Soil Microbiomes to the Service of Global Challenges

Inaugural Lecture
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Rector Magnificus, esteemed colleagues, students, friends and family present here and online, I am honored to deliver my inaugural lecture on the topic of soil microbiomes and their role in addressing global challenges. Today it is a great opportunity to explain to my family and friends what my research is about. When they ask me: “what do you do?”, I usually give a concise response: “I study beneficial soil microbes, including bacteria and fungi.”

As a professor in Microbial Community Ecology & Environmental Genomics at Utrecht University, my passion lies in trying to understand the ecology of soil microbiomes, how do microbiomes function, how do microbes interact with each other and how do environmental changes impact the microbiome. And, taking this a step further, how we can apply such fundamental knowledge to tackle pressing sustainability problems, such as climate change and food security. With a growing global population and the increasing pressures on the natural resources of our planet, it is more important than ever, to focus on these critical global concerns – and I do believe that soil microbiomes will be critical to dealing with these global challenges.

Let’s begin by understanding what the microbiome is. Look around you, the ceiling of this amazing room, the windows, the floor, the person sitting next to you, and on the screen if you are watching this lecture online...

They all are full of microbes, these various assemblages of microbes are collectively called microbiomes. The microbiome is made up of bacteria, fungi, protists, and viruses, each with their own taxonomy and functions.

As I have said, microbes are everywhere - in humans, insects, animals, plants, air, water and soil.

For instance, in terms of cell numbers, each of you is more microbial than human. And plants have a so-called second genome, microbes that live in and on plants. These microbes have their own set of genes that can provide additional functionality beyond what is encoded in the plant’s own genome.
These invisible tiny creatures are collectively very powerful. Take the gut microbiome for example, where microbial metabolism and signaling contribute not only to digestion and health, but also to brain function and behavior.

The gut microbiome is diverse and amazing, but it is nothing in comparison with the soil microbiome. Have you ever thought about what’s happening underground, specifically in the soil beneath your feet? Or in the soil of your beautiful garden or in the pot with your favorite plant?

**We live in a microbial world**

![](image1)

Soil is not boring. It is a dynamic and fascinating environment! It hosts a huge diverse community of microorganisms, the soil microbiome. Just one gram of soil, equivalent to a teaspoon, contains as many microbes as the total human population on Earth!

**Soil microbiome ecosystem services**

![](image2)
So, without even realizing it, beneath our feet there is an entire universe that is bustling with activity. The soil microbiome plays a crucial role in maintaining soil health, soil structure, and fertility by cycling nutrients and promoting plant growth and health.

Nutrients, like Nitrogen, Phosphorus, Potassium, and micronutrients are essential for plant growth. The quality of these nutrients is related to the diversity of the material being cycled.

Quality of nutrients: aboveground diversity

Consider a natural ecosystem, with minimum anthropogenic disturbance, such as a pristine forest or grassland, where there is a large diversity of plant species. Different plant species offer diverse qualities of nutrients, and when their leaves die, the microbes decompose them, providing diverse qualities and quantities of nutrients in the soil. This is of course a very different story in ecosystems with limited aboveground diversity, such as a monoculture.

Nitrogen is one of the most important nutrients that microbes provide to plants, so I think it is worth taking a look at the nitrogen cycle for a minute.

The nitrogen cycle is complex with many processes, but to summarize it, I have illustrated the main processes in this simple cartoon.

Nitrogen cycle

The Nitrogen gas $N_2$ is emitted into the atmosphere and is the most abundant gas on Earth, representing 78% of our atmosphere. This gas is very stable, and generally inert. It would be a great source of Nitrogen to the plants but unfortunately, plants cannot uptake it in this form. However, bacteria can help! Bacteria living in soil or in symbiosis with plants within root nodules, can convert Nitrogen gas to form of nitrogen available to plants. This process is called nitrogen fixation.
There are bacteria and archaea in the soil that transform ammonium to nitrate, a process called nitrification.

This nitrate can then be leached into the soil, taken up by plants, or used by bacteria and fungi to produce nitrous oxide (N₂O) gas, a greenhouse gas, or nitrogen gas, N₂, via steps referred as denitrification. Interestingly, some microorganisms produce nitrous oxide greenhouse gas but there are some others that can consume this gas. Denitrification process closes the nitrogen cycle beautifully, taking us back to N₂ gas! In environments that are not under disturbances, we expect these different processes of the nitrogen cycle to be in balance.

Also, in the case of phosphorus, most of phosphorus present in soils is not readily available to plants. However, bacteria and fungi can produce acids and other compounds that have the ability to convert unavailable forms of phosphorus into a soluble form that can be utilized by plants.

These phosphorus solubilizing bacteria live in soils and can be associated with the roots of plants.
Most relevant here is an amazing group of fungi called the Arbuscular Mycorrhizal Fungi (AMF) that live in symbioses with more than 80% of terrestrial plant species. Plants provide them with carbon and energy, and in return, they provide phosphorus to the plants. Not only that, but this fungus and other fungi can make a huge network of hyphae that can even be used for communication between plants. This communication between plants and trees through fungal hyphae is especially intense in natural systems. These networks of hyphae carry different bacteria and other organisms like protists that also play a role in maintaining the functionality of the ecosystem.

Microbiomes are also essential for the dynamics of organic matter in soil. They not only decompose organic matter and convert it into a stable form, but they also contribute significantly to the total amount of organic matter in the soil when they die and leave behind their necromass.
Microbiomes also contribute to improving soil quality and structure. Fungi enmesh soil aggregates with their hyphae, while bacteria generate biofilms and exopolysaccharides that act as binding agents like glue, enhancing soil aggregation and stability. This results in the retention of water, nutrients and fractions of organic matter in the soil aggregates, which is crucial for plant growth and soil quality. Furthermore, the increased soil stability also reduces the risk of erosion and nutrient loss in the environment.

As you can see, the soil environment is highly dynamic and teeming with life. Although we recognize its importance, there is still much to learn about it. The soil is a complex environment due to the constant interaction between its microbiome (bacteria, archaea, fungi, and protists) and soil chemical properties. However, despite the significance of these microbes, less than 3% of them have been successfully cultivated, leaving the remaining, more than 97%, yet to be discovered. This presents an exciting and significant challenge for microbiologists, microbial ecologists, and of course our students!

Nevertheless, different methods and approaches based on DNA, RNA and proteins extracted from soils, have been developed to understand the diversity and function of the unculturable microbiome. They include advanced techniques in molecular biology, metagenomics, post-metagenomics, next-generation sequencing, bioinformatics, and modeling.

My research

Global warming: agriculture and deforestation

It is clear that we are facing a climate crises! According to the IPCC, global greenhouse emissions can be categorized by economic activity. The primary source of emissions is electricity and heat production, mainly from burning coal, natural gas, and oil.
Intensive agriculture, including both cultivation of crops and livestock production, is a major global contributor to emissions, and deforestation is also contributing significantly to rising CO₂ levels in the atmosphere.

With this in mind, I would like to concentrate this part of my lecture on the topic “Climate Change: Deforestation and Land Use Change”. I will share my research insights of deforestation and land use change on the soil microbiome. Then, we will move to the topic of “Sustainable Agriculture and the Nitrogen cycle”.

A. Climate Change: Deforestation and Land Use Change

If you look at a picture of Amazon forest, or if you are actually there, like our PhD Marcio Leite was, it is easy to imagine that, with all this amazing plant diversity, the Amazon soil must be very rich in nutrients! Look at this rich liter composition that Marcio is collecting for analysis in the right corner of this slide! Please remember what we have discussed about aboveground diversity and quality of nutrient cycling.

However, the fertility of Amazon forest soil is a complex phenomenon. The Amazon forest is a diverse ecosystem that contributes to nutrient cycling and soil fertility through a combination of various factors, such as the different sizes and shapes of trees with their different types of rooting systems, including deep roots that are capable of pumping nutrients up from deep layers of the soils. Thus, these different trees have different nutrient contents in their biomass. Once the leaves of the trees die, making this huge amount of litter, the microbes do their job recycling these nutrients, making them again available for growing plants. The forest canopy that intercepts rainfall, reduces soil erosion and nutrient leaching, and provides a shaded and humid environment that promotes the growth of microorganisms that enhance nutrient recycling, thereby providing nitrogen, phosphorus, and potassium that are essential for plant growth.
In summary, most of the carbon and essential nutrients are locked up in the living vegetation, dead wood, and decaying leaves. However, when the aboveground vegetation is gone, the Amazon soil becomes very poor and infertile.

**What is the impact of deforestation on soil microbiome?**

Thus, deforestation and land use change can have a great impact on soil microbiomes. Deforestation has become a significant issue, particularly in the tropics, with agriculture being the primary cause of disturbance. So, what happens to the soil microbiome after deforestation?

**Loss of organic matter reshapes microbial interactions**

A former PhD Acacio Navarrete, found that deforestation led to a decrease in soil organic matter content and drastic changes in soil acidity, pH and chemical properties. Slash-and-burn clearing of forest, resulted in an increase in soil nutrient availability. This is because burning of the diverse vegetation results in nutrient-rich ash that is deposited on the soil. These changes in soil chemical factors, and
loss of organic matter, reshape the interactions between microbes by changing their composition, structure and functions, reflecting adaptations of the microbiome in cleared forest soil (Navarrete et al., 2015).

**Acidobacteria**

Let's take the story of Acidobacteria for instance. We found that the Acidobacteria is one of the most abundant group of bacteria in forests soils. In fact, this group of bacteria has been found in various different forests all over the world, including Dutch forest soils, such as Wolfheze shown here. Ohana Costa showed in her PhD research that these bacteria have important interactions with other bacteria and fungi in forest soils, where they produce many different enzymes responsible for organic matter decomposition (Ohana Y. A. Costa et al., 2020; Ohana Y.A. Costa et al., 2020). So, this bacterial group plays an essential role in carbon cycling in forest ecosystems.
Acacio discovered that certain subgroups of Acidobacteria, indicated as “Gp” in this slide, respond differently to changes in soil factors caused by deforestation of Amazon forest for soybean cultivation. This discovery opens up new possibilities for exploring acidobacterial subgroups as early-warning bioindicators of agricultural soil management effects in the Amazon area (Navarrete et al., 2013).

Deforested areas in the Amazon region are subjected to constantly changing pressures. During his PhD research, Lucas Mendes found that different land uses significantly impacted the soil bacterial communities. Forest soils had higher levels of certain bacterial groups, while agricultural and pasture soils had greater microbial functional redundancy. This indicates that different microorganisms or microbial communities can perform similar functions in these soils, allowing for ecosystem functioning even if one group is lost or reduced. These functions include DNA, RNA and protein metabolism and cell division, which are critical for maintaining the high activity and growth of microbes necessary for soil system functioning (Mendes et al., 2015). However, if the microbial community reaches a tipping point, beyond which it cannot sustain the necessary functions to maintain the ecosystem, it may be almost impossible to reverse the damage.
A proposed solution to mitigate the degradation of Amazon soil due to deforestation is the implementation of Agroforest systems. Agroforest systems combine crops with fruit trees and animals in an attempt to mimic the natural plant-soil interactions of mature forests. However, very little is known about the impacts of Agroforestry on the soil microbiomes that determine and maintain soil-plant interactions. Our former PhD Marcio Leite sought to address this issue by asking: is agroforestry a suitable solution for the restoration of the Amazon forest?

To answer this question, we had many trips to the jungle with our motivated team of professors, master and PhD students and even, my family members helped us in one of these campaigns.

**Sampling – great team!**
These campaigns included plant ecologists, plant taxonomists, soil scientists, entomologists, microbiologists, microbial ecologists and of course our students. It was a lot of hard work, but teamwork and effort paid off in the end.

Samples were taken from different agroforest systems, successions of secondary forest and mature forest across an area of 1.5 times bigger than this country.

**Data integration: Agroforestry is a different group**

When we integrated all the different data such as litter biomass and nutrient composition, soil factors, tree species, AMF composition and diversity, fungal and bacterial communities, the Agroforest systems form a different cluster than secondary succession and mature amazon forest.

**Agroforest systems do not mimic the mature Amazon forest’s plant-soil interactions**

The answer to our question is, that Agroforest systems do not mimic the mature Amazon forest’s plant-
soil interactions. Instead they reshape these interactions by altering the aboveground biomass, soil abiotic properties and soil microbiome.

Agroforest systems foster more bacteria in soil, which is very different from the fungi-rich soils of mature Amazonia.

Moreover, our mathematical simulations indicate that Agroforest systems would require many changes in soil and microbial factors to truly mimic Amazon Forest.

In conclusion, agroforest systems could be a potential alternative to less sustainable land management in Amazonia. However, it is necessary to make this practice more sustainable and eco-efficient by adjusting and improving its plant-soil-microbiome interactions (Leite et al., 2023).

B. Sustainable Agriculture and the Nitrogen Cycle

"Unleashing the hidden power of soil: revolutionizing sustainable agriculture with microbiome"

Now let’s move on to the second topic of my lecture: Sustainable Agriculture and the Nitrogen cycle. My focus will be on microbial processes of the Nitrogen cycle and how these microbial functions are related to nitrous oxide greenhouse gas emissions and potential mitigation strategies.

Why am I interested in Nitrogen?

We all need Nitrogen. Nitrogen is essential for all living organisms, including microbes. It is a critical building block for proteins and genetic material, including DNA and RNA, and plays a key role in the growth and development of living organisms. In addition, nitrogen is vital for maintaining ecosystem health and productivity, especially for plant growth.

In conventional agriculture, nitrogen fertilization is commonly used to fulfill the nitrogen needs of plants. However, mismanaging nitrogen in agricultural systems leads to significant greenhouse gas emissions, especially nitrous oxide, which I will refer as N₂O. N₂O is around 300 times more potent than carbon dioxide, CO₂ as a greenhouse gas. As I previously mentioned, soil microbiomes are critical to driving the nitrogen cycle, including the production and consumption of greenhouse gases. Understanding the mechanisms and identifying microorganisms responsible for these processes is essential to implementing sustainable agricultural practices.

The use of organic residues is an interesting sustainable practice in agriculture. This practice contributes to a circular economy management. It can be used instead of, or in addition to, inorganic fertilizer to reduce inorganic fertilizer use. There are many different residues that can be used, including composts, algae, straw, chitin sources from shrimp, insects and fungi, liquid residues from industries of food and so on. They are not only source of nutrients, specially nitrogen for plants, but they enhance soil quality and health, through the soil engineering activities of the Microbiome, leading to soils with higher organic matter content and more resistance to pathogen outbreaks.
For instance, our PhD Manoeli Lupatini has shown that applying chitin from residues of shrimp to soil can modulate and steer the microbial community and select for microbes capable to producing chitinases, an important group of enzymes that can control pathogenic nematodes and pathogenic fungi *Verticillium* (Lupatini et al., 2017, 2019).

**N fertilizer + organic wastes (vinasse and straw)**

In sugarcane, the use of liquid residue is used as nutrient amendment, resulting in lower reliance on inorganic nitrogen fertilizer. However, we observed that combining nitrogen fertilizer with organic wastes like liquid organic vinasse and sugarcane straw lead to highest emissions of N\textsubscript{2}O, as you can see in the red bars in the side. Furthermore, liquid residue vinasse, straw, applied separated or in combination in soils, modulates different microbial community compositions and functions, as represented by different colors illustrated in the graph on your right-hand side (Pitombo et al., 2016).
We then sought to determine the main biological processes responsible for N\textsubscript{2}O production. This was far from a trivial task given the fact that no previous studies have been carried out on microbiological processes of the Nitrogen cycle in these tropical soils with sugarcane. Our PhD Késia Lourenço was brave enough to accept this challenge and attempted to address this issue. By conducting many large field experiments in different seasons and years and by quantifying the microbial genes of the nitrogen cycle using molecular tools, we identified, for the first time, that nitrification was the main process related to N\textsubscript{2}O production. I want to stress that it is typically assumed that N\textsubscript{2}O is produced during denitrification, but we found that N\textsubscript{2}O was actually, produced by the organisms that are responsible for nitrification under these specific field conditions.

Of course, in science, one answer often leads to many other questions!
Thus, our next question was: who are these nitrifier bacteria? Késia together with my other PhD Noriko Cassman, a bioinformatician, answered this question by sequencing the ammonia monooxygenase gene \((amoA)\) from nitrifier populations of all the experimental field soils. They found *Nitrosospira* sp. colored green in this phylogenetic tree to be the dominant ammonia-oxidizing bacteria in the soil, with their density correlated with \(\text{N}_2\text{O}\) emissions.

By identifying *Nitrosospira* sp. as the primary contributor to \(\text{N}_2\text{O}\) emissions, effective management practices can be developed to mitigate the environmental impact of this gas during sugarcane production and promote sustainable agriculture.

Commercial inhibitors of nitrification, such as DMPP and DCD, can block the ammonia monooxygenase activity, thereby reducing \(\text{N}_2\text{O}\) production.

Although these inhibitors have been demonstrated to be effective in temperate soils, their impact on tropical soils, especially in sugarcane production, was unknown until our PhD Johnny Soares studied them. He applied these nitrification inhibitors to soil with urea and measured their effect on the nitrifying community by quantifying the \(amoA\) gene. He found that both inhibitors decrease 95% of \(\text{N}_2\text{O}\) emissions as compared to urea fertilizer, which caused the highest \(\text{N}_2\text{O}\) emissions (Soares et al., 2016). He also observed a reduction in ammonia volatilization.

### \(\text{N}_2\text{O}\) reduction by Nitrification Inhibitors

In addition to identifying *Nitrosospira* sp. as the primary contributor to \(\text{N}_2\text{O}\) emissions, our research team conducted a field experiment where we applied nitrogen fertilizer and organic residue inputs at different times to reduce the activity of these bacteria and decrease \(\text{N}_2\text{O}\) production (Cassman et al., 2019) (Lourenço et al., 2018). By steering nitrifiers to slow down their activity using nitrification inhibitors and applying inorganic and organic fertilizers at different times, we can prevent nitrogen losses through \(\text{N}_2\text{O}\) and ammonia volatilization into the atmosphere. This approach based on our fundamental research was a valuable tool for policy makers, and is currently contributing to sustainable agriculture practices in sugarcane production in Brazil.
Another example of sustainable agricultural management practice is Conservation Tillage, which is a farming practice that involves reducing soil disturbance during crop planting and management to minimize soil erosion and improve soil quality and health.

I have vivid memories of my father, a farmer, always implementing these practices in his farming techniques. In Brazil, the country I came from, conservation tillage practices were first introduced in the 1970s by Franke Dijkstra a Dutch immigrant and Hebert Bartz, a German immigrant. They were losing fertile soils due to erosion. They were called crazy farmers because of planting crops on straw. Today, this country leads in conservation agriculture. We even have a museum of Conservation Tillage! There are numerous living labs across the country in various research institutions and universities that provide valuable long-term sites for us scientists!

Nevertheless, our understanding of the impact of conservation tillage practices on soil microbiome diversity and functions and nitrogen cycle processes, especially in tropical regions, is still in its infancy.

**Palisade grass cover crop**

Promotes:

- Soil microbiome diversity
- Soil microbiome functions
- Carbon storage
- Nutrient availability
- Reduced N losses
- Boost rice & maize productivity

Moneeva et al. 2012, Agri-Ecosystems
In the tropics, cover crops like palisade and ruzigrass grasses, are commonly used in no-till cropping systems. They produce long, deep, fine roots that naturally exude biological nitrification inhibitor compounds. In her PhD, Letusa Momesso found that palisade grass can improve soil carbon storage, increase bacterial and fungal abundances, enhance microbiome diversity and functionality, reduce nitrogen losses due to microbial processes, promote a nutrient-rich soil environment, and boost crop productivity (Momesso et al., 2022).

Another sustainable agriculture practice is the use of beneficial microbes that naturally exist in soils as inoculants, which can reduce reliance on fertilizers and consequently decrease N2O emissions.

Luiz Moretti in his PhD, conducted a long-term experiment with soybean in a non-till system to understand the mechanisms by which such beneficial microbes influence not only plants, but also their associated root microbiome. Luiz found that inoculation of a microbial consortium with various traits such nitrogen fixation, plant growth promotion, and metabolites against pathogens, modulated the microbial community composition that established on the roots of soybean. These changes increased root activity, root nodulation, plant development, and improved grain protein quality and yield. (Moretti et al., 2020a, 2020b).

This change in the microbial community composition reflected changes in their functions related to nutrient metabolism, microbe growth, and interactions between microbes and plants. These functions are critical for the delivery of important services to the plant.

Furthermore, the use of an engineered microbial consortium helped plants alleviate the impact of drought stress during dry spells. (Moretti et al., 2021)(Moretti et al., 2021).
However, if inorganic nitrogen fertilizer is applied together with these microbes, the nitrogen input weakens the associations between microbes and plant biomass and nutrients.

This is because plants that received nitrogen fertilizer and inoculated with beneficial microbes have a different metabolite exudate in their roots compared to plants that didn’t received fertilizer. Nitrogen input reduces the diversity of metabolites in plants. These metabolites influence the recruitment of microbiome in the root and inside the plants.

Therefore, reduced fertilization is essential for these beneficial microbes to have a greater impact on the plant microbiome, both in the roots and inside the plants, allowing them to deliver their services for plant growth and health (Leite et al., 2021).
In conclusion, the soil microbiome holds immense potential to help address global challenges such as land restoration and sustainable agriculture. However, human activities such as deforestation and land use change can significantly impact soil microorganisms, leading to soil degradation and decreased ecosystem functioning.

Our research has shown that understanding the soil microbiome ecology, we can steer and modulate them through sustainable agricultural practices such as the use of organic residues, management and conservation tillage practices, and the use of beneficial microbes as inoculants. These approaches increase the diversity and functionality of the soil microbiome, thereby directly promoting plant growth and health, and mitigating the negative environmental consequences.

Nevertheless, it is crucial to continue fundamental research focused on understanding the mechanisms by which soil microorganisms are impacted by abiotic factors, such as inorganic nitrogen fertilization, not only in specific regions but worldwide. By doing so, we scientists can contribute to developing effective management practices that promote sustainable agriculture. While agroforest systems hold promise as a tool in land restoration, our research highlights the need to improve and adjust its plant-soil-microbiome interactions toward more sustainable and eco-efficient practices.

Overall, adopting sustainable agricultural practices that promote soil microbiome diversity and function can contribute to mitigating the impact of agriculture on the environment, and promoting sustainable and resilient food systems for the future, thus contributing to the achievement of global challenges such as food security and environmental protection.

As part of my future plans, in addition to being embedded within the Institute of Environmental Biology, I look forward to having my chair in Microbial Community Ecology & Environmental Genomics contribute to the Utrecht University’s strategic theme of ‘Pathways to Sustainability’, especially through the Future Food Utrecht initiative. At the same time, contribute to Netherlands Institute of Ecology on Climate Change and Sustainable Land use themes. One of my main goals, is to integrate microbiome studies into an integrated ecosystem perspective, which also links above and belowground ecosystem drivers. Thus, using the amazing developing omics toolbox, together with ecological theory and links with stakeholders to help unlock the power of the microbiome for a more sustainable future.
Words of thanks

Ladies and gentlemen, I would like to thank all those who have contributed to my appointment. I am grateful to the Board of Biology, the nomination advisory committee led by professor Corné Pieterse, the Faculty of Science, our esteemed Dean professor Isabel Arends, and the Board of Governors of our university for entrusting me with this honor. I also have a special feeling of gratitude for Professor Rens Voesenek. I of course wish he could have been here today with us – his confidence in me and support were very important to me, as were our enjoyable conversations filled with positive energy and motivation.

I would like to express my heartfelt appreciation to all the amazing students, PhDs, postdocs, bioinformaticians and technicians who have been part of my research group, both in the past and present. I also want to thank Agaat Pijl, who is a crucial support to everyone in my group. I appreciate the hard work and dedication you all have shown in the lab and field. Our lively and engaging discussions, on both scientific and everyday topics, have created a positive and enjoyable work environment. Your contributions have been instrumental in the success of my research, and it’s an honor that you’ve chosen to be part of my group.

I express my sincere appreciation to Professor Hans van Veen, whose impact on my career in the Netherlands has been invaluable. As a postdoc in the Ecogenomics program at Netherlands Institute of Ecology, his dedication to high-quality science, and critical thinking inspired me to push my boundaries. His confidence in me was a significant milestone when he appointed me as a group leader in the Ecolinc and BeBasic programs and supported me to create international research collaborations. I am deeply grateful for his continued support throughout my career, and it is an honor to have him as my mentor, colleague and friend.

I am deeply grateful to professor George Kowalchuk. As a postdoc in his group, I was constantly inspired by his expertise and enthusiasm, and credit him with igniting my own passion for the field of Microbial Ecology.
I want to express my deep gratitude to professor Riks Laanbroek for his tremendous support to become a professor at Utrecht University. It is my great honor to be following his footsteps in the field of nitrogen cycle research!

I’d like to thank all of my colleagues in the Department of Biology and the Ecology & Biodiversity group of Utrecht University as well as all my colleagues of the Netherlands Institute of Ecology. I especially appreciate the support of professor Geert de Snoo, my colleagues in the Department of Microbial Ecology and professor Jos Raaijmakers for his exceptional support and trust.

I’d like to express my sincerest gratitude to all of my esteemed national and international collaborators from various parts of the world. Building a great team of multidisciplinary collaborators is essential for advancing great science.

I want to extend an enormous thank you to my brothers Jenio, Tiuji and Eizo, my sister Mayury, my sister-in-law Wakana, my brother-in-law Marcos and other members of our family and friends who are here with me today, either in person or online. I also want to thank my nephew Thomas who came all the way from Brazil to surprise me. I feel fortunate to have such a wonderful group of people in my life.

Finally, I want to express my deep gratitude and appreciation to my beloved family - Ayumi, Kenzo, and Joop - for being here with me today. Ayumi, I was convinced that you would join us online, but what a fantastic surprise it was, when you came all the way from Saba, without me knowing and joined us in person at the last minute! Thank you all for your constant support in my passion for exploring the fascinating and microscopic world around us. I am grateful for each and every one of you, and I look forward to continuing to share my journey with you.

And last but not least, I dedicate my inaugural lecture to my parents, Japanese immigrants who devoted their lives to farming. They taught us the importance of soil as the foundation of life.

Ik heb gezegd.
References


