





Samen werken aan diergezondheid



Microbiële *Eco-systemen op melkveebedrijven*

Ynte Schukken



Samen werken aan diergezondheid



Microbiële *Eco-systemen*

- Introductie
- Microbiële Eco systemen
Uier, darm
- Dynamiek van Microbiële Eco systemen
Voeding, Ab, Superinfectie, Omgeving
- Resilience
- Conclusies

Samen werken aan diergezondheid

GD

Free available online

Microbial Diversity of Bovine Mastitic Milk as Determined by Pyrosequencing of Metagenomic 16S rDNA

Ynte Hein Schukken, Rodrigo C. Bicalho, Georgios Oikonomou, Vinicius Silva Machado, Carlos Carvalho

Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, Ithaca, New York, United States of America

Identified as causative agents of mastitis in a metagenomic study of healthy and mastitic milk

www.nature.com/scientificreports

SCIENTIFIC REPORTS

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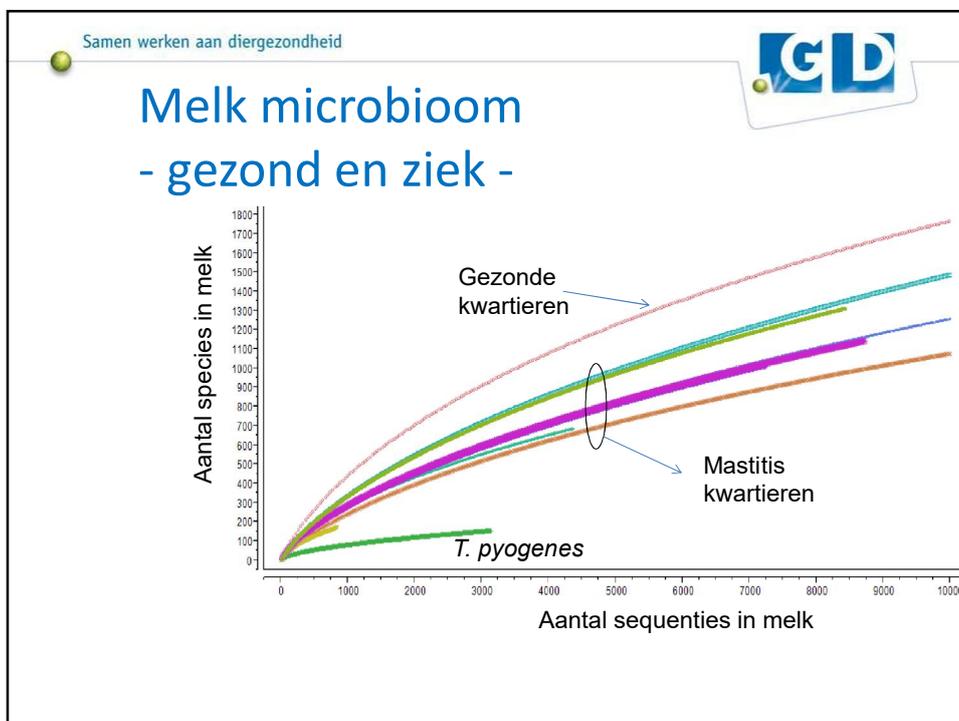
Longitudinal metagenomic profiling of bovine milk to assess the impact of intramammary treatment using a third-generation cephalosporin

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Erika K. Ganda¹, Rafael S. Bisinotto^{1,2}, Svetlana F. Lima³, Kristina Kronauer¹, Dean H. Dectel¹, Georgios Oikonomou^{1,2}, Ynte H. Schukken¹ & Rodrigo C. Bicalho¹

Antimicrobial usage in food animals has a direct impact on human health, and approximately 80% of the antibiotics prescribed in the dairy industry are used to treat bovine mastitis. Here we provide a longitudinal description of the changes in the microbiome of milk that are associated with mastitis and antimicrobial therapy. Next-generation sequencing of 16S rRNA gene quantitative real-time PCR, microbiome. Cows diagnosed with clinical mastitis associated with Gram-negative pathogens or

Abstract
Dairy cow mastitis is an important disease in the dairy industry and is traditionally diagnosed by culture of bacteria. The results of pyrosequencing of bacterial 16S rRNA genes from mastitic milk samples were compared with those from healthy milk samples. The results showed that the most clearly differentially amplified genes were those of *Streptococcus dysgalactiae* and *Streptococcus agalactiae*, which were the second most abundant genera in the mastitic milk. *Staphylococcus aureus* and *Streptococcus agalactiae* were the most abundant genera in the mastitic milk. These results suggest that *Streptococcus agalactiae* and *Streptococcus dysgalactiae* are important pathogens in bovine mastitis.



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Wat is het melk microbioom?

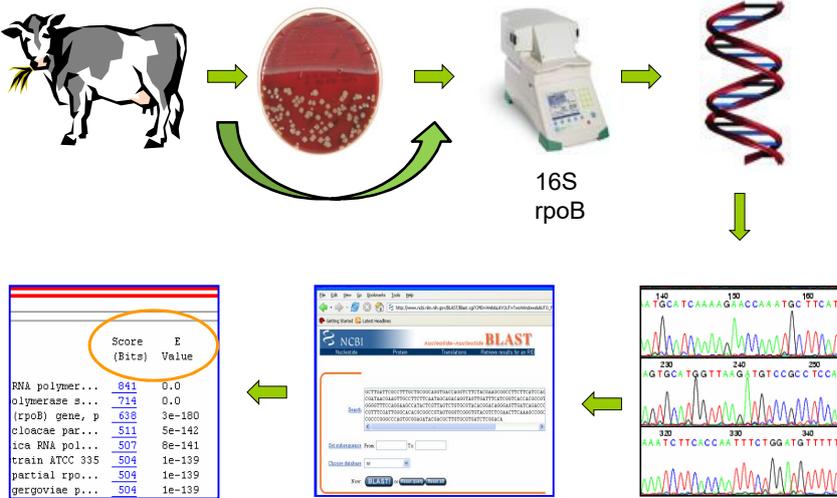
Melk microbieele samenstelling zoals gevonden met next generation of pyro-sequencing.

De populatie van bacterieele species gevonden met 16S sequencing van DNA geïsoleerd uit melk

Gemiddeld 7000 bacterieele 16S sequenties corresponderend met ~1000 bacterieele species per melk monster, en waarschijnlijk meer in melk van gezonde kwartieren.

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Bacterieele identificatie met 16S DNA Sequencing



16S rpoB

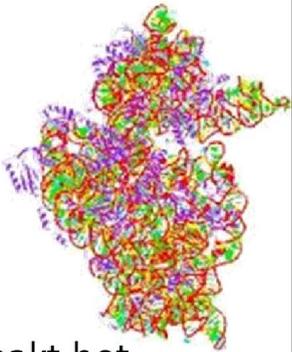
	Score (Bits)	E Value
RNA polymer...	841	0.0
polymerase s...	714	0.0
(rpoB) gene, p	535	5e-180
cloacae par...	511	5e-142
ica RNA pol...	507	8e-141
rxain ATCC 335	504	1e-139
partial rpo...	504	1e-139
gergoviae p...	504	1e-139

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16S ribosomaal RNA

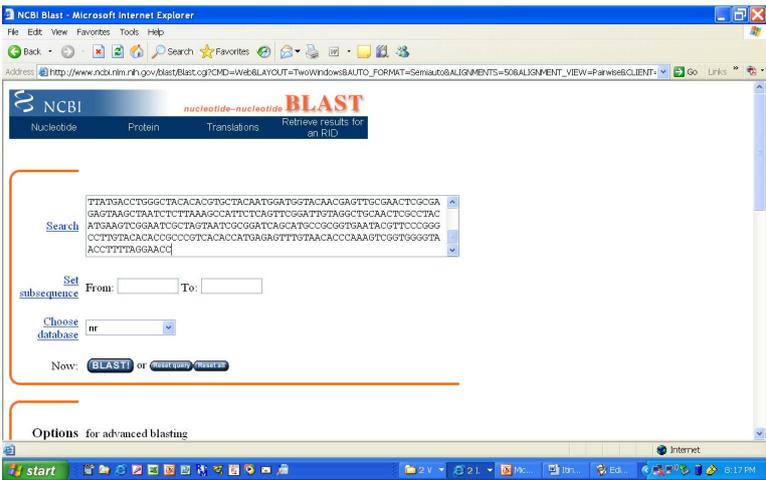
- Hoog geconserveerde regio
 - Gebruikt voor primers
- Variabele regionen
 - Tussen species variatie
- Bruikbaar voor phylogeny
- Next-generation-sequencing maakt het mogelijk grote aantallen te vinden:



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Sequentie resultaten, BLAST



NCBI *nucleotide-nucleotide* **BLAST**
Nucleotide Protein Translations Retrieve results for an RID

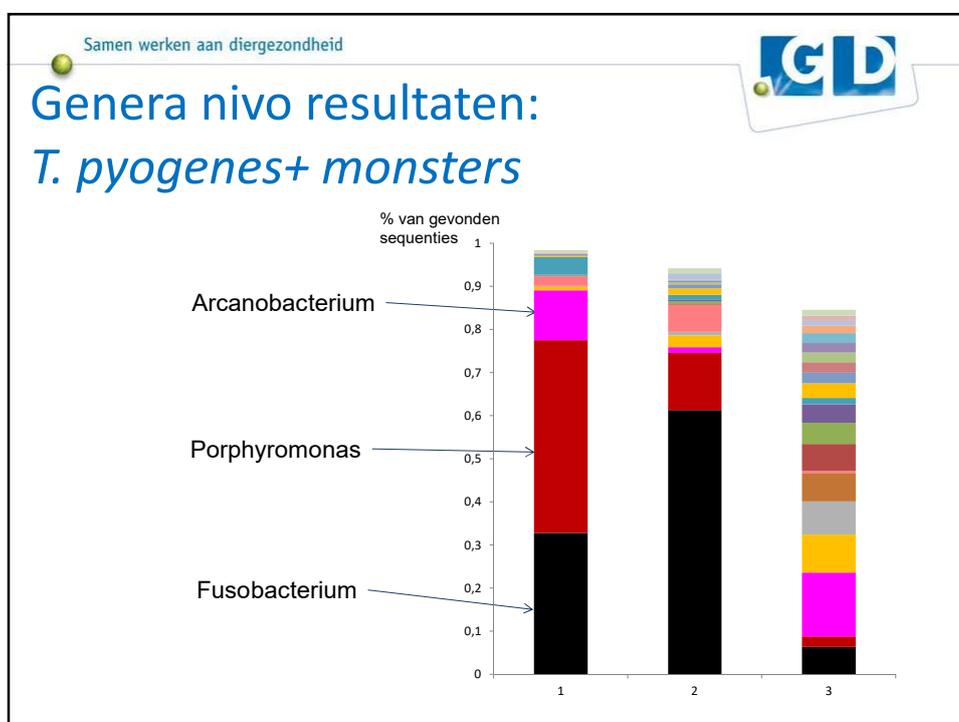
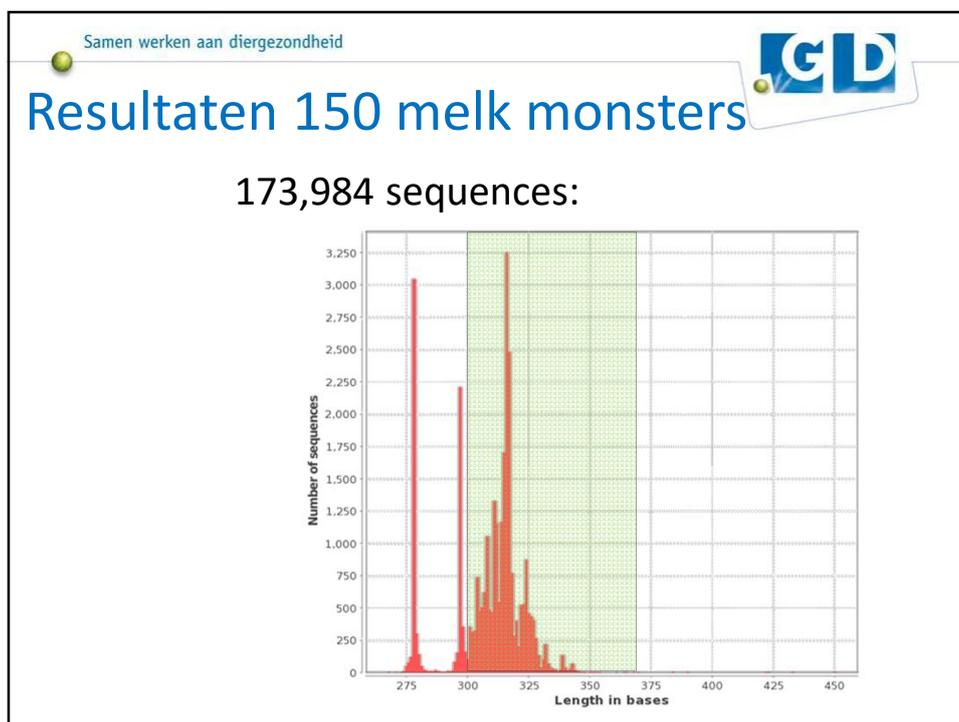
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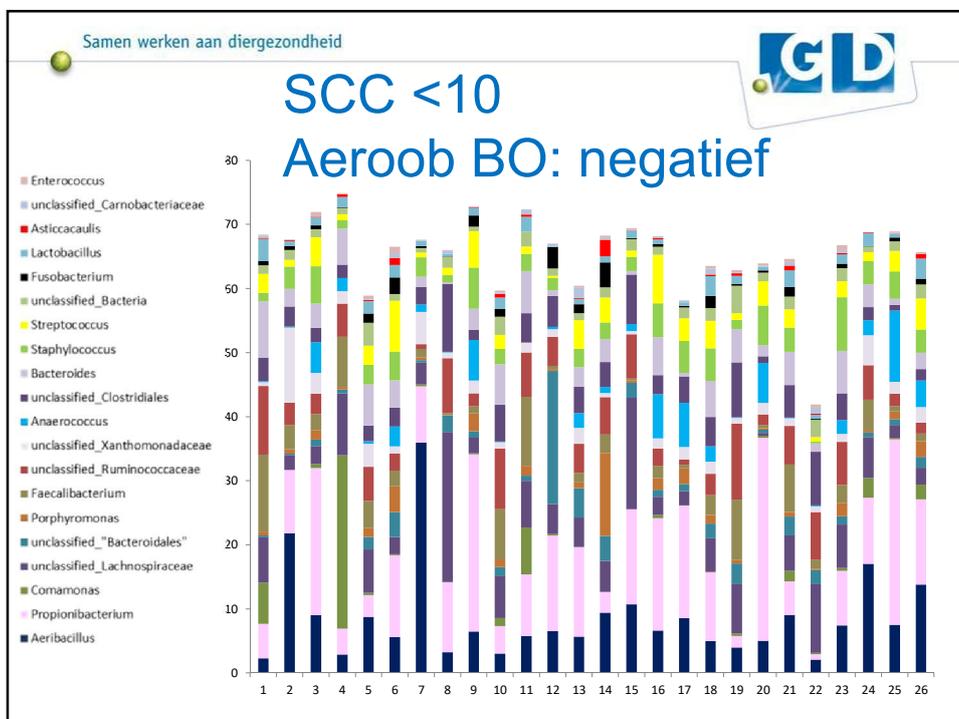
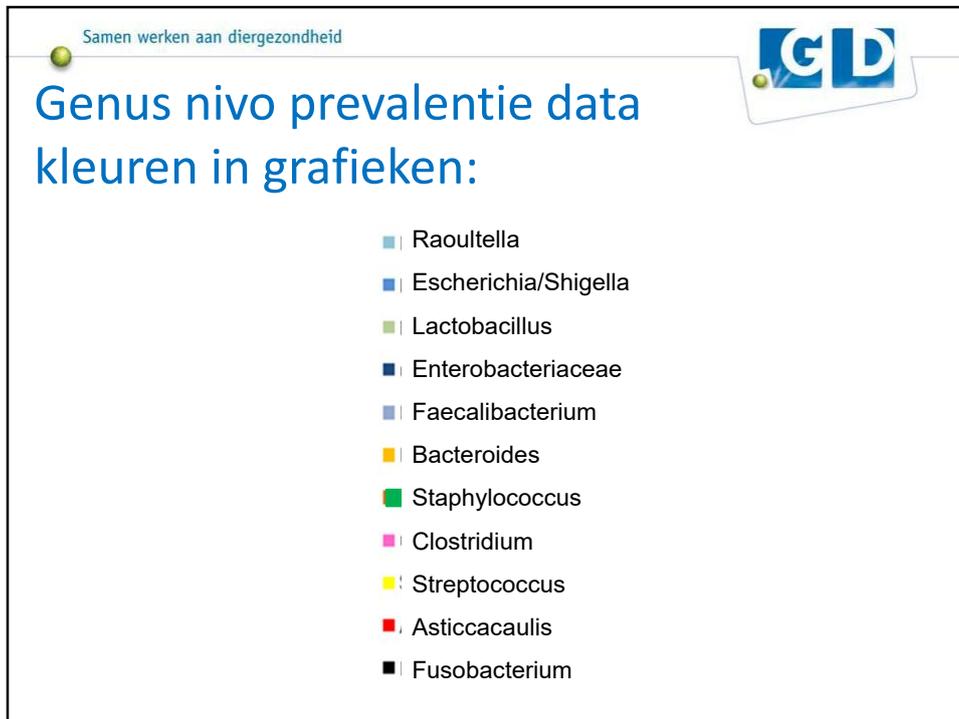
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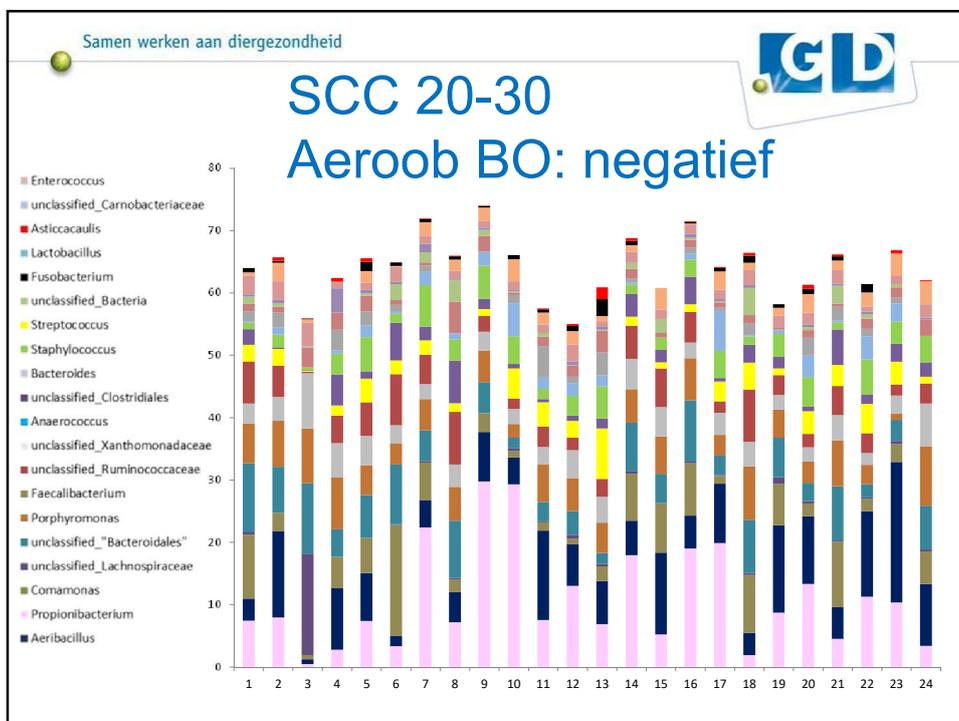
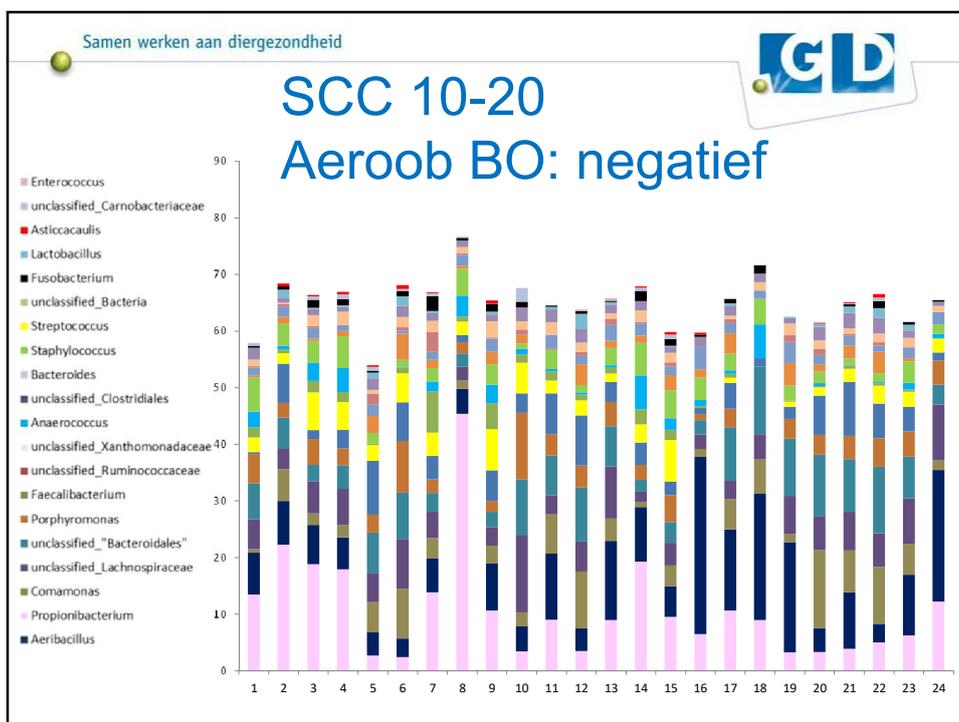
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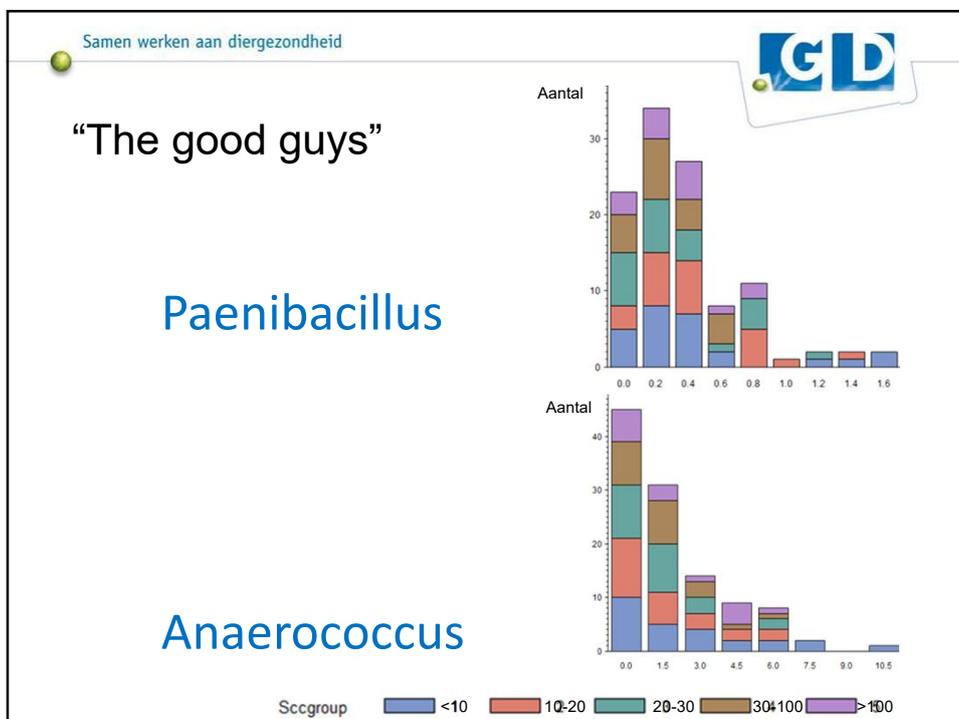
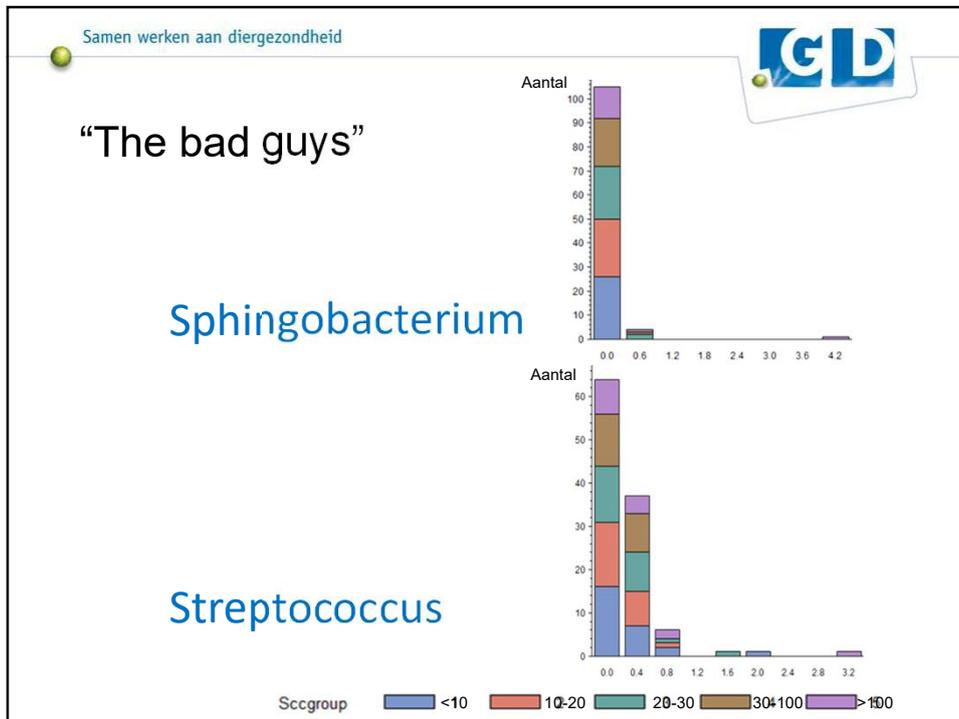
Now:

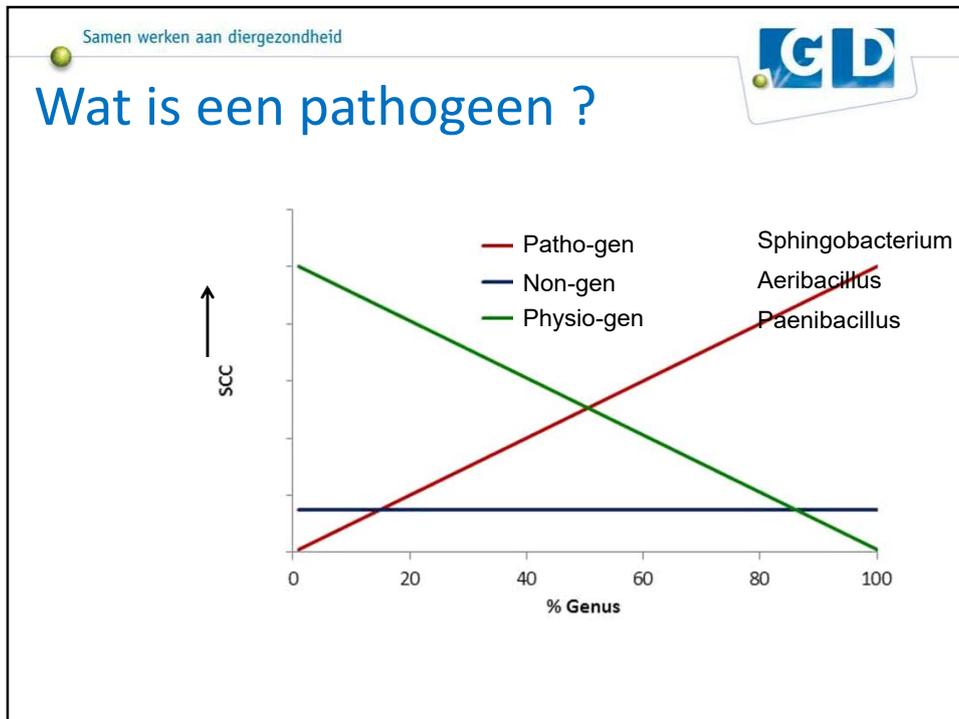
Options for advanced blasting









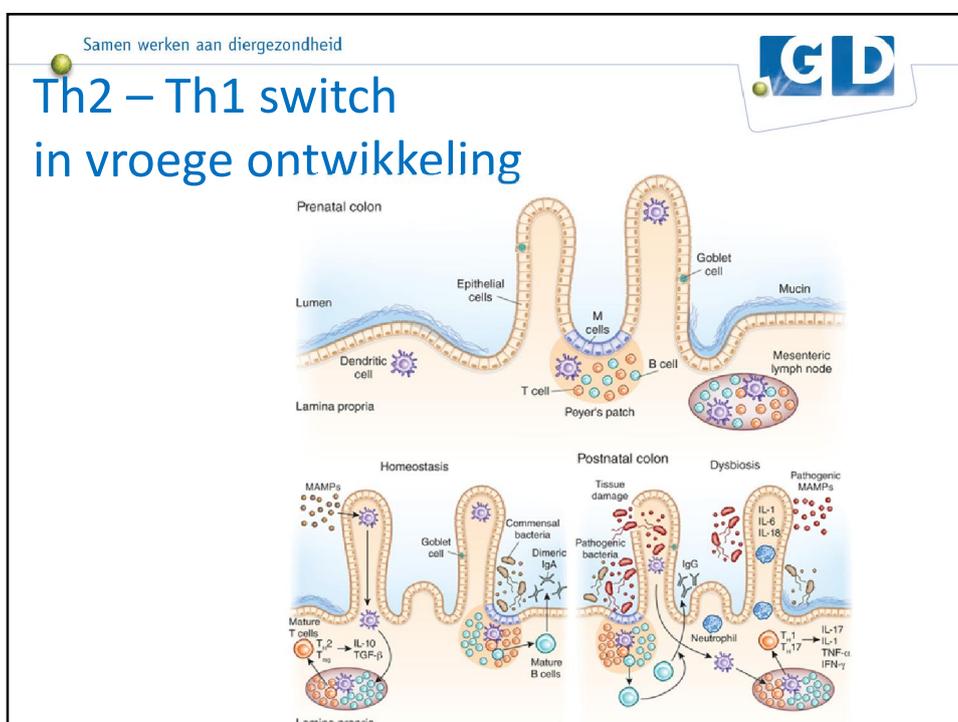
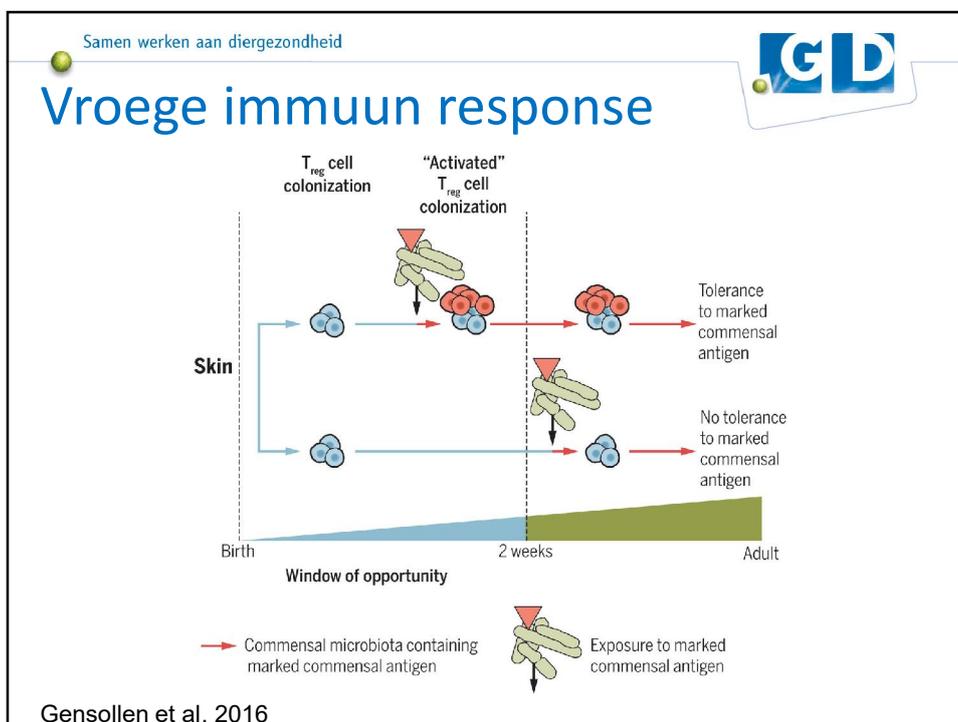


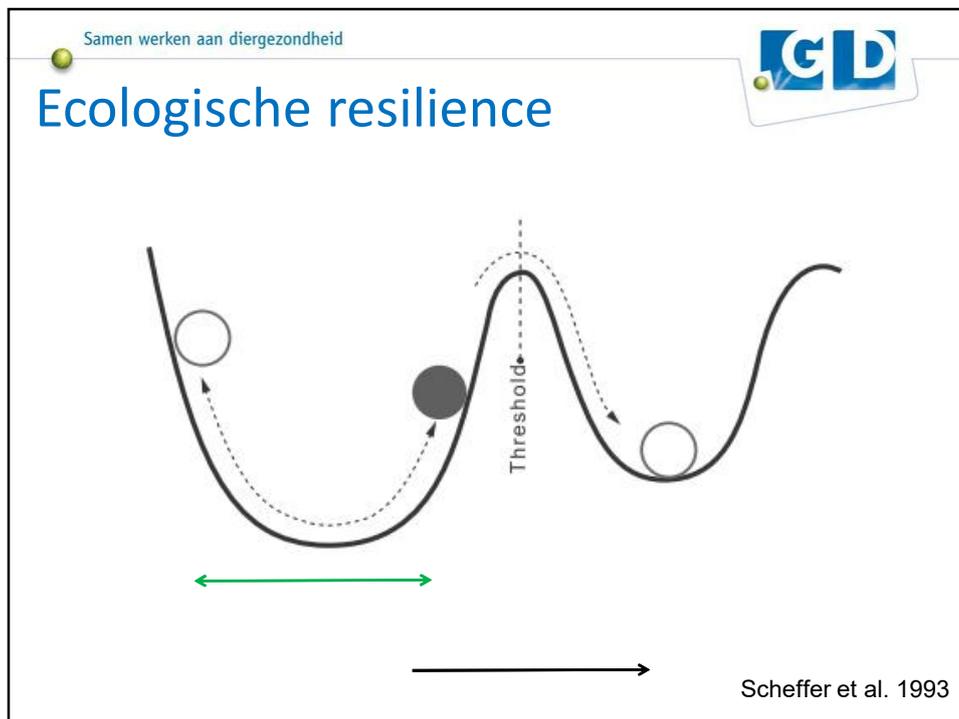
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G.D.

Self vs non-self

- Grote aantallen bacterieele species zijn aanwezig in een gezond kwartier met geen aanwijzing voor een immuun response.
- Zijn dit niet immunogen species of is er een andere reden voor het herkennen van deze 'self' populatie ?



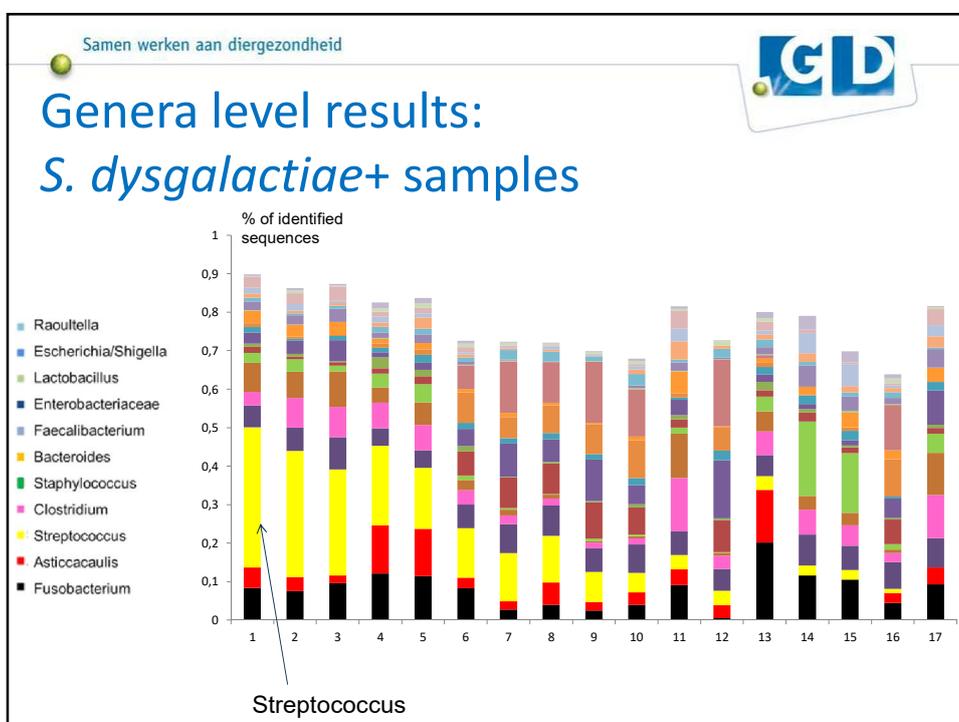
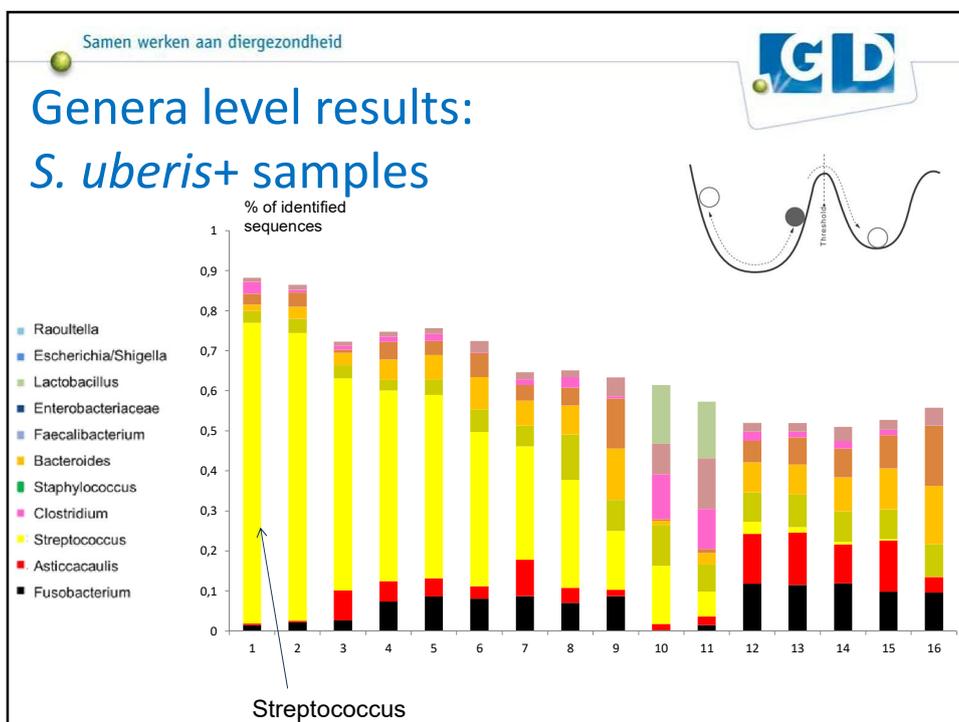


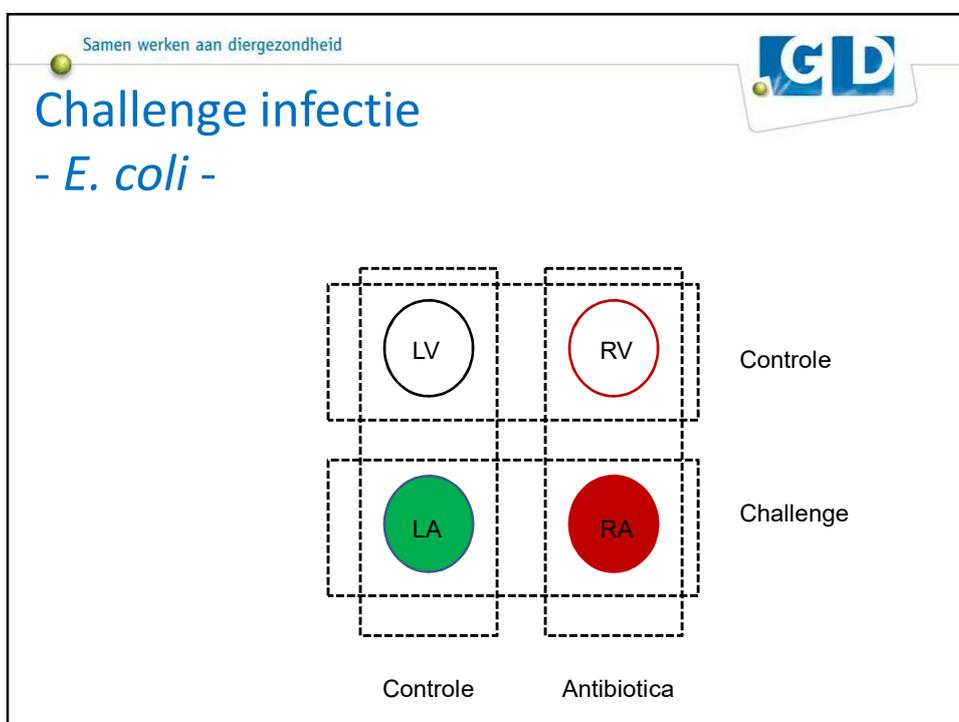
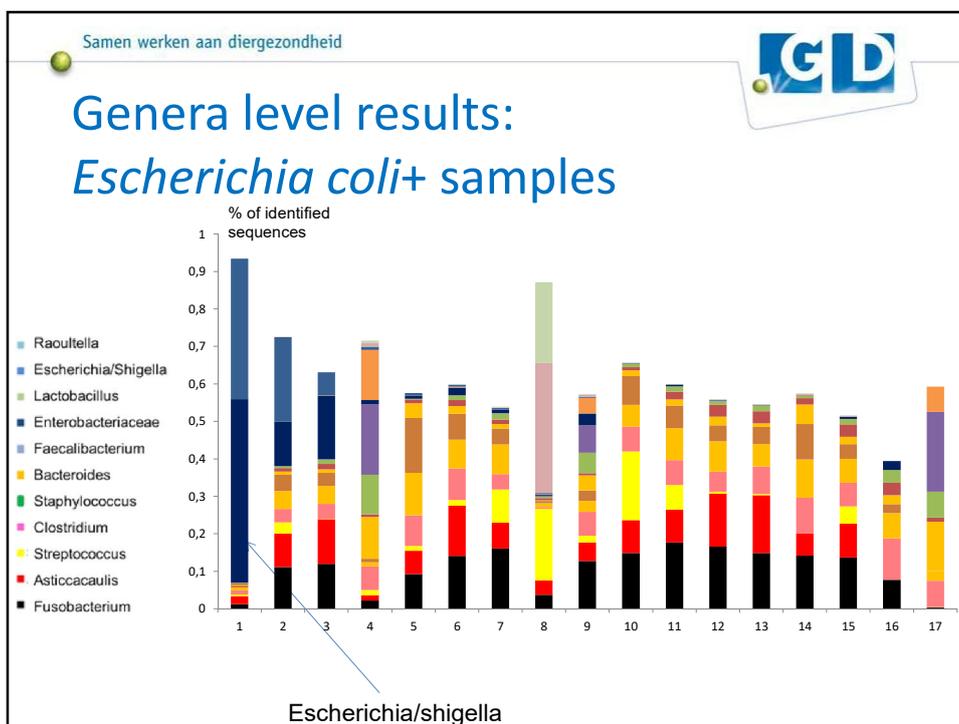
Samen werken aan diergezondheid

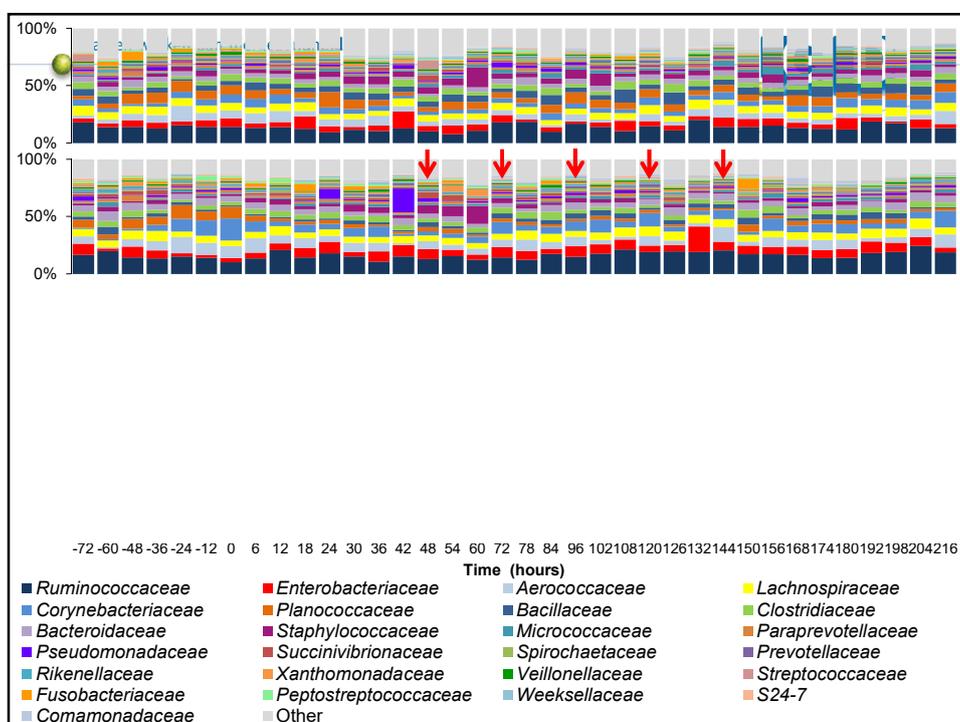
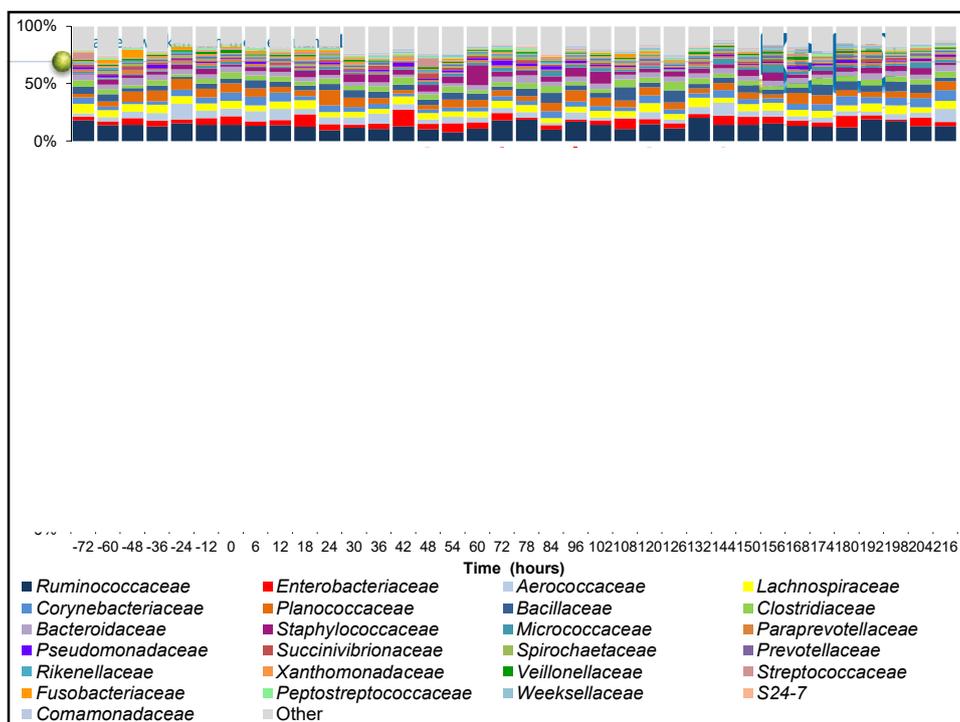
GD

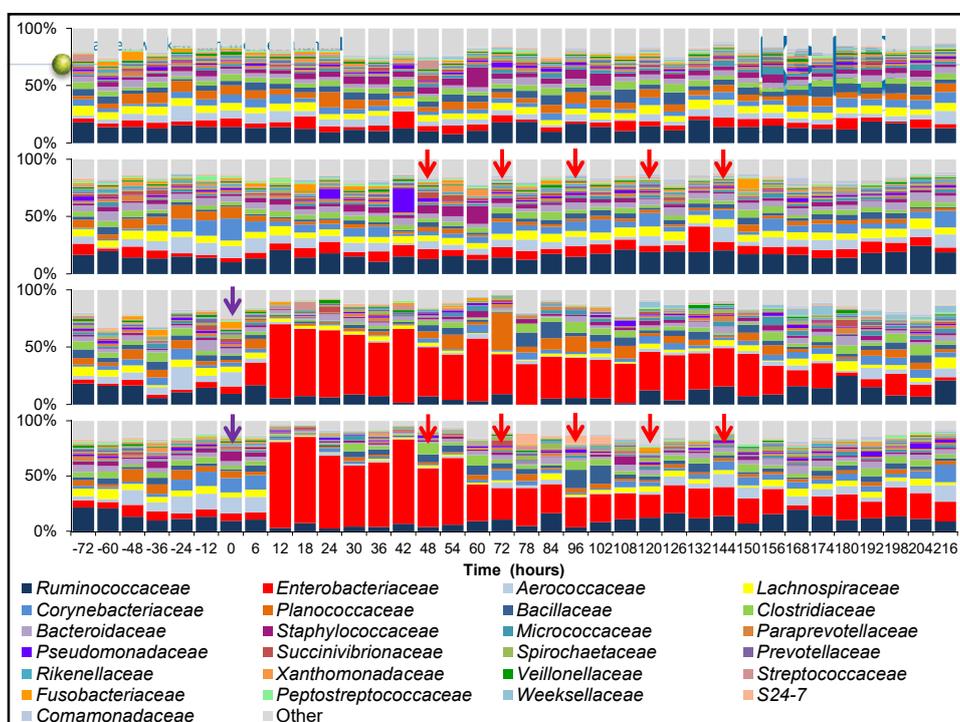
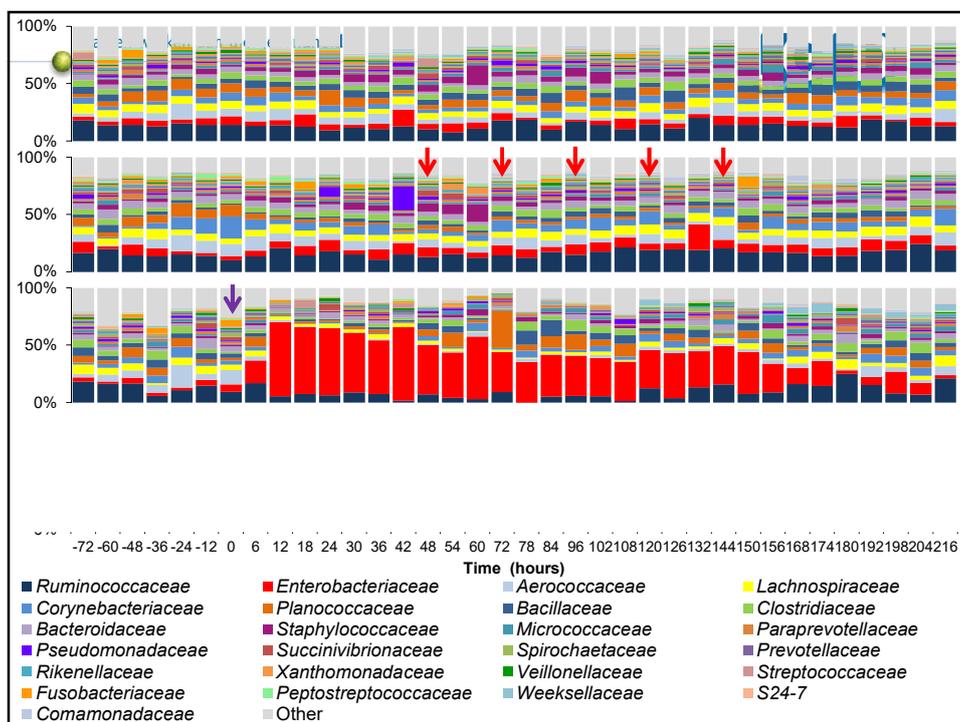
Dynamiek van Eco-systemen

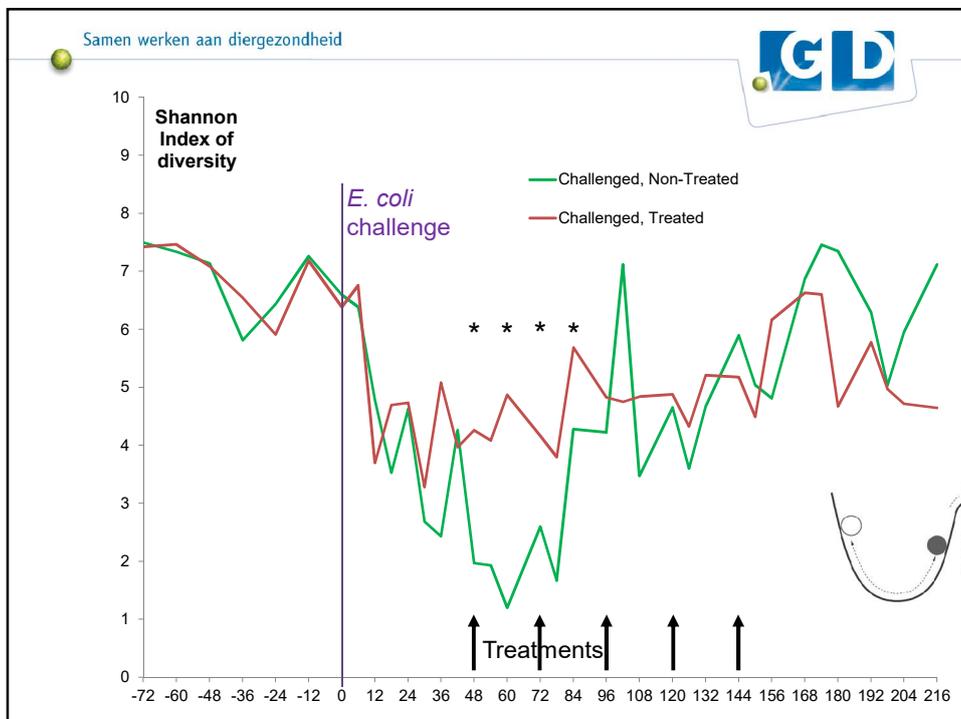
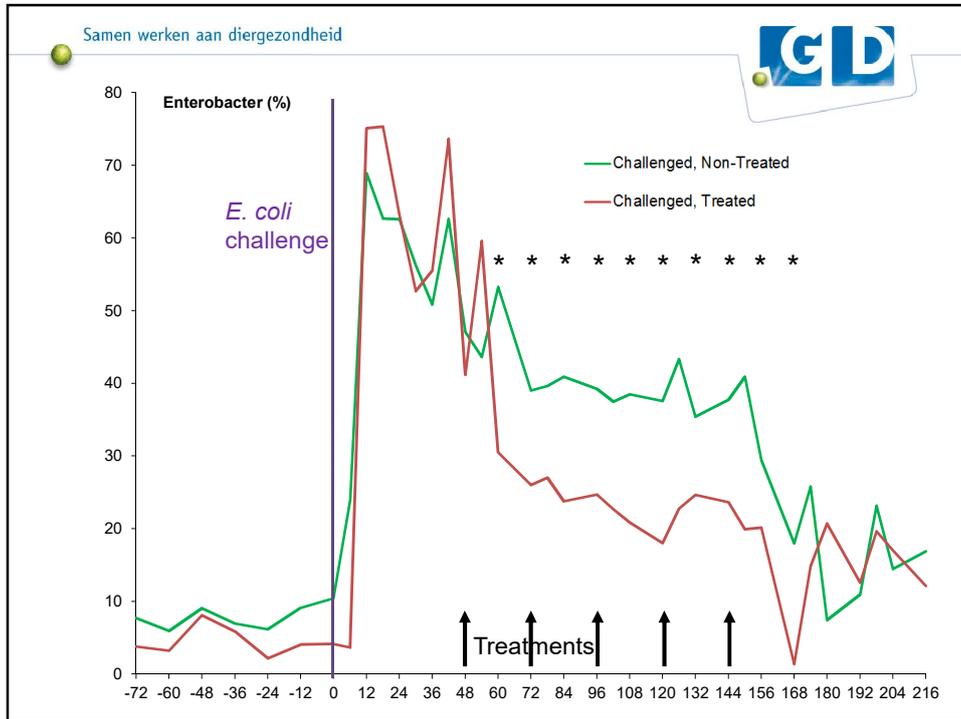
- **Superinfectie met pathogenen**
- Dieet
- Expositie op jonge leeftijd
- Antibiotica
- Gastheer
- Omgeving

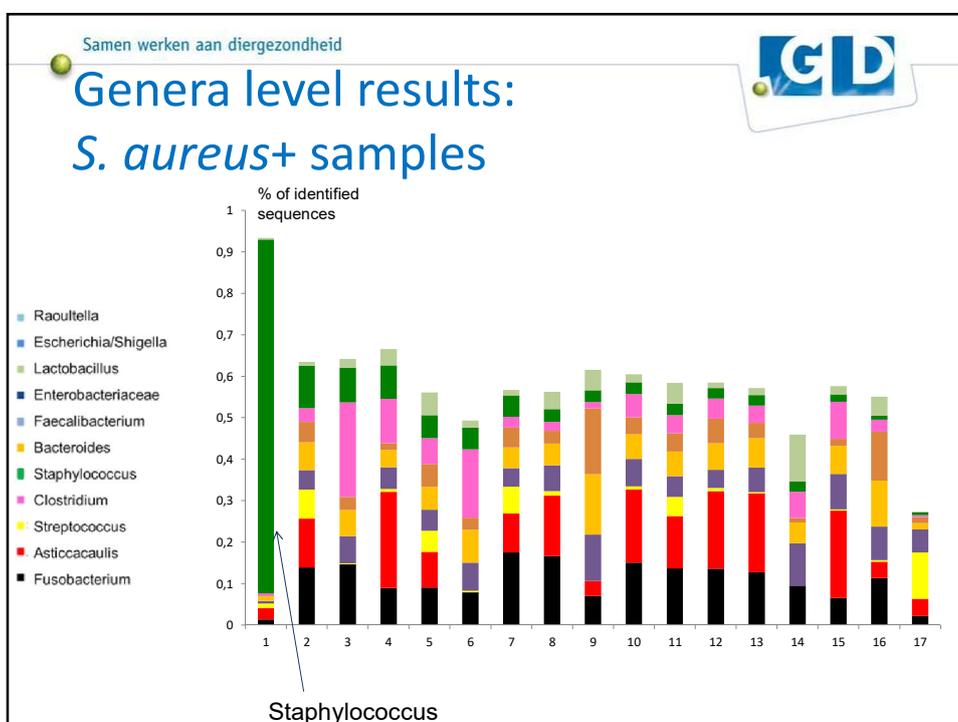
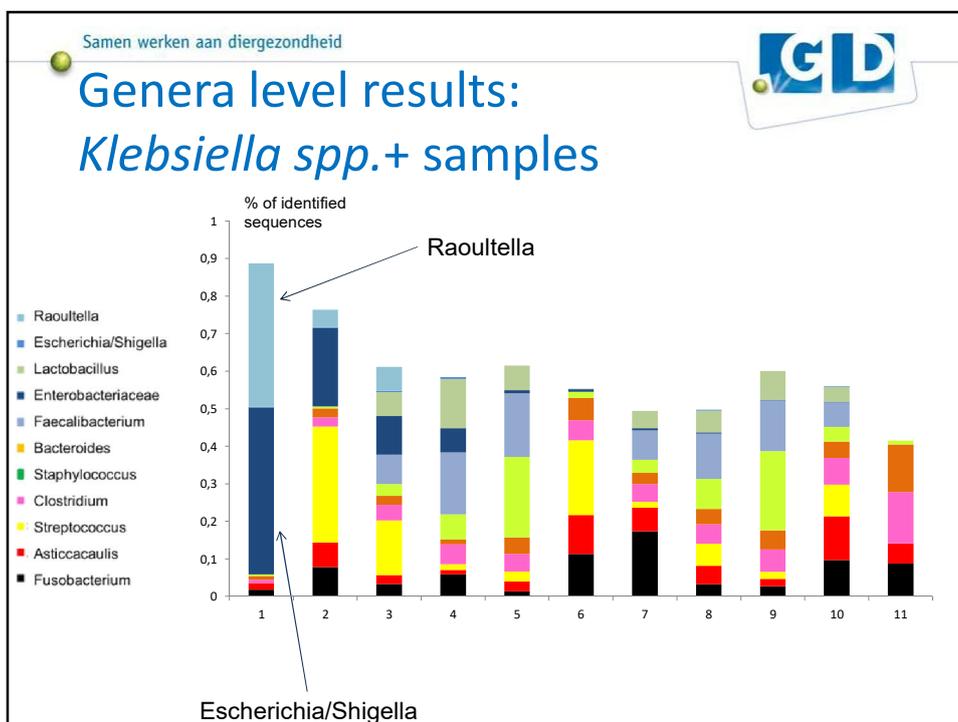


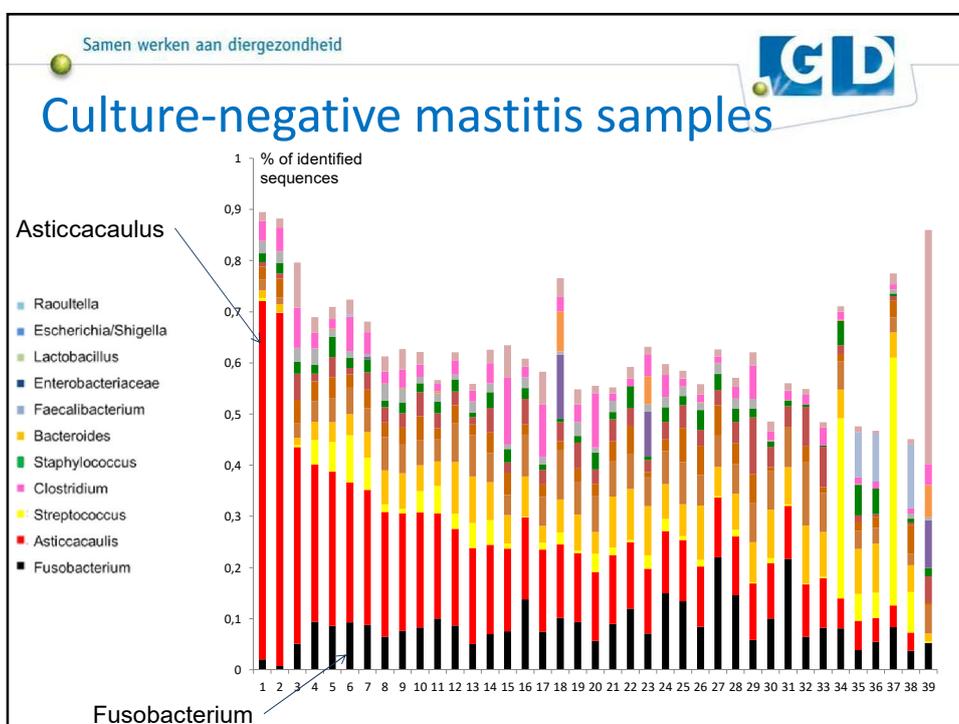
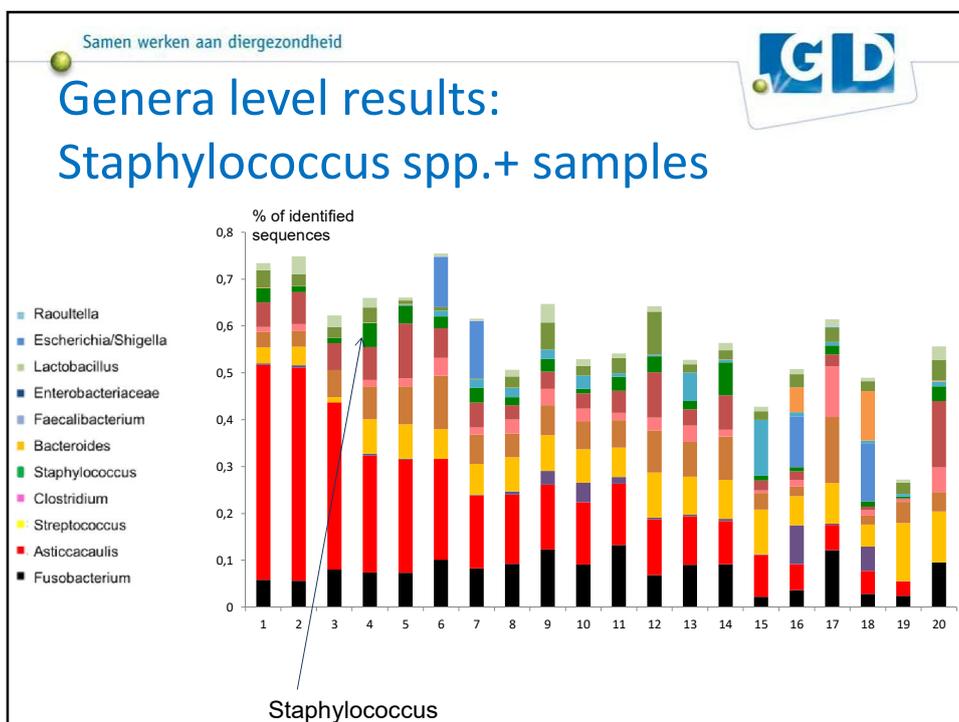


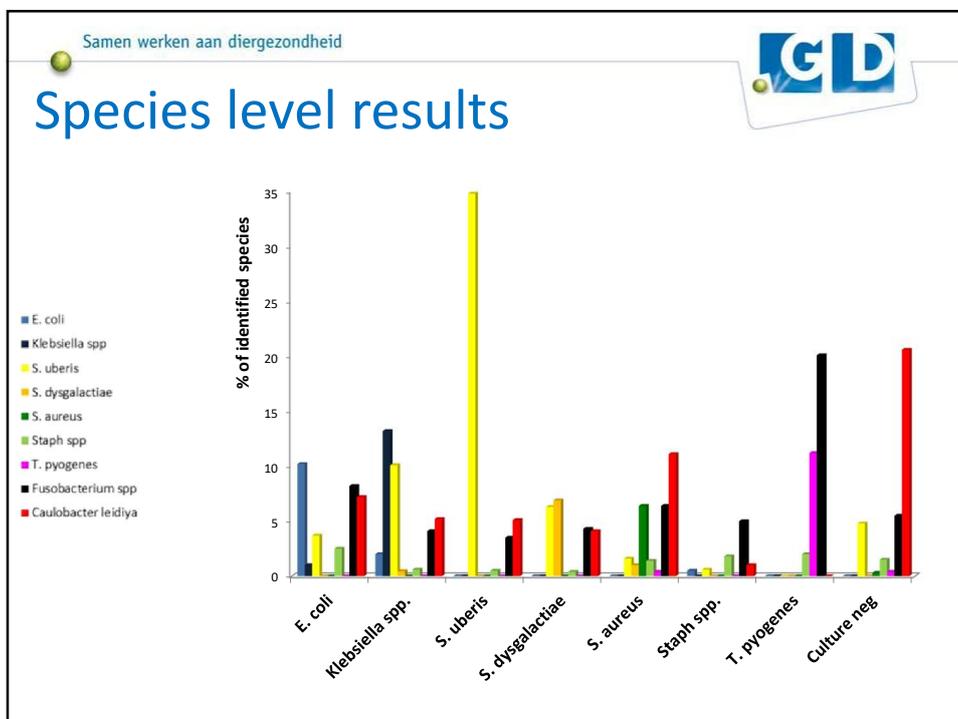
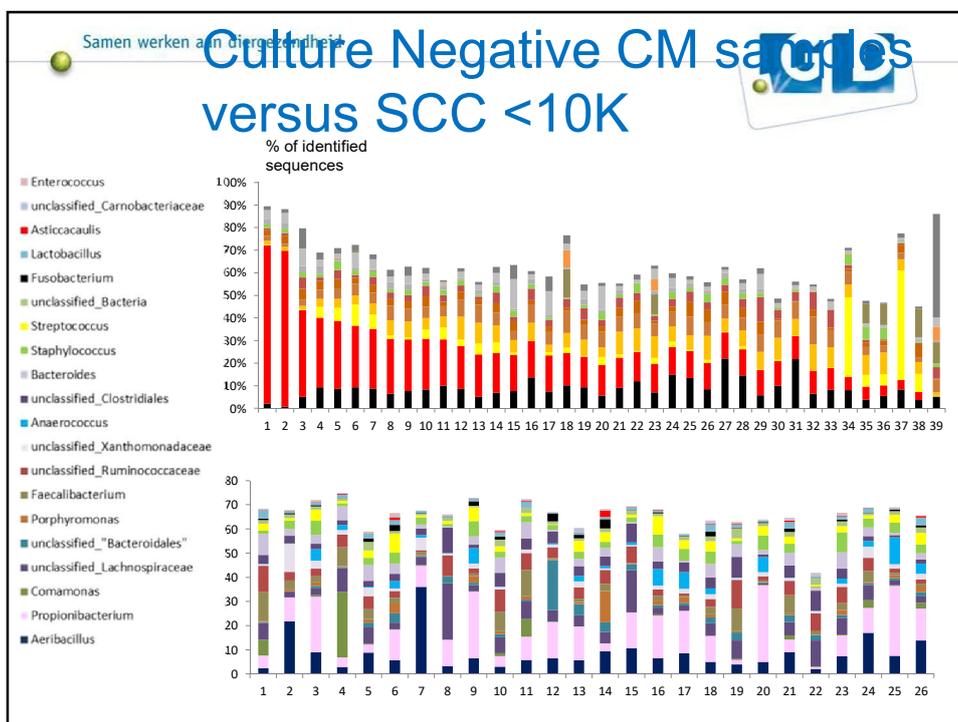


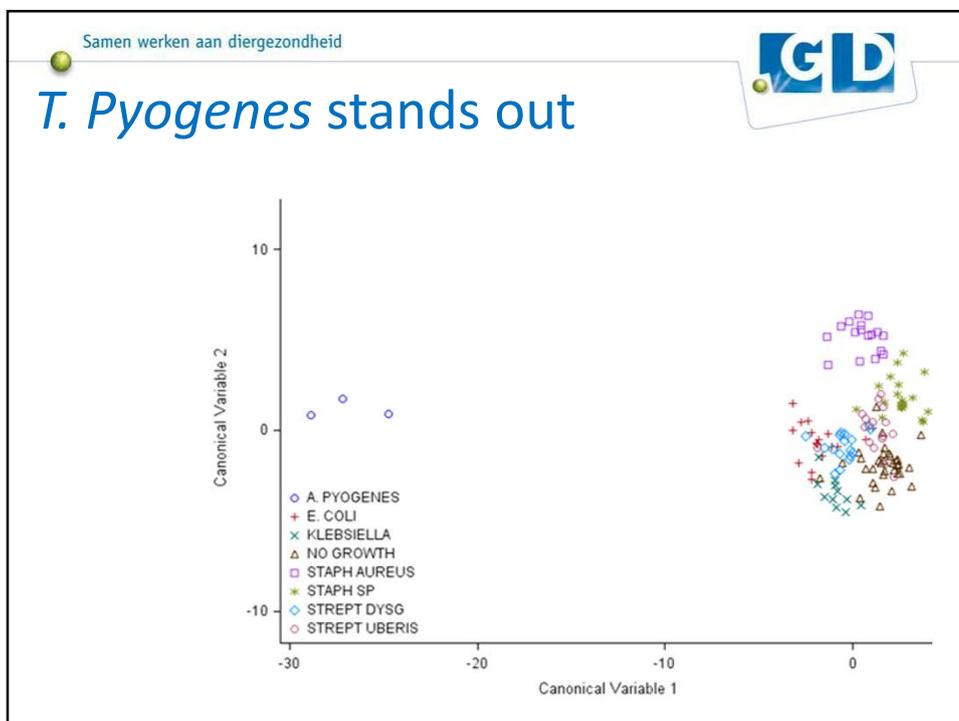
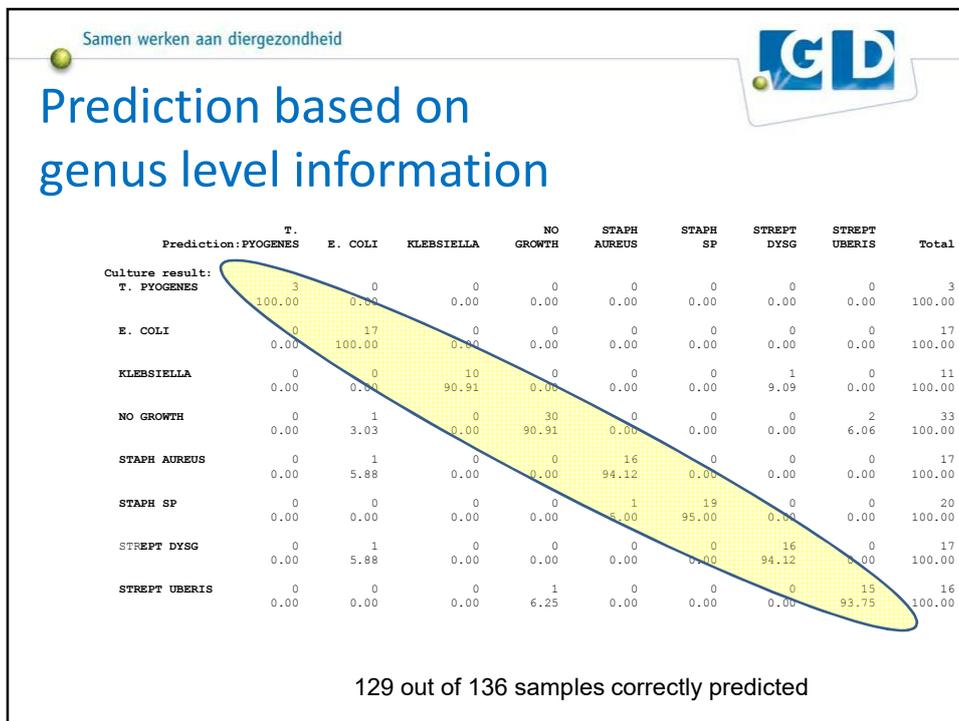


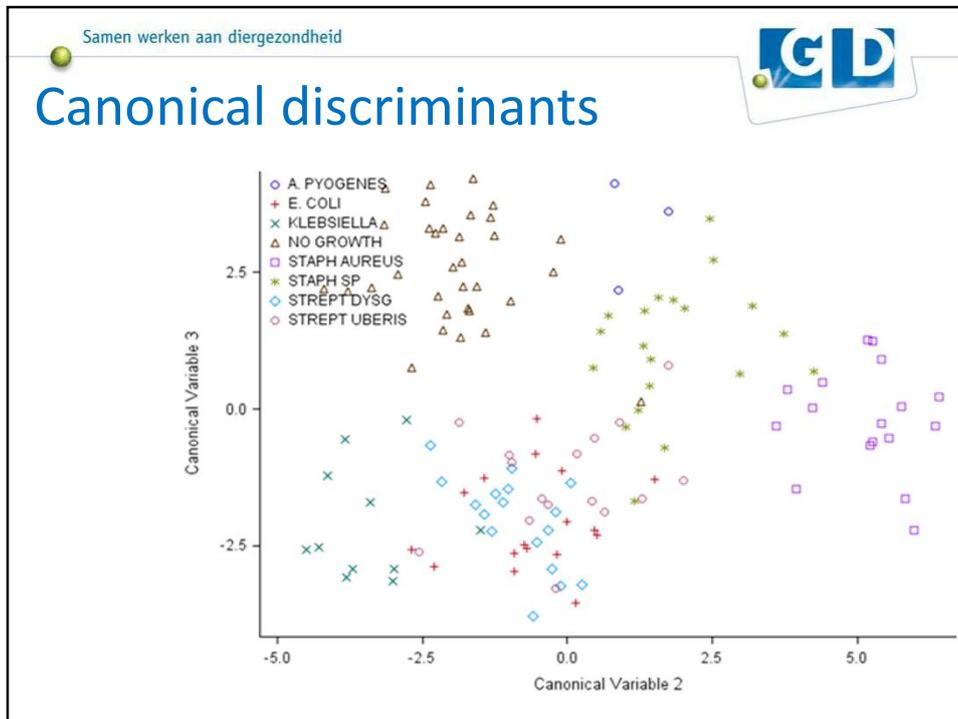










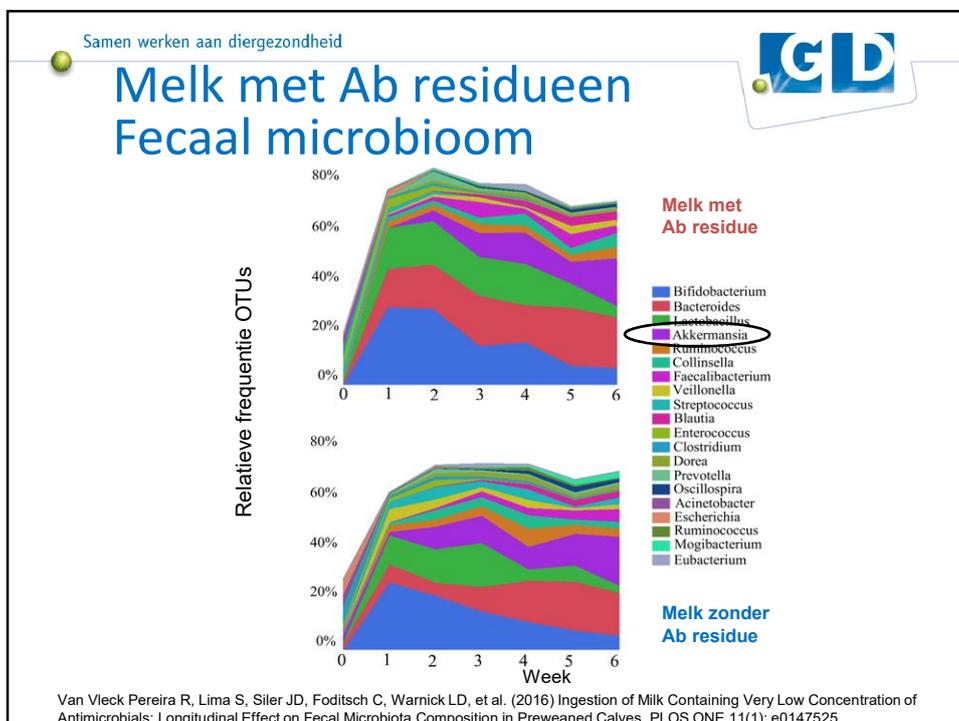
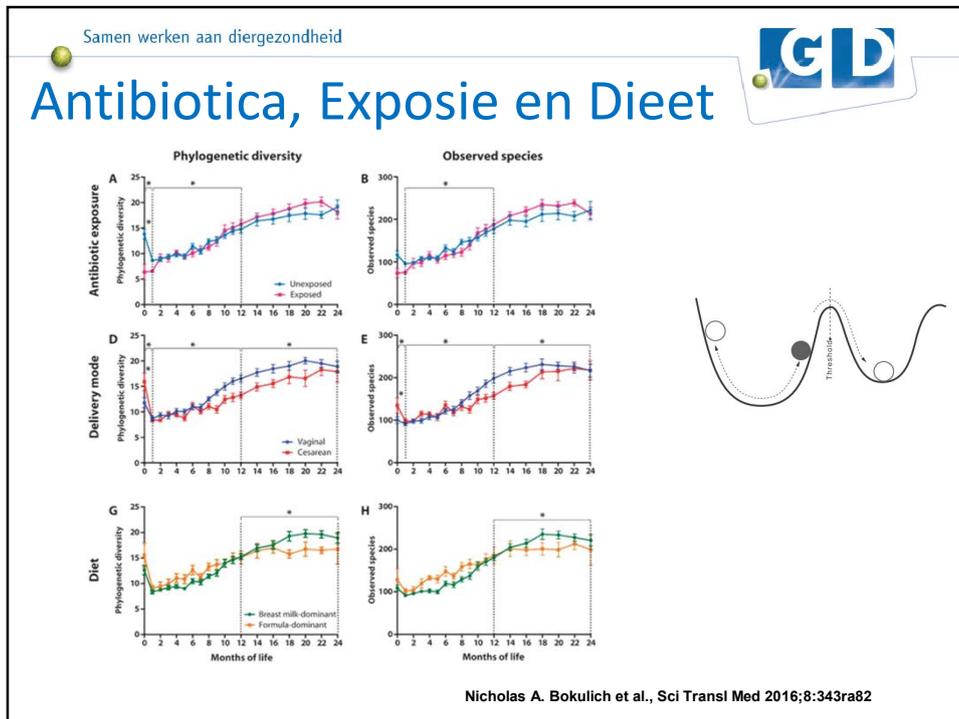


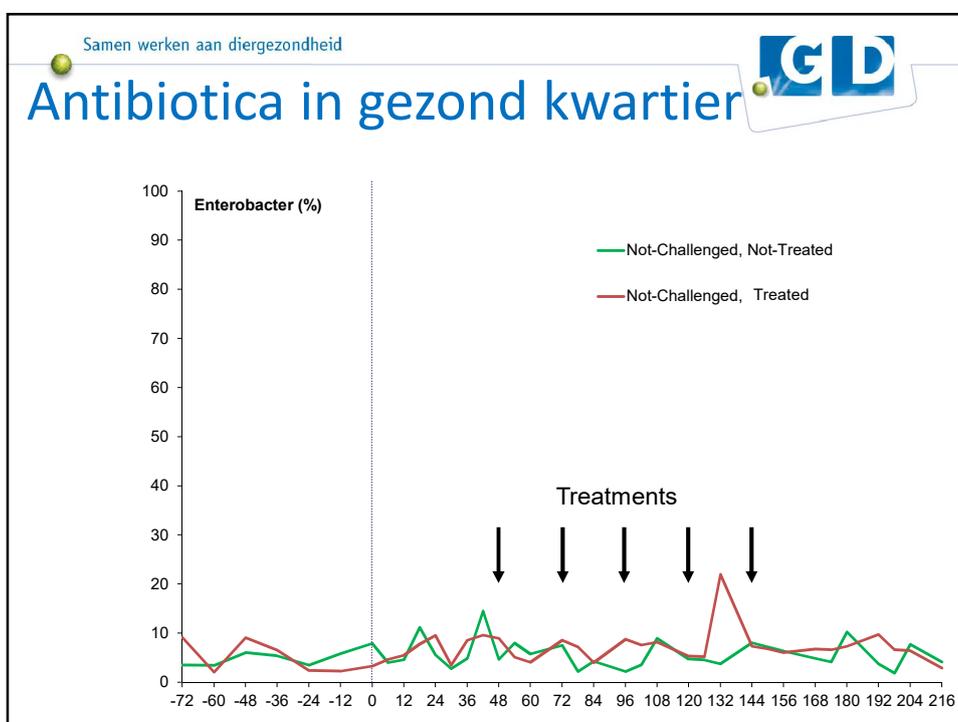
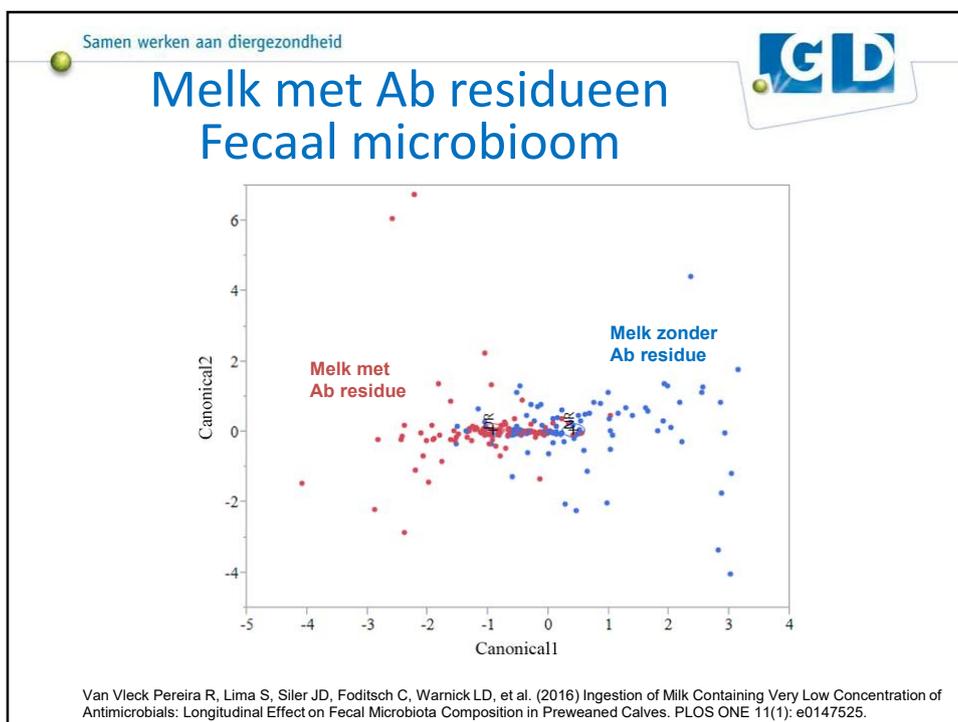
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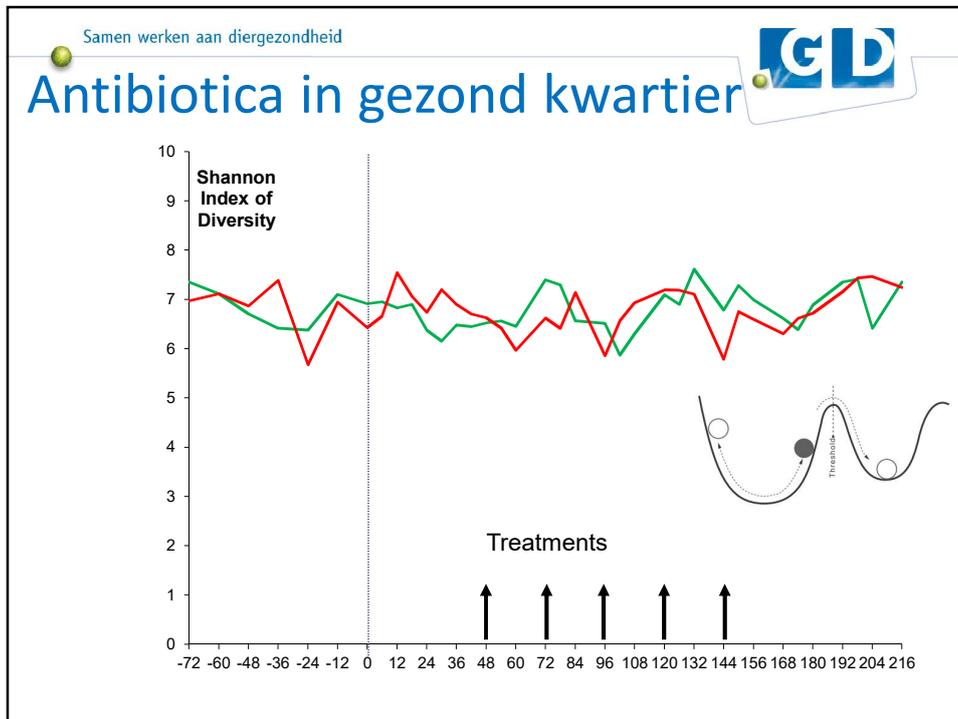
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Dynamiek van Eco-systemen

- Infectie met pathogenen
- **Dieet**
- **Exposie op jonge leeftijd**
- **Antibiotica**
- Gastheer
- Omgeving





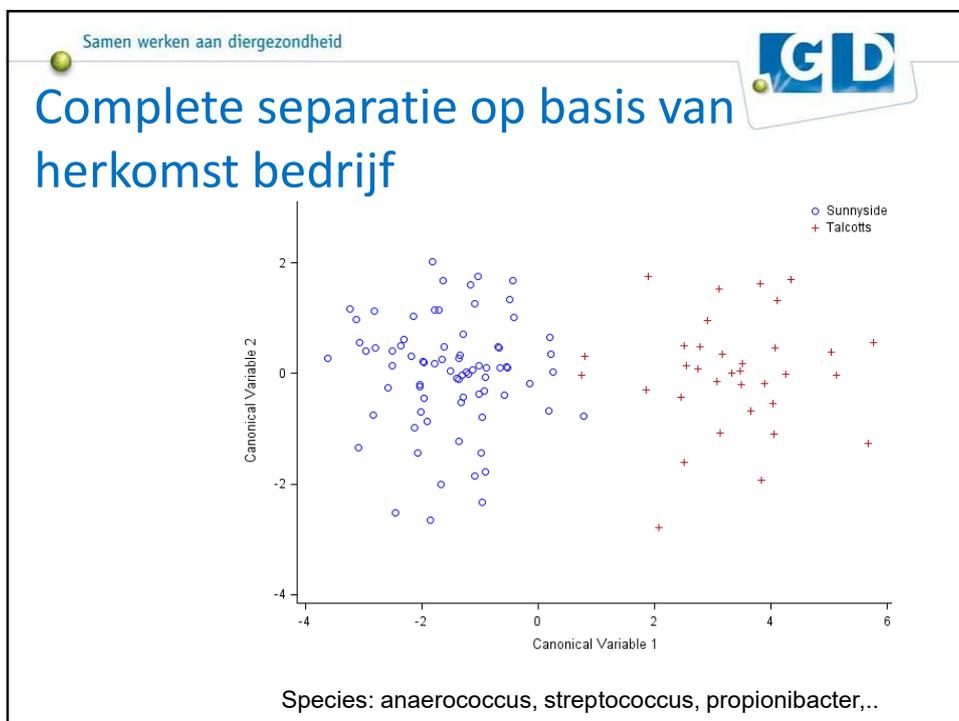
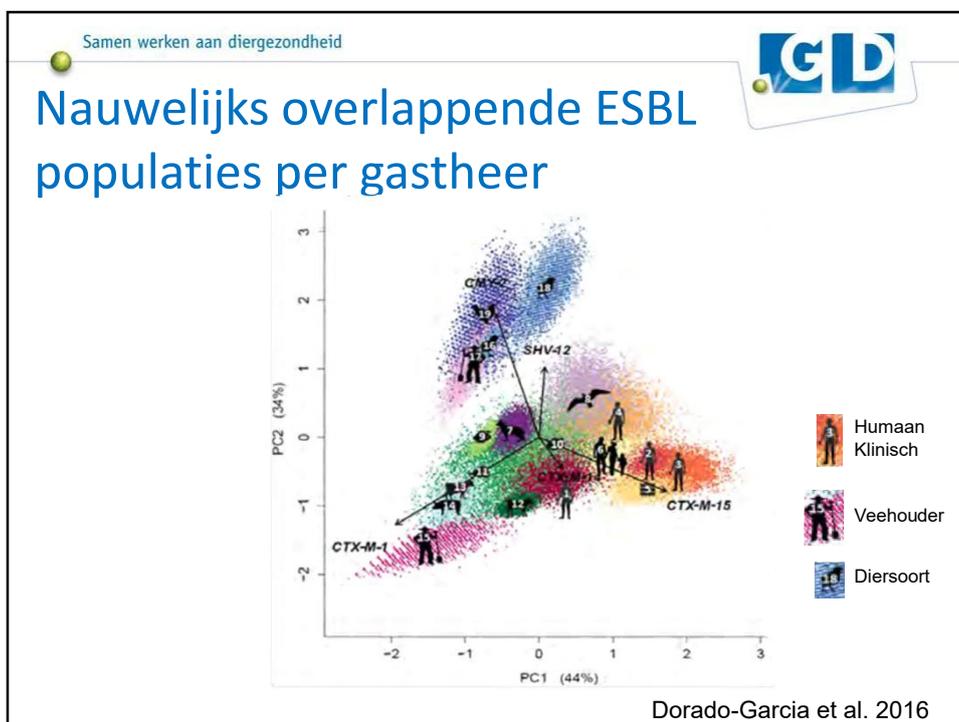


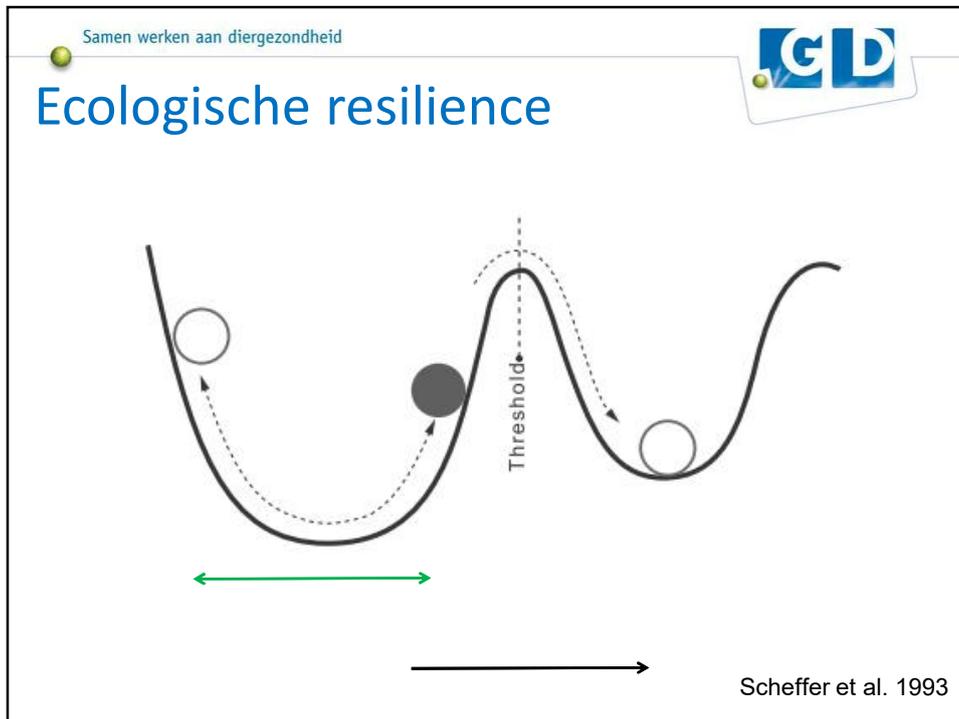
Samen werken aan diergezondheid

GD

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- Infectie met pathogenen
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- Antibiotica
- **Gastheer**
- **Omgeving**





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Microbiële Eco-systemen

- *Management van microbiom versus bestrijden van pathogenen.*
- *Microbiële Eco-systemen spelen een belangrijke rol in uier, darm, ...*
- *Belangrijke beïnvloeding door:*
 - *Voeding, omgeving, superinfecties, Ab, gastheer, ...*
- *Belangrijke kiemen:*
 - *Paenibacillus, Akkermansia*
- *Veel mogelijkheden voor nieuwe benaderingen, focus op **Eco-systeem management***

