



**Western Cape  
Government**

**FOR YOU**



**Agriculture**

**CONSERVATION TILLAGE PRACTICES FOR POTATO PRODUCTION  
AND THE ASSOCIATED BACTERIAL AND FUNGAL COMMUNITY  
ANALYSIS SPANNING THREE PRODUCTION CYCLES**

**23-26 June 2024**

**Jacques van Zyl**



# Introduction



**Conservation Agriculture** is a way of farming that **combines** the best-known **traditional** and **modern practices** to manage the **natural capital** of agriculture, namely **soil, soil organic matter, water** and **biodiversity** simultaneously.

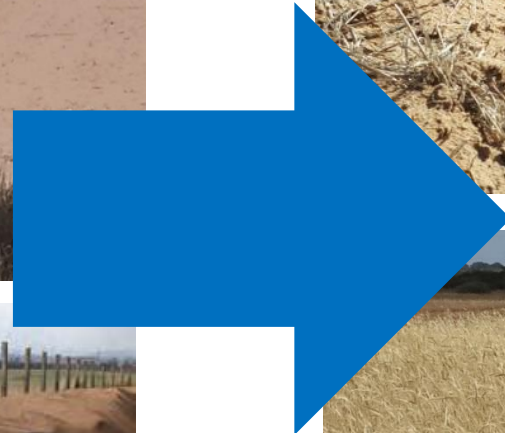
**Conservation farming practices for potato production in the Sandveld region of South Africa**



# Main Objective

From

To





# Bacteria

Bacteria are the most abundant microbes in the soil

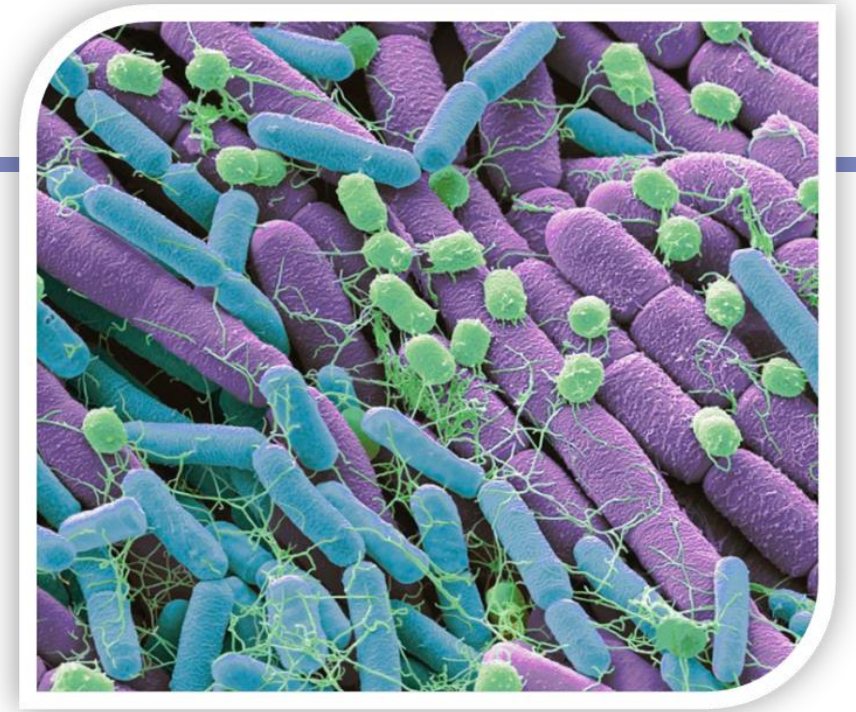
Single celled organisms

Billions of bacteria in a single gram of soil

Populations of bacteria can change in few days

Some bacteria species are very fragile whereas others are extremely tough

Some bacteria are dependent on specific plant species



Bacteria breaks down organic residues in the soil

Bacteria, such as **Rhizobium**, convert atmospheric nitrogen into a form that plants can use - **Nitrogen fixation**

Bacteria like **Nitrosomonas** and **Nitrobacter** convert ammonia into nitrite and then to nitrate - **Nitrification**

Bacteria like **Pseudomonas** and **Clostridium** convert nitrate back into nitrogen gas - **Denitrification**

Some bacteria produce **antibiotics** that **protect** plants from disease-causing organisms

Bacteria help form stable aggregates in the soil

# Fungi

Soil fungi are microscopic plant-like cells

Single celled (e.g. yeast)

Long threadlike structures or hyphae that make a mass called mycelium

Can be symbiotic with plant roots

Not as dependent on specific plant species as some bacteria

Populations are slower to develop

Most soil fungi *decompose* organic matter

Play a crucial role in *recycling nutrients*

Form symbiotic relationships with plants – **mycorrhizae**

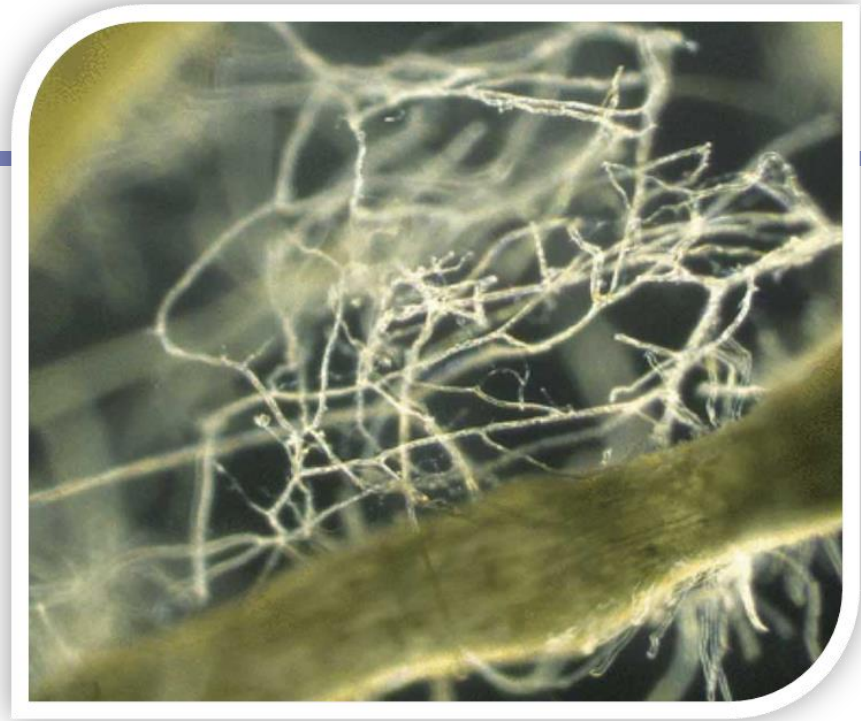
Aggregate soil particles - **hyphae**

Some suppress plant diseases

Improve plant nutrient uptake, especially in stressed conditions

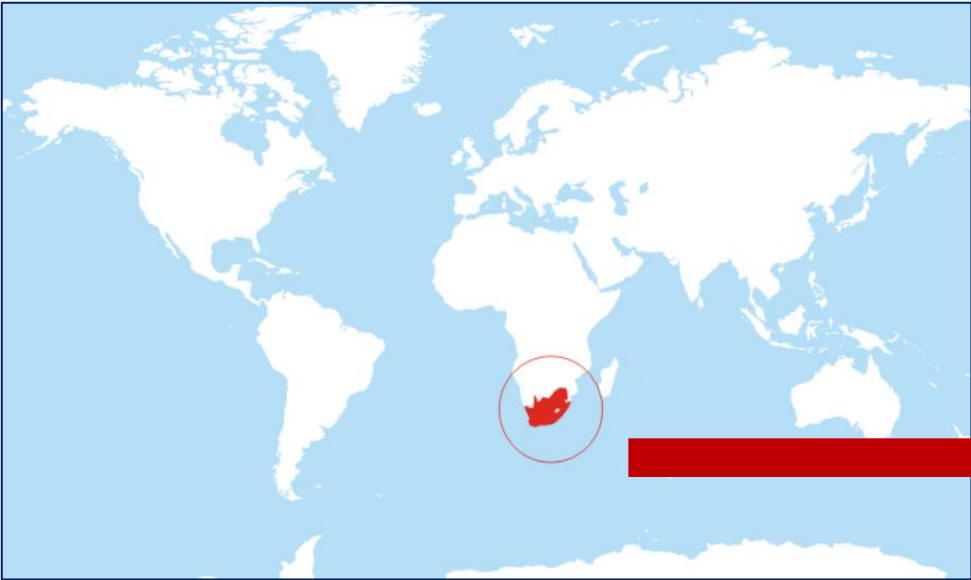
Transport water from the soil to the plant

Contribute to soil **carbon sequestration**

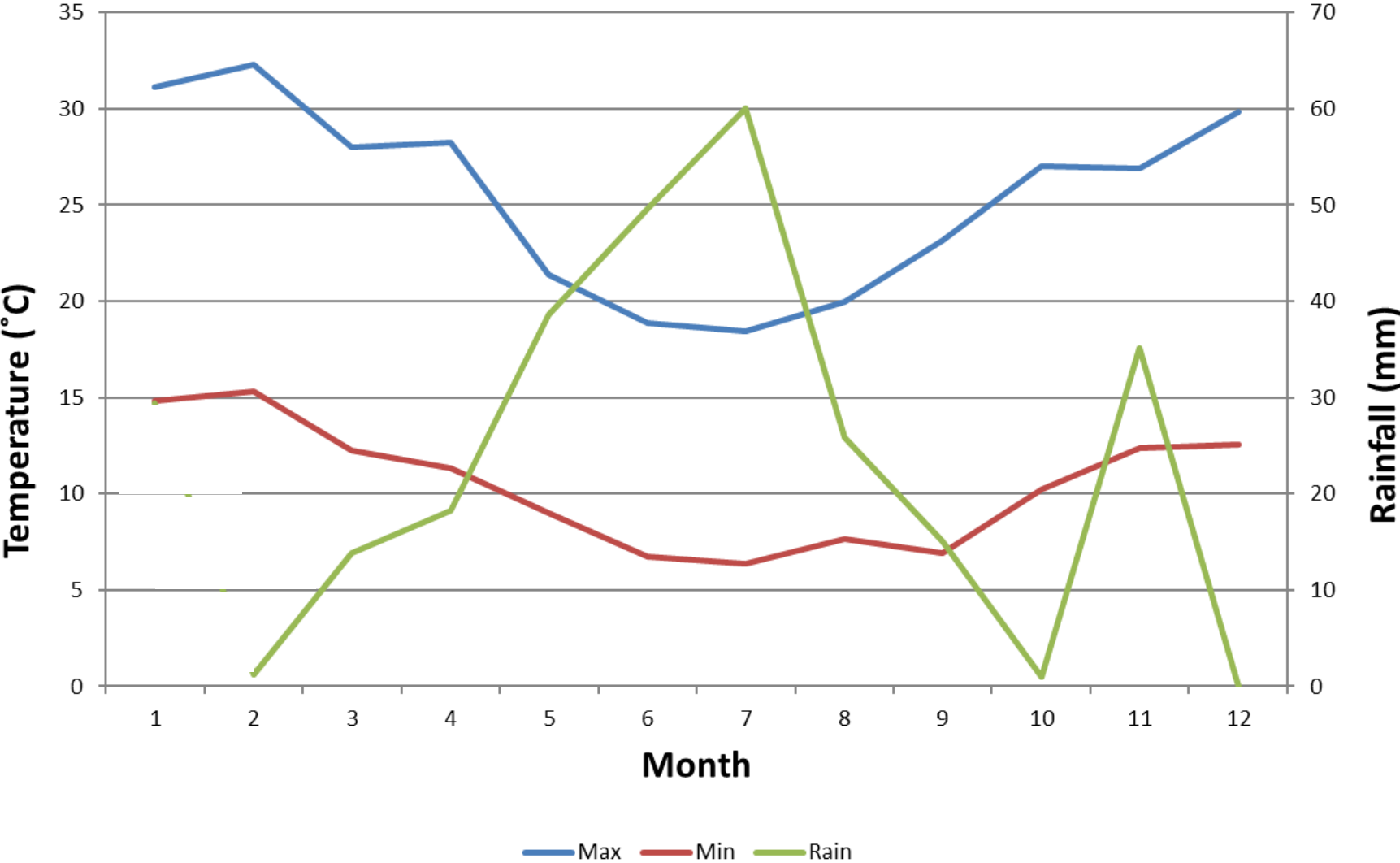




# Materials and Methods:Location



# Climate - Aurora



# Materials and Methods:

## Trial layout- Randomised complete block with 3 experimental units

Rep.	Conventional tillage			Conservation tillage: Paraplow						Conservation tillage: Rip		
	12 m											
	4 m	4 m	4 m									
1	1	2	3	10 m	25	26	27	49	50	51		
2	4	5	6		28	29	30	52	53	54		
3	7	8	9		31	32	33	55	56	57		
4	10	11	12		34	35	36	58	59	60		
5	13	14	15		37	38	39	61	62	63		
6	16	17	18		40	41	42	64	65	66		
7	19	20	21		43	44	45	67	68	69		
8	22	23	24		46	47	48	70	71	72		



# Materials and Methods: Tillage



## Conventional tillage: Mouldboard

Irrigate up to field water capacity (FWC) before tilling  
Mouldboard plough up to a depth of **350 mm**  
Level with a ghrop and broadcast fertiliser  
Rip **600 mm** deep between planting rows  
Plant potatoes  
Rip **600 mm** deep after plant in tyre tracks



## Conservation tillage: Rip

Irrigate up to FWC before tilling  
Broadcast fertiliser + scarify  
Rip **600 mm** deep in planting rows  
Plant potatoes  
Rip **600 mm** deep after plant between rows



## Conservation tillage: Paraplough

Irrigate up to FWC before tilling  
Broadcast fertiliser + scarify  
Plant potatoes  
Paraplough **600 mm** deep over two planting rows

# Materials and Methods:

## Microbial community analysis

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**Fluorescently labelled primers** - amplified the Internal transcribed spacer (ITS) regions

**Determined the community structure** by using Automated Ribosomal Intergenic Spacer Analysis (ARISA)

**The amplicons of the samples were run** on an ABI 3010XL Genetic analyser to obtain electropherograms

**The ARISA PCR samples were run** with the LIZ1200 size standard

**Genemapper 5 software** converted the fluorescent data to peaks of different fragment lengths

These peaks of different fragment lengths are termed **operational taxonomic units (OTUs)**

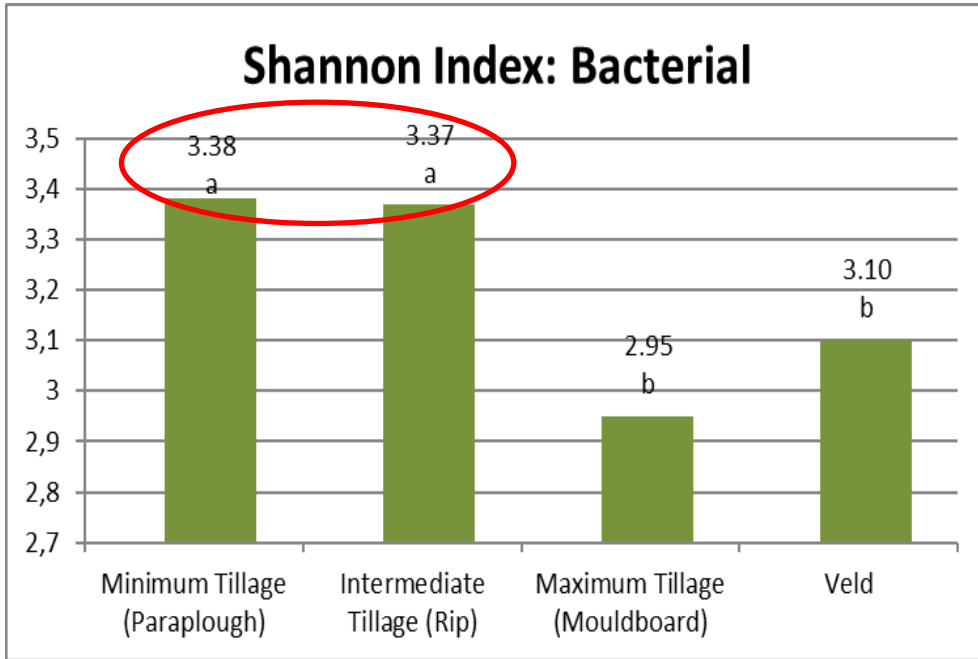
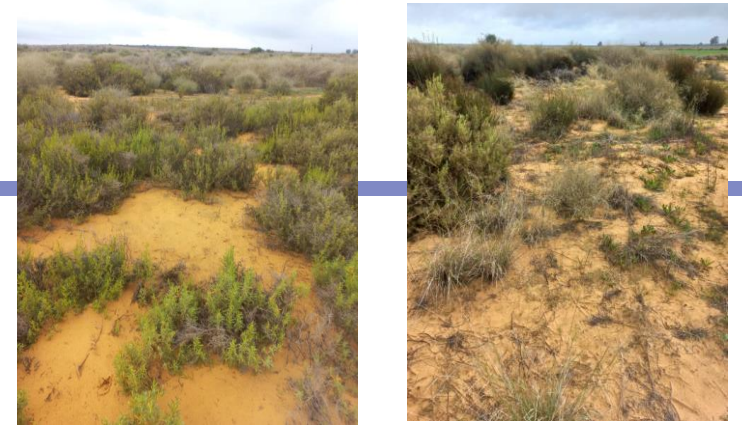
**Peak heights** are used to indicate the **relative abundance** of the fragments in the samples

**Only fragment sizes between 100 and 1000 base pairs and peak heights above 150 fluorescent units** were used for analysis as OTUs

**A bin size of 3 bp** was used to minimize inaccuracies of the ARISA profile  
(Brown et al., 2005; Slabbert et al., 2010)

All **alpha** (Shannon and Simpsons) and **beta diversity** (NMDS graphs) calculations, and statistical analyses were performed using the **'microeco'** (Liu et al. 2021) and **'vegan' packages** (Oksanen et al. 2020)

# Bacterial Community Analysis



## Shannon index

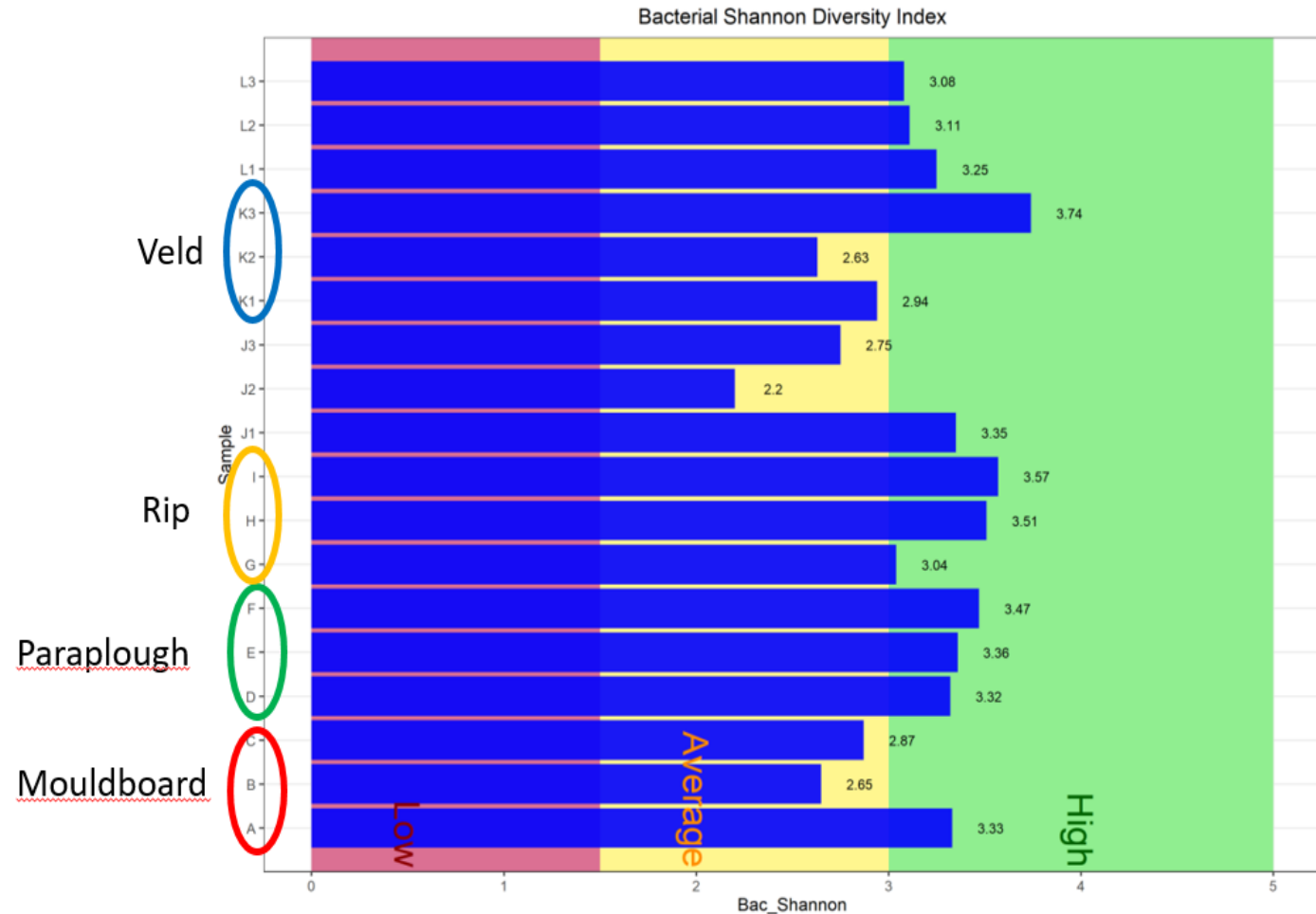
This index is used to observe the richness and evenness of the microbial community within a sample.

Values typically lie between 1.5 and 3.5, but can reach above 4 in rare occasions.

It is calculated by looking at the number of different species and their abundance.

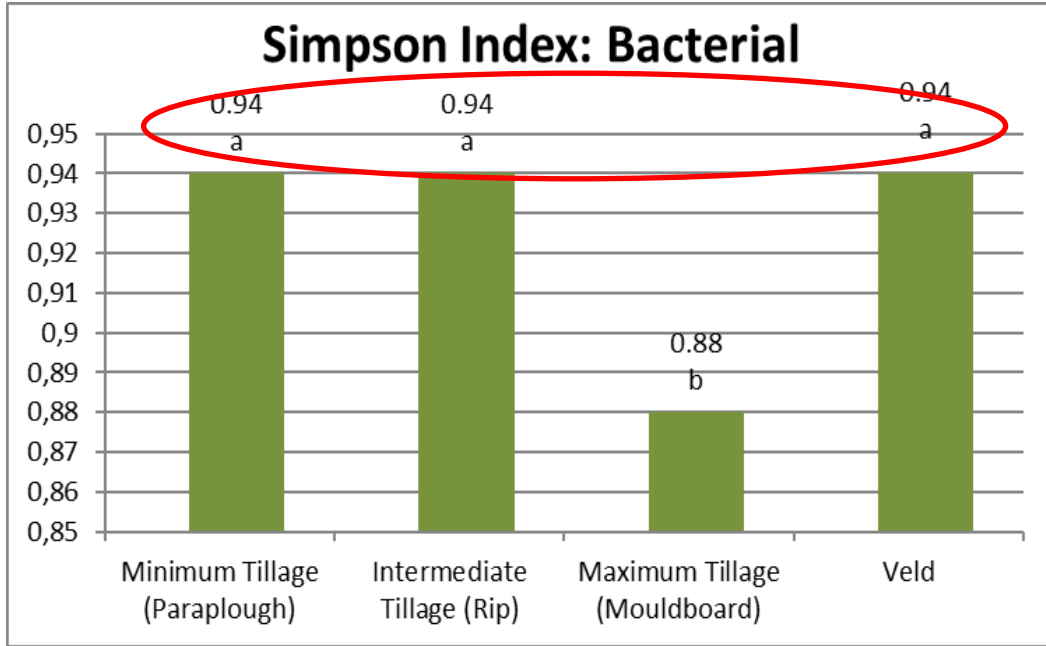
A high Shannon index indicates that the microbial community is even.

A low value indicates that there is a dominating effect happening within the sample.





# Bacterial Community Analysis



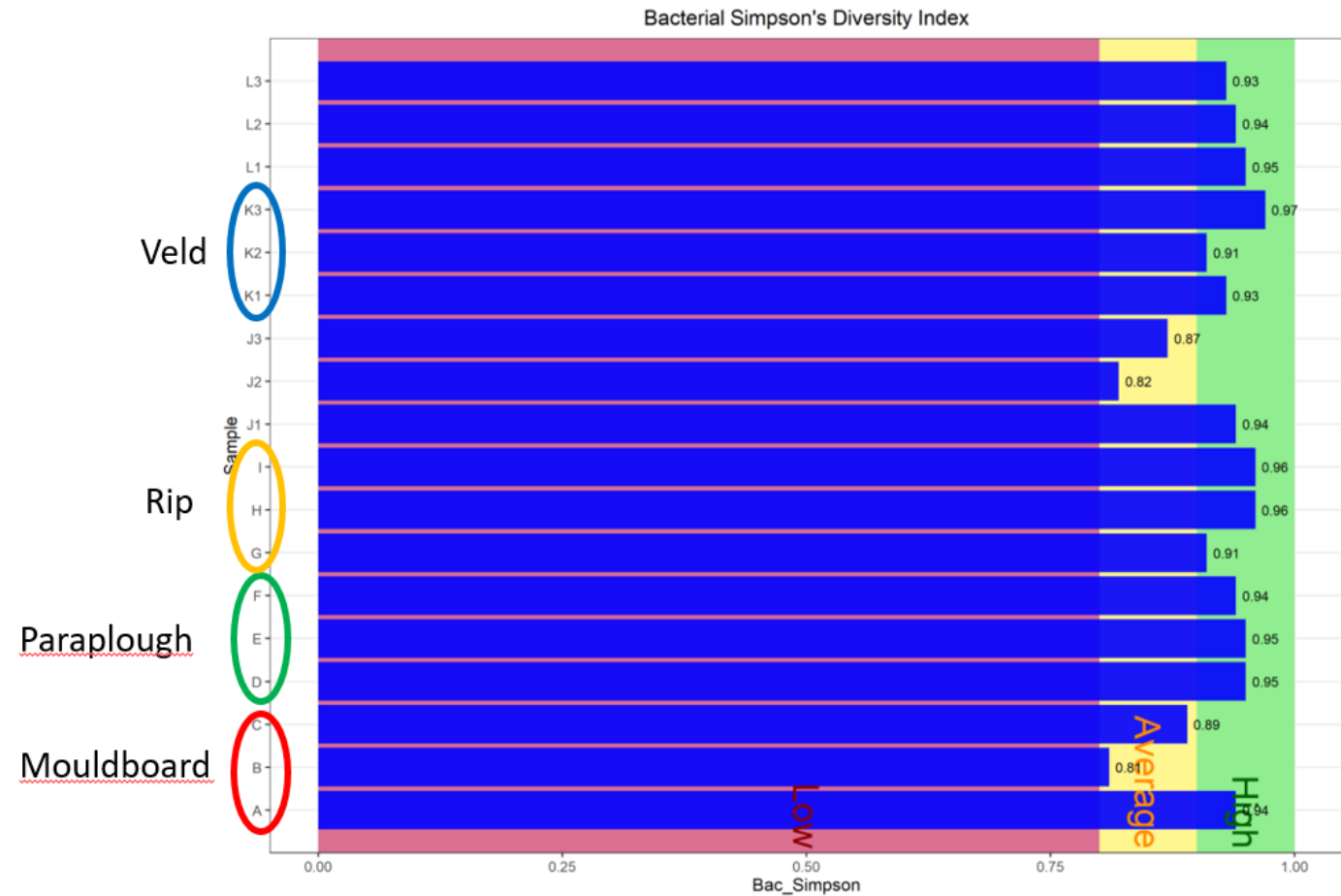
## Simpson's index

This index is used along with the Shannon index to describe the microbial evenness within a sample.

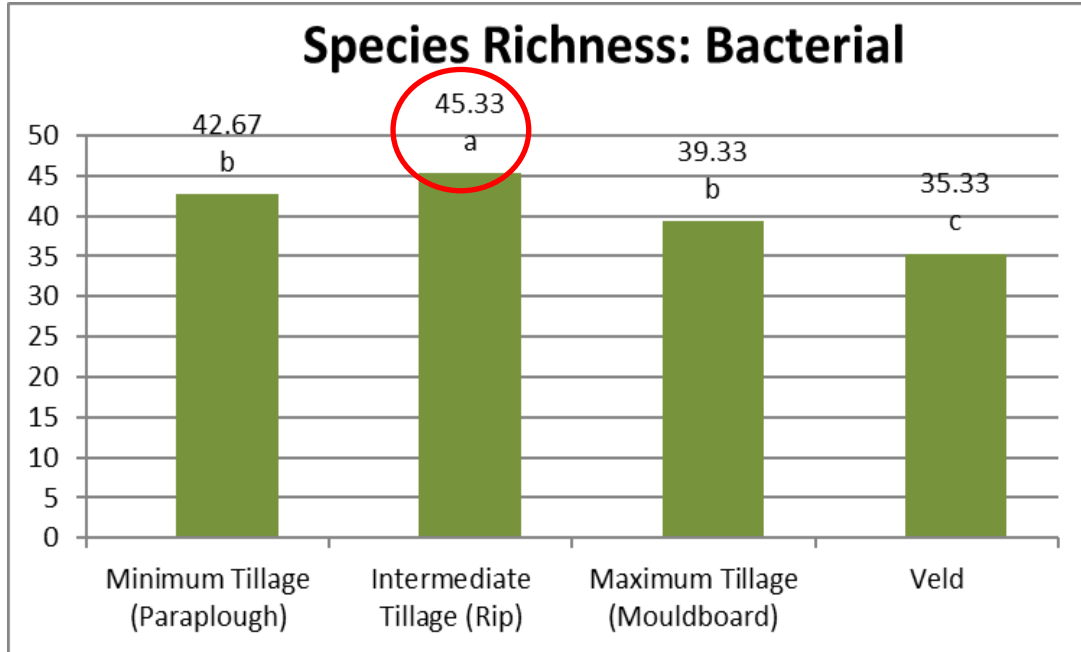
These values will always fall between 0 and 1.

A value close to 1 indicates low dominance.

A value of 0 indicates that the microbial community within the sample is dominated by one, or very few, microorganisms.



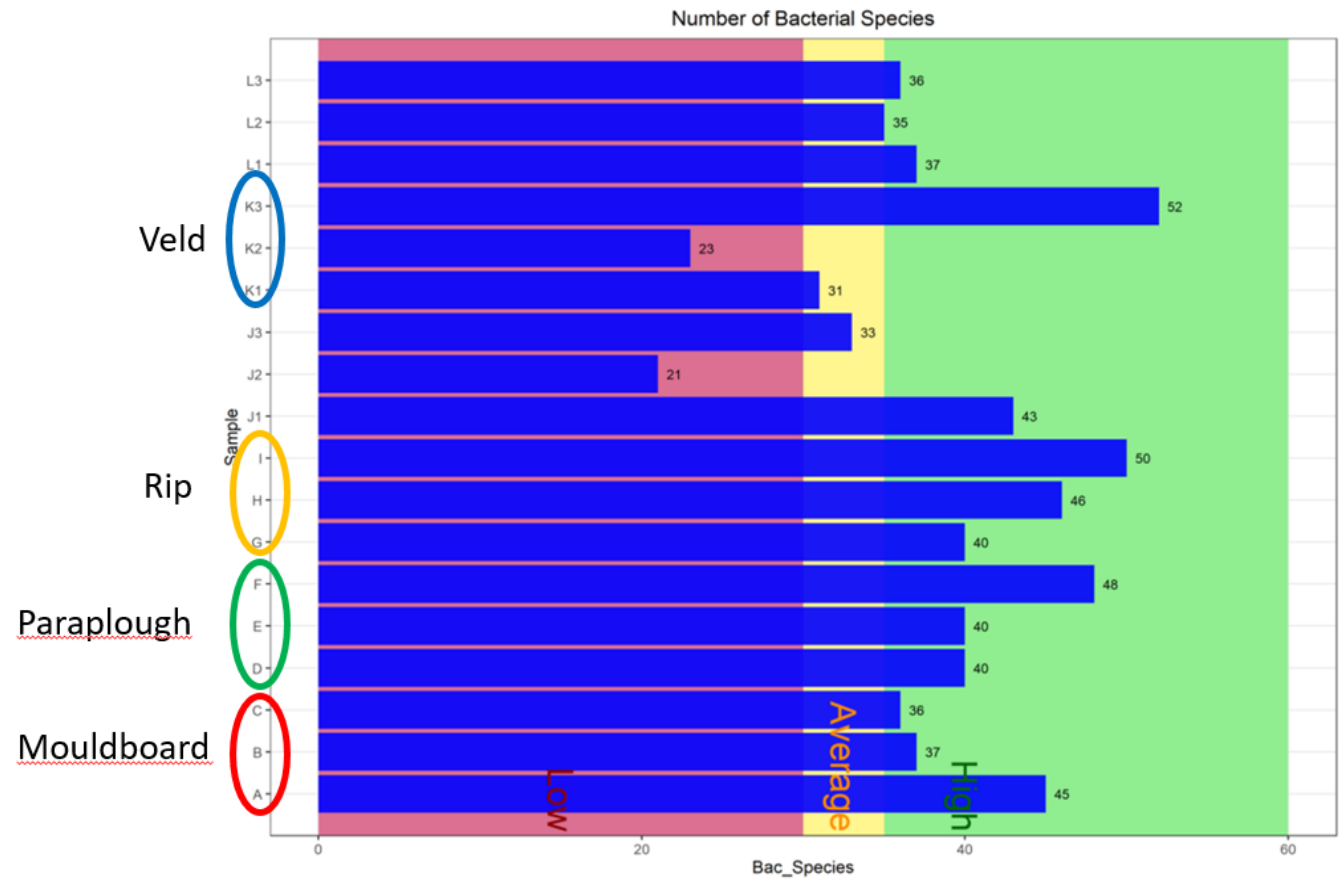
# Bacterial Community Analysis



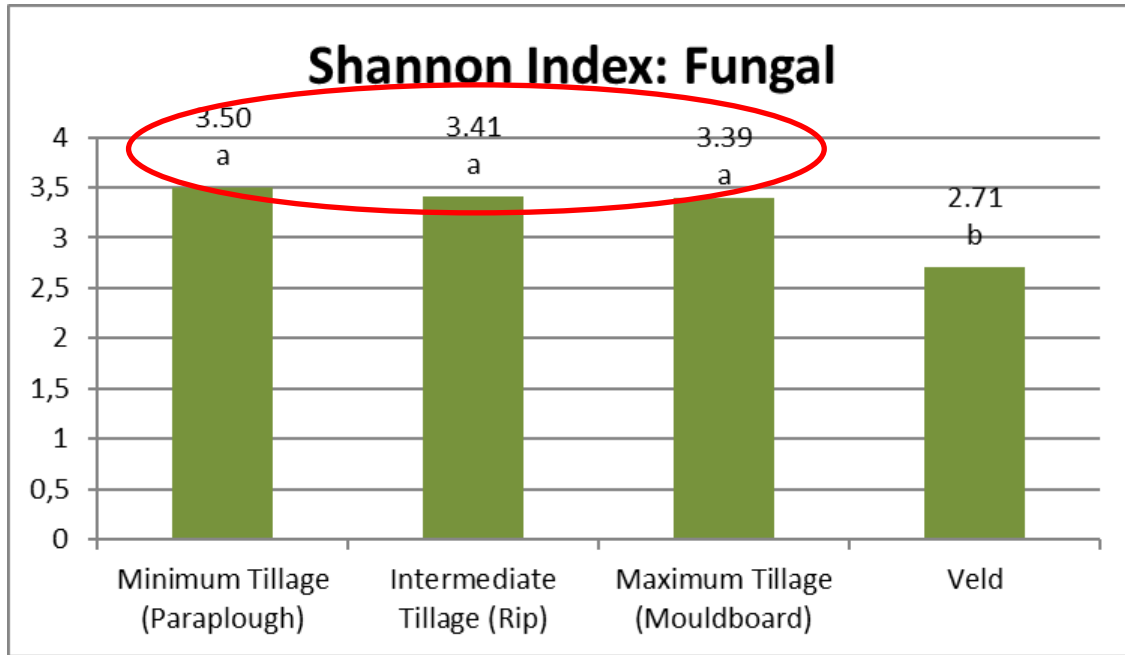
## Species richness

This value shows the number of Operational Taxonomic Units (OTUs).

A higher OTU value indicates a high level of diversity, but it should be uniquely interpreted for every case as the environment determines what the highest diversity limit could be.



# Fungal Community Analysis



## Shannon index

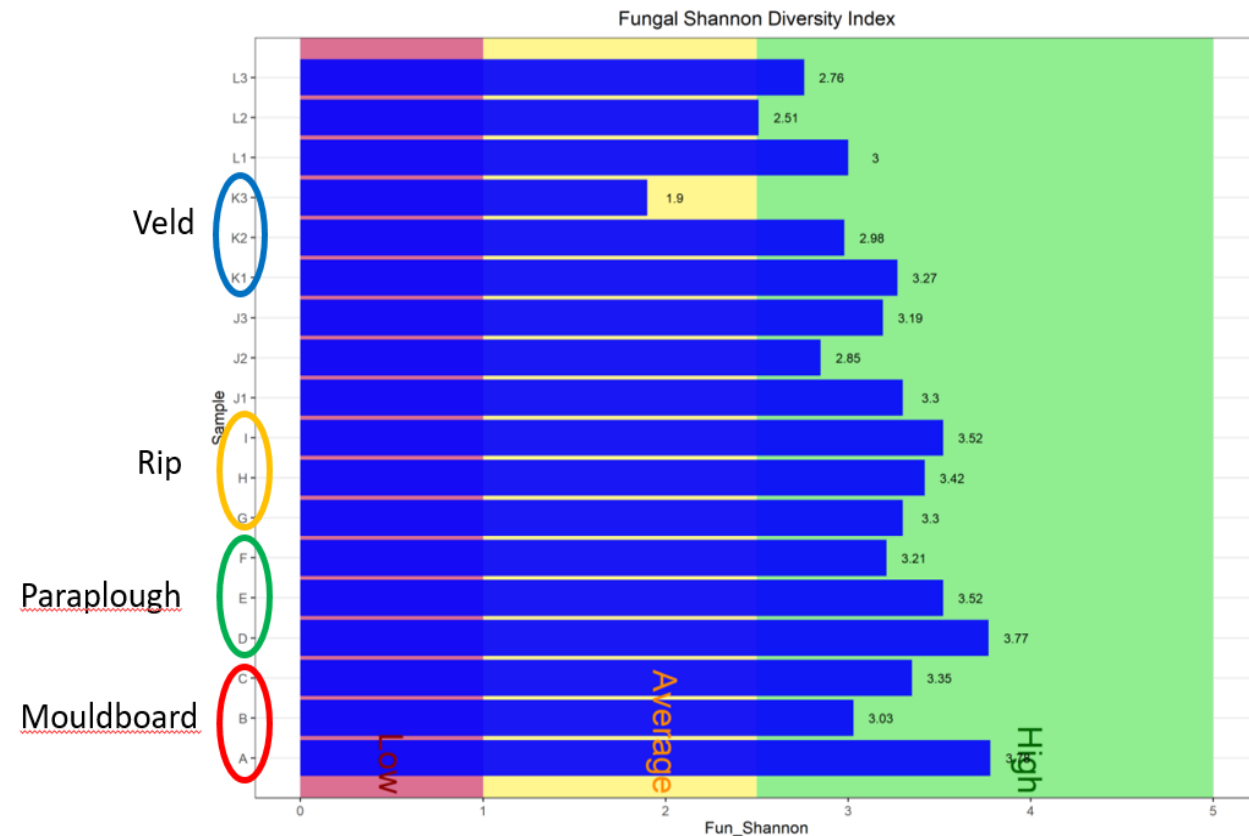
This index is used to observe the richness and evenness of the microbial community within a sample.

Values typically lie between 1.5 and 3.5, but can reach above 4 in rare occasions.

It is calculated by looking at the number of different species and their abundance.

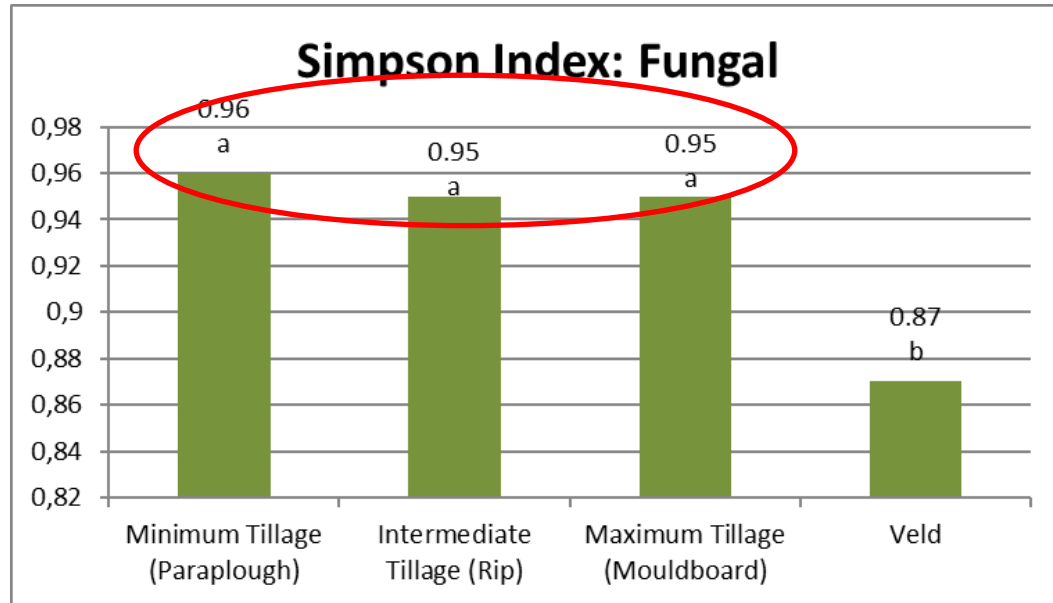
A high Shannon index indicates that the microbial community is even.

A low value indicates that there is a dominating effect happening within the sample.





# Fungal Community Analysis



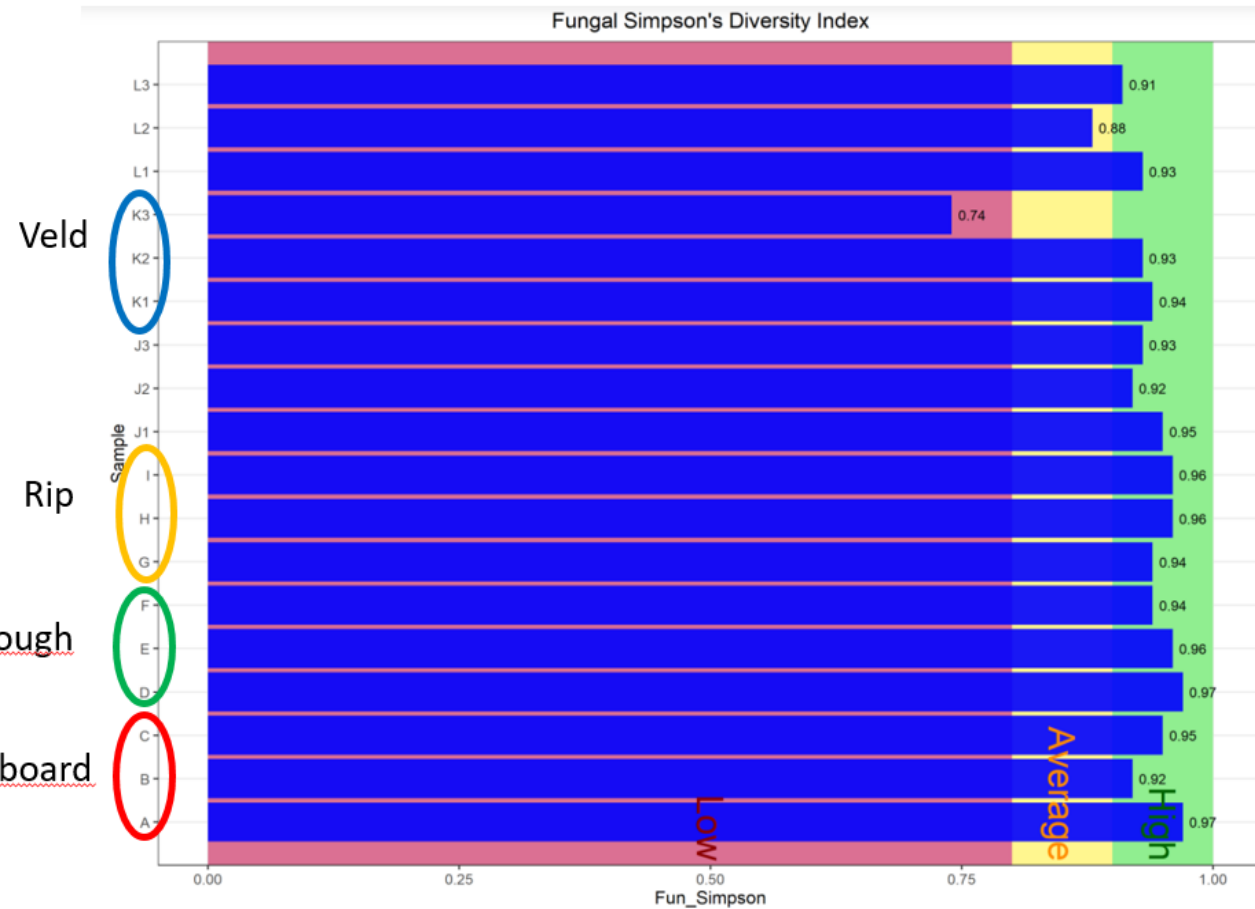
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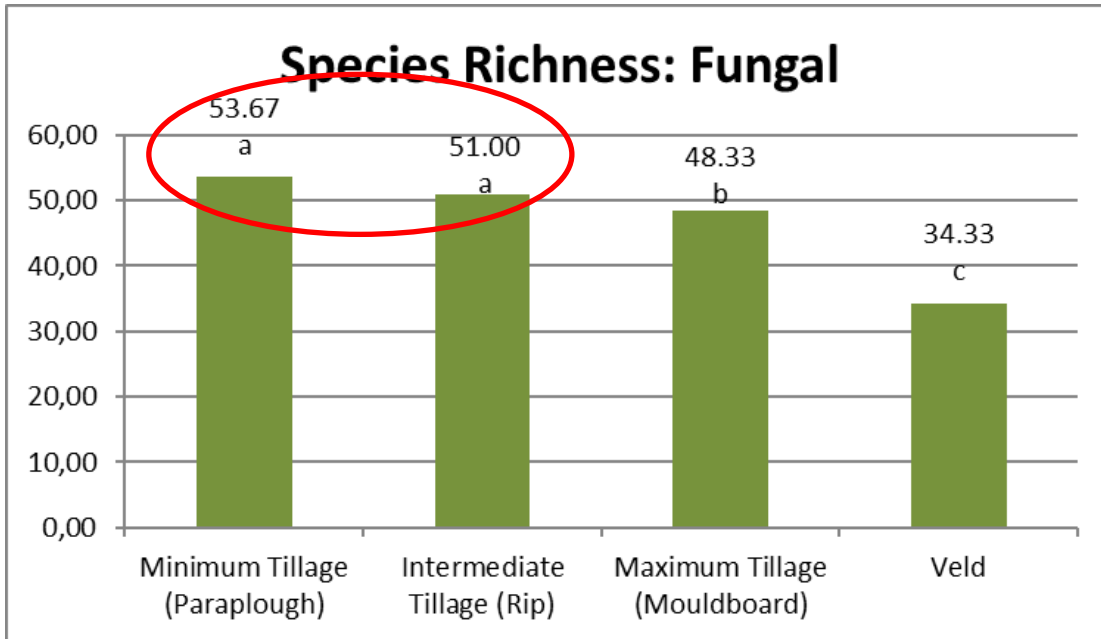
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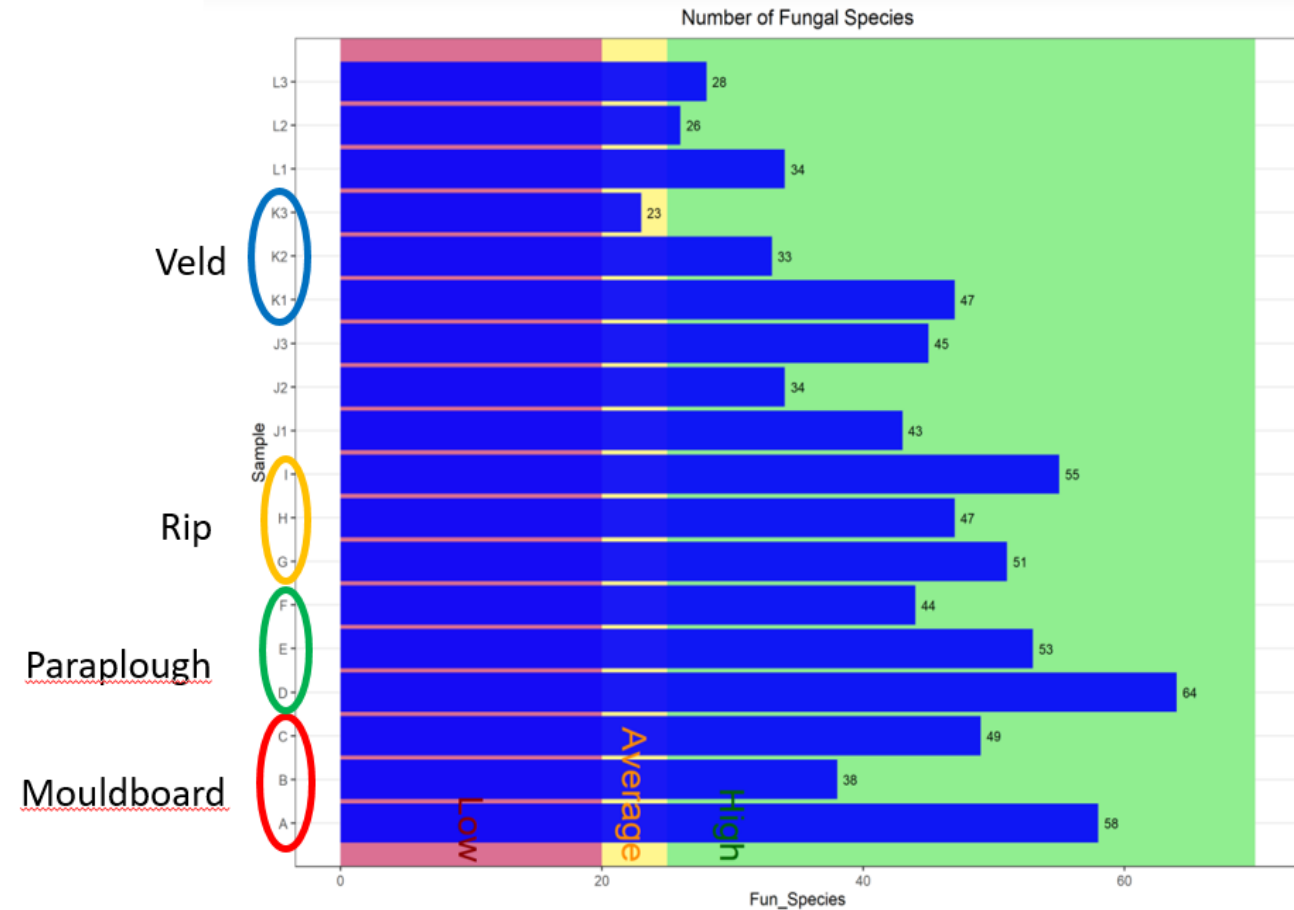
# Fungal Community Analysis



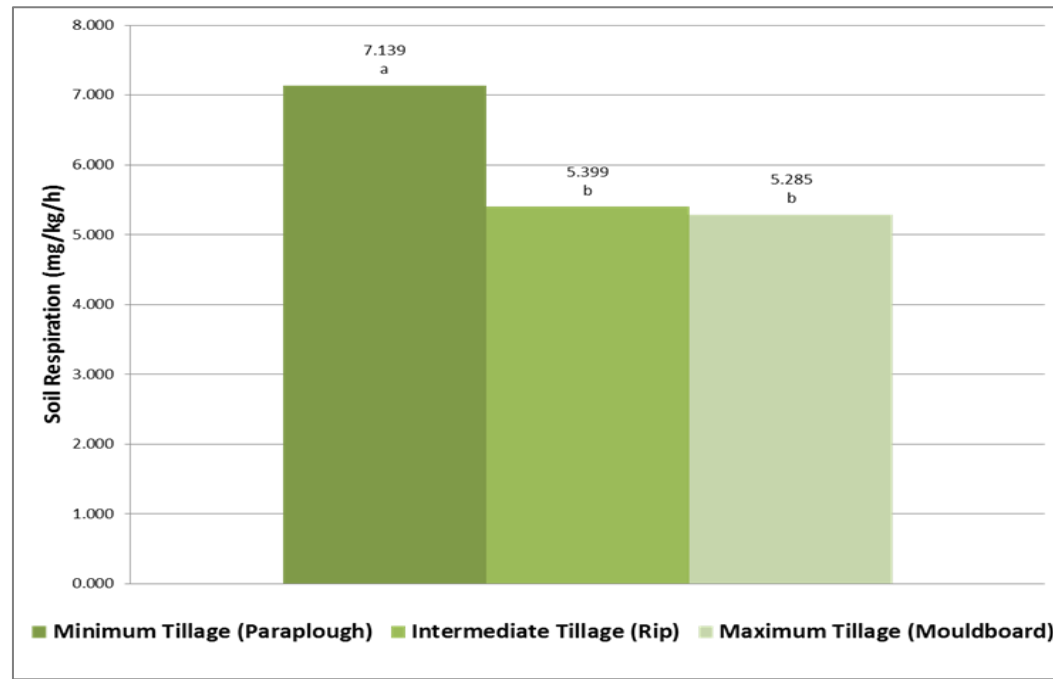
#### Species richness

This value shows the number of Operational Taxonomic Units (OTUs).

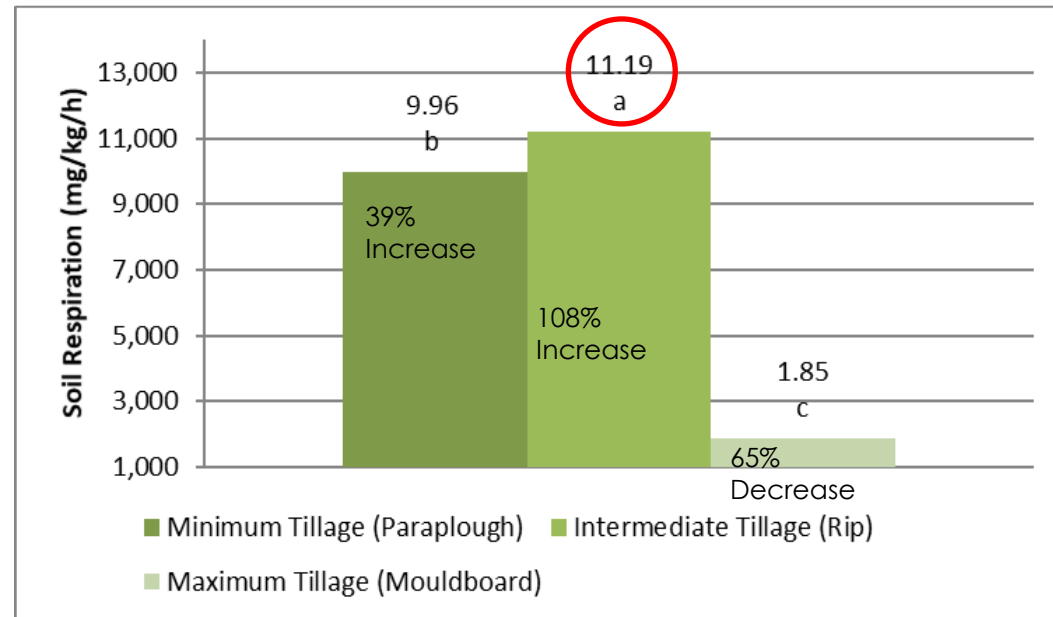
A higher OTU value indicates a high level of diversity, but it should be uniquely interpreted for every case as the environment determines what the highest diversity limit could be.



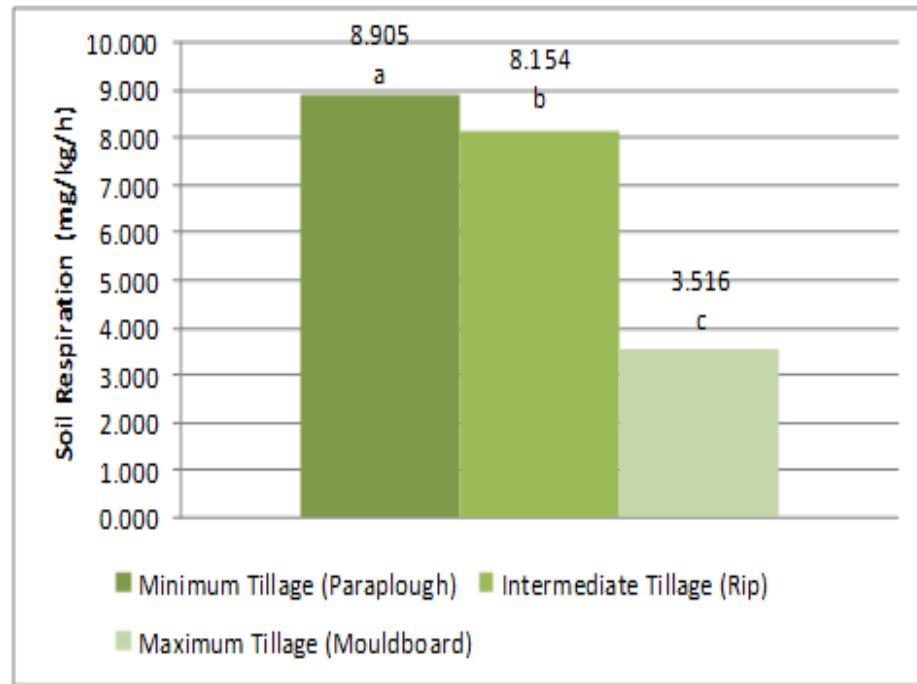
# Soil Respiration mg/kg/h



2014



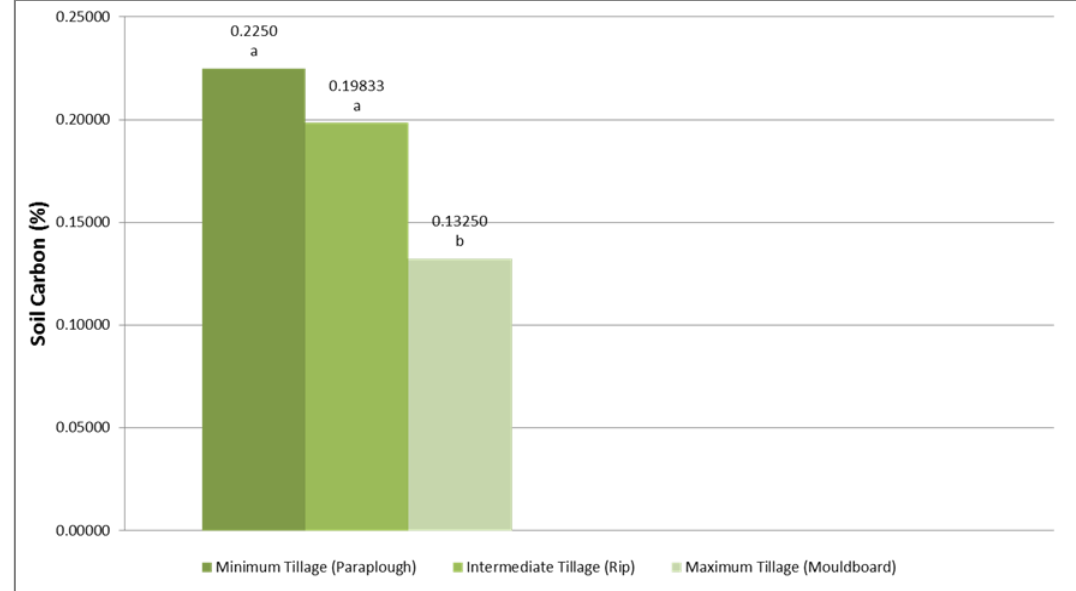
2022



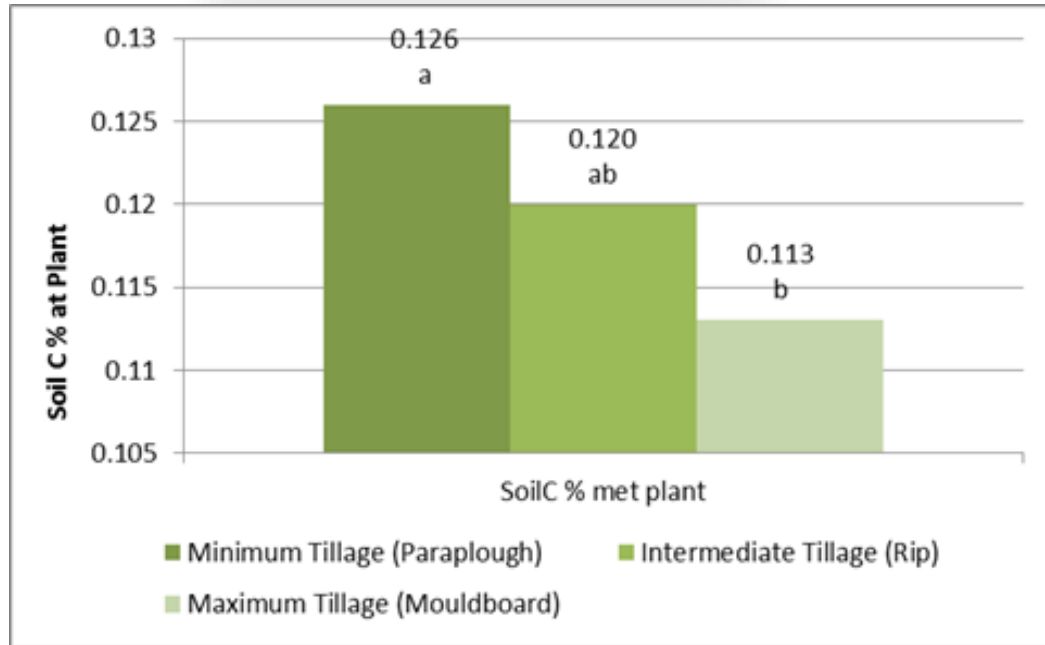
2018



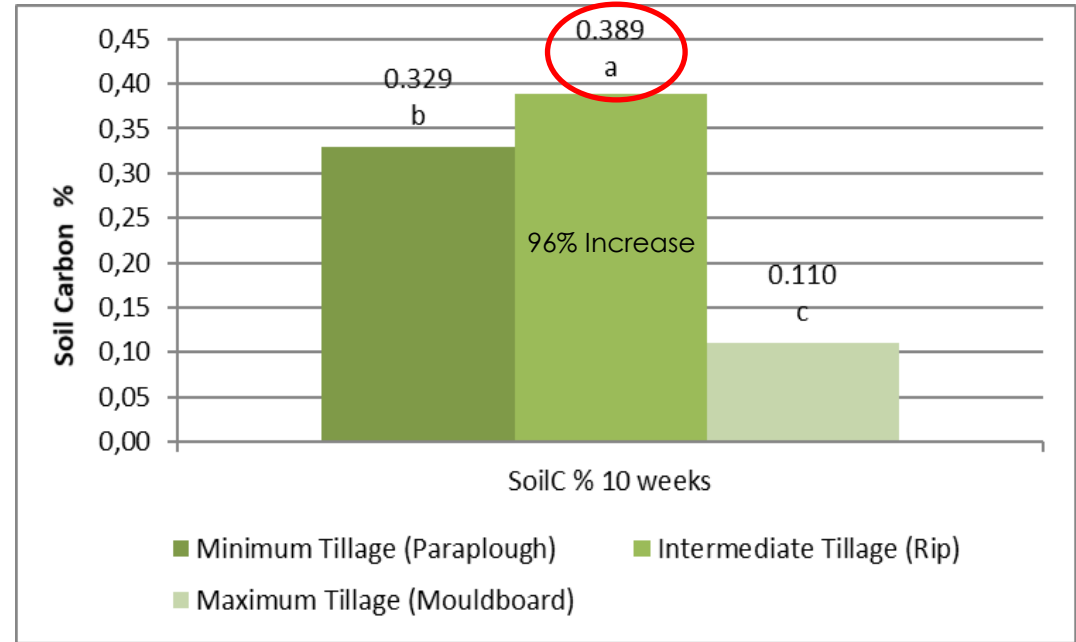
# Soil Carbon %



2014

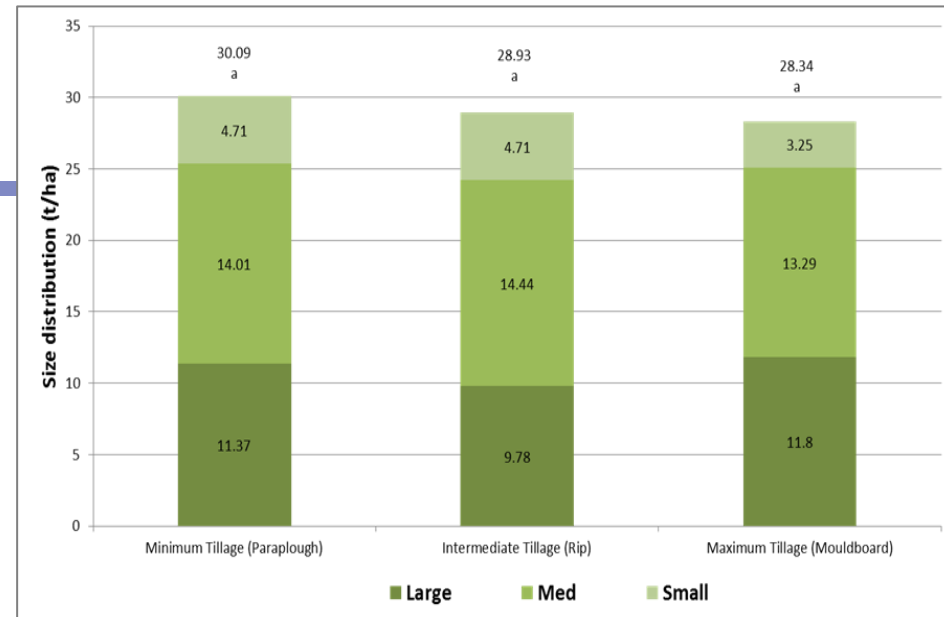


2018

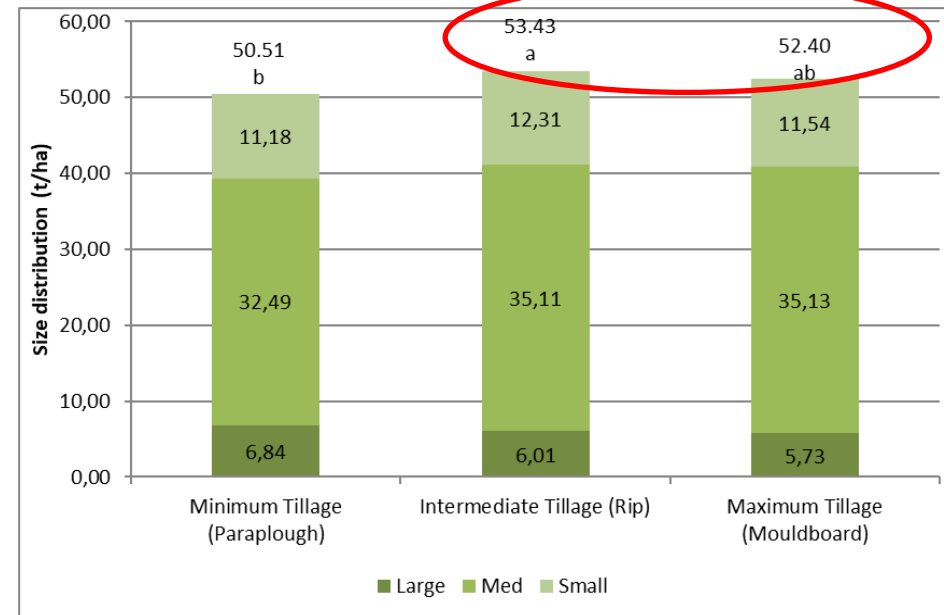


2022

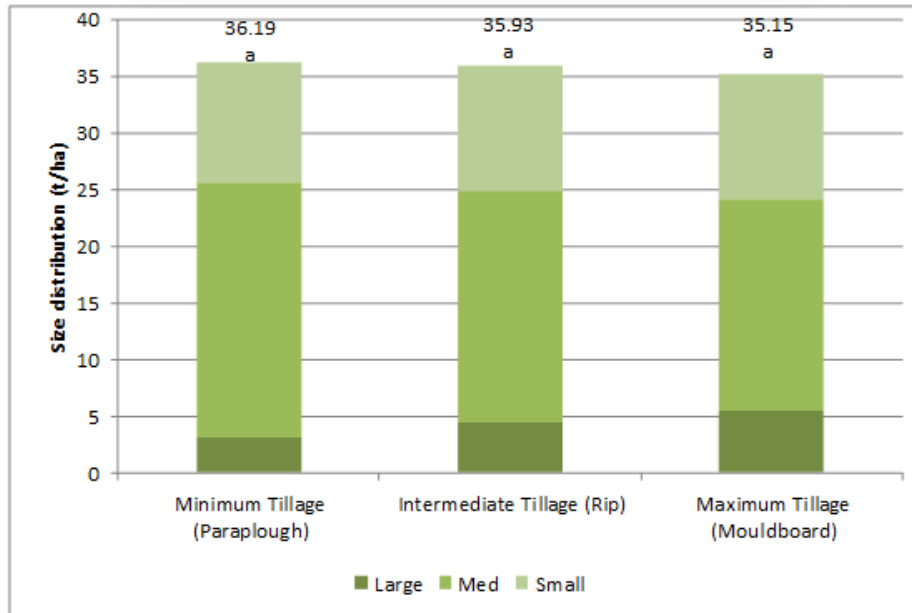
# Yield and Size distribution



2014

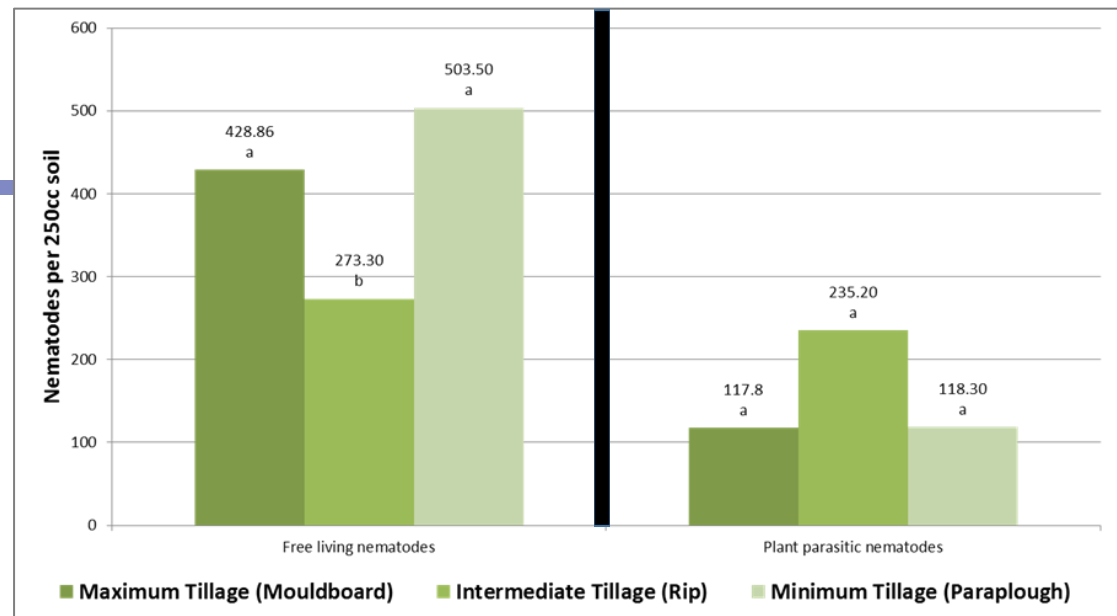


2022

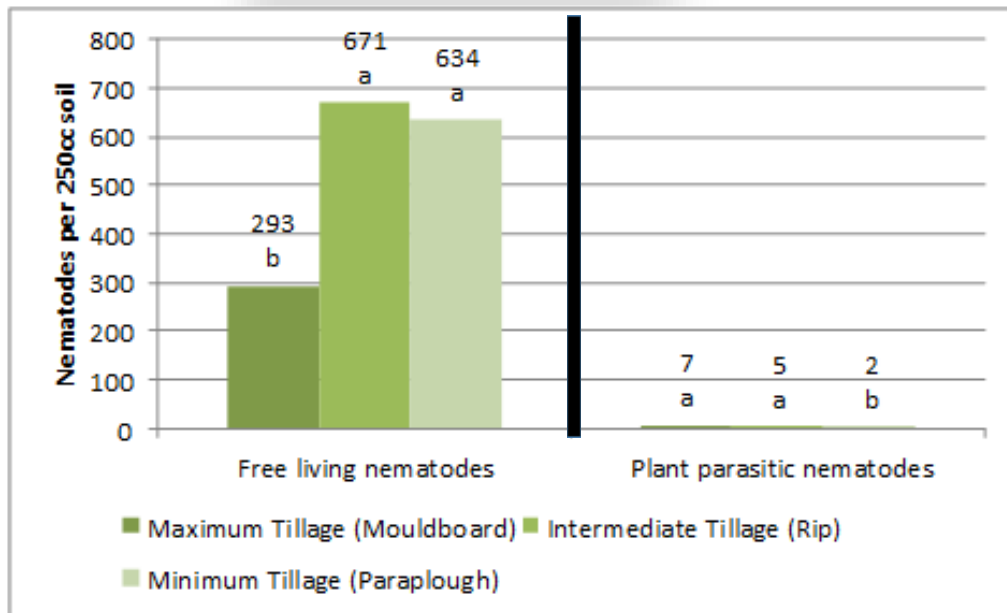


2018

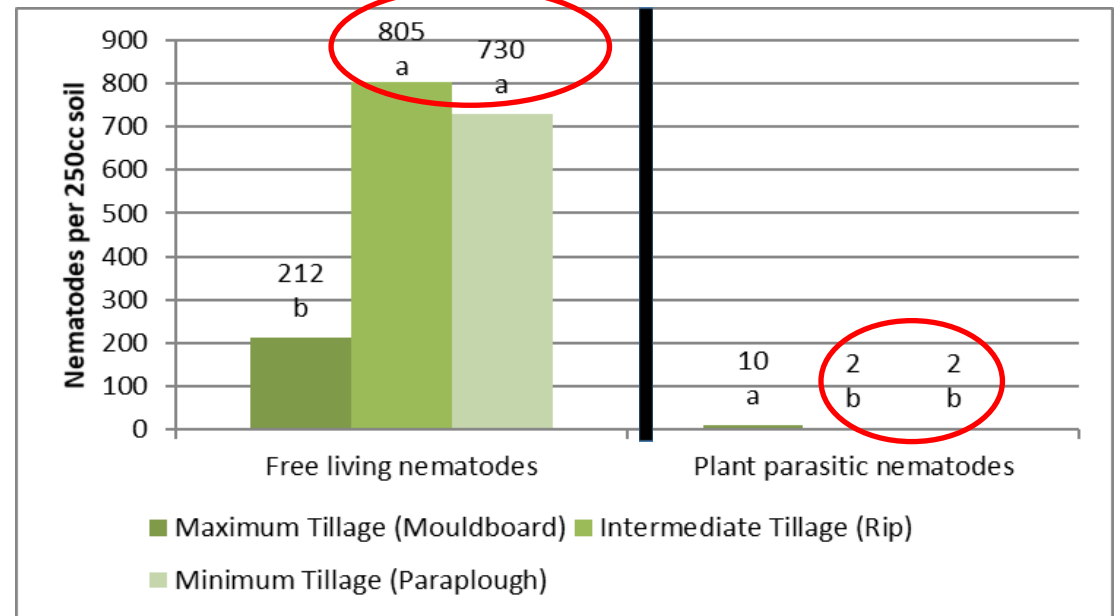
# Nematodes



2014



2018



2022

# Conclusion:



	Parapl	Rip	Mouldb
<b>Bacterial: Shannon</b>	★	★	
<b>Bacterial: Simpson</b>	★	★	
<b>Bacterial: Species Richness</b>		★	
<b>Fungal: Shannon</b>	N/S	N/S	N/S
<b>Fungal: Simpson</b>	N/S	N/S	N/S
<b>Fungal: Species Richness</b>	★	★	
<b>Soil Respiration</b>		★	
<b>Soil Carbon</b>		★	
<b>Yield</b>		★	★
<b>Nematodes: Free Living</b>	★	★	
<b>Nematodes: Plant Parasitic</b>	★	★	



# Acknowledgements

- Co-worker: Albert de Villiers
- Potatoes South Africa
- Heinrich van Zyl
- Western Cape Department of Agriculture



# Contact Us



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