Safe Foods - So Common yet So Unpredictable?

Prof.dr Heidy M. W. den Besten

Inaugural lecture upon taking up the position of Professor of Ecology of Foodborne Pathogens at Wageningen University & Research on 30 November 2023

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Thank you Rector Magnificus, esteemed colleagues, dear family and friends.

We all love good food, food that is tasty and nutritious, and we can really enjoy eating good food. We all also need food to support our health, and actually, we do not consider unsafe food to be food. Consuming healthy and safe food is a primary requirement in all our lives. And this triggered my interest in food science when I was a teenager, and it drove me to do a Bachelor in Food Technology after my secondary school.

Food safety affects us all

Microorganisms play an important role in making good food, and when you consume food, you consume many microbes. The feta cheese and olives in a Greek salad, for example, are produced with microorganisms, as well as the vinegar to flavour a salad. Microorganisms can also spoil our products, and when they are present in high amounts, we can smell it and taste it. High concentrations of spoilage microorganisms in food are unwanted. When foods get spoiled, we will waste the food, which is unsustainable, economically not profitable, and may affect food security. Although spoilage microorganisms may affect the quality of our food, they do not directly affect the safety of our food. The real threat to food safety, however, are the foodborne pathogenic microorganisms that can make us ill. In fact, according to the estimations of the World Health Organization (WHO), one in ten persons per year fall ill after eating food contaminated with pathogens (WHO, 2022). But when you take into account that in the Netherlands more than 17 million people consume three meals a day, most people do not get sick, and most meals we consume, therefore, are safe to eat.

Food safety affects us all, and it is an important focus of governmental agencies and the food industry. The safety of our foods also attracts the keen interest of consumer

organisations, newspapers, and news websites. Generally, food safety only reaches the news when major problems occur. Different types of microorganisms can cause foodborne diseases, and if this had been an interactive lecture, I would have asked you whether you could mention a foodborne pathogen, because most of us know one or more pathogens. But as this is not an interactive lecture, I will give some answers. *Salmonella*, EHEC, or *Listeria monocytogenes* are names of pathogens that you may have heard of. Usually, infections result in the mild health effects of gastroenteritis, and people recover within a few days. Besides these mild effects, however, there are also a few hundred cases of severe illnesses and even deaths in the Netherlands each year (RIVM, 2006).

Before a pathogen reaches the human host, it has been able to survive not only in food, but also in soil and on raw food ingredients. And it is only the most robust pathogen that will be able to survive from soil to humans. This brings me to the key research question I am working on: how do pathogens survive from soil to humans? In some niches they will grow, in others they will be inactivated, and only the most robust organism will finally reach the intestine of the human host in sufficient quantity to cause disease. It is my ambition to predict the path of pathogens along the food production chain. Next to being a food microbiologist, therefore, this also makes me a food detective. As a food detective, I want to find out what drives the suspect to commit its crime and how it can remain under the detection radar and attack its victims. Collecting the pieces of the puzzle on the suspect's behaviour and combining these pieces to predict whether a pathogen can reach the human host is real detective work, and is rather challenging.

Challenges in food safety prediction

Predicting the prevalence and behaviour of pathogens is challenging for several reasons (Figure 1). First of all, not all pathogens behave the same (Figure 1A). Perpetrators use different methods, and this also goes for microorganisms. There are differences between bacterial strains and between single cells, and these impact their survival along the food chain. Secondly, pathogens are like humans: they can be resistant, and they are resilient (Figure 1B). Resistant means that microorganisms are able to cope with adverse conditions, and when they are more resistant, they can survive better along the food chain. Pathogens are also resilient, because they can recover from adverse conditions. Much like our behaviour is influenced by our roots, the behaviour of pathogens is also influenced by their previous experiences. Let me take you back to my roots, because the third challenge we face in the field of food safety is illustrated by a picture from my roots. I was raised on a cattle farm in the western part of the Netherlands. Figure 1C

shows the haystack where my parents stored the hay for our cows, and this haystack illustrates the third challenge: detecting pathogens in foods is like finding a needle in a haystack. We want as few pathogens as possible in our foods, and so, we must be able to detect very low quantities in food. For pathogens, absence testing is often required in one or several samples of 25 grams of food. This means that when one or more pathogenic cells are present in 25 grams of food sample, the test should result in a positive test outcome. When you have a positive outcome, action must be taken, resulting, for example, in the withdrawal of a batch of products from the market. The detection of one cell in 25 grams of foods is not an easy task. Bacterial cells are extremely small and should be isolated from a relatively enormous food volume. Let us do a small calculation together. Generally, the length and width of a bacterial cell is in the range of a few micrometers. A typical mass of one bacterial cell would then be around 3 picogram.

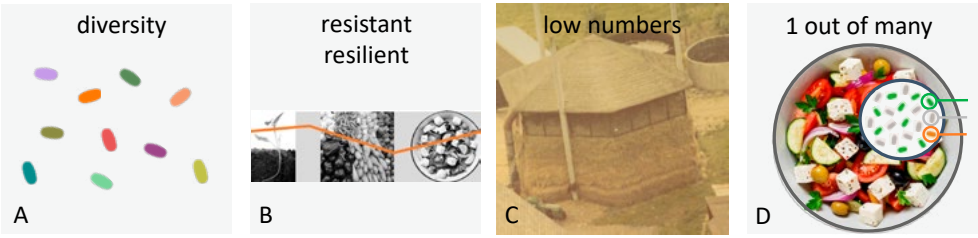

Figure 1: Challenges in food safety testing and prediction: strain and single cell diversity (panel A), resistance and resilience of pathogens (panel B), low concentrations of pathogens in food (panel C), and, pathogens represent only a fraction of the total food microbiota (panel D).

When you want to find such a bacterium in 25 grams of food, you must be able to find one part out of ten trillion parts. And this is, indeed, the same as finding a small needle in the haystack. To date, no method has proved to be sensitive enough to directly detect such low concentrations. In order to detect pathogens in food, therefore, we have to artificially enrich pathogens during our detection procedure in an enrichment step. In the enrichment step, we create an optimal environment such that the target pathogen can multiply to detectable levels. Later in my lecture, I will touch on this special ecosystem we have to create to detect pathogens from foods. Last but not least, pathogens are present in food with many other non-pathogenic organisms (Figure 1D). Pathogens represent only a small fraction of the total microbiota, and the background microbiota can influence the behaviour of the pathogenic microorganism. In sum, then, the realistic prediction of pathogens along the food chain is challenging because pathogens are there

in low levels with lots of other microorganisms. Moreover, pathogens may be different from each other and adapt to new environments. Together, these features influence the likelihood that we can detect pathogens and the possibility that pathogens cause disease. Let me get back to the title of my lecture: Safe foods – so common yet so unpredictable? One side of the coin says that we can take the safety of food for granted. The other side says that food safety appears to be very difficult to test for and to predict. And this touches on the challenges I am working on, and I believe that in order to address these challenges, we need a quantitative and multi-level approach from genome level to ecosystem level (Figure 2).

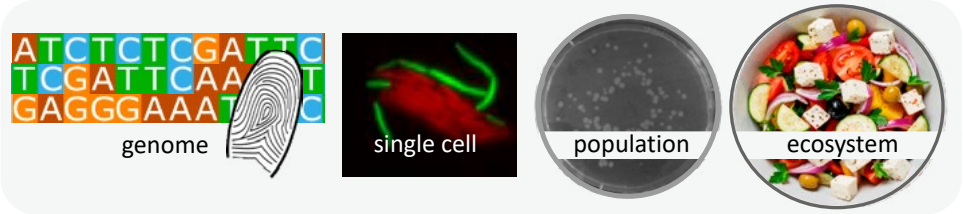

Figure 2: Quantitative, multilevel research approach: from genome to ecosystem level.

Information on the molecular level gives me the genetic fingerprint of microorganisms, just what a food detective needs, and this information helps me to understand how individual cells in a population behave and, therefore, how the population as a whole behaves. Pathogens live and grow in ecosystems such as foods and enrichments, and my aim is to understand and predict the behaviour of pathogens in these ecosystems. By linking different functional levels, I can understand why different strains behave differently, and this will also give leads to genetic biomarkers for robust performance along the chain. My research approach not only generates understanding of the biology of pathogens, which gives us fundamental knowledge, we also want to translate this fundamental knowledge into strategies that we can take up to control food safety.

Societal and industrial trends that affect food safety

I mentioned at the start of my talk that almost one in ten people fall ill every year after eating contaminated food. And this number is expected to increase because the sensitive population, in particular the elderly, is increasing. Also other developments in our environment put food safety under pressure. One-third of all food produced globally is wasted between farm and fork (FAO, 2011). At the same time, the world's population is growing rapidly. It is estimated that by 2050, around 9 billion people will be living on this

planet (UN, 2022), and they will all need access to sufficient nutritious and safe food. We cannot feed this growing population using the methods used to grow food to date: we are depleting natural resources too much and water sources will become less and less available. The production of food must become more sustainable without compromising the quality and safety of food. We should transition towards a more circular economy with less food waste, reusing water, eating more plant-derived proteins, and producing food with technologies that demand less energy input. In its Green Deal, the European Commission described how they propose to make our food production more sustainable in the near future by reusing side streams and bringing these back into the food production system (EC, 2020). In this way, our production system will change from linear production chains to more circular production loops. To make this successful, the ways we value food side-streams need to change drastically. Currently, food-grade edible side-streams are transformed into bioenergy or reused to feed livestock. However, the opportunity to valorize food-grade side-streams to consumer food is virtually unexplored, and we do not know much about food safety when using side-streams and closing loops. In the past, we made food production systems linear to better control food safety. So when we are moving to more circular food production systems, the control of food safety is a clear consideration. Our group will explore how we can sustainably reuse food-grade side-streams in a safe way, and we will interact with Wageningen colleagues from social sciences with key expertise in consumers' behaviour to explore opportunities along this avenue in the coming years.

Our group is already actively contributing to develop research that supports the sustainable transition of our current food system. Since 2021, I have coordinated TRANSIT, a Horizon Marie Curie International Training Network. TRANSIT focuses on sustainable processing technologies, such as Non-Thermal Plasma. These technologies can offer consumers clean-label foods with extended shelf life. Currently, however, we do not know how pathogens are killed when we preserve foods with these technologies. In the years to come, therefore, we will work on answers to this question in order to stimulate the uptake of sustainable technologies into our food systems.

From molecule to management

In my research, I integrate the fields of microbiology and mathematics to predict the behaviour from molecular to management level. In my first Bachelor year, my interest in microbiology was triggered, because microbiology is dynamic as microbes are able to grow and adapt to different environments. At the end of my first Bachelor year, I was happy with my study programme, but I missed the quantitative part and the joy of

playing with numbers, which is why I decided to do another Bachelor in mathematics. In my current research, I combine my passion for tasty and healthy food with my two favorite disciplines: microbiology and mathematics.

Since the eighties, empirical predictive models have been developed to predict microbial behaviour at the macro-level along the food chain. To ensure that these models can be used to realistically predict the growth or inactivation of pathogens in food, they should include variability based on the biology. If you ask me whether we can trust models, then my answer will be yes. But as a scientist, I will add a critical subordinate clause here, namely: models cannot give us absolute accuracy. To illustrate this caveat, I would like to recall the extreme weather we had on my birthday this year. The Netherlands was battered by a rare and powerful summer storm. Storm Poly hit our country with heavy rain and winds, and Poly was the strongest summer storm on record in our country. Had rough weather been predicted? Yes. To this extent? No. Are weather forecast models therefore wrong? No. Models do not give absolute accuracy. It is useless to maintain that we can build models to predict accurately: this is impossible. Biology is variable, and we must include this variability in our predictions to build realistic models. Even if we include variability, we will still not be able to predict an outcome with 100% certainty, but we can use models to compare scenarios and to give relative accuracy. By using models in this manner, models give us valuable insights into how we can improve and finetune processes and what interventions will be most effective to control food safety.

Quantitative microbiology and the use of models are powerful tools, and I want to share two examples of work in our group. These examples illustrate how we use models to understand and predict the resistance and growth of pathogens in different ecosystems, and how our approach answers both fundamental and practical questions.

My first example focuses on the steps we took to better understand how diverse microorganisms are in terms of their resistance. When we collect information at molecular level, what can it give us? How can we use genetic information? As in humans, the genetic information of microorganisms is stored in their DNA. The DNA of most bacteria is contained in a single molecule, called the bacterial chromosome, built with four different nucleotides. Whole-genome sequencing of the DNA gives us an unprecedented view of the genetic potential of a bacterial strain, and provides us with the genetic fingerprint of a pathogen. We can use this genetic fingerprint for strain identification, much like a detective searches for fingerprints to identify the perpetrator of a crime. To prove that a food isolate is the causative strain of a foodborne disease, the genetic fingerprint of the pathogen isolated from the food and the isolate from the

patient must be compared, which basically means that millions of base pairs must be compared. And if there is a perfect match, then you have the proof at hand that the food isolate did indeed cause the disease, which is the ultimate outcome of the detective work. A *Salmonella* outbreak occurring between 2015-2018 was the first published outbreak in the European Union where whole-genome sequencing was used to prove the source of the outbreak (Pijnacker et al., 2019). Besides providing the fingerprint of a pathogen, the DNA can give much more information. In my work, I use the genetic information to better understand the behaviour of pathogens. Microorganisms are diverse, and I use the genetic information to unravel why microorganisms behave differently. To do so, we work with strains that have been collected from different sources, such as raw materials, food production environments, foods, and also from patients, and we try to link specific characteristics of strains to their genetic fingerprint in order to understand why strains behave differently.

One of our previous PhD students, Diah Chandra Aryani, quantified the heat resistance of 20 *Listeria monocytogenes* strains (Aryani et al., 2015). We expressed the heat resistance of the strains in the *D*-value, which is the time required to reduce the number of cells with a factor 10, or 1 $\log_{10}$. We demonstrated that different *L. monocytogenes* strains vary enormously in their heat resistance. Because we collected the *D*-values of so many strains, a solid quantification of the impact of strain variability could be made, which was expressed in the standard deviation of the *D*-value (Figure 3). Next to *L. monocytogenes*, also the *D*-values of 20 *Lactiplantibacillus plantarum* strains were determined (Aryani et al., 2016). And surprisingly, the standard deviation of the *D*-value was rather comparable for the two bacterial species (Figure 3).

This raised the question whether the impact of strain variability was preserved among bacterial species. In collaboration with NIZO Food Research, we quantified the variability in heat resistance of bacterial sporeformers (Berendsen et al., 2015; Den Besten et al., 2017b; Den Besten et al., 2018; Wells-Bennik et al., 2019). Figure 3 shows the standard deviation of the *D*-value for the different sporeformers. This is a very clear picture based on a lot of data, showing that strain variability for the different bacterial species had the same order of magnitude. Note that one bacterial species, namely *Bacillus subtilis*, has been grouped into two groups. Indeed, the *B. subtilis* strains could be grouped into a group of strains that produced high-level heat resistant spores, and a group of strains that produced low-level heat resistant spores, and the *D*-values of these two groups clearly differed in their heat resistance. This ringed the bell whether the difference in heat resistance among the *B. subtilis* strains had a genetic reason. Hence, our NIZO colleagues sequenced all *B. subtilis* strains, and they demonstrated that all strains

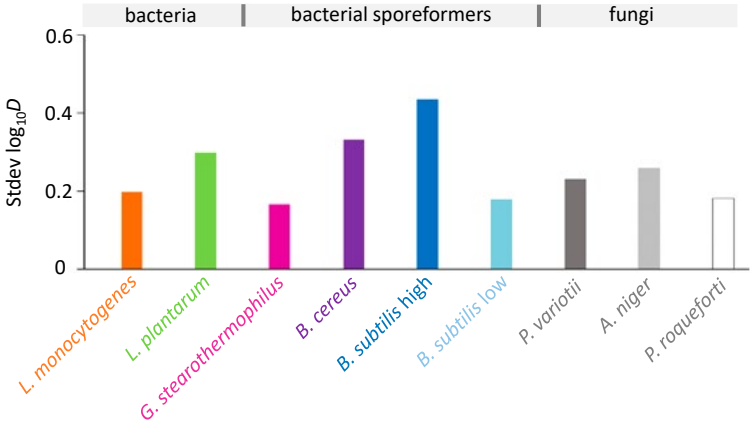

Figure 3: Comparison of strain variability in heat resistance among microbial species. Listeria monocytogenes *cells (orange),* Lactiplantibacillus plantarum *cells (green),* Geobacillus stearothermophilus *spores (pink),* Bacillus cereus *spores (purple),* Bacillus subtilis *high-level heat resistant spores (dark blue),* Bacillus subtilis *low-level heat resistant spores (light blue),* Paecilomyces variotii *conidia (dark gray),* Aspergillus niger *conidia (light gray),* Penicillium roqueforti *conidia (white). Adapted from Van den Brule et al., 2022.*

that produced high-level heat resistant spores harboured a specific genetic biomarker, which was absent in strains that produced low-level heat resistant spores (Berendsen et al., 2016). To confirm that this genetic element was responsible for this increased heat resistance, they integrated this specific DNA sequence into the genome of a low-level heat resistant strain. As expected, this mutant strain jumped from the low-level heat resistant group to the high-level heat resistant group, confirming the importance of this genetic biomarker for heat resistance. This demonstrates how a quantitative approach leads to biological insight, and in the coming years we will follow this road to search for other biomarkers for stress resistance.

The strain variability of the bacterial species had the same order of magnitude, and this remarkable finding led to the question whether this points to a biological signature over microbial kingdoms. My group works on bacteria, not on other types of microorganisms. In order to answer this fundamental question, I joined the project on fungal diversity of the Top Institute of Food and Nutrition (TIFN). Three PhD students working at Utrecht University, Leiden University, and the Westerdijk Fungal Diversity Institute dedicated time together with Wageningen Master thesis students to quantify the heat resistance of the fungal strains they were working with. And as shown in Figure 3, it indeed seems to be the case that strain diversity is rather preserved over

microbial kingdoms. This answers a fundamental question in microbiology on how preserved diversity is, and this remarkable finding was published last year with our TIFN colleagues (Van den Brule et al., 2022).

And how can we use this information to manage the safety of our foods? Our approach gives us necessary quantitative information to make our predictive models realistic. We can include this biological variability in our models, to realistically estimate the kinetics over the food chain (Figure 4), and to evaluate which interventions are most effective to reduce the chance to get sick. In our research, we also compare different sources of variability. The example I just shared focused on variability in resistance, but we also look at variability in growth. Comparison of the impact of different sources of variability is very important, and we expressed this message in one of our article titles, in the spirit of George Orwell: 'All variabilities are equal but some are more equal than others' (Den Besten et al., 2017a).

Figure 4: Simplified illustration of predicting the behaviour of pathogens from soil to humans.

My second and last example of how our approach answers both fundamental and practical questions focuses on growth in an ecology we create to detect pathogens, namely enrichments. As I mentioned earlier, we should be able to detect very low levels of pathogens in food. The food testing procedures that are globally used by governments and industries have been standardised by the International Standardization Organization, the ISO. The ISO methods are accepted as the golden standard to isolate a specific pathogen from a food. The enrichment aims to provide an ideal environment for the target microorganism to recover from possible cell injury induced during food processing. The enrichment also stimulates the target pathogen to grow massively to much higher levels to allow for subsequent detection. The chosen enrichment media are pathogen-specific and supplemented with selective

antibiotics to suppress background microbiota. While the enrichment step forms the basis of the detection procedure to recover the target pathogen and to allow it to grow to detectable levels, the ecology of these enrichments are fairly unexplored. So you will understand that this topic drew our attention. Our PhD student Jasper Bannenberg worked on the enrichment ecology of *Listeria monocytogenes*. As I mentioned earlier, legislation stipulates that we should be able to detect one cell in 25 grams of food. In the enrichment step, cells repair damage during the lag phase, and multiply to detectable levels. Our approach was to first quantify how different strains are. We quantified the lag phase of 23 *L. monocytogenes* strains, and the lag phase varied among the strains, especially when the strains were stressed. This quantitative approach allowed us to predict not only the growth kinetics of the fast growers with a short lag phase, but also that of intermediate and slow growers (Figure 5) (Bannenberg et al., 2021). Because we quantified the kinetics, we could also predict the fail chance of the current detection method, and we could demonstrate that the current fail chance is 20%. Based on the quantified kinetics, moreover, we could demonstrate how we can adapt the procedure to increase the detection chance. So quantitative microbiology expresses behaviour in terms of numbers and chances, and this gives us a solid foundation for understanding. But we also want to generate knowledge of the biology behind this behaviour.

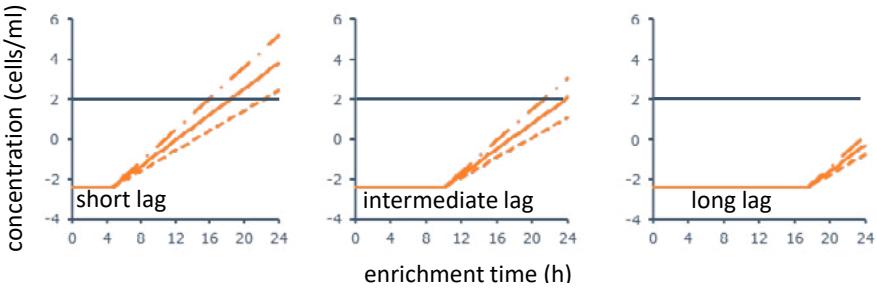

Figure 5: Prediction of growth and detection chances in enrichment-based detection procedures. Adapted from Bannenberg et al., 2021.

The next step we took, therefore, was to understand how cells adapt during the lag phase at the molecular level. We looked at all intercellular proteins that were expressed by the cells during the lag phase, to understand what factors are involved in damage repair (Bannenberg et al., 2024). We demonstrated that, in both slow-growing and fast-growing cells, generic stress factors are upregulated to repair damage. And this answers a fundamental question in food microbiology on how cells can recover from damage. Insights we obtained in this project also have a clear societal and economic relevance. Based on the publications from this

project, I was invited to join an ISO working group as an expert. This working group is responsible for revising the current *Listeria* detection procedure that is globally used to detect *L. monocytogenes* in food, and the knowledge gained in the project will help us to revise this international test procedure. This example shows what I am doing it for: to work on relevant food safety issues, and to actively disseminate our research results to the scientific community and societal organisations to enhance the field of food safety.

New directions for research

The field of ecology of foodborne pathogens is a very exiting field and in the coming years we will perform research to address the challenges for the future. Currently, we are already facing the challenges of climate change, and we are living in a world that is moving towards greater sustainability and circularity. We are facing more frequent periods of droughts and floods, and this may increase the prevalence of pathogens in our future food systems. An increasing number of consumers are adopting plant-based diets and buying mildly processed foods, and food safety is an absolute requirement to valorize these trends. Therefore, ensuring the safety of these foods will be an important item on the research agenda for us in the years to come.

In my lecture today I mentioned that the standard procedures for food testing are pathogen specific, and these only allow the detection of one pathogen. However, we also know that foods are sometimes contaminated with multiple pathogens, and when only one food testing method is applied, other pathogens remain under the detection radar. Last year, therefore, we launched two PhD projects in collaboration with Wageningen Food Safety Research and the RIVM to develop a test procedure that detects multiple pathogens in a single test procedure. This will help to ensure that all pathogens are detected from food.

By working from molecule to management, our approach opens up opportunities to revisit our current way of assessing microbiological risks at the management level. Quantitative microbiological risk assessments are used to estimate the risk of illness when a population or individual is exposed to a pathogen in the food. In these assessments, quantitative models are used to describe microbial behaviour from food production to food consumption. Current quantitative microbiological risk assessments, however, do not take into consideration that specific subtypes of pathogens may be overrepresented in specific food commodities, while this is relevant when you want to evaluate the efficacy of interventions. As an expert group member of the WHO and FAO,

I evaluated how data based on whole-genome sequencing could enrich the risk assessments of the future (FAO & WHO, 2022). This area of research will have our attention in the years to come, in which I will team up with international colleagues to explore this new avenue of food safety risk assessment.

Education and dissemination

With this lecture today, I officially take up my position as a professor. Let me finish off with a question I asked myself when I took up this role. What am I doing it for? How can I create impact, and how can I make a valuable contribution to the society in this position?

With my research, I want to generate knowledge that we can use to make our food safer. But research does not change the world. What changes the world? It is the people, you and me, who can change the world. When you translate the word "professor" into Dutch, you would call me "hoogleraar". And I want to emphasize the last part, "leraar", meaning "teacher, educator". The primary aim for me as a "leraar" is to provide students with a solid knowledge base, and to foster skills and attitudes for their professional as well as their personal lives, such as critical thinking, self-motivation and creativity. I teach six courses, in both Bachelor and Master programmes, and supervise PhD students. This gives me ample opportunity to enthuse students and, more importantly, to attend to their development path. To answer the urgent questions we have in our field, it is essential, in my view, to work together. Therefore, I actively seek to collaborate with colleagues in and outside the Netherlands. This joining of forces is essential to take big steps in our rapidly changing world. Wageningen University strongly positions itself as an independent partner that seeks collaboration, and the projects I initiate often involve industrial partners, research institutes, governmental bodies, and other public entities. This results in consortia with broad combinations of expertise and ensures that pre-competitive, new knowledge can actually be followed up by the partners, resulting in the wide dissemination of research results. Dissemination of research output is vital to ensure that you can create impact with your research. I consider it my duty to participate in working groups outside the academic bubble. As a researcher, I take up a societal role by working together in consortia, and acting as an expert in nationally and internationally renowned institutes such as the Gezondheidsraad and the WHO. I think that we as researchers have to actively share our knowledge beyond the academic bubble. When opinions differ, one may be tempted to get cynical, a liability for all of us: researchers, media, politicians, and consumers. As researchers we can stimulate critical discussion and provide essential nuance.

Taking up an active role outside the academic bubble is also needed to provide good teaching. Here in Wageningen we are in a privileged position, because we are a university that attracts students from all over the world. A few years ago, I counted the number of nationalities in the classroom of our introductory course on Food Microbiology, and I counted almost 30 nationalities, so a small world in one classroom.

When I was finishing my Bachelor's in Food Technology in 2000, I was in Mongolia to do an internship. I was teaching nomads in rural Mongolian areas how to preserve food. I had the ambition to work in the field of food safety in developing countries in Asia or Africa and to discover the world. The director of the Mongolian institute I was working at was a Swiss agronomist, with a PhD in his field. He was a man I really admired, because he was truly recognised by the Mongolians because of his experience. He saw my ambition and my wish to work in developing countries, and gave me unexpected but wise advice: go back to school and get your PhD, because in positions where you can have an impact, you often need a PhD. I was lucky that after completing my Master in Food Technology, I found a PhD project in the laboratory of Food Microbiology where I could combine my interests in mathematics and food microbiology. In the course of this PhD project, my supervisor Professor Marcel Zwietering said that, here in Wageningen, we teach the teachers of the future. This made me realise that I had found the place where I could flourish, where I could work in a field I really like, and where I can make a valuable contribution to society.

Words of gratitude

These sentences merge seamlessly with my final words of gratitude.
Dear parents, dear sisters and brother, dear in-laws and dear friends. Many thanks to all of you. Over the past years, I learned that it takes a whole community to raise a professor.

The two people who gave me the room to flourish and to develop myself into the person I am today, are my former supervisors and dear colleagues Professor Marcel Zwietering and Professor Tjakko Abee. You formed the two strong shoulders I could stand on to grow as researcher and supervisor during my tenure track years. Marcel, as chair of our group, you lead by example, and in this way I learned so many things from you. Thanks for being a mirror and a guide to me all those years. Tjakko, your creativity is a continuous source of inspiration to me. Our complementary way of working helped me to develop myself as researcher and supervisor. You are a great supporter. Together, you are the best coaches I could have had.

The laboratory of Food Microbiology is a very pleasant working environment. Dear colleagues, we are a very good team together. The team spirit we have, gives me a lot of energy, many thanks for that.

My final words of gratitude go to the four main men in my life: Reindert, Ruben, Bram, and David. You are the foundation of my joy and happiness. Ruben, Bram and David, you were already there when I was a PhD student, and now, 12 years later, you are taller and stronger than I am. All three of you have your own sparkling personality. You make me a very proud mom.
Reindert, without your ever-lasting support and love I would not stand here today. You anchor and balance us as a couple. I am very blessed to have you as my husband.

Ik heb gezegd.

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Consuming healthy and safe foods is a primary requirement for everyone. Foods can get contaminated with pathogens along the food production chain. To understand and predict the behaviour of pathogens along the food chain, the field of ecology of foodborne pathogens integrates the domains of food technology, microbiology, and mathematics. Knowledge at the molecular level provides explanations for the behaviour of pathogens in ecosystems, such as food. Quantification of this behaviour based on the underlying biology gives us valuable insights into how we can improve and finetune food production processes to control the safety of our foods.