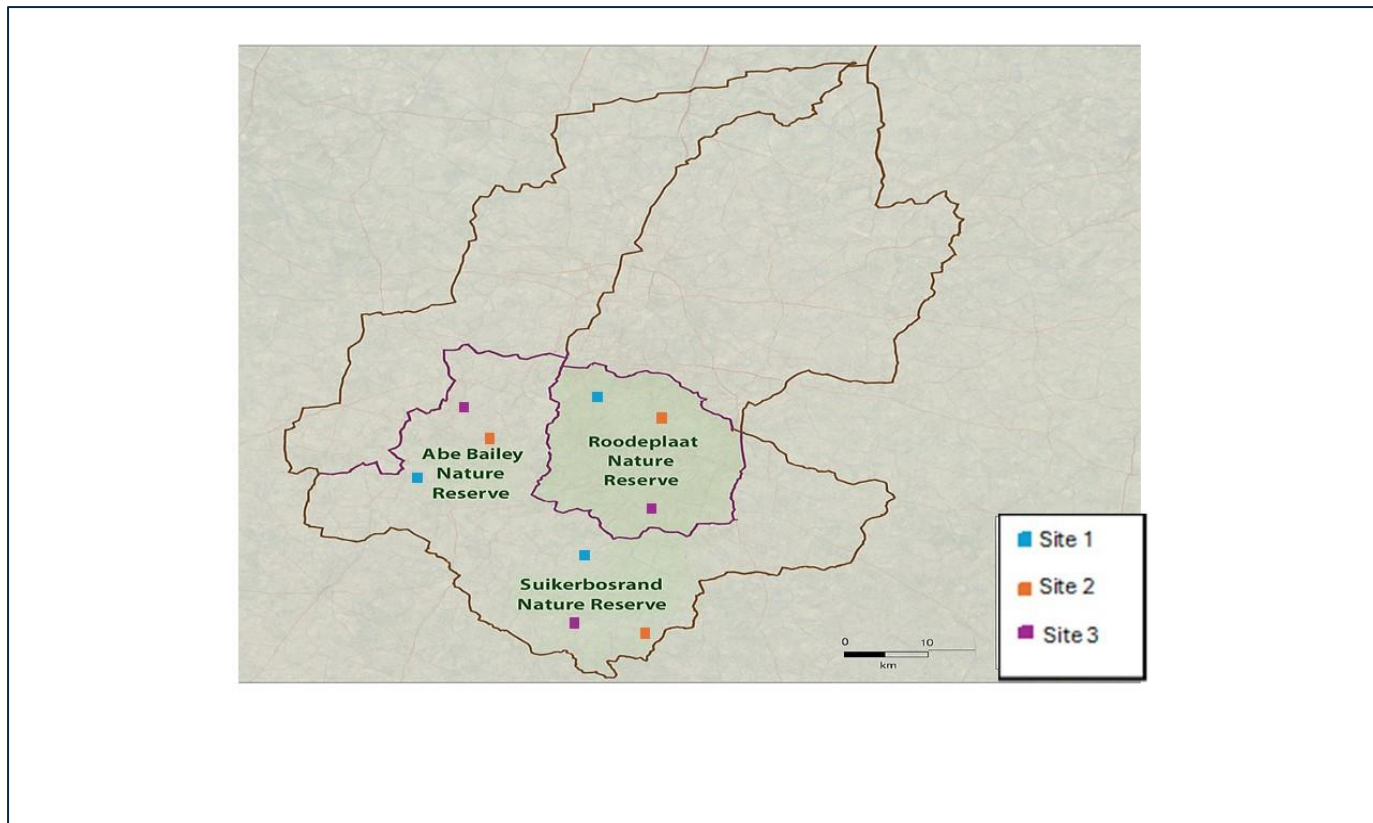


Figure 3.1: Map of Gauteng province showing all three nature reserves and their three study sites in each reserve.

3.1.1 Abe Bailey Nature Reserve study location

Abe Bailey Nature reserve is situated in Carletonville, a small gold mining town and is adjacent to Khutsong township in Merafong local Municipality. It was named after Abe Bailey who was a pioneering mining magnate who lived, farmed, and hunted in the area in the 19th century. It is approximately 4200 hectares. There are approximately 220 species of both wetland and grassland birds. This Nature reserve is a mixture of wetlands, bushveld, and grasslands. The mean annual rainfall is about 655-668 mm (Davis et al., 2005). We prepared our study sites and they are presented below (Figure 3.1.1). Each site is a 50 m x 20 m, with 12 small (1 m x 1 m) sub-sample plots inside each site. The orange plots represent the ungrazed plots, fenced-off (grazing cannot take place) and the plain ones represents the grazed plots (grazing animals can access plants). The number within the plots represents voucher number for each plot.

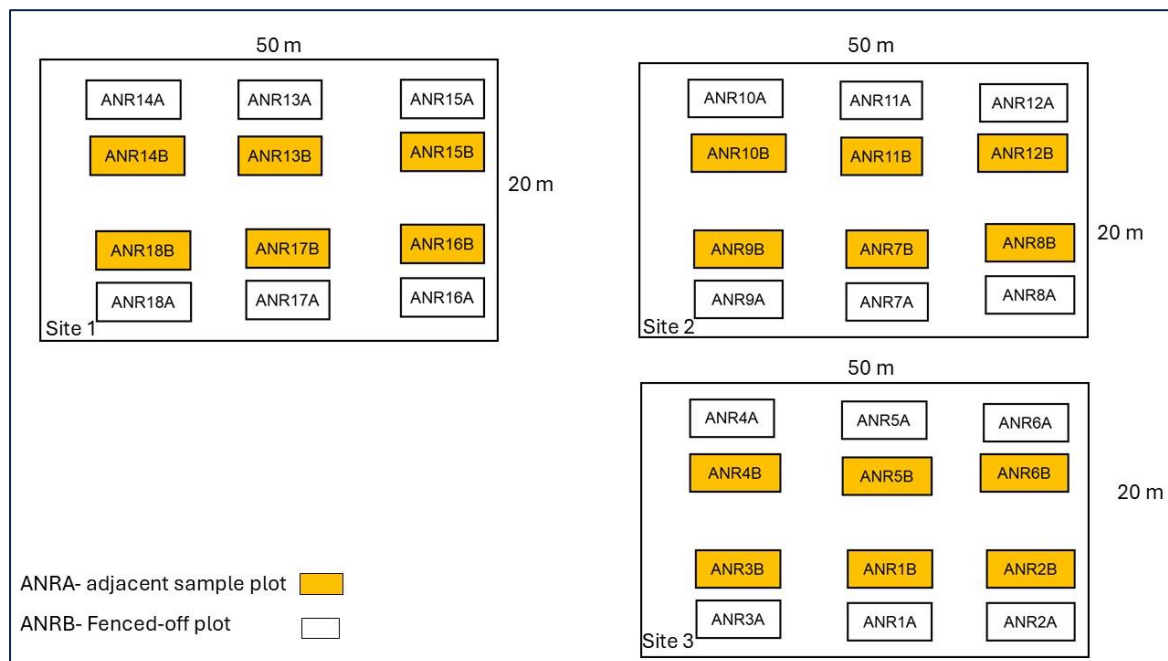


Figure 3.1.1: An indication of study sites (site 1, 2 and 3) within the Abe Bailey Nature Reserve.

Site 1 had animal droppings, trampling's, and paths on the ground. Large grazing animals were seen on the site vicinity. The grazing animals that were seen were cattle, zebra, hartebeest, and black wildebeest. There were some few ant mounds and some bare ground with less vegetation. The dominant grass species was *Erigeron canadensis*. There were ant mounds and few bare grounds with vegetation patches on site 2. There were some powerlines, graves and the site were situated opposite the main road. Animal dung, tracks, paths, trampling, and burrows were seen on the study site vicinity. There were lot of cattle's movement closer to the study site. The site was dominated by *Eragrostis curvula*. Site 3 had animal droppings, trampling, burrows, and animal paths which indicates the presence of grazing animals. Grazing animals that were seen in the site vicinity were zebra, cattle, kudu, springboks, and hartebeest. The dominant grass species was *Eragrostis cillianesis*.

3.1.2 Suikerbosrand Nature Reserve study location

Suikerbosrand Nature reserve is situated close to Heidelberg town in Lesedi local municipality. It is one of the most idyllic game reserves in Gauteng. It was named Suikerbosrand because of the Sugarbush/Transvaal suikerbosrand which is found in abundance in the area. It is approximately 11 595 ha It harbours about 200 various species of birds. Some of the fauna that can be spotted here include steenbok, baboon, zebra, black wildebeest, and kudu. The plants include vast number of grasses species and trees such as *Vachellia karoo*, *Euclea undulata*, *Cussonia paniculata* and *Celtis africana*. The average rainfall is about 706-733 mm annually (Davis et al., 2005). The study sites within the vicinity of Suikerbosrand Nature reserve are presented in Figure 3.1.2 below. Each site is a 50 m x 20 m, with 12 small (1 m x 1 m) sub-sample plots inside each site. The orange plots represent the ungrazed plots (fenced-off) and the plain plots represents grazed plots (grazing animals can access plants). The number within the plots represents voucher numbers.

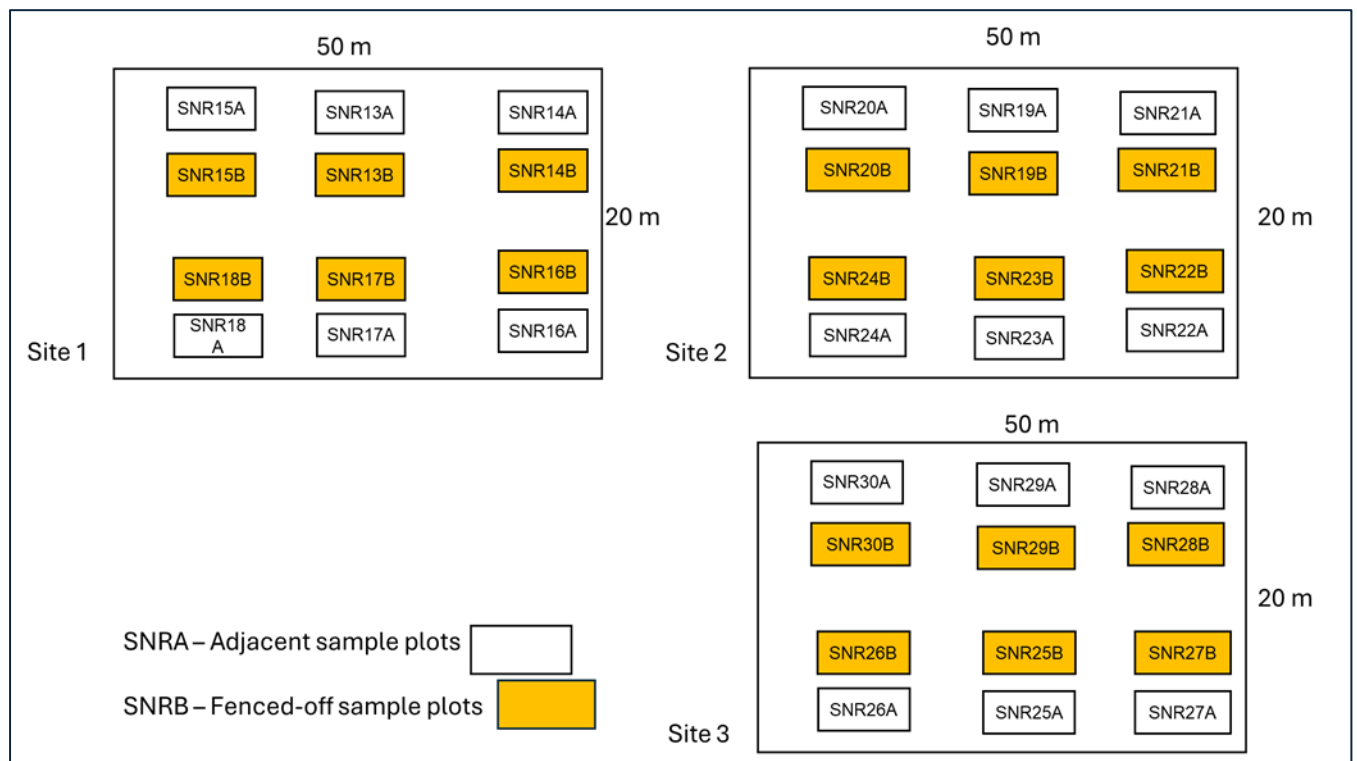


Figure 3.1.2: An indication of study sites (site 1, 2, and 3) within the Suikerbosrand nature reserve.

The Site 1 showed to have recently been burnt and there was lot of bare ground with few vegetation patches, had animal droppings, tracks, trampling and few animal burrows. The site was close to the wetland/ stream where animals drink water. There were some graves close to the study site. There were some grazing animals in the site vicinity such as Zebra, kudu, hartebeest, and zebra. Animals' paths could be clearly seen headed towards the wetland/ streams where they drink water. There were some powerlines on the study site. The site was dominated by the grass *Heteropogon contortus*. Site 2 was closer to a small valley. Animal droppings, burrows, and tracks were present at the site. There were few ants' mounds presence and animal's pathways were also seen. Some of the animals that were seen at the study vicinity were impalas, springboks, zebra, and baboon. The site was dominated by the *Cynodon dactylon*. Animal dung, trampling, tracks, burrows, and paths were present indicating the presence of grazing animals in site 3. There were some very few ants' mounds preset. Grazing animals that were seen on the site vicinity were zebra, impala, and kudu. *Themeda triandra* was the dominant grass species on the site.

3.1.3 Roodeplaat Dam Nature Reserve study location

Roodeplaat Dam Nature reserve is located about 22 km north-east of Pretoria. It is a 200 000-ha reserve. There are more than 250 bird species found in this reserve. Some of the animal species that can be spotted include kudu, zebra, warthogs, impala, and water birds. The mean annual rainfall is about 655-660 mm (Davis et al., 2005). The study sites are presented in Figure 3.1.3 below. Each site is a 50 m x 20 m, with 12 small (1 m x 1 m) sub-sample plots inside each site. The orange plots represent ungrazed plots (grazing cannot take place) they are fenced-off and the plain ones represents the grazed plots (grazing animals can access plants). The numbers within the plots represents voucher numbers.

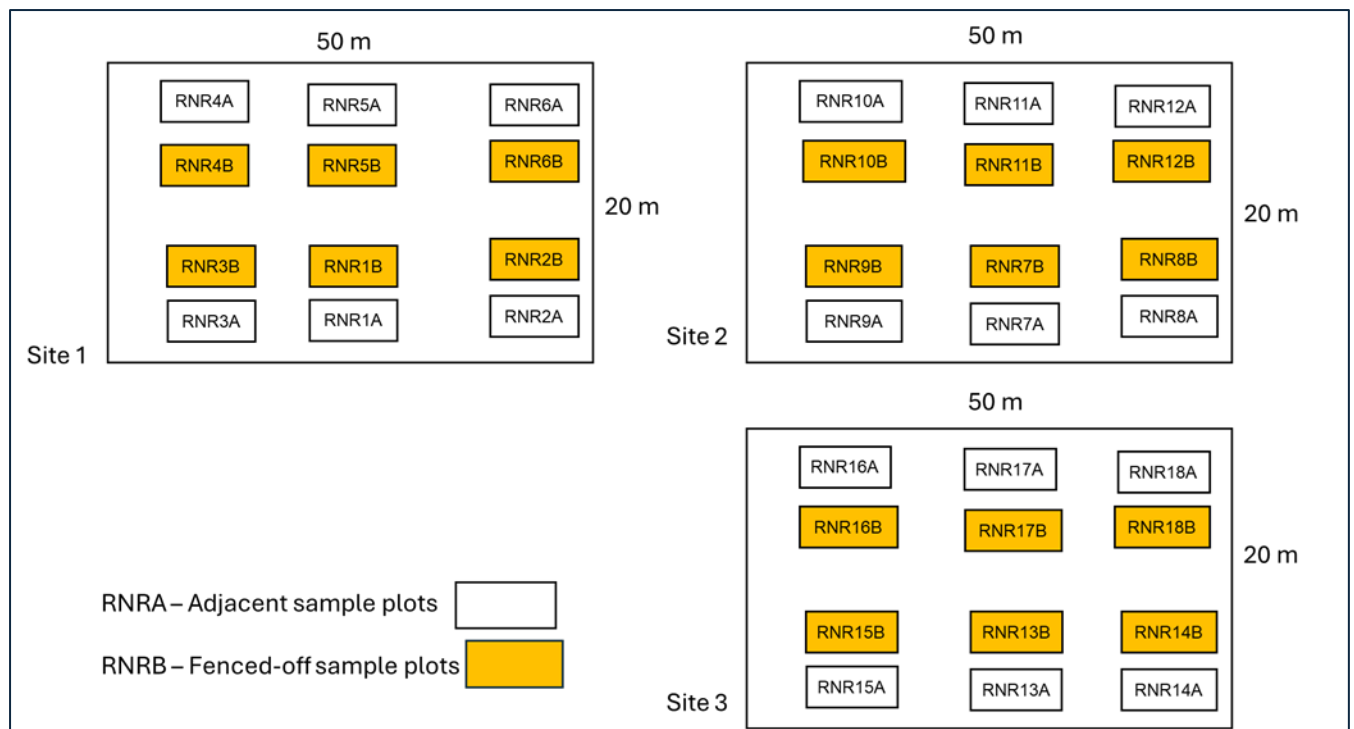


Figure 3.1.3: An indication of study sites (site 1, 2, and 3) within the Roodeplaat Dam Nature reserve.

The Site 1 had animal dung, burrows and tracks that indicated the presence of grazing and other animals. The site had many ant mounds. Various grazing animals that were spotted across the site vicinity were giraffes, zebra, kudu, impala, and springboks. The dominant grass was *Eragrostis curvula*. Animal droppings, track and trampling were present at site 2 indicating the presence of grazing animals, however there were few anima' paths seen due to a lot of loose stones/rocks present within the site vicinity. *Setaria parviflora* was the dominant grass species. Site 3 had very few animal droppings, trampling, tracks, and burrows. There were no animal paths in the site vicinity though few animals were seen across the site vicinity such as giraffe, zebra, and eland. There was lot bare ground with very few vegetation patches. The dominant grass species was visually estimated as *Setaria parviflora*.

3.3 Topography and Vegetation

3.3.1 Abe Bailey Nature reserve

The landscape is primarily flat and consists mainly of Mispash soils alongside dolomite and Glenrosa soils. You can identify quartzite areas, which are different from the more fertile, low-lying regions characterized by Hutton soil (Dzerefos and Witkowski, 2001). There are many small habitats with a mix of very shallow and deep soils located nearby (O'Connor and Bredenkamp, 1997).

The area is characterized by Rocky Highveld Grassland, specifically referred to as Western Bankenveld (Acocks, 1988; Van Rooyen and Bredenkamp, 1996). This type of vegetation acts as a transition between sour veld and Cymbopogon-Themeda veld. It features a variety of plant species that coexist, resulting in high floristic diversity, with no one species dominating the landscape (O'Connor and Bredenkamp, 1997). The average rainfall is 646 mm in Carletonville, and it occurs mainly in summer. The altitude is between 1460 m and 1520 m (Dzerefos and Witkowski, 2001).

3.3.2 Suikerbosrand Nature reserve

The topography of the area is mainly determined by its geology. There are two geological formations in the reserve which are Witwatersrand system in the eastern and Ventersdorp system in the west. (Bredenkamp and Theron, 1976). Of the two geological formations, Witwatersrand is the older formations, and it consist of quartzite sediments which have gone through faulting, severe folding, and extensive erosion (du Toit, 1954), hence it has led to complex, broken topography of the reserve. The quartzite rocks have been worn to coarse Sandy loam soil. There are rocky hills enclosed with small flat area of the grassland and woody vegetation. Grassland can be found at the rocky hill foot, an altitude of about 1525 m to 1600 m and high-altitude plateau of 1700 m to 1750 m (Bredenkamp and Theron, 1976). The Witwatersrand vegetation has lower grazing potential and is in poor condition because of poorer, shallower, and sandier soils derived from the sandier soils derived from the quartzite

sediments than the Ventersdorp system. The soil in the Ventersdorp differ from sandy clay to clay loam and are usually more clayey than the soils in Witwatersrand system (Bredenkamp and Theron, 1976). Ventersdorp system communities are related and can be grouped as *Trachypogon spicatus*, *Themeda trianda* grassland (Bredenkamp, 1975).

The Ventersdorp has been deposited on top of Witwatersrand and originated from a volcano (Mountain, 1968). The lavas are largely andesitic or basaltic in nature (Nel and Jansen, 1957) and weather to a clay loam or sand clay loam soil. The sour grassland vegetation has good grazing during summer when in good condition but little potential in winter. The woody vegetation usually occurs in the patches in protected valleys and kloofs (Bredenkamp and Theron, 1976).

3.3.3 Roodeplaat Dam Nature Reserve

Roodeplaat Dam nature reserve is situated on the verge of Roodeplaat Dam and the build-up areas which are not dense. Some part of the land is used for smaller farming purposes (Mucina and Rutherford, 2006). The average rainfall is 655-660 mm per year (Davis et al, 2005). The landscape is slightly surging with valleys and hills and is characterised by open *Vachelia karoo* woodland (Mucina and Rutherford, 2006). Roodeplaat is a bushveld reserve which comprises open woodland with many strongly shaded thickets, isolated and few patches altered to grassland on the deep finer-grained soils that are rocky and shallow on the stony outcrops nearby to the edge of Roodeplaat Dam (Davis et al., 2005). Some of the plants and includes *Themeda trianda*, *Setaria sphacelate*, *Ziziphus mucronata* and *Barleria macrostegia* (Mucina and Rutherford, 2006).

3.4 Climate

The daily mean summer and winter temperatures vary in Gauteng between 25.5°C in January and 15°C in July (SAWS, 2022). Most of the Highveld Grassland is relatively cool with mean annual temperatures of about 22°C south of Gauteng but increasing to 25°C in the north. The annual rainfall varies between 700 mm on the Witwatersrand (about 1 700 masl) and 600 mm north of the Magaliesberg (about 1 100 masl) (Ajikah et al., 2023). The long-term climate data provided focuses on the 2021 to 2023 rainfall

and temperature (Table B1a; Figure B1a; Table B1b; Figure B1b; Table B2a; Figure B2a; Table B2b, Figure B2b, Table B3a; Figure B3a; Table B3b; Figure B3b).

3.4.1 Abe Bailey Nature Reserve

The monthly rainfall in ANR in late spring (October 2021) was 48 mm. In summer (December 2021), the monthly rainfall was 79 mm. The monthly rainfall in winter (July 2022) was 34 mm (Table B1a & Figure B1a). The average daily minimum temperature was 9.1°C and the average maximum temperature was 25°C for late spring (October 2021) and summer (December 2021). The average daily minimum temperature was 8°C and the average maximum daily temperature was 23°C for winter (July 2022) (Table B1b & Figure B1b).

3.4.2 Suikerbosrand Nature Reserve

The monthly rainfall in SNR in late spring (October) was 0 mm meaning there was no rainfall at all in October 2021. The monthly rainfall in summer (December 2021) was 139 mm and the monthly rainfall in winter (July 2022) was 0 mm (Table B2a & Figure B2b). The average daily temperature was the same for late spring (October 2021) and summer (December 2021) with the average minimum daily temperature of 7°C and the maximum temperature of 24°C. The average daily minimum temperature was 8°C and the maximum temperature was 23°C for Winter (July 2022) (Table B2b & Figure B2b).

3.4.3 Roodeplaat Dam Nature Reserve

The monthly rainfall in RNR in late spring (October 2021) was 103 mm. The monthly rainfall in summer (December 2021) was 74 mm and the monthly rainfall in winter (July 2022) was 0.2 mm (Table B3a & Figure B3a). The average daily minimum and maximum temperature was the same for late spring (October 2021) and summer (December 2021) with minimum temperature of 10 °C and the maximum of 26 °C. However, the average daily minimum temperature for winter (July 2022) was 9 °C and the maximum temperature was 26 °C (Table B3b & Figure B3b).

3.5. Data collection and Processing

Data sampling was accomplished by using Modified-Whittaker-Plot (MWP) technique developed by Whittaker (Shmida, 1984). The MWP was measured into 50 m x 20 m (Figure 3.1.1, Figure 3.1.2, and Figure 3.1.3) with 6 adjacent/grazed sample plots (1 m x 1 m sub-sample plots) to allow herbivore grazing paired with 6 fenced-

off/ungrazed sample plots (1 m x 1 m sub-sample plots) to exclude herbivore grazing in each study site.

3.5.1 Plant productivity

Above-ground biomass was harvested by near ground clippings of 0.5 m x 0.5 m within each 1 m x 1 m sample plot, per season during the month of October, December and July. The harvested plant material was sorted into species (only during summer sampling), placed in labelled paper bags and brought to the laboratory. The samples were then dried in an oven at a temperature of 65°C for 72 hours, after which they were weighed using a scale. Plant productivity was determined using repeating biomass clippings over three seasons Summer (December), Winter (July) and late Spring (September/October).

3.5.2 Plant functional traits

All plant species present in each plot were recorded and four individuals of each species were collected and analyzed for the spinescence availability in the field and plant height.

3.5.2.1 Plant height

The height of plants is usually measured towards the end of the growth season and is regarded as the shortest distance between ground level and the highest photosynthetic tissue in the canopy (Cornelissen et al., 2003). The height was measured for 4 healthy adult plants of each species that were fully exposed to the sun, using tape measure.

3.5.2.3 Spinescence

Spinescence is closely associated with grazing, as spines and thorns serve as physical defenses against herbivores. Data on spinescence were collected to better understand plant defense mechanisms against herbivory. The spinescence data were collected in the field as recommended by Perez-Harguindeguy et al., (2013). The spinescence is the presence of spines, thorns or prickles which are sharp appendages that protect plants from herbivore grazing. Data were collected qualitatively by visually estimating the density of spines present on a plant as follows: no spines, low/high density of soft spines, and low/high density of hard, sharp spines (Perez-Harguindeguy et al., 2013).

3.6 Soil sampling and microbial analysis

Three soil samples were taken from 0 to 10cm depth in each sample plot and a composite was created from all three soil samples taken in each site. The soil was then analysed for microbial presence following standard protocols of DNA extraction, amplification and sequence processing. The microbes analysed were bacteria and fungi. The gene regions used to analyse the microbes were QC 16s PCR and QC fungal ITS PCR. The 16s was used to identify all the bacteria species available in the soil samples and ITS was used to identify fungi species in the soil samples. Next Generation Sequencing (NGS) was used to sequence the whole genome in this study and it usually involves several steps such as DNA fragmentation, library preparation, and massive parallel sequencing, bioinformatics analysis and data interpretation. NGS can sequence millions of genomes in a short period of time (Satam et al., 2023). Soil samples were sent to Inqaba Biotechnical Industries, a commercial NGS service provider for sequencing.

3.6.1 DNA Extraction

The Genomic DNA was extracted using the ZymoBiomics DNA Miniprep Kit following the standard protocol of ZymoBiomics Kit at Inqaba Biotechnical Industries.

3.6.2 PCR amplification

Genomic DNA samples were amplified using a barcoded universal primer pair 27F and 1492R (12x 27F barcoded primers and 8x 1492R barcoded primers), targeting the V1 – V9 region of the bacterial 16S rRNA gene. The resulting barcoded amplicons were individually quantified, pooled equimolar and Ampure PB bead-based purification step was performed on the pool. The pooled sample was then used to prepare SMRTbell library following manufacturer protocol pool and cleanup, repair and a-tailing, adapter ligation and cleanup, and lastly nuclease treatment and cleanup. The SMRTbell library was qualified using Fragment Analyzer (Agilent) and quantified using Qubit HS dsDNA Assay (Thermo Fisher). The annealing of the sequencing primer and polymerase binding steps were performed following PacBio SMRT link v13.1 software protocol (browser based) to prepare the library for sequencing.

DNA sequences were amplified following a standard procedure for PCR. The first step was denaturation where DNA strands were separated at 92°C to 98°C for about 30 seconds to a minute. The second step was annealing; the primers anneal to

complementary DNA sequence at 37°C to 65° C for 30 seconds to a minute. The third step was elongation; new DNA strands are formed at 72°C for 30 seconds to a minute. Lastly, all the three steps were repeated for about 20 to 30 times (Suchman, 2016). The PCR amplification is repeated for 20-30 times/ cycles to produce effective DNA by doubling the targeted DNA amount.

3.6.3 DNA Sequencing

DNA sequencing determines the order of nucleotide in DNA molecule. Next generation sequencing has been successfully utilized for the identification of *Bacillus anthracis* bacteria from the soil samples (Fazil et al., 2024). NGS is vital for determining the microbial communities of soil samples (Soliman et al., 2017). The samples were sequenced using PacBio Revio system using SMRT cell 2.

3.7 Data analysis

3.7.1 Plant productivity

Plant biomass was analysed by calculating the summary statistics using excel formula function for mean, standard deviation, minimum, maximum and standard errors. Paired t-test was conducted to determine if there's a significant difference between grazed and ungrazed mean biomass. One- way ANOVA was also conducted to check if there's a significance differences between the means in October (late spring), December (summer) and July (winter). Paired t-test was also conducted to determine if there is a significance differences between grazed and ungrazed mean biomass throughout all three seasons.

3.7.2 Soil microbes

QIIME 2 (Quantitative Insights into Microbial Ecology) is a microbiome bioinformatics platform which adapts the raw data to understandable conception (Fung et al., 2021). QIIME 2 was used to analyse the bacteria data (16S rRNA). The soil samples for ITS were classified on the Revio system by PacBio. The raw sub-reads were handled by the SMRTlink (v25.1) Acicular Consensus Sequences (CCS) algorithm to generate extremely accurate reads (>QV40). The exceptionally accurate reads were processed by search and other in-house software at Inqaba biotec laboratory and the ITS data were determined.

3.7.3 Jaccard dissimilarity index

Jaccard dissimilarity index is a measure of the similarity concerning two groups of data (Verma and Aggarwal, 2020). Jaccard dissimilarity index was used to determine species composition between all three nature reserves. The index ranges from 1 to 0. If the two groups are closer to 1, the more similar the two groups of data. The similarity index will be 1, if the two data groups share equal numbers. If there is no common members, then the similarity will be 0. Jaccard dissimilarity index was used to determine the species composition across all three reserves.

Jaccard's index is expressed as: $J = |A \cap B| / |A \cup B|$

where

$|A \cap B|$ is the number of basics to both groups

$|A \cup B|$ is the total number of unique basics across both groups

3.7.4 Shannon- Weiner diversity indices

There are many different ways to define and measure species diversity, these include Shannon-Weiner diversity index. Diversity indices provide crucial data about rarity and the commonness of species in a community (Magurran, 2004). Shannon-Weiner signifies the proportions of the individual of each species in a sample plot (Fowler et al., 1998). When the value of H' is higher, it means the plant diversity is also higher in that particular community. The lower value of H' shows lower plant diversity in a certain community. A value of $H'=0$ indicates a community that has only one species. The Shannon- Weiner diversity index (H') were calculated for each reserve to determine the plant diversity.

The equation used to calculate Shannon- Weiner index was :

$$H' = -\sum p_i * \ln(p_i)$$

where

Σ is the sum

p_i is the proportion of the entire community made up of species i

$\ln$ is Natural log

CHAPTER 4: RESULTS

4.1 Plant productivity

Plant productivity is the amount of biomass plants add over time due to photosynthesis. The plant biomass between ungrazed and grazed plots differs significantly. The plant biomass in ungrazed plots is generally higher than the plant biomass in the grazed plots. Grazing plays a role in influencing biomass in grazed and ungrazed plots. The grazed plots usually have plants with shorter height compared to plant in ungrazed plots which usually have plant with high height. This section will address plant productivity between grazed and ungrazed plots.

4.1.1a Abe Bailey Nature Reserve

The mean biomass in the grazed sample plots in ANR in late spring (October 2021) was $47 \pm 20 \text{ gm}^{-2}$ and in the ungrazed sample plots the mean biomass was $56 \pm 34 \text{ gm}^{-2}$. The plant biomass in the grazed plots ranged between minimum of 18 gm^{-2} to maximum of 84 gm^{-2} and in the ungrazed sample plots plant biomass ranged from minimum of 17 gm^{-2} to maximum of 134 gm^{-2} (Table 4.1.1a and Figure 4.1.1).

The mean biomass in the grazed sample plots in ANR in summer (December 2021) was $48 \pm 26 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $47 \pm 15 \text{ gm}^{-2}$. In the ungrazed sample plots the minimum plant biomass ranged from 12 gm^{-2} to maximum of 112 gm^{-2} and in the grazed sample plots plant biomass ranged from a minimum of 9 gm^{-2} to maximum of 77 gm^{-2} (Table 4.1.1a and Figure 4.1.1).

The mean biomass in the grazed sample plots in ANR in winter (July 2022) was $25 \pm 14 \text{ gm}^{-2}$ and in the ungrazed sample plots the mean biomass was $26 \pm 17 \text{ gm}^{-2}$. In the ungrazed sample plots the plant biomass ranged from minimum of 11 gm^{-2} to a maximum of 81 gm^{-2} . The plant biomass ranged from a minimum of 11 gm^{-2} to maximum of 68 gm^{-2} in the grazed sample plots (Table 4.1.1a).

The mean biomass grazed in late Spring (October) was $47 \pm 20 \text{ gm}^{-2}$ and ungrazed mean biomass was $59 \pm 34 \text{ gm}^{-2}$, $t_{(17)}=1.5$, $p=0.1$. The mean biomass grazed in summer (December 2021) was $48 \pm 26 \text{ gm}^{-2}$ and ungrazed mean biomass was $47 \pm 15 \text{ gm}^{-2}$, $t_{(17)}=-0.1$, $p=0.9$. The mean biomass grazed for winter (July 2022) was $25 \pm 14 \text{ gm}^{-2}$ and ungrazed mean biomass was $26 \pm 17 \text{ gm}^{-2}$, $t_{(17)}=0.2$, $p=0.8$. The p-values

shows that there were no significant differences between the grazed and ungrazed conditions in late spring (October 2021), summer (December 2021) and winter (July 2022) Table 4.1.1a.

Table 4.1.1a: Paired t-test summary stats for grazed and ungrazed sample plots in Abe Bailey Nature Reserve

Dates	Late Spring (October 2021)		Summer (December 2021)		Winter (July 2022)	
Sample plots	Ungrazed	Grazed	Ungrazed	Grazed	Ungrazed	Grazed
Min	17	18	9	12	11	11
Max	134	84	77	112	81	68
Mean	59	47	47	48	26	25
Std.dev	34	20	15	26	17	14
df	17	17	17	17	17	17
t	1.5		-0.1		0.2	
p	0.1		0.9		0.8	

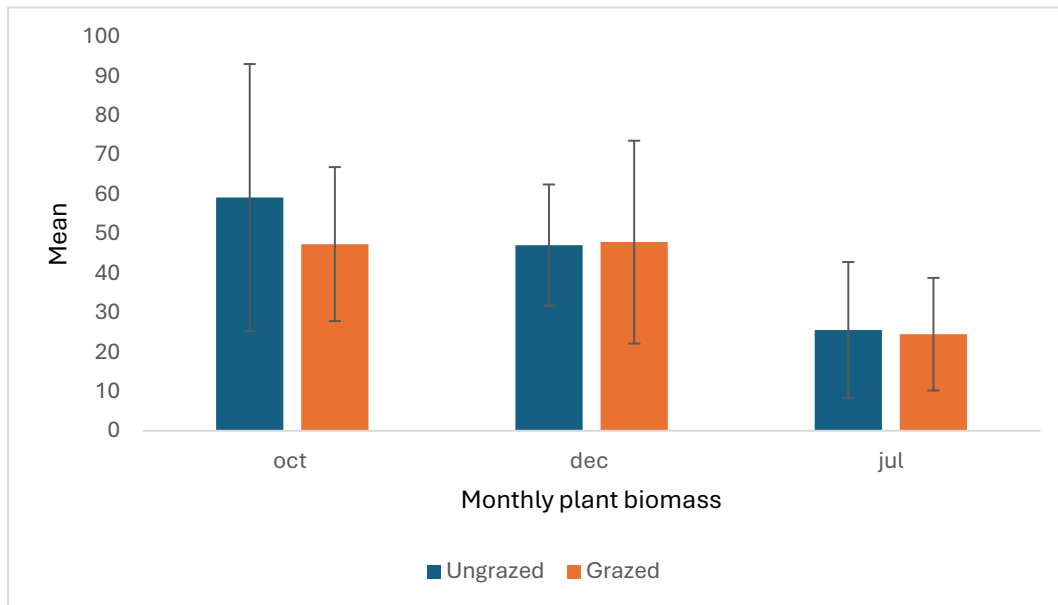


Figure 4.1.1: The mean plant biomass for the ungrazed and grazed plots with standard errors within the vicinity of Abe Bailey nature reserve.

4.1.1b: Analysis of Variance for Abe Bailey Nature Reserve

There was a significant difference in plant productivity measured in late spring (October 2021), summer (December 2021) and winter (July (2022) at $p < 0.05$ [$F(2, 105) = 16. p < .05$). The F-value calculated is greater than the F-critical (3.1) confirming the differences throughout all season's late spring (October 2021), summer (December 2021) and Winter (July 2022) (Table 4.1.1b).

Table 4.1.1b: Analysis of Variance for Abe Bailey Nature Reserve.

Source of Variation	Sum of squares	Df	MS	F	P-value	F critical
Between Groups	16015	2	80007	16	<<0.05	3.1
Within Groups	5118	105	486			
Total	67133	107				

4.1.2a Suikerbosrand Nature Reserve

The mean biomass in late spring (October 2021) in SNR in the grazed sample plots was $3 \pm 3 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $2 \pm 2 \text{ gm}^{-2}$. The plant biomass ranged from minimum of 0 gm^{-2} to maximum of 15 gm^{-2} in the grazed sample plots and it also ranged from minimum of 0 gm^{-2} to maximum of 7 gm^{-2} in the ungrazed sample plots (Table 4.1.2a and Figure 4.1.2).

The mean biomass in summer (December 2021) in SNR in the grazed sample plots was $108 \pm 68 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $117 \pm 61 \text{ gm}^{-2}$. The plant biomass ranged from minimum of 42 gm^{-2} to maximum of 258 gm^{-2} in the grazed sample plots and it ranged from minimum of 30 gm^{-2} to maximum of 292 gm^{-2} in the ungrazed sample plots (Table 4.1.2a and Figure 4.1.2).

The mean biomass in winter (July 2022) in SNR in the grazed plots was $47 \pm 19 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $71 \pm 44 \text{ gm}^{-2}$. The plant biomass ranged from minimum of 19 gm^{-2} to maximum of 82 gm^{-2} in the grazed sample plots and the plant productivity ranged from minimum of 27 gm^{-2} to maximum of 182 gm^{-2} in the ungrazed sample plots (Table 4.1.2a).

The grazed mean biomass in late spring (October 2021) was $3 \pm 3 \text{ gm}^{-2}$ and ungrazed mean was $2 \pm 2 \text{ gm}^{-2}$, t-test $t_{(17)}=-0.1$, and with the p-value of $p=0.35$. The grazed mean biomass in summer (December 2021) was $108 \pm 68 \text{ gm}^{-2}$ and ungrazed mean biomass was $117 \pm 61 \text{ gm}^{-2}$, t-test $t_{(17)}=1$, and with the p-value of $p=0.50$. The grazed mean biomass in winter (July 2022) was $47 \pm 19 \text{ gm}^{-2}$ and ungrazed mean biomass was $71 \pm 44 \text{ gm}^{-2}$, t-test $t_{(17)}=2$ and the p-value of $p=0.03$. The p-values shows that there was no statistical significance between the grazed and ungrazed conditions in late spring (October 2021) and summer (December 2021). However, there was a

statistical significance differences between the ungrazed and grazed conditions in winter (July 2022) Table 4.1.2a.

Table 4.1.2a: Paired t-test summary for grazed and ungrazed sample plots in Suikerbosrand Nature Reserve.

Dates	late Spring (October 2021)	Summer (December 2021)	Winter (July 2022)			
Sample plots	Ungrazed	Grazed	Ungrazed	Grazed	Ungrazed	Grazed
Min	0	0	34	30	19	27
Max	15	7	258	292	82	182
Mean	2	3	117	108	71	47
Std.dev	2	3	61	68	44	19
df	17	17	17	17	17	17
t	0.1		1		2	
p	0.35		0.50		0.03	



Figure 4.1.2: The mean biomass for the ungrazed and grazed plots with standard errors within the vicinity of Suikerbosrand nature reserve.

4.1.2b. Analysis of Variance for Suikerbosrand Nature Reserve

There was a significant difference in plant productivity measured in late Spring (October 2021), Summer (December 2021) and Winter (July (2022)). They had a significance different of $p < 0.05$ [$F(2, 105) = 61$]. $p < 0.05$. The F-value (61) calculated was found to be much greater than the F-critical value (3.1) confirming that the differences are not due to random chances. There was a significant relationship between biomass throughout late Spring (October 2021), Summer (December 2021) and Winter (July 2022) (Table 4.1.2b).

Table 4.1.2b: Analysis of Variance for Suikerbosrand Nature Reserve.

Source of Variation	SS	Df	MS	F	P-value	F critical
Between Groups	218287	2	109143	61	<<0.05	3.1
Within Groups	187296	105	1784			
Total	405583	107				

4.1.3a Roodeplaat Dam Nature Reserve

The mean biomass in the grazed sample plots of RNR in late spring (September/October 2022) was $66 \pm 41 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $74 \pm 39 \text{ gm}^{-2}$. The plant biomass ranged from a minimum of 12 gm^{-2} to maximum of 149 gm^{-2} in the grazed sample plots and the plant biomass ranged from minimum of 19 gm^{-2} to maximum of 158 gm^{-2} in the ungrazed sample plots (Table 4.1.3a and Figure 4.1.3).

The mean biomass in the grazed sample plots of RNR in summer (December 2021) was $81 \pm 39 \text{ gm}^{-2}$ and the mean biomass was $81 \pm 29 \text{ gm}^{-2}$ in the ungrazed sample plots. The plant biomass ranged from minimum of 30 gm^{-2} to maximum of 162 gm^{-2} in the grazed sample plots and the plant biomass ranged from minimum of 43 gm^{-2} to a maximum of 132 gm^{-2} in the ungrazed sample plots (Table 4.1.3a).

The mean biomass in the grazed sample plots of RNR in winter in the grazed sample plots was $41 \pm 27 \text{ gm}^{-2}$ and the mean biomass in the ungrazed sample plots was $47 \pm 22 \text{ gm}^{-2}$. The plant biomass ranged from a minimum of 13 gm^{-2} to maximum of 113 gm^{-2} in the grazed sample plots and ranged from minimum of 19 gm^{-2} to maximum of 87 gm^{-2} in the ungrazed sample plots (Table 4.1.3a).

The mean biomass for the grazed in late spring (September/October 2021) was found to be $66 \pm 41 \text{ gm}^{-2}$ and ungrazed mean was $74 \pm 39 \text{ gm}^{-2}$, $t_{(17)}=1.1$ and with the p-value of $p=0.3$. The mean biomass for the grazed in summer (December 2021) was $81 \pm 39 \text{ gm}^{-2}$ and ungrazed mean was $81 \pm 29 \text{ gm}^{-2}$, $t_{(17)}=-0.1$ with the p-value of $p=0.9$. The grazed mean biomass for winter (July 2022) was $41 \pm 27 \text{ gm}^{-2}$ and ungrazed mean biomass was $47 \pm 22 \text{ gm}^{-2}$, $t_{(17)}=0.9$, with the p-value of $p=0.4$. There were no

statistically significant differences between grazed and ungrazed in late spring (September/October 2021), summer (December 2021) and winter (July 2022) (see Table 4.1.3a).

Table 4.1.3a: Paired t-test summary stats for grazed and ungrazed sample plots for Roodeplaat Dam Nature Reserve

Dates	Late Spring (October 2021)		Summer (December 2021)		Winter (July 2022)	
Sample plots	Ungrazed	Grazed	Ungrazed	Grazed	Ungrazed	Grazed
Min	19	12	43	30	19	13
Max	158	149	132	162	87	113
Mean	74	66	81	81	47	41
Std.dev	39	41	29	39	22	27
df	17	17	17	17	17	17
t	1.1		-0.1		0.9	
p	0.3		0.9		0.4	

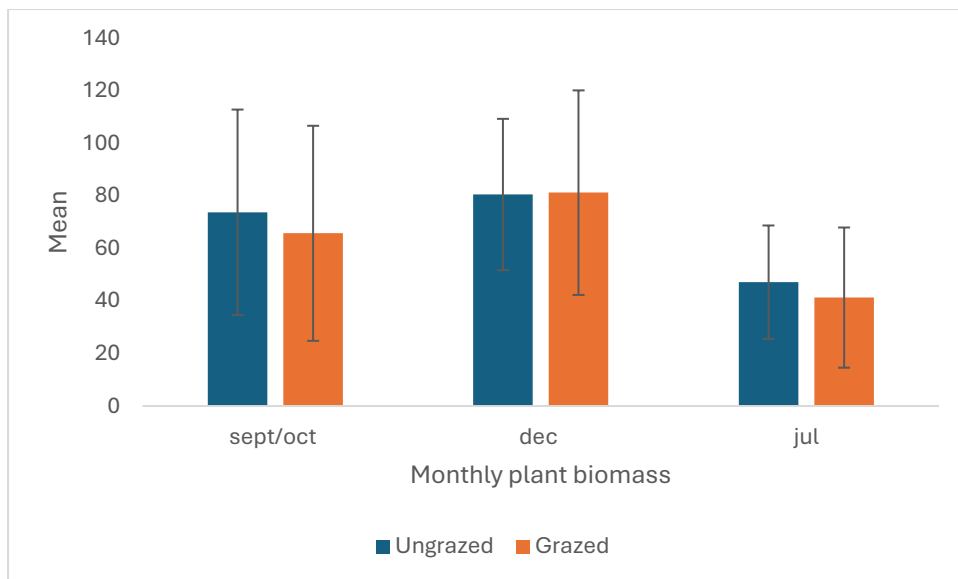


Figure 4.1.3: The mean biomass for the ungrazed and grazed plots with standard errors within the vicinity of Roodeplaat Dam nature reserve.

4.1.3b Analysis of Variance for Roodeplaat Dam Nature Reserve

There was a statistically significant difference in plant productivity measured in late Spring (October 2021), Summer (December 2021) and Winter (July (2022)). They had a p-value of $p < 0.05$ [$F(2, 105) = 12. p < .05$] between all three seasons (late Spring, Summer, and Winter). The F-value calculated was found to be higher than the F-critical (3.1) thus confirming the differences between all three seasons means. There was a relationship between plant productivity throughout late Spring, Summer, and Winter (July 2022) (Table 4.1.3b).

Table 4.1.3b: Analysis of variance for Roodeplaat Dam Nature Reserve.

Source of Variation	SS	df	MS	F	P-value	F critical
Between Groups	25488	2	12744	12	<<0.05	3.1
Within Groups	115378	105	1098			
Total	140867	107				

4.3 Plant functional traits

4.3.1 Abe Bailey Nature Reserve

The species that were recorded in ANR includes *Erigeron canadensis*, *Pseudognaphalium obtusifolium*, *Tagetes erecta*, *Ruellia humilis*, *Setaria parviflora*, *Eragrostis curvula*, *Plantago major*, *Bidens bipinnata*, *Vaccium darrowwi*, *Panicum oligosanthos*, *Jacobae vulgaris*, *Chamaecrista fasciculata*, *Plantago lanceolata*, *Lepidium didymium*, *Croton glandulosus*, *Polypremum procumbens*, *Heteropogon contortus*, *Eragrostis spectabilis*, *Sabatia angularis*, *Bouteloua curtipendula*, *Nassella pulchra*, *Asclepias Asperula*, *Salvia sage*, *Melinis repens*, *Helichrysum luteoalbum*, *Tanacetum vulgare*, *Panicum scoparium*, *Lysimachia arvensis*, *Cyanotis arachnoidea*, *Cologania angustifolia*, *Eragrostis cillianensis*, *Asclepias viridis*, *Gazania linearis*, *Panicum oligonthes*, *Plantago aristate*, and *Ziziphus mucronata* (Table C1 on Appendix C).

The site 1 in the Abe Bailey Nature reserve consisted of a mixture of plant families mostly from Astraceae and Poaceae with species such as *Erigeron canadensis*, *Pseudonaphalium obtusifolium*, and *Bidens bipinnata*. The height ranged significantly, with some species such as *Eragrostis curvula* reaching up to 190 cm. Similarly, site 2 was dominated by the Poaceae and Astraceae with species like *Eragrostis curvula* which also displayed a substantial height variability. However, site 3 was largely dominated by Poaceae species such as *Panicum scoparium* and *Eragrostis cillianensis* that are widespread. The plant height in site 3 was trending with lower plant height compared to site 1 and 2. The various height recorded ranged from very

small plants, (*Salvia sage*- 2 cm) in site 2 to a very tall tree such as *Ziziphus mucronata* reaching up to 250 cm on site 3. *Erigeron canadensis* was the most dominant plant species across all sites with different heights. *Ziziphus mucronata* was the only plant species in ANR with spines serving as structural defence against grazing. (Table C1 on Appendix C).

4.3.2 Suikerbosrand Nature Reserve

The plant species that were recorded in SNR were *Lomatium utriculatum*, *Lepidium latifolium*, *Imperata cylindrica*, *Centranthus ruber*, *Schizachyrium scoparium*, *Verbana halei*, *Gazania rigens*, *Juncus tenuis*, *Sisyrichium angustifolium*, *Ajuga genevensis*, *Comandra umbellata*, *Verbana rigida*, *Ipomoea aquatica*, *Euphorbia corollata*, *Antennaria spicata*, *Echinaceae angustifolia*, *Helenium autumnale*, *Ajuga reptans*, *Lomatium dissectum*, *Helenium flexuosum*, *Themeda triandra*, *Anaphalis margaritacea*, *Cynodon dactylon*, *Croton glandulosus*, *Echinocloa crusgalli*, *Ulex europaeus*, *Koeleria macrantha*, *Aloe maculata*, *Crotalaria tinctoria*, *Sorghastrum nutans*, *Helenium amarum*, *Sida spinosa*, *Lantana montevidensis*, *Vachellia confusa*, *Bothriochloa ischaemum*, *Artemisia ludoviciana*, *Sisyrinchium officinale*, *Linaria vulgaris*, *Echium vulgare*, *Epipactis helleborine*, *Dalea purpurea*, *Ptela trifoliata*, *Lavandula angustifolia*, *Helichrysum luteoalbum*, *Verbana bonariensis*, and *Grangea maderaspatana* (Table C2 on Appendix C).

Site 1 in Suikerbosrand Nature reserve was dominated with families such as Poaceae, Astraceae, Fabaceae and Lamiaceae. The presence of common species like *Anaphalis margaritacea* indicates a potential for environmental softness. While site 3 was dominated with species in the Asteraceae family such as *Artemisia rigida*, *Tanacetum vulgare*. Plant heights ranged from 1 cm to 150cm in species such as *Ptela trifoliata* and *Verbana bonariensis*. This offers crucial microhabitats for various species and contribute to a covered environment structure that supports various flora and fauna. Poaceae and Astraceae were the most dominant plant families across all the three sites followed by Lamiaceae and Fabaceae. Only *Ziziphus mucronata* had spines to protect against grazing (Table C2 on Appendix C).

4.3.3 Roodeplaat Dam nature reserve

The species that were recorded in RNR are *Anemarrhena asphodeloides*, *Verbana stricta*, *Eleocharis acicularis*, *Hexasepalum teres*, *Danthonia spicata*, *Indigofera miniata*, *Cyperus brevifolius*, *Danthus armeria*, *Erigeron canadensis*, *Erigeron bonariensis*, *Eupatorium capilifolium*, *Mimosa pudica*, *Paspalum notatum*, *Ruellia nudiflora*, *Lepidium didymium*, *Spiraea tomentosa*, *Eragrostis secundiflora*, *Vachellia dealbata*, *Clematis vitalba*, *Achnatherum pekinense*, *Ambroisa artemisiifolia*, *Phyllanthus urinata*, *Fimbristylis littoralis*, *Festus idahoensis*, and *Urena lobata* (Table C3 on Appendix C).

The most dominant plant families across all the three sites (1, 2 & 3) were Poaceae and Astraceae. Dominant plant species such as *Setaria parviflora* and *Tagetes erecta* were found Site 1 was dominated with *Verbana rigida* from Verbanaceae followed by *Heteropogon contortus* from Poaceae (Table 4.3.3). However, site 2 was dominated with Poaceae species such as *Eragrostis curvula* and *Cynodon dactylon* while site 3 was dominated by *Artemisia ludoviciana* from Astraceae family. The plant height varied significantly among species across all the sites, with plant heights ranging from as small as 2 cm to 200 cm in species such as *Indigofera miniata* and *Clematis vitalba* (Table C3 on Appendix C).

4.3.4 Analysis of Variance for Plant height

ANR had the highest mean of 67 ± 49 , followed by RNR with a mean of 58 ± 27 and lowest in SNR with a mean of 42 ± 25 . Additionally, ANR also had a maximum plant height of 365, followed by SNR with a maximum height of 136 and lastly, RNR had a maximum plant height of 110. The minimum height in SNR and RNR were the same plant height of 9, however, the minimum plant height in ANR was 7. The standard error shows that the plant height in SNR and RNR were likely the same across the grass species, however standard error in ANR suggests that the plant height in grass species in that reserve likely differ from the other reserves (Table 4.3.4 & Figure 4.3.4).

Table 4.3.4a: Statistical data showing mean, standard deviation, standard error, minimum and maximum plant height across the three reserves

Nature Reserve	mean	sd	se	min	max
ANR	67	49	6	7	365
SNR	42	25	3	9	136
RNR	58	27	3	9	110

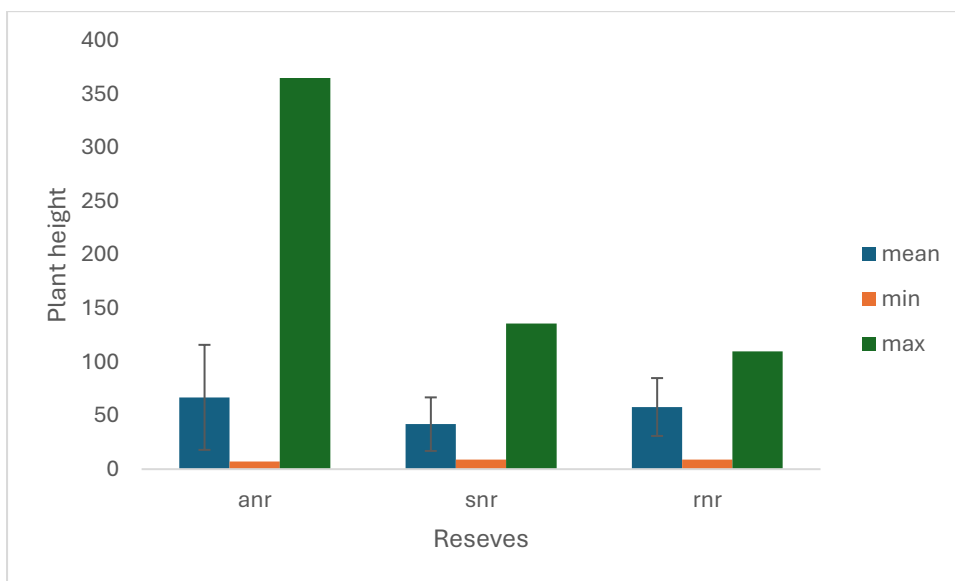


Figure 4.3.4: Plant height across all three reserve

There was a statistically significant difference in plant height measured in all three reserves. They had a p-value of $p < 0.05$ [$F(2, 178) = 8.80221$ across all three reserves. The F-value calculated was higher than the F-critical (3.04672), thus confirming the differences in plant height across all three reserves means (Table 4.4.3B).

Table 4.4.3b: Analysis of Variance for all three nature reserves

Source of Variation	SS	Df	MS	F	P-value	F-critical
Between Groups	15789.2	2	7894.59	8.80221	0.00023	3.04672
Within Groups	159646	178	896.887			
Total		175435	180			

4.4 Species composition

4.4.1 Jaccard dissimilarity index

The Jaccard dissimilarity values amongst all the reserves (0.8889 – 0.9620) shows that the species composition varies sturdily across all the study sites. All reserve has a different vegetation structure which might have been moulded by a limited biological settings and regulation regimes. ANR & SNR high Jaccard dissimilarity shows that their species composition varies significantly. It shows restrained edge, probably due to some common species. SNR & RNR has a higher dissimilarity than all the other reserves paired together. Their species composition is very different as they have the slightest species that coincide. Additionally, it shows a sturdy biological variance such as the intensity of grazing, soil type, disturbance history and moisture. RNR & ANR shows lower dissimilarity, though species composition still distinct, they somehow share slightly more species compared to other pairs. They may share more environmental conditions such as the intensity of grazing, plant communities, fire regimes history and the soil type. SNR has the most unique species composition due to its high dissimilarity over ANR & RNR. Hence, ANR & RNR seems to share the most similar species composition (Table 4.4.1).

Table 4.4.1: Jaccard Dissimilarity index in ANR, SNR, and RNR

Nature Reserve	Jaccard dissimilarity index (J')
ANR & SNR	0.9041
SNR & RNR	0.9620
RNR & ANR	0.8889

4.4.2 Plant diversity

Shannon diversity index value showed a distinguished differences in plant species diversity among the three nature reserves. Plant diversity was highest in SNR ($H'=3.932$), followed by ANR ($H'=3.367$), and lowest in RNR ($H'=3.434$). The high diversity found in SNR shows a well-stable and unique plants community which is sustained by low grazing pressure which assist the co-occurrence of many plant species. ANR H' shows moderate diversity which means in ANR grazing levels were moderate. The lower diversity in RNR may be due to strong grazing activities where constant grazing compression may have instigated the deterioration of edible species and promoting of grazing-tolerant plants. The H' establishes the way heavy grazing can reduce plant diversity, change community composition, and decline ecosystem strength (Table 4.1.2).

Table 4.4.2: Shannon-Weiner diversity index for all three reserves

Nature Reserve	Shannon- Weiner index (H')
ANR	3.367
SNR	3.932
RNR	3.434

4.5. Soil microbial analysis

4.5.1 Abe Bailey Nature Reserve

Site 1 in ANR grazed sample plots was found to have a variety of soil microbes (bacteria) belonging to phylum Acididobacteriota, Domibacterota, Proteobacteria, Actinobacteriota, Firmicutes, Eremiobacteriota, Gemmatimonadota,

Verrucomicrobita, Myxococcota, Chloroflexota, Bdelloviobionota and Planctomycetota with species such as *Jatrophihabitans endophyticus*, *Xlanimonas cellulosilytica*, *Elarobacter winogradskyi*, *Cohnella parcavi*, *Mycobacterium pulveric* and *Lactobacillus crispatus*. The ungrazed sample plots in ANR site 1 also had a wide variety of soil microbes (bacteria) belonging to phylum similar to the grazed sample plots. Additional species in the ungrazed sample plot included *Phytohabitans rumicis*, *Catenullispora polymorpha*, *Byssovorax cruenta*, *Niastella yeongjuensis* and *Roserarcus fermentans* (see Figure D1 & D2 on Appendix D).

Site 2 in ANR grazed sample plots, had a wide variety of soil microbes (bacteria) belonging to phylum Actinobacteriota, Eremiobacterota, Acidobacterota, Proteobacteria, Gemmatimonadota, Bacteriodota, Myxococcota, Domibacterota, Chloroflexota, Firmicutes, Bdellovibrionota and Verrumicrobiota with species such as *Aldersonia kummmingensis*, *Byssovorax cruenta*, *Cellumonas compositi*, *Terrabacter lapilli* and *Trebonia kvetii* (Table 4.4.1). The ungrazed sample plots also had similar phylum to the one in the grazed sample plots with species such as *Norcardiodes cynachi*, *Terrabacter lapilli*, *Mycobacterium brisbanenses*, *Methylobacterium nodlans*, *Actinoplanes digitatis* and *Methylobacterium oxadalis* (see Figure D3 & D4 on Appendix D).

The ITS region (Fungi) results showed the relative abundance of various phylum in Site 1, 2 and 3 in ANR. The most dominant phylum in the grazed sample plots was Ascomycota followed by Basidiomycota with a relative abundance of more than 30%. Phylum such as Mortierellomycota, Kickxellomycota, Glomeromycota, Chytridiomycota, Mucoromycota, Fungi phy Incertae Sedis, Zoopagomycota, Rozellomycota and Calcarisporiellomycota had a relative abundance of less than 1%. In the ungrazed sample plots the dominant phylum was Ascomycota followed by Basidiomycota with relative abundance of more than 20%, Phylum such as Kickxellomycota, Mortierellomycota, Chytridiomycota, Fungi phy Incertae sedis, Mucoromycota, Rozellomycota, Zoopagomycota and Glomeromycota had relative abundance of less than 4%. The phylum Calcarisporiellomycota was only found in the grazed sample plots.

The study sites showed no difference in fungal composition between grazed and ungrazed plots. The pre-dominant phylum was Ascomycota followed by Basidiomycota and Mortierellomycota on overall grazed and ungrazed plots. Phylum such as Chytridiomycota, Fungi phy Incertae Sedis, Kickxellomycota, Rozellomycota, Zoopagomycota, Mucoromycota, Calcarisporiellomycota, and Glomeromycota had overall relative abundance of less than 2% which could imply that they play a lesser role in plant productivity in ANR (see Table E1 & Figure E1 on Appendix E).

4.5.2 Suikerbosrand Nature Reserve

Site 1 in SNR grazed sample plots had wide variety of soil microbes (bacteria) belonging to phylum Acidobacteriota, Myxococcota, Planctomycetota, Eisenbacteria, Cyanobacteria, Nitrospirota, Desulfobacterota, Gemmatimonadota, Firmicutes, Chloroflexota, Bacteriodota, Actinobacteriota, Proteobacteria and Verrucomicrobiota with species such as *Mamoricola solisivae*, *Lichenicoccus roseus*, *Planosporangium mesophilum*, *Rhodopila globiformis*, *Reyranella massilensis* and *Microcystis aeroninosa*. The ungrazed sample plots also had a wide variety of soil microbes (Bacteria) from phylum Cyanobacteria, Nitrospirota, Desulfobacterota, Gemmatimonadota, Firmicutes, Chloroflexota, Bacteriodota, Actinobacteriota, Proteobacteria and Verrucomicrobiota with species such as *Streptomyces odonnelli*, *Micromonospora rosaria*, *Kitasatospora griseola*, *Rhodopila globiformis*, *Micromonospora crainellae* and *Rhizobium altiplani* (see Figure D5 & Figure D6 on Appendix D).

Site 2 in SNR had wide variety of soil microbes (bacteria) belonging to phylum Firmicutes, Actinobacteriota, Verrucomicrobiota, Proteobacteria, Gemmatimonadota, Chloroflexota, Myxococcota, Cyanobacteria, Bacteriodota, Desulfobacterota, Acidobacteriota, Eremiobacterota and Deinococcota with species such as *Neobacillus soli*, *Ureibacillus yapensis*, *Lapillicoccus jejuensis*, *Knoellia remsis*, *Xylanimonas cellulosilytica* and *Deinococcus ficus*. The ungrazed sample plots had phylum such as Proteobacteria, Actinobacteriota, Verrucomicrobiota, Firmicutes, Myxococcota, Eremiobacterota, Bacteriodota, Chloroflexota, Acidobacteriota and Nitrospirota with species such as *Ureibacillus halotolerans*, *Nocardioides ungokensis*, *Polymorphospora rubra*, *Segetibacter koreensis*, *Staphylococcus aureus*,

Mycobacterium helvum and *Solibacterium usitatus* (see Figure D7 & Figure D8 on Appendix D).

Site 3 in SNR grazed sample plots also had wide variety of soil microbes (bacteria) belonging to the phylum Firmicutes, Verrucomicrobiota, Actinobacteriota, Proteobacteria, Desulfobacterota, Acidobacteria, Chloroflexota, Eisenbacteria, Bacteriodota, Nitrospirota and Myxococcota with species such as *Hyalangium minutum*, *Mycobacterium sphaagni*, *Corallococcus coralloides*, *Mycobacterium canariasense*, *Legionella cherrii* and *Rhodopia giobiformis*. The ungrazed sample plots had soil microbes (bacteria) belonging to phylum Firmicutes, Actinobacteriota, Verrucomicrobiota, Gemmatimonadota, Desulfobacterota, Chloroflexota, Proteobacteria, Bacteriodota, Myxococcota, Nitrospirota, Cyanobacteria, Eremiobacterota and Domibacterota with species such as *Trebonia kvetii*, *Pseudomonas kunmingensis*, *Micromonospora auratinigra*, *Phthohabitans rumicis*, *Phthohabitans flavus*, *Manganitrophus noduliformans* and *Elorobacter winogradski* (see Figure D9 & Figure D10 on Appendix D).

The ITS data region showed the relative abundance of all the phylum that were found in SNR Site 1, 2 and 3. The dominant phylum in the grazed sample plots was Ascomycota followed by Basidiomycota with relative abundance of more than 10% whereas phylum such as Mortierellomycota with, Rozellomycota, Fungi phy Incertae Sedis, Chytridiomycota, Kickxellomycota, Zoopagomycota, Glomeromycota, Mucoromycota, Monoblepharomycota and Entorrhizomycota had less than 2% relative abundance. The dominant ITS (Fungi) on the ungrazed sample plots was also Ascomycota followed by Basidiomycota with relative abundance of more than 5% and all other phylum such as Mortierellomycota, Fungi phy Incertae sedis, Kickxellomycota, Rozellomycota, Entorrhizomycota Glomeromycota, Monoblepharomycota and Zoopagomycota had less than 2% relative abundance (see Table E2 on Appendix E).

The study sites 1 and 3 in SNR showed no differences in fungal composition between grazed and ungrazed plots. Ascomycota was the most dominant phylum followed by Basidiomycota in site 2 but followed by Mortierellomycota in site 1 (see Table 4.4.2). However, phylum such as Chytridiomycota, Kickxellomycota, Entorrhizomycota, Fungi phy Incertae Sedis, Monoblepharomycota, Rozellomycota, Glomeromycota,

Olpidiomycota and Zoopagomycota had overall relative abundance of less than 2% (See Table E2 & Figure E2 on Appendix E).

4.5.3 Roodeplaat Dam Nature Reserve

Site 1 in RNR grazed sample plots had only two phylum (Pseudomonodota and Bacillota) with species such as *Klebsiella variicola*, *Enterobacter kobei*, and *Citrobacter braakii*. The ungrazed sample plots in RNR site 1 had species only belonging to Pseudomonodota phylum, with species such as *Klebsiella variicola*, *Enterobacter kobei*, *Enterobacter cloacea*, *Enterobacter dissolvens* and *pseudomonas aeruginosa* (see Figure D11 & Figure E12 on Appendix E).

Site 2 in RNR grazed and ungrazed sample plots had similar phylum with wide variety of bacteria. The phylum included Pseudomonodota, Actinomycetota, Myxococcota, Acidobacterota with species such as *Kribbella soli*, *Psuedomonas ecoli*, *Luteimonas mephitis* and *Vibrio viridaestus* (see Figure D13 & Figure D14 on Appendix D).

Site 3 in RNR grazed plots had wide variety of soil microbes (bacteria). The grazed and ungrazed sample plots had species belonging to the same phylum. The phylum in this site were Pseudomonodota, Actinomycetota, Bacillota, Cyanobacteria, Myxococcota, Acidobacteriota and Gemmatimonadota, however the most dominant phylum was Pseudomonodota. Pseudomonodota, Bacillota, Acidobacteriota, Nitrospirota, Myxococcota had species such as *Klebsilla quasipneumoniae*, *Citrobacter freundii*, *Enterobacter mori*, *Paracoccus chinensis* and *Myxococcus xibeiensis* (see Figure D15 & Figure D16 on Appendix D).

The ITS data region showed relative abundance of various Phyla in Site 1, 2 and 3 in RNR. The Ascomycota is the dominant phylum in the grazed sample plots followed by Chytridiomycota with more than 1% relative abundance and all other phylum such as Basidiomycota, Mortierellomycota, Fungi phy Incertae sedis, Rozellomycota, Monoblepharomycota and Mucoromycota had relative abundance of less than 1% (see Table E3 on Appendix E). In the ungrazed sample plots, Ascomycota was dominant followed by Chytridiomycota, Basidiomycota with relative abundance of

more than 2% and all other phylum such as Mortierellomycota, Fungi phylum Incertae sedis, Mucoromycota, Monoblepharomycota and Zoopagomycota had less than 2% of relative abundance (see Table E3 on Appendix E).

There was no difference in fungal composition between grazed and ungrazed plots. Ascomycota was the most dominant phylum followed by Chytridiomycota, Basidiomycota and all other phyla had overall relative abundance of less than 1% except for Mortierellomycota with relative abundance of 3.2% in site 2 (see Table E3 & Figure E3 on Appendix F3).

4.6 Validity and reliability of the results

The results of the study are trustworthy, reliable and valid. The scientific techniques such as Shannon-Weiner, Jaccard dissimilarity index and QIIME2 were used. To provide the accurate measures for species composition and plant diversity; Shannon-Weiner and Jaccard dissimilarity index were used. Soil microbial diversity were analysed precisely using QIIME2. The results validity was enhanced by comparison between the ungrazed and grazed plots in all the reserves, however the results may have been impacted by periodic fluctuations and soil form in a specific site. The results are trustworthy because the statistical analysis such as t-test and ANOVA were conducted. Generally, the study results are valid and reliable for understanding the impact of plant productivity and soil microbes in the Grassland biome.

CHAPTER 5: DISCUSSION

5.1. Plant productivity and grazing

The overall ungrazed and grazed plant productivity was found to be higher in late spring (September/October 2021) and summer (December 2021) in ANR and RNR (Figure 4.2.1 & Figure 4.2.3). However, in SNR the ungrazed and grazed plant productivity in late spring (October 2021) was found to be incredibly low and high in summer and winter month (July 2022; Figure 4.2.2). This result is similar to the findings reported by Hurtado-Uria et al. (2013), which states that in late spring and early summer productivity is highest but declines late in summer. Plant productivity fluctuated with weather (monthly rainfall and average daily minimum and maximum temperature). Numerous studies have found comparable results whereby plant productivity differs in response to temporal fluctuations in weather (Knapp and Smith, 2001, Tilman et al., 2006).

In ANR, ungrazed plant productivity was higher than grazed plant productivity in late spring (October 2021), summer (December 2021) and the ungrazed plant productivity in winter (July 2022) was slightly lower than the grazed plant productivity. In SNR, the ungrazed plant productivity was higher than plant grazed plant productivity in summer (December 2021), winter (July 2022). Again, the ungrazed plant productivity was slightly lower than the grazed plant productivity in late spring (October 2022).

In RNR, the ungrazed plant productivity was higher than grazed plant productivity in late Spring (September/October 2021), Winter (July 2022) and the ungrazed and grazed plant productivity was similar in Summer (December 2021). The ungrazed plant productivity tends to be higher than the grazed plant productivity because of grazing impact on plant growth when pressure of grazing is high. Similar research findings of Zhang et al., (2023) and Xiang et al., (2023) have shown that the ungrazed plant productivity is higher than the grazed plant productivity.

Ungrazed plots indicated the exclusion of herbivores thus allowing the plants to grow unhindered by the grazing compression. There are usually more plant species in the ungrazed plots because the competitive relations are less skewed by grazing, and this could lead to higher plant productivity (O'Connor et al., 2011). Grazed plots are

subjected to natural grazing pressures which usually reduce the plant biomass, and moderate grazing can also stimulate growth in some conditions leading to modified grasslands changes (Milchunas & Lauenroth, 1993).

5.2 Plant functional traits and grazing

The plant functional traits in the grasslands play a significant role in the changes of ecosystems particularly in the context of grazing. In South Africa, areas such as Suikerbosrand Nature Reserve, Abe Bailey Nature Reserve and Roodeplaat Dam Nature Reserve are a home to various grasslands environments that are shaped by different ecological processes such as herbivore grazing. A study by Niu et al. (2015), signified that plant functional traits can be altered by long-term grazing.

Grazing is an important ecological process that enhances plant communities and their functional traits (Anderson et al., 2006). Grazing also has an advantage in plant diversity by hindering dominant species from surpassing others (Olf & Ritchie, 1998). However, biodiversity can be reduced by overgrazing (Neke & Du Plessiss, 2004, O'Connor et al., 2011). Also, grazers can impact nutrient dynamics in the ecosystems over their waste disposal which can improve soil fertility but contrarily affecting functional traits of plant communities (Dingaen et al., 2016; Franzluebbers, 2005).

5.2.1. Spinescence

In some plants, spinescence serves a structural defense against large herbivore grazers, however some herbivores may be able to feed on spineless plant species of the same plant species with spines (Godwa, 1996). Spinescences tend to reduce the rate at which herbivores feed on them and reduces the bite size. Our study found that *Ziziphus mucronata* had spines to protect against grazers. *Ziziphus mucronata* uses spines to protect against herbivore grazers, however they are still prone to grazing because ungulates such as Giraffes have some mouth features that allows to feed on trees with spines (Mogonong et al., 2023).

5.2.2. Plant height

Results from ANR showed that grazing reduced plant height which concur with that of Zuo et al., (2018). Zuo et al.,(2018), study found that grazing decreased plant height in all four grasslands where Zuo study was conducted. (Wardle et al., (1998) found that plant species such as *Cynodon dactylon* with short height can be easily overlooked or ungrazed by animals and this result was found to be similar to ours. Therefore, this indicates a of negative relationship between animal grazing and plant height, (Zuo et al., 2018). Similarly, Diaz et al., (2001) indicated that plants that are resistant to grazing have small soft leaves and are usually short in height. Plants with tall heights has advantage in light thus influencing grasslands changes, (Dingaan et al., 2016). Shorter and tall plant species and coexist by occupying various niches within the vertical levels (Dingaan et al.,2016) and also, plant height influenced plant-animal interactions which includes herbivory pressures (Roem & Berendse, 2000).

5.3 Soil microbial analysis and plant productivity

In our results, we found various soil microbes that promotes plant productivity across all three Nature Reserves (ANR, SNR and RNR). Usually, soil microbes enhance plant productivity through direct and indirect mechanisms. The microbes residing in the soils regulate plant growth by promoting plant supply and nutrient cycling and they also produce hormones and vitamins to enhances plant productivity (Yadav et al., 2021). The microbes as biofertilizers promote plant productivity in a bearable manner without causing harm to the environment. The biofertilizers helps to improve plant productivity as well as soil fertility (Kour et al., 2020). The biofertilizers enables plants to access nutrients. Some microbes that act as biofertilizers includes nitrogen fixing soil bacteria such as *Azotobacter*, *Rhizhobium*, *Azospirillum*, and *Azolla*; nitrogen fixing cyanobacteria like *Anabaena*, phosphate solubilizing bacteria like *Pseudomonas sp* and arbuscular fungi (Malyan et al., 2020; Yadav et al., 2021).

5.3.1 Abe Bailey Nature Reserve

The grazed and ungrazed sample plots in ANR had wide variety of soil microbes (bacteria) coming from different taxonomic phylum, families, orders and class suggesting a rich microbial environment in ANR. The Actinobacteriota formerly known

as Actinobacteria was the most dominant phylum across all the sample plots in the grazed and ungrazed sample plots. Actinobacteria promotes the nutrient availability of soil which enhances plant growth leading to increased plant productivity (Scagliola et al., 2016). They also provide phytohormones and protect plants against phytopathogens enhancing plant growth (Boukhatem et al., 2022). Additionally, they promote nutrient availability such as phosphorus, iron, and nitrogen complex. Actinobacteria protects plants under severe ecological situations such as drought, nutrients deficits, salinity and soil that are heavily polluted by metals and promote plant growth (Yadav et al., 2021). Species such as *Streptomyces* and *Micromonospora* produces hormones such as gibberellins that protects plants from pathogens and promote plant growth (Bottini et al., 2004).

The Firmicutes known as the “*Bacillus*” act as nitrogen-fixing bacteria that’s convert nitrogen into ammonia, which is used by plants, and promote phosphorus uptake in plant growth which increase plant productivity (Lau et al., 2020). These bacteria decomposes soil organic matter, enhances cycling of nutrients and plant growth leading to increase in plant productivity (Huang et al., 2023). The Verrumicrobiota bacteria (found ANR and SNR) enhances cycling of nitrogen leading to plant growth (Bunger et al., 2020). These bacteria decompose soil organic matter and enhances nutrient cycling and plant growth in plants (Zhang et al., 2025). The Gemmatimonadota (found in ANR and SNR) promotes growth of the plants and protects them against pathogens and improves stress tolerance (Mujakic et al., 2022) and enhances soil health which increases plant productivity (Reddy, 2012).

The Myxococcota and Chloroflexota indirectly decomposes soil organic matter (Dworkin and Falkow, 2006; Zhang et al., 2025); and promotes nitrogen cycling (Bovio-Winker et al., 2024). Myxococcota, Bacillota, Acidobacteriota, Verrumicrobiota and Ascomycota play role in promoting nutrients uptake in plants (Zhang et al., 2025). The *Rhizobium* convert nitrogen into ammonia or nitrate which is usable by plants and promotes nitrogen cycling and enhances plants growth (Orozco-Mosqueda et al., 2023). The Rhizobiales from the Proteobacteria serve as nitrogen-fixing bacteria which promotes plant growth as well as soil fertility enhancing plant productivity (Denison and Kiers, 2011). The *Rhizobium* and *Azospirillum* forms symbiotic relations with grasses and legumes to convert nitrogen to ammonia usable by plants, therefore increasing plant growth which in turn also enhances plant productivity (Graham and

Vance, 2003). The Cyanobacteria are biofertilizers which serve as nitrogen fixers which enhances soil health (Ammar et al., 2022). Acidobacteriota decomposes soil organic matter, promotes nutrient cycling of phosphorus and nitrogen (Thanh et al., 2025).

The ungrazed and grazed sample plots in ANR had wide variety of similar fungi except that the Calcarisporiellomycota was only found in the grazed sample plots. The fungi phylum found in ANR includes Ascomycota, Basidiomycota, Mortierellomycota, Kickxellomycota, Glomeromycota, Chytridiomycota, Mucoromycota, Fungi phylum Incertae Sedis, Zoopagomycota and Calcarisporiellomycota with species such as *Agaricomycetes species*, *Penicillium annulatum*, *Pezizomycotina species*, *Entoloma*, *Eurotiomycetes species*, *Penicillium simplicissimum*, *Mortierella rishikeshia*. The Ascomycetes forms symbiosis relations with plants especially the mycorrhizal fungi which improves Phosphorus uptake which increases plant growth and productivity (Smith and Read, 2008) and also breakdown soil organic matter (Wan-Mohtar et al., 2023). The Ascomycetes play a crucial role in breaking down organic materials, nutrients recycling in the soil leading to an increase in plant productivity (Wan-Mohtar et al., 2023). The Basidiomycota comprises several ectomycorrhizal fungi (ECM) which forms symbiotic relations with root promoting nutrients uptake such as Phosphorus and Nitrogen thereby increasing plant growth and productivity (Read, 1991). Basidiomycota, Kickxellomycota, Zoopagomycota, and Mortierellomycota play a role in decomposing organic matter, and cycling of nutrients (Hodge, 2000).

5.3.2 Suikerbosrand Nature Reserve

The samples in grazed and ungrazed plots had a wide variety of soil microbes from various taxonomic phylum, classes, and orders suggesting that SNR is rich in microbial diversity similar to ANR. The Actinobacteriota was the dominant phylum in SNR.

The Verrucomicrobiota and Bacteriota decomposes soil organic matter enhancing plant productivity (Rakitin et al., 2024; Wolinska et al., 2017). Acidobacteriota produces plant hormones such as indole-3-acetic acid (IAA) which enhances plant growth directly, and nutrient availability which in turn improves plant productivity (Desai and Amaresan, 2022). They also protect plant health from stresses like nutrient

deficiency, and drought therefore indirectly increasing plant productivity (Ebrahimi-Zarandi et al., 2023). Acidobacteriota promotes nutrients cycling and decomposition of soil organic matter (Chen et al., 2021) and they promote plant growth which enhances plant productivity (Kielak et al., 2016). Actinobacteria breakdown down soil organic matter enabling plant to take the particles up again. They improve plant growth and soil health by endorsing diverse plant growth trait like phosphorus, potassium, iron, plant hormone and nitrogen even under harsh environment (Hozzein.2022). Actinomycetes have many useful qualities which enhances plant productivity (Muleta and Assefa, 2018).

Cyanobacteria facilitate nutrients uptake acting as a mycorrhizae and improves plant growth thus increasing plant productivity (Faghihinia et al., 2004). Planctomycetota, cyanobacteria and Nitrospirota enhances nitrogen supply in the soil which leads to more nitrogen being supplied to the soil which then increases plant growth and productivity (Zhang et al., 2025). Cyanobacteria fix nitrogen into ammonia and ammonium using the nitrogenase enzyme, this promotes plant productivity (Pahari et al., 2021). It improves soil fertility and enhances microbial diversity (Mao et al., 2024). The Cyanobacteria produces compounds that enables plants to tolerate stress such as environmental drought, providing better nutrient-uptake, growth-promoting materials and helping plants survive with various environments (Gr et al., 2021). They improve soil structure, and water retention which increases plant productivity (Costa et al., 2018).

The Desulfobacteriota are sulfate-reducing bacteria. They use protein such as sulfate adenylyltransferase (Sat), adenylyl sulfate reductase (Apr) and dissimilatory sulfite reductase (Dsr) to reduce sulfate to sulfide in the soils which increases the availability of Sulfur to plants as Sulfur is crucial for plant health and increases plant productivity (Langwig et al., 2022). The Chloroflexota promotes soil structure, water retention in soil, nutrient cycling in the soil and plant growth which enhances plant productivity (Freches and Fradinho, 2024). Proteobacteria such as *Azospirillum*, *Bacillus* and *Pseudomonas* produces hormones like cytoknins, gibberellins and auxins which promotes plant growth. These hormones stimulate shoot and roots growth which increases plant productivity (Cruz-Hernandez et al., 2022). Proteobacteria such as *Rhizobium*, *Sinorhizobium* and *Mesorhizobium* suppress plant pathogens (Preston et al., 2005). The proteobacteria promotes soil health, nutrient availability of Pottassium

and Phosphate, decomposition of soil organic matter, fixes nitrogen into ammonia which is usable for plants which promotes plant productivity (Zhang et al., 2022).

The ungrazed and grazed sample plots in SNR had a wide variety of similar soil microbes. The fungi phylum found in SNR includes Ascomycota, Basidiomycota, Mortierellomycota, Rozellomycota, Fungi phy Incertae Sedis, Chytridiomycota, Kixkxellomycota, Zoopagomycota, Glomeromycota, Mucoromycota, Monoblepharomycota and Entorrhizomycota with species such as *Chloridium aseptatum*, *Lasionectriopsis spinosa*, *Agaricales species*, *Humicola repens*, *Humicola ovivacea*, *Penicillium sacculum* and *Arxiella terrestris*. Ascomycota improves the breakdown of plant biomass, nitrogen cycling and intracellular relations with plants (Challacombe et al., 2019). Ascomycota improves decomposition of organic matter and increases plant growth leading to an increase in plant productivity (Smith and Read, 2008). However, there are some Ascomycetes such as *Aspergillus* which are plant pathogens which causes diseases that reduces plant health and growth which leads to decrease in plant productivity (Sampson, 2024). The Entorrhizomycota promotes nutrient availability which improves plant growth and plant productivity (Bauer et al., 2015). Glomeromycota and Monoblepharomycota improve plant growth, enhances water uptake leading to increased plant productivity (Smith and Read, 2008; Sun et al., 2018). The Mucoromycota consists of the Arbuscular fungi (AMF) which promotes Phosphorus, water uptake which are crucial for plant growth thus promoting soil health and lead to an increase in plant productivity (Weber et al., 2025).

5.3.3 Roodeplaat Dam Nature Reserve

The samples in grazed and ungrazed plots had a wide range of bacteria coming from various taxonomic families, orders and this suggests a rich microbial environment in Roodeplaat Dam Nature Reserve. Sites 2 and 3 had a wide variety of bacteria unlike site 1 which only had two phyla namely Pseudomonadota and Bacillota. *Enterobacter* and *Pseudomonas* species are prominent for their ecological significance and distinct roles in the ecosystem. The “Unassigned” categories indicate the sequences/samples that could not be classified into a specific group.

Soil microbes such as rhizobia bacteria act as a determinant or drivers of plant diversity and plant community structure, (Van der Heijden et al., 2006). Bacteria contribute more biomass than protists and archaea, Timmusk et al., (2023) had similar results to our research. Plant productivities were found to be higher where the rhizobia bacteria are diverse (Van der Heijden et al., 2006). The legumes increase plant productivity in species-rich grasslands (Hooper and Dukes, 2004; Van der Heijden et al., 2006). Soil microbes have positive and negative effects on plant productivity (Van der Heijden et al., 2008) and rhizobacteria directly and indirectly promotes plant growth (Timmusk et al., 2023). Some bacteria from the Rhizobiales order forms symbiotic relations with the plants to fix atmospheric nitrogen enriching the soil with nitrogen which is important for plant growth or plant productivity (Timmusk et al., 2023). Rhizobia increase the availability of nitrogen in the soil which facilitates the growth of some plant species (Van der Heijden et al., 2006).

Enterobacter and *Klebsiella* species promote plant growth by producing the phytohormones such as auxins, enhances the availability of nutrients and improves root health leading to the increase of plant biomass and improved nutrient uptake (Hayat et al., 2010). The increase of plant biomass might have led to an increase of plant productivity in RNR. However, bacteria such as *Pseudomonas* species suppress the plant pathogens, for example, *Pseudomonas aeruginosa* produces the secondary metabolites that prevent the growth of harmful fungi and bacteria which results in health plants and improved yield (Brierley, 1985; Ehrlich.1990; Hayat et al., 2010). *Pseudomonas aeruginosa* and *Bacillus subtilis* enhances soil structure, water retention which make soil more productive leading to increased productivity (Martens and Frankenberg, 1992).

However, some bacteria from the Entrobacteriaceae like *Klebsiella* and *Citrobacter* can be pathogenic to plants by causing diseases that affect plant health. For instance, *Klebsiella variicola* is a plat pathogen that causes wilting and some other symptoms that impact plant growth negatively (Sun et al., 2023). Species that are pathogenic overshadow the bacterial ones when bacteria compete for resources, leading to reduced plant health and productivity.

The ungrazed and grazed sample plots in RNR had wide variety of similar fungi except that the Mucoromycota was only found in grazed sample plots and the

Zoopagomycota was only found in the ungrazed sample plots. The fungi phylum that was found in RNR sites includes Ascomycota, Chytridiomycota, Basidiomycota, Mortierellomycota, Fungi Phy Incertae sedis, Rozellomycota, Monoblepharomycota, and Mucoromycota with species such as *Aspergillus*, *Pseudothielavia*, *Chatothyriales gen Incertae sedis*, *Pseudothielavia Subhyalodema*, *Pezizales fam Incertae sedis*, and *Dothideomycetes fam incertaceae sedis*. The Fungi phy Incertae sedis refers to the uncertain taxonomic placement and their effects on plant productivity may vary depending on individual species with the effects ranging from beneficial to detrimental.

Ascomycota was the most dominant phylum in RNR with variety of fungi which includes many that forms important symbiotic relations with plants such as mycorrhizal fungi. Mycorrhizal fungi improve the nutrient uptake, especially Phosphorus and Nitrogen which are important for plant growth. Ascomycota also decomposes soil organic matter, recycle nutrients back into the soil and enhances soil fertility which boosts plant productivity (Smith and Read, 2008).

The Chytridiomycota negatively affects plant health by promoting disease, however there are few Chytrids that enhance plant growth by controlling the soil-borne pathogens such as *Lecanicillium psallotae* (Zhang et al., 2017, Hanrahan-Tan et al., 2022). However, the chytridiomycota low abundance in this study dataset suggests that they may play a lesser role in the ecosystem of RNR study location. The Basidiomycota acts similar to Ascomycota whereby they enhance nutrient uptake for particular plants, improve soil structure, and facilitate water retention, therefore promoting plant productivity (Smith and Read, 2008).

The Mortierellomycota also contributes to the nutrient cycling of Phosphorus and iron in the soil, improves soil structure (Ozimek and Hanaka, 2021) hence they have an incredibly low effects when compared to Ascomycota and Basidiomycota. The Monoblepharomycota is less studied; however, they are involved decomposition of soil organic materials (Burgess et al., 2019) and their effect on plant productivity in this study is likely limited due to their very low relative abundance. The relative abundance of Zoopagomycota in this suggests an insignificant role that they play in plant productivity either as a pathogen or as a competitor.

5.4 Soil microbial diversity, plant productivity and grazing

The soil microbial diversity sustains the plant productivity under various grazing levels in the Grassland biome. The soil microbial groups influences the cycling of nutrients, decomposition of organic matter, and the relations of root-micro-organism which enhances rejuvenation after grazing. Moderate grazing conditions restores the microbial diversion and sustain soil productiveness which leads to high plant productivity. Nevertheless, heavy grazing pressures decrease vegetation, biological process and soil composition which reduces the availability of nutrients leading to decreased plant productivity. Hence, moderate grazing sustains the steadiness amongst microbial variety and soil nourishment changes, enhancing strong and high-yielding grassland biome.

The proper control of grazing conditions is crucial for sustaining the grassland substantiality. Grazing should be revolving allowing intermission and herbivore grazers needs to be controlled in order to allow the plant communities to recuperate. Rotational grazing, recessing phases and controlling of herbivore grazers prevents the deprivation of soil, stimulate compost collection, and boost nutrient stability, which together sustain productivity. The preservation of grazing also adds to a sustained environment resilience. These prevents the decline in nutrient, erosion by ensuring that the soil process remain balanced. Furthermore, microbial activity maintains decarbonisation required for the reduction of climatic changes and soil sustainability.

CHAPTER 6: CONCLUSION AND RECOMMENDATIONS

The plant height results signified a rich diversity of plant species, family diversity across all three study sites, with substantial variability in plant height. Height variability illuminates the co-occurrence of both short and tall species which contribute to habitat convolution. The data revealed the dynamic influential within these ecosystems, illuminating the plausible influences of ecological factors on species distribution and development. The interaction amongst the plant functional traits and grazing in South Africa's grassland ecosystems shows the complex dynamics of these environments. Higher grazing pressure enhances plant community variation and intense grazing changes vegetation structure which leads to irregular species dispersal. Proper grazing management is crucial for ecology to preserve both high plant diversity and community constancy across grassland. The overall ungrazed plant productivity was higher than the overall grazed plant productivity in all three Reserves (ANR, SNR &RNR). Grazing significantly reduces plant productivity. The plant productivity fluctuates with monthly rainfall, average daily minimum and maximum temperature. The effects of bacteria found in ANR, SNR and RNR on plant productivity was complex and can encompass positive or negative aspects in the ecosystem. Our study found that soil microbes might be the drivers of plant productivity. Understanding the impacts of soil microbes is important for agricultural practices which are aimed at improving plant health which leads to maximized plant productivity through microbial management.

The dominance of Ascomycota and Pseudomonodota indicates a positive effects of soil microbes on plant productivity through soil health, enhanced nutrient uptake and processes of decomposition. The lesser abundant groups of fungi may contribute to certain ecological functions which are important in plant productivity maintenance in the ecosystem.

- Further research might focus on the specific conditions that affects these particular heights such as moisture levels, interspecies competition and soil composition.

- Further research on identifying the soil microbes(bacteria) that are harmful and beneficial for plants in order to enhance plant productivity is crucial.
- Further studies on fungal pathogens that are beneficial and detrimental to ungrazed and grazed plant productivity is important.
- The reason behind fungal and bacterial communities being similar in the ungrazed and grazed plant productivity in the Grassland biomes in Gauteng in South Africa can also be investigated.

Limitations of the study

- There was only 3 grasslands reserve, it would have been better to have 9 grasslands sites reserves.
- There were only three seasons, four seasons could have been done for two years, but because it is a master's degree, time was limited.
- More plant functional traits such as leaf size, specific leaf area, leaf dry matter content, specific root length, root biomass and root mass fraction. These functional traits were not done due to lack of proper equipment to measure them. This led to limited data that could have helped in determining the trait based metrics.
- In addition to grazing, fire could have also been done since fire is important determinant in grasslands.
- Soil microbe microbes were collected once; it would have been better if they were collected for four seasons when collecting biomass. It would have also made it possible to do correlation analysis.
- In addition to soil microbe, soil property could also have been done

CHAPTER 7: REFERENCES

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Appendices

Appendix A: Ethics Approval Letter



UNISA-CAES HEALTH RESEARCH ETHICS COMMITTEE

Date: 10/08/2021

Dear Ms Netangula

**Decision: Ethics Approval from
05/08/2021 to 31/07/2024**

NHREC Registration # : REC-170616-051
REC Reference # : 2021/CAES_HREC/115
Name : Ms P Netangula
Student # : 62065130

Researcher(s): Ms P Netangula
nadia.netangula@gmail.com

Supervisor (s): Dr M Dingaan
dingam@unisa.ac.za; 011-471-3580
Prof R Adeleke
Rasheed.adeleke@nwu.ac.za; 018-299-2495

Working title of research:

The effect of soil microbial diversity on plant productivity in the grassland biome of South Africa

Qualification: MSc Life Science

Thank you for the application for research ethics clearance by the Unisa-CAES Health Research Ethics Committee for the above mentioned research. Ethics approval is granted for three years, **subject to further clarification and submission of yearly progress reports. Failure to submit the progress report will lead to withdrawal of the ethics clearance until the report has been submitted.**

The researcher is cautioned to adhere to the Unisa protocols for research during Covid-19.

Due date for progress report: 31 July 2022

Please note the points below for further action:



University of South Africa
Preller Street, Muckleneuk Ridge, City of Tshwane
PO Box 392 UNISA 0003 South Africa
Telephone: +27 12 429 3111 Facsimile: +27 12 429 4150
www.unisa.ac.za

Appendix B: Climate

Abe Bailey Nature Reserve

Table B1a: Monthly rainfall recorded in a 14-year (2010 – 2023) period at Fochville-Police-Ars weather station within the vicinity of Abe Bailey Nature Reserve study location.

Year	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
2010	290	129	33	0	26	0	0	0	0	0	88	248
2011	123		16					0	0	1	4	21
2012	5	13	22	5	0	0	0.2	0.2	0.2	97	65	176
2013	151	22	27	36	3	0	0	0	0	0	0	61
2014	58	104	121	7	0.4	0	0	0.6	12	27	0	0
2015	0	0	0	0	0	0	0	0	0	11	48	89
2016	162	84	91	28	95	10	45	0	0.2	92	218	257
2017	178	146	78	88	18	0	0	0	14	70	145	81
2018	105	272	173	49	29	0.4	8	0	15	46	52	286
2019	157	46	13	213	0	0	0	0	3	0.4	111	193
2020	89	149	101	111	0	24	0	1	10	120	124	128
2021	351	85	102	6	18	1	0	7	49	48	6	79
2022	185	90	130	253	55	32	3	6	0	65	217	0
2023	0	0	1	3	7	3	5	0	3	33	4	171

Data source: South African Weather Service

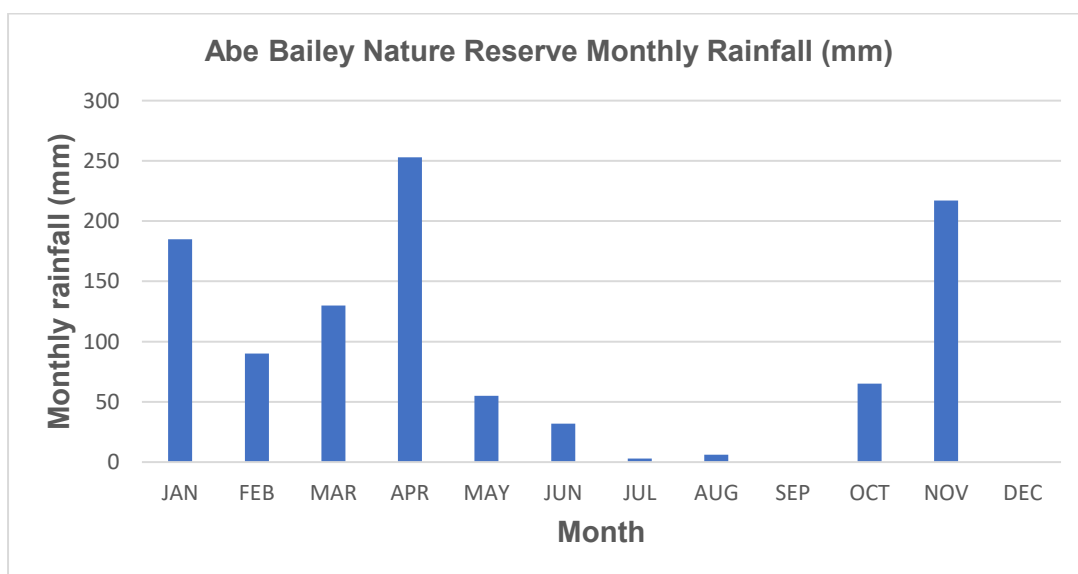


Figure b1a:monthly rainfall (mm) data for station – fochville- police ars measured at 08:00 for abe bailey nature reserve.

Table B1b: Average Daily temperatures recorded over 14-year (2010 – 2023) period at Zuurbekom Aws for Abe Bailey Nature Reserve.

YEAR	AVERAGE MAXIMUM TEMPERATURE (°C)	AVERAGE MINIMUM TEMPERATURE (°C)
2010	24	8
2011	23.5	10
2012	24	9
2013	25	10
2014	24	9
2015	26	9.1
2016	24.1	8
2017	25	9
2018	25.3	9
2019	27	10
2020	25	10
2021	25	9.1
2022	23	8
2023	26	11

Average Daily temperatures Data for station – ZUURBEKOM AWS

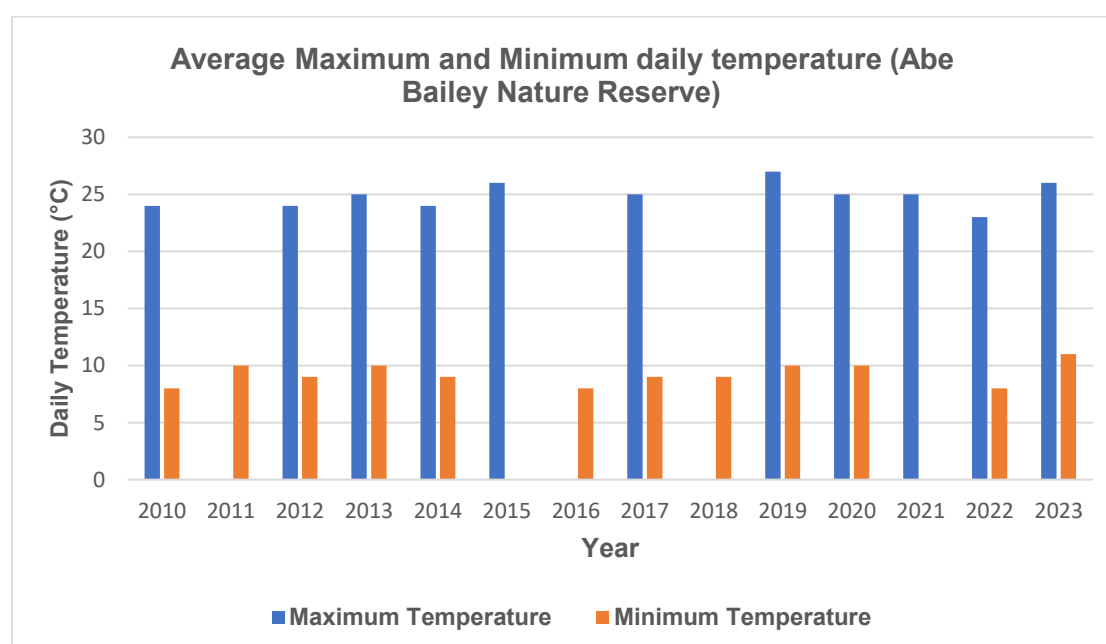


Figure B1b: Average Daily temperatures recorded over 14-year (2010 – 2023) period at Zuurbekom Aws - Measured at 8:00 for Abe Bailey Nature Reserve.

Suikerbosrand Nature Reserve

Table B2a: Monthly rainfall recorded in a 14-year (2010 – 2023) period at Schikfontein weather station within the vicinity Suikerbosrand Nature Reserve study location.

Year	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
2010	321	170	41		25	0	0	0	0	0	90	215
2011	164	25	20	59	16	10	0	0	47	0	84	113
2012	81	88	64	0	0	0	0	0	69	55	59	90
2013	192	52	42	167	0	0	0	7	0	113	169	237
2014	69	96	77	12	0	0	0	13	0	90	166	183
2015	129	24	98	8	0	0	11	0	71	18	98	10
2016	134	102	82	17	68	4	11	0	0	84	141	180
2017	50	219	44	45	49	0	0	0		67	79	95
2018	31	88	173	54	5	3		0	3	60	34	70
2019	54	185	23	48	0	0	0	0	0	0	63	
2020	73	82	113	49	0	0	0	0	16			
2021					0	0	0	0	14	0	146	139
2022	155	104	51	206			0	0	0		72	
2023						0	0	0				

Data source: South African Weather Service

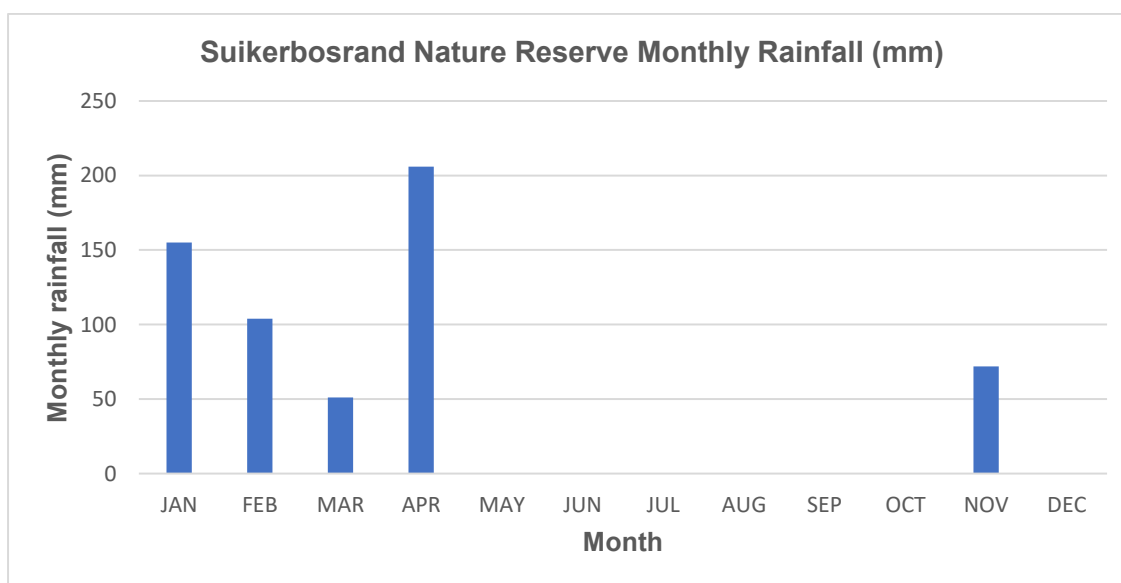


Figure B2a: Monthly rainfall (mm) Data for station – Schikfontein Measured at 08:00 for Suikerbosrand Nature Reserve.

Table B2b: Average Daily temperatures recorded over 14-year (2010 – 2023) period at Vereeniging for Suikerbosrand Nature Reserve.

YEAR	AVERAGE MAXIMUM TEMPERATURE (°C)	AVERAGE MINIMUM TEMPERATURE (°C)
2010	25	9
2011	23	7
2012	24	8
2013	25	8
2014	23.1	7
2015	26.1	10
2016	26	10
2017	25.1	10
2018	23.71	8
2019	22.1	2
2020	22.8	4
2021	24	7
2022	23.5	8
2023	26	11

Average Daily temperatures Data for station – VEREEGING weather station.

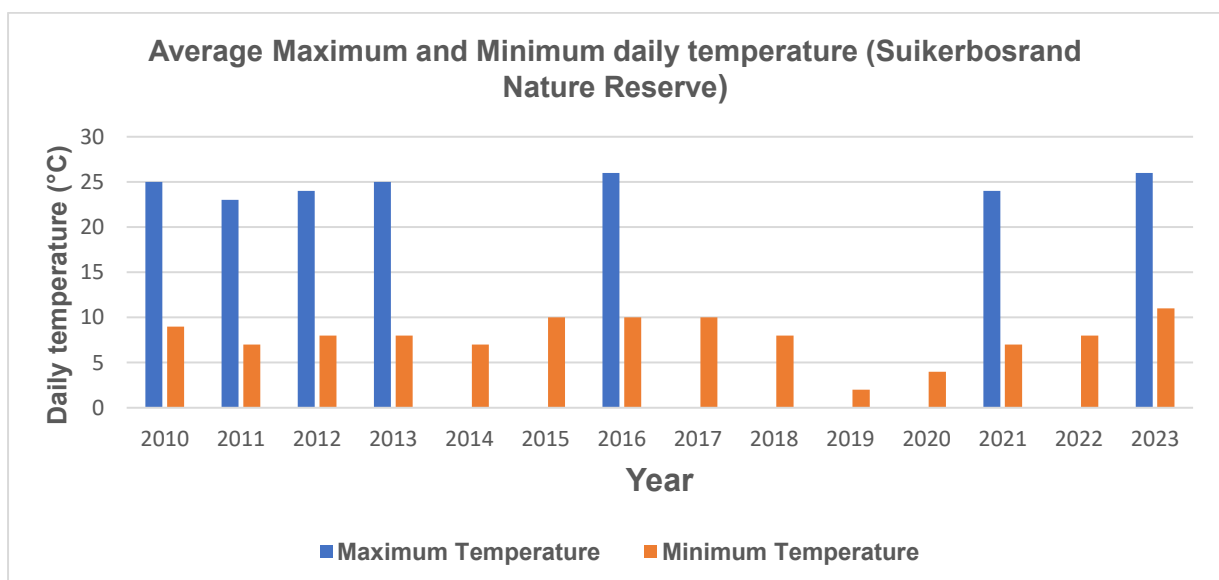


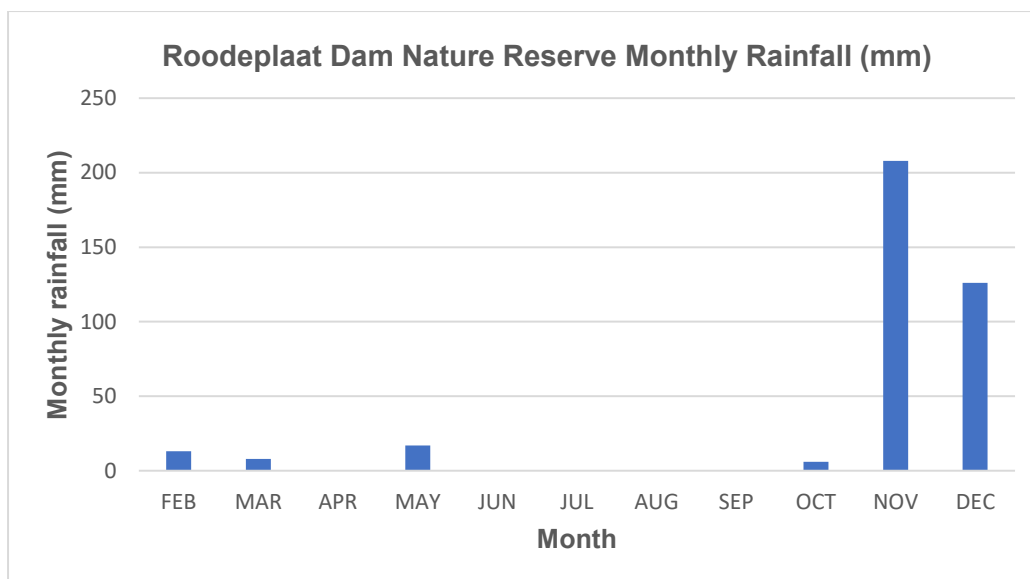
Figure B2b: Average daily temperatures recorded over 14-year (2010 – 2023) period at Vereeniging - Measured at 8:00 for Suikerbosrand Nature Reserve.

Roodeplaat Dam Nature Reserve

Table B3a: Monthly rainfall recorded in a 14-year (2010 – 2023) period at Kameeldrift- Ars weather station within the vicinity of Roodeplaat Dam Nature Reserve study location.

Year	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
2010	114	62	36	132	45	0	0	0	0	30	69	214
2011	275	46	131	97	2	14	0	7	3	39		
2012		42	67	7	0	0	0	0	96	117	7	60
2013												
2014												
2015								0		1	6	5
2016	29	1	4	7	0.2	0	0	0	0	0.2	3	1
2017	0.6	1	0.2	72	26	0	0	11	16	68	68	24
2018	45	1.4										
2019											5	34
2020	59	80	74	0.0	0.0	0	0	0	0	0.4	677	99
2021	15		2			0	0.4	0	44	59	123	74
2022		13	8		17	0.0	0.2	0.2	0	6	208	126
2023	25	232	35	14	107	2	3	2	2	40	29	45

Data source: South African Weather Service



Monthly Rain (mm) Data for station (0513550 3) – KAMEELDRIFT ARS Measured at 08:00 (Year 2022)

Figure B3a: Monthly rainfall (mm) Data for station – Kameeldrift Ars Measured at 08:00 for Roodeplaat Dam Nature Reserve.

Table B3b: Average Daily temperatures recorded over 14-year (2010 – 2023) period at Wonderboom Airport for Roodeplaat Dam Nature Reserve.

YEAR	AVERAGE MAXIMUM TEMPERATURE (°C)	AVERAGE MINIMUM TEMPERATURE (°C)
2010	27	12
2011	26	11.1
2012	26	10.1
2013	27.5	11.3
2014	27	10.3
2015	29	12.
2016	27.4	11
2017	27	10
2018	28	12
2019	0	0
2020	23	5
2021	26	10
2022	26	9.3
2023	29	17

Average Daily temperatures Data for station – WONDERBOOM AIRPORT weather station

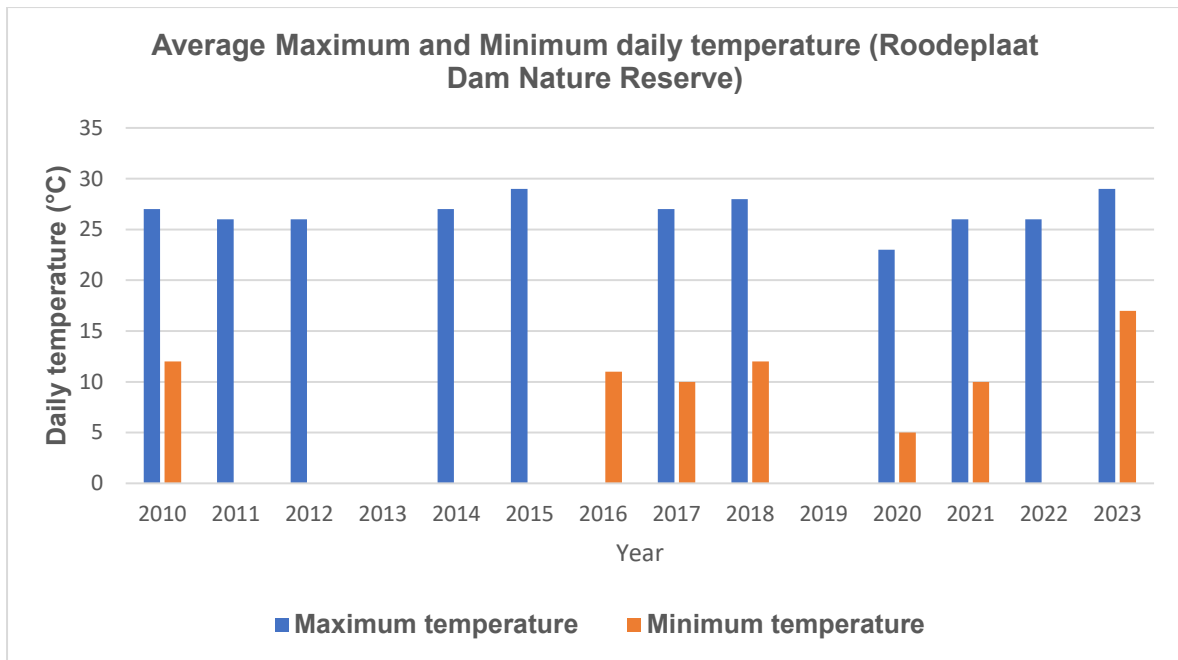


Figure B3b: Average daily temperatures recorded over 14-year (2010 – 2023) period at Wonderboom Airport - Measured at 8:00 for Roodeplaat Dam Nature Reserve.

Appendix C: Plant functional traits tables

Abe Bailey Nature Reserve

Table C1: Plant species recorded within the study sites of Abe Bailey nature reserve.

SITE 1

Sample plot	Species	Family	Plant height	Spinescence
ANR13A	<i>Erigeron canadensis</i>	Asteraceae	70cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	15cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	105cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	60cm	No spines
	<i>Setaria parviflora</i>	Poaceae	55cm	No spines
ANR13B	<i>Eragrostis curvula</i>	Poaceae	190cm	No spines
	<i>Erigeron canadensis</i>	Asteraceae	70cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	15cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	50cm	No spines
	<i>Plantago major</i>	Plantaginaceae	11cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	150cm	No spines
ANR14A	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	17cm	No spines
	<i>Erigeron canadensis</i>	Asteraceae	60cm	No spines
	<i>Vaccinium darrowii</i>	Ericaceae	120cm	No spines
	<i>Panicum oligosanthos</i>	Poaceae	50cm	No spines
ANR14B	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	72cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	100cm	No spines
ANR15A	<i>Bidens bipinnata</i>	Asteraceae	100cm	No spines
	<i>Erigeron canadensis</i>	Asteraceae	140cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	55cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	185cm	No spines

ANR15B	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	75cm	No spines
	<i>Setaria parviflora</i>	Poaceae	115cm	No spines
	<i>Erigeron canadensis</i>	Asteraceae	50cm	No spines
	<i>Jacobae vulgaris</i>	Asteraceae	30cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	150cm	No spines
ANR16A	<i>Chamaecrista fasciculata</i>	Fabaceae	50cm	No spines
	<i>Plantago lanceolata</i>	Plantaginaceae	10cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	75cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	150cm	No spines
ANR16B	<i>Erigeron canadensis</i>	Asteraceae	60cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	70cm	No spines
	<i>Setaria parviflora</i>		115cm	No spines
	<i>Jacobaea vulgaris</i>	Asteraceae	25cm	No spines
ANR17A	<i>Erigeron canadensis</i>	Asteraceae	55cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Asteraceae	20cm	No spines
	<i>Lepidium didymium</i>	Brassicaceae	40cm	No spines
	<i>Setaria parviflora</i>	Poaceae	130cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	145cm	No spines
ANR17B	<i>Tagetes erecta</i>	Asteraceae	20cm	No spines
	<i>Croton glandulosus</i>	Euphorbiaceae	60cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	150cm	No spines
	<i>Setaria parviflora</i>	Poaceae	35cm	No spines
ANR18A	<i>Polypremum procumbens</i>	Tetrachondraceae	5cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	85cm	No spines
	<i>Setaria parviflora</i>	Poaceae	115cm	No spines
ANR18B	<i>Ruellia humilis</i>	Acanthaceae	40cm	No spines
	<i>Plantago major</i>	Plantaginaceae	45cm	No spines
	<i>Eragrostis spectabilis</i>	Poaceae	70cm	No spines
	<i>Sabatia angularis</i>	Gentianaceae	35cm	No spines

SITE 2

Sample plot	Species	Family	Plant height	Spinescence
ANR7A	<i>Polypremum</i>	Tetrachondrace	30cm	No spines
	<i>procumbens</i>	ae		
	<i>Eragrostis curvula</i>	Poaceae	150cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	30cm	No spines
ANR7B	<i>Nassella pulchra</i>	Poaceae	90cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	170cm	No spines
ANR8A	<i>Pseudognaphalium</i>	Astraceae	20cm	No spines
	<i>obtusifolium</i>			
	<i>Bouteloua curtipendula</i>	Poaceae	20cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	110cm	No spines
	<i>Asclepias Asperula</i>	Apocynaceae	25cm	No spines
ANR8B	<i>Eragrostis curvula</i>	Poaceae	85cm	No spines
	<i>Pseudognaphalium</i>	Astraceae	22cm	No spines
	<i>obtusifolium</i>			
	<i>Polypremum</i>	Tetrachondrace	5cm	No spines
	<i>procumbens</i>	ae		
ANR9A	<i>Eragrostis curvula</i>	Poaceae	25cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	31cm	No spines
	<i>Salvia sage</i>	Laminaceae	2cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	25cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	145cm	No spines
ANR9B	<i>Eragrostis curvula</i>	Poaceae	110cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	25cm	No spines
	<i>Pseudognaphalium</i>	Astraceae	150cm	No spines
	<i>obtusifolium</i>			
ANR10A	<i>Eragrostis curvula</i>	Poaceae	180cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	140cm	No spines
	<i>Pseudognaphalium</i>	Astraceae	140cm	No spines
	<i>obtusifolium</i>			
ANR10B	<i>Erigeron canadensis</i>	Astraceae	110cm	No spines
	<i>Pseudognaphalium</i>	Astraceae	150cm	No spines
	<i>obtusifolium</i>			
	<i>Eragrostis curvula</i>	Poaceae	190cm	No spines

	<i>Chamaecrista fasciculata</i>	Fabaceae	40cm	No spines
ANR11A	<i>Erigeron canadensis</i>	Astraceae	150cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Astraceae	112cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	155cm	No spines
ANR11B	<i>Plantago lanceolata</i>	Plantaginaceae	5cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	18cm	No spines
	<i>Pseudognaphalium obtusifolium</i>	Astraceae	150cm	No spines
ANR12A	<i>Eragrostis curvula</i>	Poaceae	100cm	No spines
	<i>Melinis repens</i>	Poaceae	101cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	92cm	No spines
	<i>Helichrysum luteoalbum</i>	Astraceae	22cm	No spines
ANR12B	<i>Tanacetum vulgare</i>		55cm	No spines
	<i>Helichrysum luteoalbum</i>	Astraceae	55cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	25cm	No spines
SITE 3				No spines
Sample plot	Species	Family	Plant height	Spinescence
ANR1A	<i>Eragrostis cilianensis</i>	Poaceae	41cm	No spines
	<i>Panicum scoparium</i>	Poaceae	150cm	No spines
	<i>Lysimachia arvensis</i>	Primulaceae	21cm	No spines
	<i>Cyanotis arachnoidea</i>	Commelinaceae	20cm	No spines
	<i>Cologania angustifolia</i>	Fabaceae	42cm	No spines
ANR1B	<i>Eragrostis cilianensis</i>	Poaceae	42cm	No spines
	<i>Panicum scoparium</i>	Poaceae	150cm	No spines
	<i>Asclepias verticillata</i>	Apocynaceae	71cm	No spines
ANR2A	<i>Eragrostis cilianensis</i>	Poaceae	21cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	20cm	No spines
	<i>Panicum scoparium</i>	Poaceae	90cm	No spines
ANR2B	<i>Eragrostis cilianensis</i>	Poaceae	40cm	No spines
	<i>Panicum scoparium</i>	Poaceae	72cm	No spines
	<i>Melinis repens</i>	Poaceae	51cm	No spines

ANR3A	<i>Eragrostis cilianensis</i>	Poaceae	10cm	No spines
	<i>Panicum scoparium</i>	Poaceae	55cm	No spines
ANR3B	<i>Eragrostis cilianensis</i>	Poaceae	41cm	No spines
	<i>Asclepias viridis</i>	Apocynaceae	60cm	No spines
	<i>Gazania linearis</i>	Asteraceae	2cm	No spines
	<i>Panicum scoparium</i>	Poaceae	23cm	No spines
ANR4A	<i>Bouteloua curtipendula</i>	Poaceae	30cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	41cm	No spines
	<i>Panicum oligosanthos</i>	Poaceae	50cm	No spines
ANR4B	<i>Panicum scoparium</i>	Poaceae	120cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	41cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	12cm	No spines
ANR5A	<i>Eragrostis cilianensis</i>	Poaceae	10cm	No spines
	<i>Panicum scoparium</i>	Poaceae	110cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	25cm	No spines
ANR5B	<i>Panicum scoparium</i>	Poaceae	150cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	50cm	No spines
	<i>Melinis repens</i>	Poaceae	101cm	No spines
	<i>Plantago aristate</i>	Plantaginaceae	41cm	No spines
ANR6A	<i>Ziziphus mucronata</i>	Rhamnaceae	200cm	Spines
	<i>Eragrostis cilianensis</i>	Poaceae	50cm	No spines
	<i>Panicum scoparium</i>	Poaceae	12cm	No spines
	<i>Eupatorium capillifolium</i>	Astrearaceae	30cm	No spines
ANR6B	<i>Ziziphus mucronata</i>	Rhamnaceae	250cm	Spines
	<i>Panicum scoparium</i>	Poaceae	22cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	10cm	No spines

Suikerbosrand Nature Reserve

Table C2: Plant species recorded within the study sites of Suikerbosrand nature reserve.

SITE 1				
Sample plot	Species	Family	Plant height	spinescence
SNR13 A	<i>Lomatium utriculatum</i>	Apiaceae	15cm	No spines
	<i>Lepidium latifolium</i>	Brassicaceae	50cm	No spines
	<i>Imperata cylindrica</i>	Poaceae	60cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	52cm	No spines
	<i>Centranthus ruber</i>	Caprifoliaceae	50cm	No spines
SNR13 B	<i>Schizachyrium scoparium</i>	Poaceae	121cm	No spines
	<i>Verbena halei</i>	Verbenaceae	20cm	No spines
	<i>Gazania rigens</i>	Asteraceae	50cm	No spines
	<i>Eragrostis spectabilis</i>	Poaceae	70cm	No spines
	<i>Juncus tenuis</i>	Juncaceae	25cm	No spines
	<i>Sisyrinchium angustifolium</i>	Iridaceae	47cm	No spines
SNR14 A	<i>Ajuga genevensis</i>	Laminaceae	10cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	80cm	No spines
	<i>Comandra umbellata</i>	Santalaceae	8cm	No spines
SNR14 B	<i>Verbena rigida</i>	Verbenaceae	50cm	No spines
	<i>Ziziphus mucronate</i>	Rhamnaceae	100cm	Spines
	<i>Heteropogon contortus</i>	Poaceae	21cm	No spines
	<i>Ipomoea aquatica</i>	Convolvulaceae	15cm	No spines

	<i>Schizachyrium scoparium</i>	Poaceae	72cm	No spines
SNR15 A	<i>Verbena rigida</i>	Verbenaceae	50cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	90cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	52cm	No spines
	<i>Euphorbia corollata</i>	Euphorbiaceae	61cm	No spines
SNR15 B	<i>Verbena rigida</i>	Verbenaceae	50cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	71cm	No spines
	<i>Antennaria rosea</i>	Asteraceae	6cm	No spines
	<i>Scutellaria parvula</i>	Lamiaceae	15cm	No spines
SNR16 A	<i>Heteropogon contortus</i>	Poaceae	25cm	No spines
	<i>Danthonia spicata</i>	Poaceae	20cm	No spines
	<i>Ajuga reptans</i>	Lamiaceae	15cm	No spines
SNR16 B	<i>Verbena rigida</i>	Verbenaceae	50cm	No spines
	<i>Ajuga reptans</i>	Lamiaceae	25cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	71cm	No spines
	<i>Echinacea angustifolia</i>	Asteraceae	41cm	No spines
SNR17 A	<i>Helenium autumnale</i>	Asteraceae	30cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	20cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	25cm	No spines
	<i>Plantago major</i>	Plantaginaceae	10cm	No spines
SNR17 B	<i>Aruga reptans</i>	Lamiaceae	7cm	No spines
	<i>Plantago lanceolata</i>	Plantaginaceae	15cm	No spines

SNR18 A	<i>Verbena rigida</i>	Verbenaceae	12cm	No spines
	<i>Lomatium dissectum</i>	Apiaceae	114cm	No spines
	<i>Centratherus ruber</i>	Caprifoliaceae	51cm	No spines
	<i>Eragrostis cilianensis</i>	Poaceae	41cm	No spines
	<i>Imperata cylindrica</i>	Poaceae	60cm	No spines
	<i>Helenium autumnale</i>	Asteraceae	51cm	No spines
SNR18 B	<i>Helenium flexuosum</i>	Asteraceae	30cm	No spines
	<i>Themeda triandra</i>	Poaceae	50cm	No spines
	<i>Ajuga genevensis</i>	Lamiaceae	35cm	No spines
SITE 2				
Sample plot	Species	Family name	Plant height	Spinescence
SNR19 A	<i>Anaphalis margaritacea</i>	Astraceae	50cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	56cm	No spines
	<i>Cynodon dactylon</i>	Poaceae	8cm	No spines
	<i>Tanacetum vulgare</i>	Astraceae	60cm	No spines
SNR19 B	<i>Melinis repens</i>	Poaceae	51cm	No spines
	<i>Croton glandulosus</i>	Euphorbiaceae	15cm	No spines
	<i>Anaphalis margaritacea</i>	Astraceae	51cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	120cm	No spines
SNR20 A	<i>Melinis repens</i>	Poaceae	25cm	No spines
	<i>Tanacetum vulgare</i>	Astraceae	52cm	No spines
	<i>Echinochloa crus-galli</i>	Poaceae	40cm	No spines
	<i>Ulex europaeus</i>	Fabaceae	200cm	No spines
SNR20 B	<i>Tanacetum vulgare</i>	Astraceae	50cm	No spines
	<i>Themeda triandra</i>	Poaceae	26cm	No spines

	<i>Ajuga reptans</i>	Lamiaceae	7cm	No spines
	<i>Cynodon dactylon</i>	Poaceae	10cm	No spines
	<i>Ziziphus mucronata</i>	Rhamnaceae	105cm	No spines
SNR21	<i>Koeleria macrantha</i>	Poaceae	30cm	No spines
A				
	<i>Aloe maculata</i>	Asphodelaceae	30cm	No spines
	<i>Melinis repens</i>	Poaceae	21cm	No spines
	<i>Cynodon dactylon</i>	Poaceae	5cm	No spines
SNR21	<i>Crotalaria tinctoria</i>	Astraceae	20cm	No spines
B				
	<i>Melinis repens</i>	Poaceae	21cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	15cm	No spines
SNR22	<i>Sorghastrum nutans</i>	Poaceae	150cm	No spines
A				
	<i>Heteropogon contortus</i>	Poaceae	21cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	51cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	20cm	No spines
	<i>Koeleria macrantha</i>	Poaceae	30cm	No spines
SNR22	<i>Heteropogon contortus</i>	Poaceae	15cm	No spines
B				
	<i>Eragrostis curvula</i>	Poaceae	22cm	No spines
	<i>Koeleria macrantha</i>	Poaceae	62cm	No spines
SNR23	<i>Melinis repens</i>	Poaceae	112cm	No spines
A				
	<i>Helenium amarum</i>	Astraceae	50cm	No spines
	<i>Plantago major</i>	Plantaginaceae	10cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	51cm	No spines
SNR23	<i>Plantago major</i>	Plantaginaceae	7cm	No spines
B				
	<i>Anaphalis margaritacea</i>	Astraceae	20cm	No spines

	<i>Heteropogon contortus</i>	Poaceae	22cm	No spines
SNR24 A	<i>Anaphalis margaritacea</i>	Astraceae	51cm	No spines
	<i>Sida spinosa</i>	Malvaceae	21cm	No spines
	<i>Tagetes erecta</i>	Astraceae	51cm	No spines
	<i>Cynodon dactylon</i>	Poaceae	11cm	No spines
SNR24 B	<i>Cota tinctoria</i>	Astraceae	55cm	No spines
	<i>Themeda triandra</i>	Poaceae	55cm	No spines
	<i>Lantana montevidensis</i>	Verbenaceae	30cm	No spines
SITE 3				
Sample plot	Species	Family	Plant height	Spinescence
SNR25 A	<i>Vachellia confusa</i>	Fabaceae	12cm	No spines
	<i>Bothriochloa ischaemum</i>	Poaceae	15cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	51cm	No spines
	<i>Artemisia ludoviciana</i>	Astraceae	34cm	No spines
SNR25 B	<i>Bothriochloa ischaemum</i>	Poaceae	11cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	45cm	No sines
	<i>Symphytum officinale</i>	Boraginaceae	50cm	No spines
	<i>Linaria vulgaris</i>	Plantaginaceae	55cm	No spines
SNR26 A	<i>Artemisia ludoviciana</i>	Astraceae	51cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	48cm	No spines
	<i>Themeda triandra</i>	Poaceae	33cm	No spines
	<i>Tanacetum vulgare</i>	Astraceae	128cm	No spines

SNR26 B	<i>Artemisia ludoviciana</i>	Astraceae	51cm	No spines
	<i>Echium vulgare</i>	Boraginaceae	26cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	55cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	32cm	No spines
	<i>Epipactis helleborine</i>	Orchidaceae	21cm	No spines
	<i>Dalea purpurea</i>	Fabaceae	30cm	No spines
SNR27 A	<i>Artemisia ludoviciana</i>	Astraceae	51cm	No spines
	<i>Themeda triandra</i>	Poaceae	33cm	No spines
	<i>Tanacetum vulgare</i>	Astraceae	51cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	21cm	No spines
	<i>Ptela trifoliata</i>	Rutaceae	2cm	No spines
SNR27 B	<i>Verbena rigida</i>	Verbenaceae	29cm	No spines
	<i>Artemisia ludoviciana</i>	Astraceae	33cm	No spines
	<i>Ptela trifoliata</i>	Rutaceae	1cm	No spines
	<i>Imperata cylindrica</i>	Poaceae	61cm	No spines
	<i>Lavandula angustifolia</i>	Lamiaceae	105cm	No spines
SNR28 A	<i>Helichrysum luteoalbum</i>	Astraceae	58cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	47cm	No spines
	<i>Verbena rigida</i>	Verbenaceae	28cm	No spines
	<i>Themeda triandra</i>	Poaceae	51cm	No spines
SNR28 B	<i>Themeda triandra</i>	Poaceae	21cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	21cm	No spines
	<i>Artemisia ludoviciana</i>	Astraceae	28cm	No spines

SNR29	<i>Artemisia ludoviciana</i>	Astraceae	51cm	No spines
A				
	<i>Themeda triandra</i>	Poaceae	23cm	No spines
	<i>Verbana bonariensis</i>	Verbenacea	150cm	No spines
		e		
	<i>Ruellia humilis</i>	Acanthacea	30cm	No spines
		e		
SNR29	<i>Ruellia humilis</i>	Acanthacea	52cm	No spines
B		e		
	<i>Themeda triandra</i>	Poaceae	38cm	No spines
	<i>Verbana rigida</i>	Verbenacea	51cm	No spines
		e		
SNR30	<i>Ruellia humilis</i>	Acanthacea	51cm	No spines
A		e		
	<i>Themeda triandra</i>	Poaceae	45cm	No spines
	<i>Verbana bonariensis</i>	Verbenacea	138cm	No spines
		e		
	<i>Grangea maderaspatana</i>	Astraceae	10cm	No spines
SNR30	<i>Verbana rigida</i>	Verbenacea	50cm	No spines
B		e		
	<i>Themeda triandra</i>	Poaceae	61cm	No spines
	<i>Grangea maderaspatana</i>	Astraceae	5cm	No spines
	<i>Verbana bonariensis</i>	Verbenacea	51cm	No spines
		e		
	<i>Ruellia humilis</i>	Acanthacea	53cm	No spines
		e		
	<i>Artemisia ludoviciana</i>	Astraceae	33cm	No spines

Roodeplaat Dam Nature Reserve

Table C3: Plant species recorded within the study sites of Roodeplaat Dam nature reserve.

SITE 1				
Sample plot	Species	Family	Plant height	Spinecesne
RNR1A	<i>Anemarrhena asphodeloides</i>	Asparagaceae	56cm	No spines
	<i>Setaria parviflora</i>	Poaceae	51cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	57cm	No spines
	<i>Sorghastrum nutans</i>	Poaceae	110cm	No spines
RNR1B	<i>Eragrostis curvula</i>	Poaceae	102cm	No spines
	<i>Verbana stricta</i>	Verbenaceae	60cm	No spines
	<i>Setaria parviflora</i>	Poaceae	41cm	No spines
RNR2A	<i>Eleocharis acicularis</i>	Cyperaceae	3cm	No spines
	<i>Hexasepalum teres</i>	Rubiaceae	41cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	51cm	No spines
	<i>Setaria parviflora</i>	Poaceae	34cm	No spines
RNR2B	<i>Setaria parviflora</i>	Poaceae	37cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	109cm	No spines
	<i>Danthonia spicata</i>	Poaceae	21cm	No spines
	<i>Indigofera miniata</i>	Fabaceae	2cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	51cm	No spines
RNR3A	<i>Themeda triandra</i>	Poaceae	51cm	No spines
	<i>Setaria parviflora</i>	Poaceae	108cm	No spines
	<i>Eragrostis spectabilis</i>	Poaceae	21cm	No spines
	<i>Cyperus brevifolius</i>	Cyperaceae	3cm	No spines
	<i>Dianthus armeria</i>	Caryophyllaceae	41cm	No spines
RNR3B	<i>Themeda triandra</i>	Poaceae	50cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	110cm	No spines
	<i>Tagetes erecta</i>	Astraceae	20cm	No spines
	<i>Danthonia spicata</i>	Poaceae	51cm	No spines
RNR4A	<i>Erigeron canadensis</i>	Astraceae	50cm	No spines

	<i>Setaria parviflora</i>	Poaceae	111cm	No spines
	<i>Eupatorium capillifolium</i>	Astraceae	51cm	No spines
	<i>Vachellia farnesiana</i>	Fabaceae	93cm	No spines
RNR4B	<i>Erigeron bonariensis</i>	Astraceae	10cm	No spines
	<i>Dianthus armeria</i>	Caryophyllaceae	51cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	48cm	No spines
	<i>Eupatorium capillifolium</i>	Astraceae	64cm	No spines
RNR5A	<i>Eupatorium capillifolium</i>	Astraceae	51cm	No spines
	<i>Setaria parviflora</i>	Poaceae	108cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	54cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	21cm	No spines
RNR5B	<i>Eragrostis spectabilis</i>	Poaceae	30cm	No spines
	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
	<i>Tanacetum vulgare</i>	Astraceae	122cm	No spines
	<i>Dianthus armeria</i>	Caryophyllaceae	15cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	71cm	No spines
RNR6A	<i>Vachellia farnesiana</i>	Fabaceae	150cm	No spines
	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
	<i>Verbena bonariensis</i>	Verbenaceae	150cm	No spines
	<i>Erigeron canadensis</i>	Astraceae	51cm	No spines
RNR6B	<i>Setaria parviflora</i>	Poaceae	51cm	No spines
	<i>Anemarrhena asphodeloides</i>	Asparagaceae	84cm	No spines

SITE 2

Sample plot	Species	Family	Plant height	Spinescence
RNR7A	<i>Schizachyrium scoparium</i>	Poaceae	31cm	No spines
	<i>Asclepias viridis</i>	Apocynaceae	45cm	No spines

	<i>Melinis repens</i>	Poaceae	51cm	No spines
	<i>Mimosa pudica</i>	Fabaceae	15cm	No spines
RNR7B	<i>Tagetes erecta</i>	Asteraceae	21cm	No spines
	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
	<i>Sorghastrum nutans</i>	Poaceae	115cm	No spines
RNR8A	<i>Setaria parviflora</i>	Poaceae	30cm	No spines
	<i>Eragrostis spectabilis</i>	Poaceae	71cm	No spines
	<i>Schizachyrium scoparium</i>	Poaceae	57cm	No spines
	<i>Eupatorium capillifolium</i>	Asteraceae	89cm	No spines
RNR8B	<i>Setaria parviflora</i>	Poaceae	51cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	28cm	No spines
	<i>Bouteloua curtipendula</i>	Poaceae	31cm	No spines
RNR9A	<i>Setaria parviflora</i>	Poaceae	111cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	51cm	No spines
	<i>Heteropogon contortus</i>	Poaceae	27cm	No spines
	<i>Eupatorium capillifolium</i>	Asteraceae	89cm	No spines
	<i>Paspalum notatum</i>	Poaceae	51cm	No spines
RNR9B	<i>Setaria parviflora</i>	Poaceae	108cm	No spines
	<i>Eragrostis curvula</i>	Poaceae	28cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	58cm	No spines
	<i>Eupatorium capillifolium</i>	Asteraceae	41cm	No spines
	<i>Koeleria macrantha</i>	Poaceae	55cm	No spines
RNR10 A	<i>Eupatorium capillifolium</i>	Asteraceae	24cm	No spines
	<i>Melinis repens</i>	Poaceae	101cm	No spines
	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	21cm	No spines
RNR10 B	<i>Setaria parviflora</i>	Poaceae	22cm	No spines
	<i>Artemisia ludoviciana</i>	Asteraceae	61cm	No spines
	<i>Ruellia nudiflora</i>	Acanthaceae	51cm	No spines

	<i>Lepidium didymum</i>	Brassicaceae	12cm	No spines
RNR11	<i>Setaria parviflora</i>	Poaceae	107cm	No spines
A				
	<i>Tagetes erecta</i>	Asteraceae	117cm	No spines
	<i>Asclepias asperula</i>	Apocynaceae	23cm	No spines
RNR11	<i>Tagetes erecta</i>	Asteraceae	141cm	No spines
B				
	<i>Setaria parviflora</i>	Poaceae	115cm	No spines
	<i>Eupatorium capillifolium</i>	Asteraceae	48cm	No spines
RNR12	<i>Ruellia nudiflora</i>	Acanthaceae	31cm	No spines
A				
	<i>Eragrostis curvula</i>	Poaceae	31cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	103cm	No spines
	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
RNR12	<i>Setaria parviflora</i>	Poaceae	115cm	No spines
B				
	<i>Tagetes erecta</i>	Asteraceae	51cm	No spines
	<i>Schizachyrium scoparium</i>	Poaceae	121cm	No spines
SITE 3				
Sample plot	Species	Family	Plant height	Spinescence
RNR13	<i>Setaria parviflora</i>	Poaceae	31cm	No spines
A				
	<i>Eragrostis curvula</i>	Poaceae	58cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	61cm	No spines
	<i>Ruellia nudiflora</i>	Acanthaceae	31cm	No spines
RNR13	<i>Tagetes erecta</i>	Asteraceae	31cm	No spines
B				
	<i>Setaria parviflora</i>	Poaceae	41cm	No spines
	<i>Schizachyrium scoparium</i>	Poaceae	28cm	No spines
RNR14	<i>Spiraea tomentosa</i>	Rosaceae	61cm	No spines
A				
	<i>Sorghastrum nutans</i>	Poaceae	150cm	No spines

	<i>Eragrostis secundiflora</i>	Poaceae	21cm	No spines
	<i>Tagetes erecta</i>	Asteraceae	109cm	No spines
RNR14	<i>Tagetes erecta</i>	Asteraceae	88cm	No spines
B				
	<i>Melinis repens</i>	Poaceae	51cm	No spines
	<i>Spiraea tomentosa</i>	Rosaceae	103cm	No spines
RNR15	<i>Tagetes erecta</i>	Asteraceae	101cm	No spines
A				
	<i>Spiraea tomentosa</i>	Rosaceae	100cm	No spines
	<i>Vachellia dealbata</i>	Fabaceae	28cm	No spines
RNR15	<i>Clematis vitalba</i>	Ranunculacea	200cm	No spines
B		e		
	<i>Tagetes erecta</i>	Asteraceae	100cm	No spines
	<i>Setaria parviflora</i>	Poaceae	58cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	60cm	No spines
RNR16	<i>Achnatherum</i>	Poaceae	60cm	No spines
A	<i>pekinense</i>			
	<i>Tagetes erecta</i>	Asteraceae	108cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	112cm	No spines
RNR16	<i>Tagetes erecta</i>	Asteraceae	101cm	No spines
B				
	<i>Ambrosia artemisiifolia</i>	Asteraceae	21cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	54cm	No spines
	<i>Achnatherum</i>	Poaceae	76cm	No spines
	<i>pekinense</i>			
RNR17	<i>Tagetes erecta</i>	Asteraceae	100cm	No spines
A				
	<i>Spiraea tomentosa</i>	Rosaceae	58cm	No spines
	<i>Eupatorium</i>	Asteraceae	51cm	No spines
	<i>capillifolium</i>			
	<i>Phylanthus urinata</i>	Phylanthacea	10cm	No spines
		e		
RNR17	<i>Setaria parviflora</i>	Poaceae	51cm	No spines
B				
	<i>Tagetes erecta</i>	Asteraceae	38cm	No spines

	<i>Achnatherum pekinense</i>	Poaceae	54cm	No spines
	<i>Bidens bipinnata</i>	Asteraceae	29cm	No spines
RNR18 A	<i>Tagetes erecta</i>	Asteraceae	117cm	No spines
	<i>Setaria parviflora</i>	Poaceae	51cm	No spines
	<i>Ruellia humilis</i>	Acanthaceae	51cm	No spines
	<i>Schizachyrium scoparium</i>	Poaceae	78cm	No spines
RNR18 B	<i>Tagetes erecta</i>	Asteraceae	105cm	No spines
	<i>Fimbrisylis littoralis</i>	Cyperaceae	5cm	No spines
	<i>Festuca idahoensis</i>	Poaceae	14cm	No spines
	<i>Urena lobata</i>	Malvaceae	68cm	No spines

Appendix D: Soil Microbes (Bacteria) results

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Figure D1: Soil microbes (bacteria) in the grazed plots in ANR site 1.

d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Acidobacteriales;f_SbA1;g_Gp1-AA122;s_Gp1-AA122 sp019244045
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Jatrophihabitantaceae;g_Jatrophihabitans;s_Jatrophihabitans endophyticus
 d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp003344625
 d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-89-9;s_3-1-20CM-4-89-9 sp013816245
 d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_Dormibacteriales;f_Dormibacteraceae;g_CF-28;s_CF-28 sp005881825
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Z2-YC6860;s_Z2-YC6860 sp001579645
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp004799405
 d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus_A;s_Bacillus_A bombysepticus
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium canariense
 d_Bacteria;p_Firmicutes;c_Bacilli;o_Paenibacillales;f_Paenibacillaceae;g_Cohnella;s_Cohnella panacari
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Dermatophilaceae;g_Knoellia;s_Knoellia remis
 d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_UBA4720;s_UBA4720 sp003134685
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium canariense_A
 d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Palsa-744;s_Palsa-744 sp013815355
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Cellulomonadaceae;g_Xylanimonas;s_Xylanimonas allomyrinae
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium diazoefficiens_A
 d_Bacteria;p_Dormibacterota;c_Dormibacteria;o_Dormibacteriales;f_Dormibacteraceae;g_40CM-4-65-16;s_40CM-4-65-16 sp005889135
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Mycobacterium;s_Mycobacterium pulveris
 d_Bacteria;p_Eremiobacterota;c_Eremiobacteria;o_Baltobacteriales;f_Baltobacteraceae;g_Elarobacter;s_Elarobacter winogradskyi
 d_Bacteria;p_Myxococcota;c_Myxococcia;o_Myxococcales;f_40CM-4-68-19;s_40CM-4-68-19 sp005879535
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Kineosporiaceae;g_R-H-3;s_R-H-3 sp002198855
 d_Bacteria;p_Chloroflexota;c_Ktedonobacteria;o_Ktedonobacteriales;f_Ktedonobacteraceae;g_UBA11361;s_UBA11361 sp005881295
 d_Bacteria;p_Actinobacteriota;c_Rubrobacteria;o_Rubrobacterales;f_Rubrobacteraceae;g_SCSIO-52909;s_SCSIO-52909 sp902812425
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Dermatophilaceae;g_Intrasporangium;s_Intrasporangium calvum
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium lablabi_C
 d_Bacteria;p_Firmicutes;c_Bacilli;o_Paenibacillales;f_Paenibacillaceae;g_Paenibacillus_C;s_Paenibacillus_C catalpae
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales;f_Streptosporangiaceae;g_Actinoallomurus;s_Actinoallomurus bryophytorum
 d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacteriales;f_Bryobacteraceae;g_Solibacter;s_Solibacter usitatus_A
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Geodermatophilaceae;g_Geodermatophilus_A;s_Geodermatophilus_A daqingensis
 d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Kineosporiaceae;g_JADJPO01;s_JADJPO01 sp016713225
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_Reyranella;s_Reyranella sp017305915
 d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp000472385

Figure D2: Soil microbes (bacteria) in the ungrazed plots in ANR in site 1.



Figure D4: Soil microbes (bacteria) in ungrazed plots in ANR site 2.

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Figure D5: Soil microbes (bacteria) in grazed plots in SNR site 1.

Unassigned; ; ; ; ; ; ; ;
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Gaiellales,f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9 sp013816245
d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacteriales,f_UBA10450;g_Udaeobacter;s_Udaeobacter sp003221195
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium lablabi_C
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp003344825
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;
d_Bacteria;p_Actinobacteriota;c_Rubrobacteria;o_Rubrobacterales,f_Rubrobacteraceae;g_SCSIO-52909;s_SCSIO-52909 sp902812425
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp00425945
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus sp000702465
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Dermatophilaceae;g_Lapillicoccus;s_Lapillicoccus jejuensis
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Propionibacteriaceae;g_Microlunatus_C;s_Microlunatus_C panaciterrae
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Rhizobiaceae;g_OAS926;s_OAS926 sp014873545
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Gaiellales,f_Gaiellaceae;g_GMQP-bins7;s_GMQP-bins7 sp004388385
d_Bacteria;p_Actinobacteriota;c_UBA4738;o_UBA4738,f_HRBIN12;g_AC-51;
d_Bacteria;p_Chloroflexota;c_Limnocyndria;o_Limnocyndrales,f_CSP1-4;g_UBA5189;s_UBA5189 sp013822395
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales,f_Streptosporangiaceae;g_Actinoallomurus;s_Actinoallomurus bryophytorum
d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacteriales,f_UBA10450;g_Udaeobacter;s_Udaeobacter sp003218815
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Micromonosporaceae;g_Rugosimonospora;s_Rugosimonospora africana
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Z2-YC6860;s_Z2-YC6860 sp001579845
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Nocardioidaceae;g_Nocardioides;s_Nocardioides anomalus
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Methylobacteriaceae;g_Methyloceanibacter;s_Methyloceanibacter sp016889535
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptomyces;s_Streptomyces cadmiisoli
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium manausense_A
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Jatrophihabitantaceae;g_Jatrophihabitans;s_Jatrophihabitans endophyticus
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Micromonosporaceae;g_Virgisporangium;s_Virgisporangium ochraceum
d_Bacteria;p_Acidobacteriota;c_Acidobacteriales,f_Acidobacteriaceae;g_KBS-83;s_KBS-83 sp000381585
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Angustibacteraceae;g_Angustibacter;s_Angustibacter sp001426435
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Nocardioidaceae;g_Marmoricola;s_Marmoricola sp000426045
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp004212635
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Niallia;s_Niallia circulans_A
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Nocardioidaceae;g_Marmoricola;s_Marmoricola solisilvae

Figure D6: Soil microbes (bacteria) in ungrazed plots in SNR site 2.

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Dermatophilaceae;g_Knoellia;s_Knoellia remisii

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Geodermatophilus_A;s_Geodermatophilus_A daqingensis

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Mycobacteriaceae;g_Mycobacterium;s_Mycobacterium morioakaense_B

d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales,f_Bacillaceae_G;g_Bacillus_A;s_Bacillus_A toyonensis

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Micromonosporaceae;g_Rugosimonospora;s_Rugosimonospora sp005885555

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Cellulomonadaceae;g_Cellulomonas;s_Cellulomonas composti

d_Bacteria;p_Acidobacteriota;c_Acidobacteriae;o_Bryobacterales,f_Bryobacteraceae;g_Solibacter;s_Solibacter usitatus_A

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales,f_Sphingomonadaceae;g_Sphingomicrobium;s_Sphingomicrobium sp009720245

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Kineosporiaceae;g_JADJPO01;s_JADJPO01 sp016713225

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Micropepsales,f_Micropepsaceae;g_Rhizomicrobium;s_Rhizomicrobium sp018449595

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Propionibacteriaceae;g_Friedmanniella;s_Friedmanniella luteola

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales,f_Reyranellaceae;g_Reyranella;s_Reyranella soli

d_Bacteria;p_Chloroflexota;c_Limnocyndria;o_Limnocyndrales,f_CSP1-4;g_UBA5189;s_UBA5189 sp013822395

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp004212635

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium jicamae_A

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Kineosporiaceae;g_R-H-3;s_R-H-3 sp002198855

d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter soli

d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales,f_Sphingomonadaceae;g_Allosphingosinicella;s_Allosphingosinicella sp003347635

d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp000425945

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Propionibacteriaceae;g_Microlunatus_A;s_Microlunatus_A endophyticus

d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales,f_UBA10450;g_Udaeobacter;s_Udaeobacter sp003218615

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Pseudonocardiaceae;g_Actinomycetospora;s_Actinomycetospora cinnamomea

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Micrococcaceae;g_Arthrobacter;_

d_Bacteria;p_Chloroflexota;c_UBA2235;o_UBA12225;f_UBA12225;g_UBA12225;s_UBA12225 sp002347925

d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales,f_70-9;g_VAYN01;s_VAYN01 sp005885405

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Actinomycetaceae;g_Georgenia;s_Georgenia thermotolerans

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Nocardioidaceae;g_Nocardioides_B;s_Nocardioides_B innotensis

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Mycobacteriaceae;g_Mycobacterium;s_Mycobacterium sp003053885

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Pseudonocardiaceae;g_Actinomycetospora;s_Actinomycetospora corticicola

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus massiliensis

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus sp00188025

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Streptosporangiales,f_Streptosporangiaceae;g_Trebonia;s_Trebonia kvetii

d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Micromonosporaceae;g_Micromonospora;

Figure D7: Soil microbes (bacteria) in grazed plots in SNR site 2.

Unassigned; ; ; ; ;
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-18226;g_Bacillus_BD;s_Bacillus_BD endozanthoxylicus
d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales;f_UBA10450;g_Udaeobacter;s_Udaeobacter sp003221195
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus sp000702465
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Gaiellales;f_Gaiellaceae;g_3-1-20CM-4-69-9;s_3-1-20CM-4-69-9 sp013816245
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales;f_Propionibacteriaceae;g_Microlunatus_C;s_Microlunatus_C panaciterrae
d_Bacteria;p_Actinobacteriota;c_Rubrobacteria;o_Rubrobacterales;f_Rubrobacteraceae;g_SCSIO-52909;s_SCSIO-52909 sp902812425
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-18226;g_Nallia;s_Nallia circulans_A
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae_G;g_Bacillus_A;s_Bacillus_A pseudomycoides_B
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Angustibacteraceae;g_Angustibacter;s_Angustibacter sp001426435
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-1321;g_Peribacillus;s_Peribacillus loiseleuriae
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-18226;g_Bacillus_BD;s_Bacillus_BD benzoovorans
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-1321;g_Peribacillus;s_Peribacillus simplex_D
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp018596315
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Dermatophilaceae;g_Lapillicoccus;s_Lapillicoccus jejuensis
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubacter;s_Solirubacter sp000425945
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium lablabi_C
d_Bacteria;p_Chloroflexota;c_Limnocyndria;o_Limnocyndrales;f_CSP1-4;g_UBA5189;s_UBA5189 sp013822395
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_Sphingomicrobium sp000620665
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_Reyranella;s_Reyranella soli
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_Solirubrobacteraceae;g_Solirubacter;s_Solirubacter sp003344625
d_Bacteria;p_Desulfobacterota_B;c_Binatia;o_UBA9968;f_UBA9968;g_DP-1;s_DP-1 sp005879605
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_Sphingomicrobium sp009720245
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_Sphingomicrobium lutea
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Microvira;s_Microvira ossetica
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter;_
d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Xanthomonas;s_Xanthomonas cissicola
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_70-9;g_VAYN01;s_VAYN01 sp005885405
d_Bacteria;p_Actinobacteriota;c_Thermoleophila;o_Solirubrobacterales;f_70-9;g_VAYN01;s_VAYN01 sp018268415
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-1321;g_Peribacillus;s_Peribacillus butanolivorans
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter_I;_
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp000472385
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_D;f_Amphibacillaceae;g_Oceanobacillus;s_Oceanobacillus zhaokaii

Figure D9: Soil microbe(bacteria) in grazed plots in SNR site 3.

Unassigned;_:_:_:_:_:_
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Bacillus_BD;s_Bacillus_BD endozanthoxylicus
d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Gaiellales,f_Gaiellaceae;g_3-1-20CM-4-89-9;s_3-1-20CM-4-89-9 sp013816245
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Niallia;s_Niallia circulars_B
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus sp004570875
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_D,f_Amphibacillaceae;g_Oceanobacillus;s_Oceanobacillus zhaokaii
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Angustibacteraceae;g_Angustibacter;s_Angustibacter sp001426435
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Propionibacteriaceae;g_Microlunatus_C;s_Microlunatus_C panaciterrae
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Niallia;_
d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Chthoniobacterales,f_UBA10450;g_Udaeobacter;s_Udaeobacter sp003221195
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium sp018598315
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Neobacillus;s_Neobacillus sp000103525
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales,f_Geodermatophilaceae;g_Blastococcus;s_Blastococcus sp000702485
d_Bacteria;p_Actinobacteriota;c_Rubrobacteria;o_Rubrobacterales,f_Rubrobacteraceae;g_SCSIO-52909;s_SCSIO-52909 sp002812425
d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp000425945
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Bacillus_BD;s_Bacillus_BD benzoovorans
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium lablabi_C
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_Bradyrhizobium;s_Bradyrhizobium canariense
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_A,f_Planococcaceae;g_Ureibacillus;s_Ureibacillus halotolerans
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_A,f_Planococcaceae;g_Psychrobacillus;s_Psychrobacillus sp000111345
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_A,f_Planococcaceae;g_Sporosarcina;s_Sporosarcina luteola
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Propionibacteriales,f_Nocardioidaceae;g_Nocardioides;s_Nocardioides anomalus
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-1321;g_Peribacillus;s_Peribacillus butanolivorans
d_Bacteria;p_Chloroflexota;c_Limnocyndria;o_Limnocyndrales,f_CSP1-4;g_C-114;s_C-114 sp015478725
d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales,f_Solirubrobacteraceae;g_Solirubrobacter;s_Solirubrobacter sp003344625
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Micrococcaceae;g_Arthrobacter;_
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Xanthobacteraceae;g_BOG-931;s_BOG-931 sp019075925
d_Bacteria;p_Actinobacteriota;c_Actinomycetia;o_Actinomycetales,f_Dermatophilaceae;g_Lapillicoccus;s_Lapillicoccus jejuensis
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-18226;g_Neobacillus;s_Neobacillus sp004341175
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-1321;g_Peribacillus;s_Peribacillus loiseleuriae
d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Gemmatimonadales,f_Gemmatimonadaceae;g_UBA4720;s_UBA4720 sp003134685
d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales,f_Rhizobiaceae;g_OAS926;s_OAS926 sp014873545
d_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales_B,f_DSM-1321;g_Peribacillus;s_Peribacillus sp000112495

Figure D10: Soil microbes (bacteria) in ungrazed plots in SNR site 3.

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas;s_Pseudomonas aeruginosa

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella variicola

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter kobei

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter asburiae_B

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter roggienkampii

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter_A;s_Citrobacter_A amalonaticus

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter pseudoroggienkampii

d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Ochrobactrum;s_Ochrobactrum intermedium

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter braakii

d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Ochrobactrum;s_Ochrobactrum sp900470195

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter dissolvens

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter mori

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter werkmanii

d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus_D;s_Enterococcus_D casseliflavus

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella quasipneumoniae

d_Bacteria;p_Bacillota_A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium_J;s_Clostridium_J sulfidigenes

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter europaeus

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Achromobacter;s_Achromobacter sp001270295

Unassigned;;;

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter portucalensis

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Achromobacter;s_Achromobacter pulmonis_A

d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus_D;s_Enterococcus_D innesii

d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Alpha-05;s_Alpha-05 sp900079695

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter freundii

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter hormaechei_B

d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Kaistiaceae;g_Kaistia;s_Kaistia geumhonensis

d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium;s_Phenylobacterium sp018240795

d_Bacteria;p_Bacillota_A;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;s_Clostridium sartagoforme_A



d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Pelomonas;_
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Steroidobacteriales;f_Steroidobacteriaceae;g_SCUD01;s_SCUD01 sp019634895
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Mesorhizobium;s_Mesorhizobium sp002294725
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium;s_Novosphingobium sp026672515
d_Bacteria;p_Actinomyetota;c_Actinomycetes;o_Actinomycetales;f_Microbacteriaceae;g_Agromyces;s_Agromyces bauzanensis
d_Bacteria;p_Actinomyetota;c_Actinomycetes;o_Mycobacteriales;f_Micromonosporaceae;g_Micromonospora;s_Micromonospora deserti
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Shinella;s_Shinella sp024704725
d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Cytophagales;f_Cyclobacteriaceae;g_Chryseolinea;s_Chryseolinea sp029360725
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Caldimonas;s_Caldimonas mangrovi
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Rhodocyclaceae;g_Desulfobacillus;s_Desulfobacillus sp002840845
d_Bacteria;p_Actinomyetota;c_Actinomycetes;o_Actinomycetales;f_Microbacteriaceae;g_Agromyces;s_Agromyces albus
d_Bacteria;p_Acidobacteriota;c_Vicinamibacteria;o_Vicinamibacteriales;f_UBA2999;g_Gp6-AA45;s_Gp6-AA45 sp020073005
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_JAEWPB01;s_JAEWPB01 sp030028905
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Mesorhizobium;s_Mesorhizobium wenxiniae
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Bejerinckiacae;g_Microvirga;s_Microvirga subterranea
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium;s_Novosphingobium sp000272475
d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_JAFAEM01;s_JAFAEM01 sp026360765
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Aquabacterium;s_Aquabacterium sp005502875
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Bejerinckiacae;g_Microvirga;s_Microvirga pudoricolor
d_Bacteria;p_Acidobacteriota;c_Blastocatellia;o_Pyrinomonadales;f_Pyrinomonadaceae;g_OLB17;s_OLB17 sp002333435
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Devosiaceae;g_Devosia_A;s_Devosia_A sp001402915
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Rhizobium;s_Rhizobium yanglingense
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Xanthomonas_A;s_Xanthomonas_A sp025665335
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Ochrobactrum;s_Ochrobactrum anthropi
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomicrobium;s_Sphingomicrobium astaxanthinifaciens_A
d_Bacteria;p_Actinomyetota;c_Actinomycetes;o_Actinomycetales;f_Microbacteriaceae;g_Microbacterium;s_Microbacterium sp001897105
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Shinella;s_Shinella zoogloeoides_C
d_Bacteria;p_Myxococcota;c_Polyangia;o_Polyangiales;f_Polyangiaceae;g_Polyangium;s_Polyangium fumosum
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Andeanibacterium;s_Andeanibacterium sp001305965
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Allosphingosinella;s_Allosphingosinella sp013816585
d_Bacteria;p_Myxococcota;c_Polyangia;o_Hallangiales;f_Hallangiaceae;g_UBA2376;s_UBA2376 sp900696455
d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Flavhumibacter;s_Flavhumibacter solisilvae

Figure D13: Soil microbes (bacteria) in the grazed plots in RNR site 2.

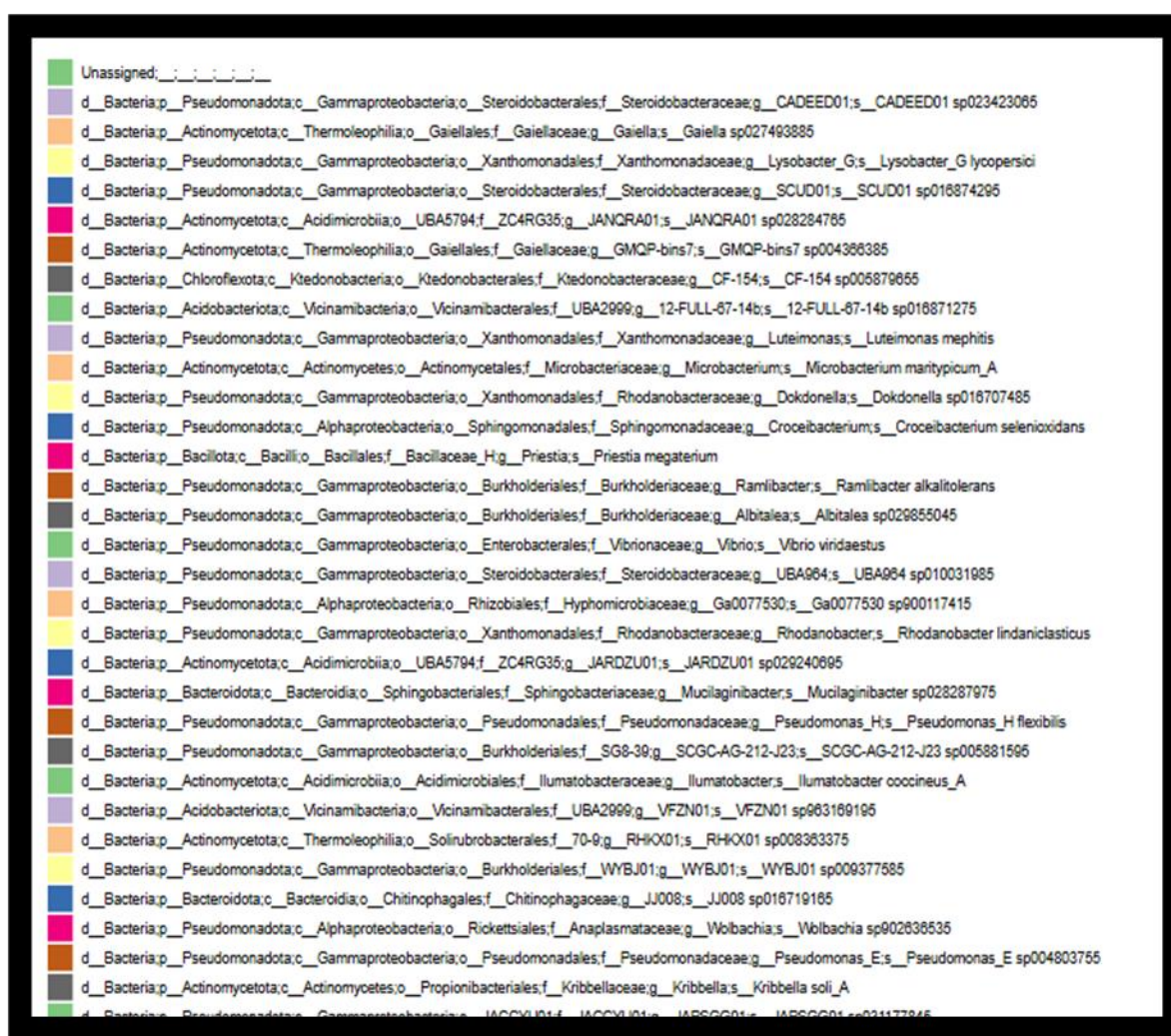


Figure D14: Soil microbes (bacteria) in ungrazed plots in RNR site 2.

d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella variicola
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter_A;s_Citrobacter_A amalonaticus
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas;s_Pseudomonas aeruginosa
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Escherichia;s_Escherichia coli
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter kobei
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella pneumoniae
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter braakii
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;_
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter portucalensis
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Atlantibacter;s_Atlantibacter hermannii_A
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;_
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas;s_Pseudomonas nitroreducens
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter asburiae_B
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhodospirillales;f_Magnetospirillaceae;g_Magnetospirillum;s_Magnetospirillum sp204707145
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Ochrobactrum;s_Ochrobactrum sp600470195
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella quasipneumoniae
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter roggenskampi
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Ochrobactrum;s_Ochrobactrum intermedium
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter europaeus
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter dissolvens
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Klebsiella;s_Klebsiella planticola
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter_A;s_Citrobacter_A sedlakii
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhizobiales;f_Pleomorphomonadaceae;g_Pleomorphomonas;s_Pleomorphomonas carboxydiphila
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Atlantibacter;s_Atlantibacter hermannii
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter freundii
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Enterobacter;s_Enterobacter mori
d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Alpha-05;s_Alpha-05 sp600079695
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Citrobacter;s_Citrobacter werkmanii
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas_F;s_Pseudomonas_F tohoni
d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g_Phytobacter;s_Phytobacter diazotrophicus
d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus_D;s_Enterococcus_D casseliflavus

Figure D15: Soil microbes (bacteria) in grazed plots in RNR site 3.



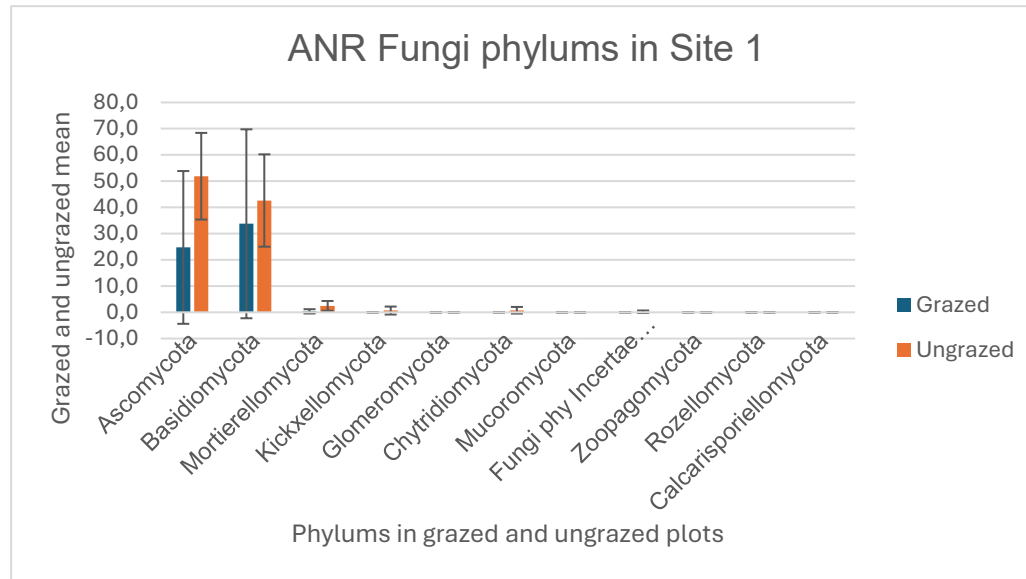
Figure D16: Soil microbes (bacteria) in ungrazed plots in RNR site 3.

Appendix E: Soil Microbes (Fungi) results

Table E1: Phyla found in grazed and ungrazed plots in ANR Study sites with their mean, standard deviation and overall relative abundance.

Site 1			
Phyla	Overall % for grazed and ungrazed	Mean & standard deviation for grazed	Mean & standard deviation for ungrazed
Ascomycota	38.3	24.7±29.1	51.9±16.5
Basidiomycota	38.15	33.7±36.0	42.6±17.6
Mortierellomycota	1.45	0.4±0.8	2.5±1.9
Kickxellomycota	0.35	0.0±0.0	0.7±1.5
Glomeromycota	0	0.0±0.0	0.0±0.0
Chytridiomycota	0.4	0.0±0.0	0.8±1.3
Mucoromycota	0	0.0±0.0	0.0±0.0
Fungi phy Incertae Sedis	0.25	0.0±0.0	0.0±0.5
Zoopagomycota	0	0.0±0.0	0.0±0.0
Rozellomycota	0	0.0±0.0	0.0±0.0
Calcarisporiellomycota	0	0.0±0.0	0.0±0.0
Site 2			
Phyla	Overall % for grazed and ungrazed	Mean & standard deviation for grazed	Mean & standard deviation for ungrazed
Ascomycota	50.95	40.7±37.3	61.2±27.0
Basidiomycota	29.1	22.6±24.8	35.6±26.3
Mortierellomycota	1.55	2.0±3.5	1.1±2.0
Chytridiomycota	0.4	0.4±0.8	0.4±0.7
Fungi phy Incertae Sedis	0	0.0±0.0	0.0±0.0
Kickxellomycota	0	0.0±0.0	0.0±0.0
Rozellomycota	0	0.0±0.0	0.0±0.0
Zoopagomycota	0	0.0±0.0	0.0±0.0
Mucoromycota	0	0.0±0.0	0.0±0.0

Site 1



Site 2

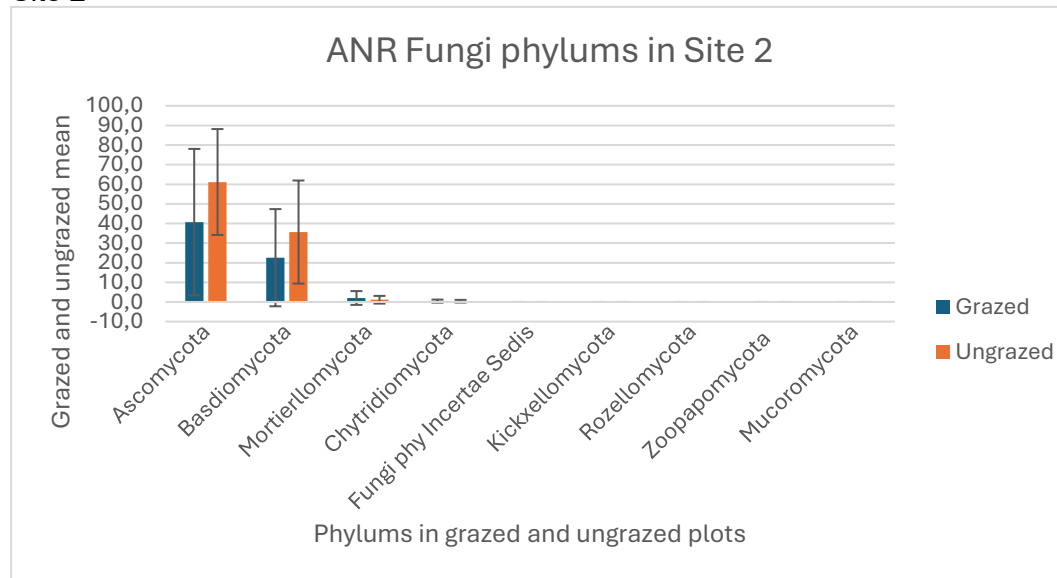
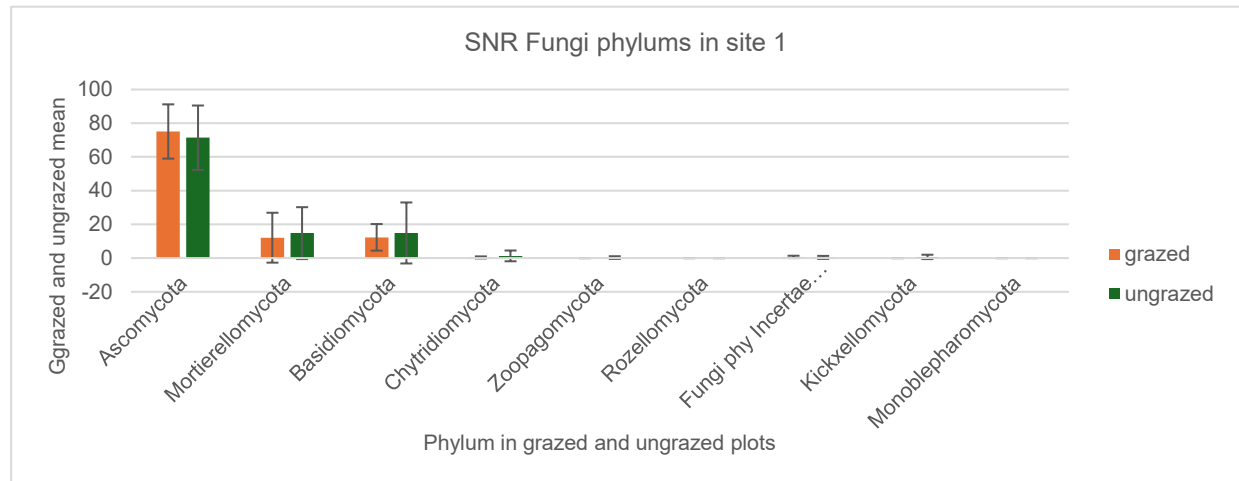


Figure E1: The fungi soil microbes in the grazed and ungrazed sample plots in RNR showing the mean and standard error bars for the grazed and ungrazed plots.

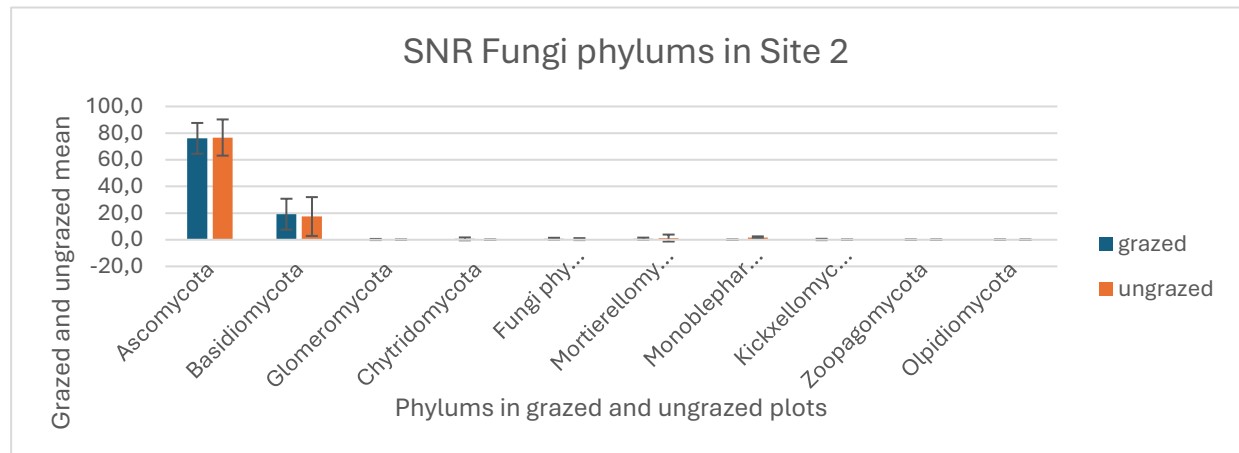
Table E2: Phyla found in grazed and ungrazed plots in SNR Study sites with their mean, standard deviation and overall relative abundance.

Site 1			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	73.25	75.1±16.1	71.4±19.1
Mortierellomycota	13.45	12.1±14.8	14.8±15.4
Basidiomycota	13.6	12.3±7.9	14.9±18.1
Chytridiomycota	0.35	0.4±0.6	1.3±3.2
Zoopagomycota	0.15	0.0±0.0	0.3±0.8
Rozellomycota	0	0.0±0.0	0.0±0.0
Fungi phy Incertae Sedis	0.55	0.7±1.8	0.4±0.9
Kickxellomycota	0.35	0.0±0.0	0.7±1.3
Site 2			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	76.4	76.1±11.6	76.7±13.6
Basidiomycota	18.3	19.2±11.6	17.4±14.6
Glomeromycota	0.1	0.2±0.4	0.0±0.0
Chytridiomycota	0.3	0.6±1.1	0.0±0.0
Fungi phy Incertae Sedis	0.6	0.7±0.8	0.5±0.7
Mortierellomycota	1	0.7±0.8	1.3±2.6
Monoblepharomycota	0.85	0.0±0.0	1.7±0.8
Kickxellomycota	0.1	0.2±0.5	0.0±0.0
Zoopagomycota	0.05	0.0±0.0	0.0±0.1
Olpidiomycota	0.1	0.0±0.0	0.0±0.2
Site 3			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	77.4	77.2±13.1	77.6±14.1
Basidiomycota	17.3	17.0±15.2	17.6±15.2
Chytridiomycota	1.85	2.1±1.3	1.6±0.6
Kickxellomycota	0.25	0.5±1.1	0.0±0.0
Mortierellomycota	1.4	1.6±2.6	1.2±1.5
Entorrhizomycota	0	0.0±0.0	0.0±0.0
Fungi phy Incertae Sedis	0.45	0.2±0.4	0.7±0.8
Monoblepharomycota	0	0.0±0.0	0.0±0.0
Rozellomycota	0.05	0.0±0.1	0.0±0.0
Zoopagomycota	0.1	0.0±0.2	0.0±0.0

Site 1



Site 2



Site 3

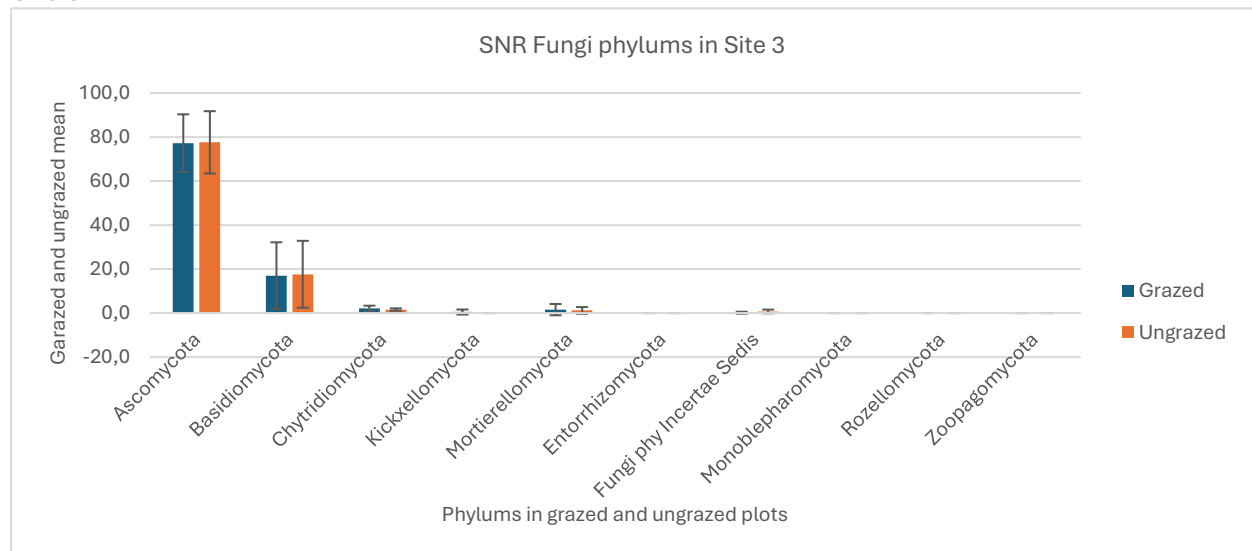
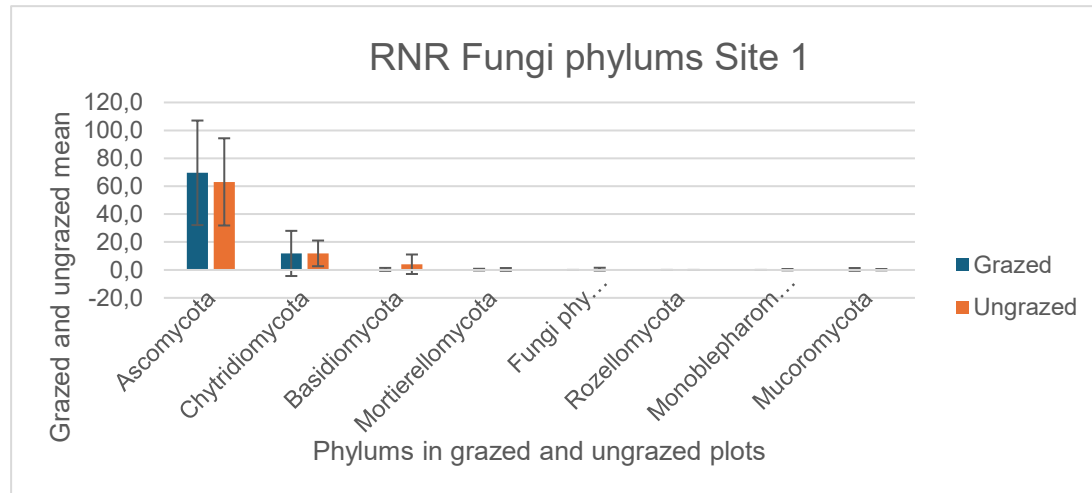


Figure E2: The fungi soil microbes in the grazed and ungrazed sample plots in SNR showing the mean and standard error bars for the grazed and ungrazed plots.

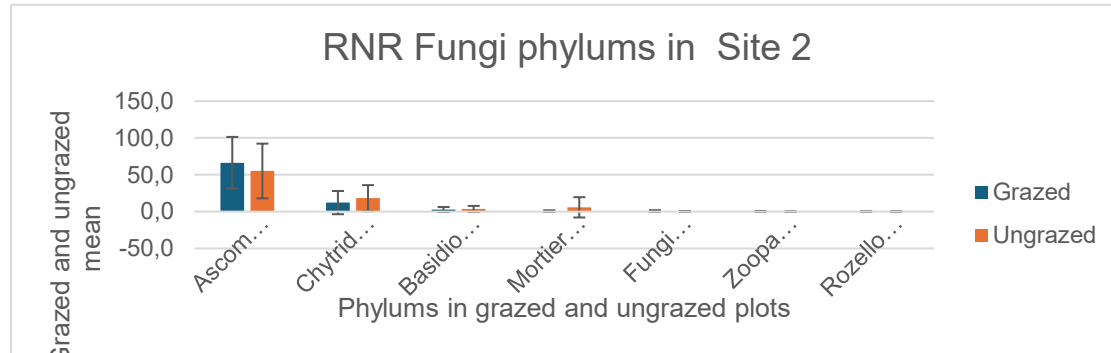
Table E3: Phyla found in grazed and ungrazed plots in RNR Study sites with their mean, standard deviation and overall relative abundance.

Site 1			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	66.35	69.6±37.4	63.1±31.2
Chytridiomycota	11.85	11.8±16.2	11.9±9.2
Basidiomycota	2.25	0.4±1.0	4.1±7.0
Mortierellomycota	0.3	0.2±0.6	0.4±1.0
Fungi phy Incertae Sedis	0.3	0.0±0.0	0.6±1.0
Rozellomycota	0	0.0±0.0	0.0±0.0
Monoblepharomycota	0.1	0.0±0.0	0.2±0.5
Mucoromycota	0.3	0.4±1.0	0.2±0.5
Site 2			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	60.8	66.4±35.0	55.2±37.1
Chytridiomycota	15.2	12.2±15.8	18.2±17.8
Basidiomycota	3.25	2.9±3.4	3.6±4.2
Mortierellomycota	3.25	0.7±1.1	5.8±13.8
Fungi phy Incertae Sedis	0.5	0.7±1.2	0.3±0.6
Zoopagomycota	0.1	0.2±0.5	0.0±0.0
Rozellomycota	0	0.0±0.0	0.0±0.0
Site 3			
Phyla	Overall % for grazed and ungrazed	Mean& standard deviation for grazed	Mean& standard deviation for ungrazed
Ascomycota	883.75	85.3±8.0	82.2±11.7
Chytridiomycota	10.4	12.5±7.7	8.3±6.9
Basidiomycota	3.6	0.9±1.2	6.3±8.1
Fungi phy Incertae Sedis	0	0.0±0.0	0.0±0.8
Mortierellomycota	0	0.0±0.0	0.0±0.0
Monoblepharomycota	0.15	0.0±0.0	0.3±0.0
Kickxellomycota	0.9	1.5±3.6	0.3±0.7
Zoopagomycota	0	0.0±0.0	0.0±0.0
Glomeromycota	0	0.0±0.0	0.0±0.0
Mucoromycota	0	0.0±0.0	0.0±0.0

Site 1



Site 2



Site 3

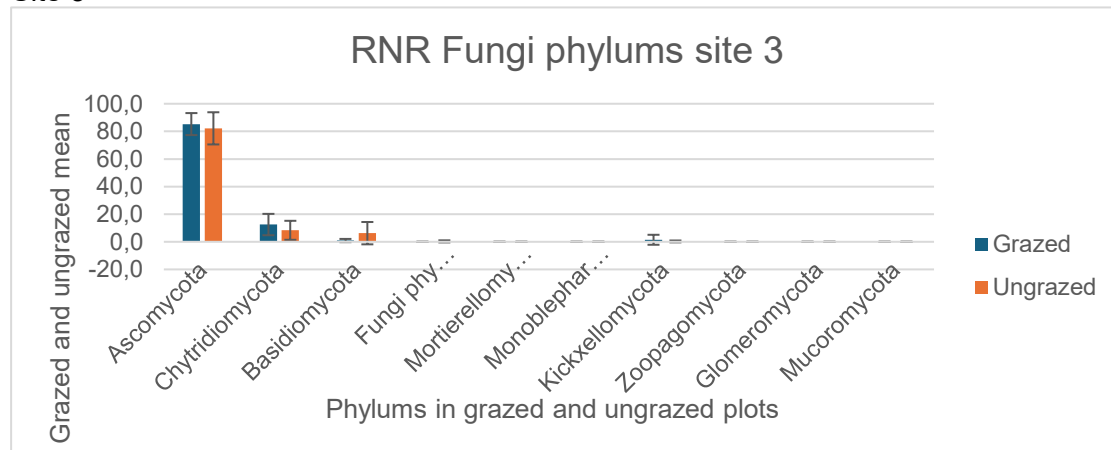


Figure E3: The fungi soil microbes in the grazed and ungrazed sample plots in RNR showing the mean and standard error bars for the grazed and ungrazed plots.

