



# The OMICS revolution in agrifood chain research

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# Scientific coevolution is a success principle of modern research



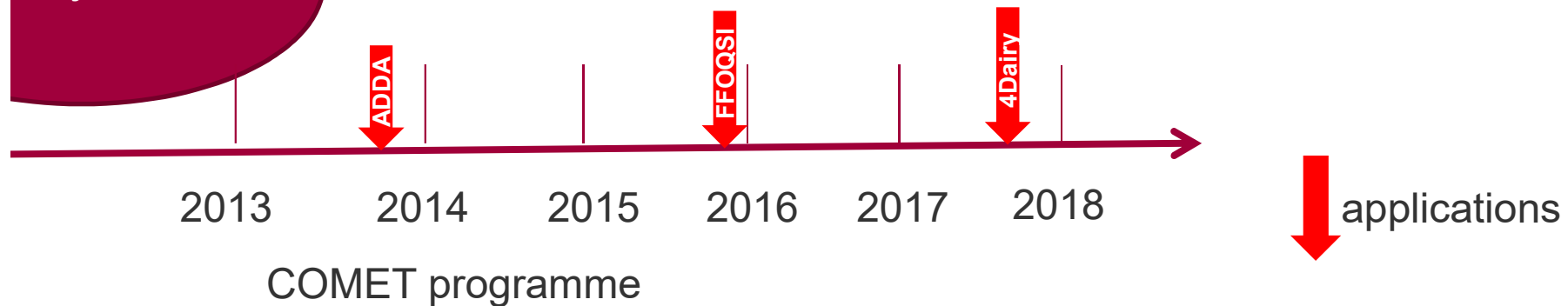
K1 Center  
FFOQSI

K Project  
D4Dairy

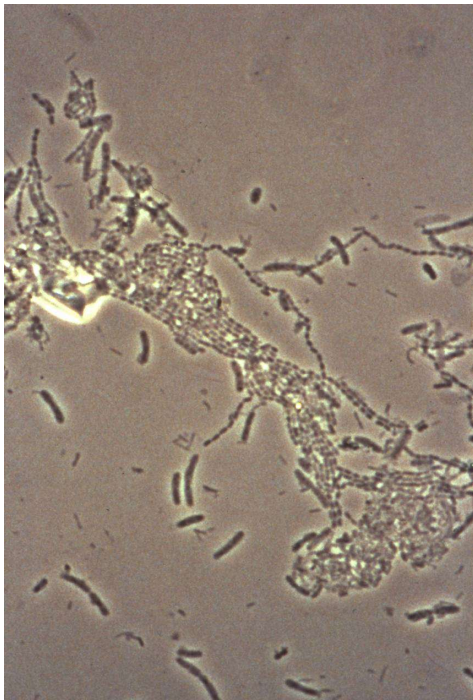


K Project ADDA

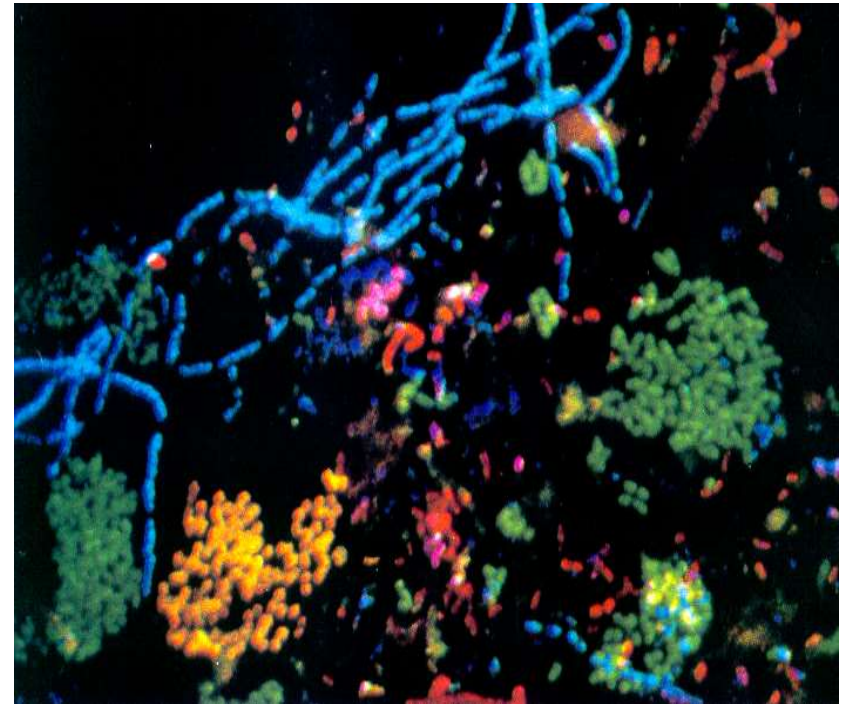
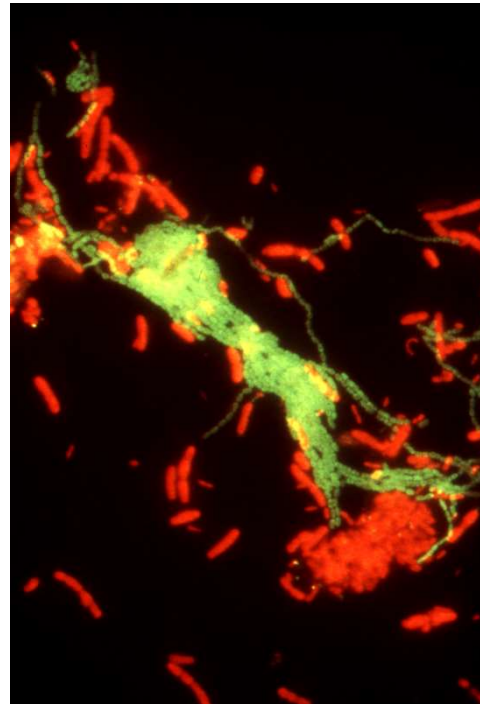
Project PVM



## (Microbial) coevolution is a success principle of life



Stoecker et al. PNAS 2006



Amann, et al, J. Bacteriol., 1996



# *Omics technologies: tool box*

*Omics* technologies...analysis of a biological totality by holostic analysis of a multitude of basic components of the same character

## *Technical Level*

Genomics

Transcriptomics

Proteomics

Metabolomics

## *Biological Level*

Secretome

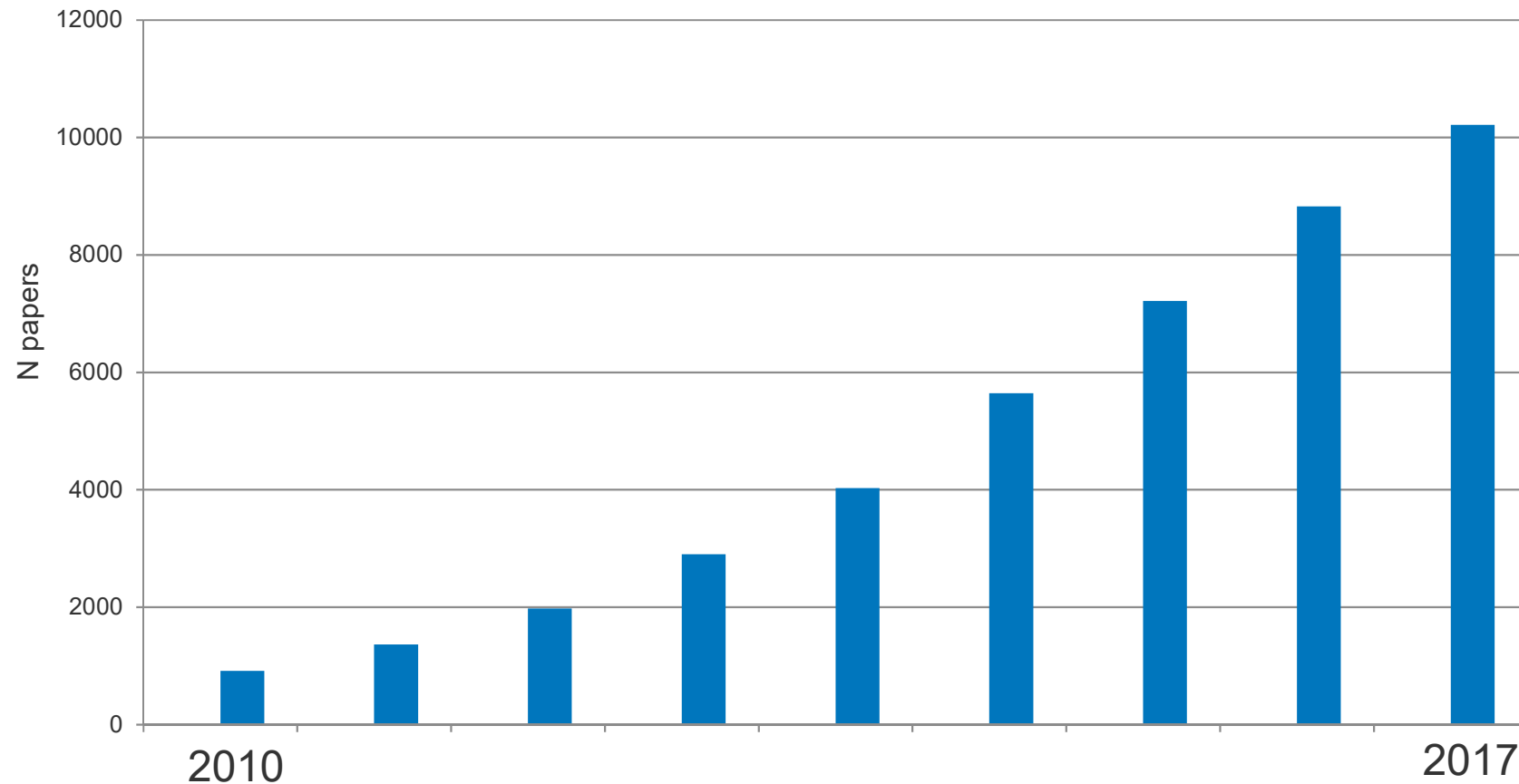
Resistome

Microbiome

Inflammasome

e.g.

# Scientific revolution as shown by number of papers



Pubmed Search 30.11.2018; search items Microbiome and year

# Omics technologies combine biology and mathematics



[www.beckmann73.de/hochzeit/wp-content/uploads/2006/06/hochzeitspaar.jpg](http://www.beckmann73.de/hochzeit/wp-content/uploads/2006/06/hochzeitspaar.jpg)

A high through-put technology generates a mass  
of raw data (sequences, mass peaks, spectra)  
from a sample

Raw data processing

Quality checks (piece control)

Data alignment (pieces to bytes)

Statistics

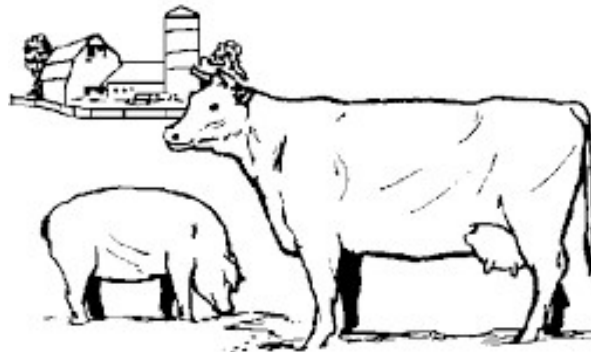


## ...Nucleic acids as an analytical target along the agrifood chain



### Microbe-plant interaction

- Impact on growth
- Sensoric Properties



### Microbe-animal interaction

- Impact on health
- Impact on performance
- Impact on treatment
- Impact on environment



### Microbe-food interaction

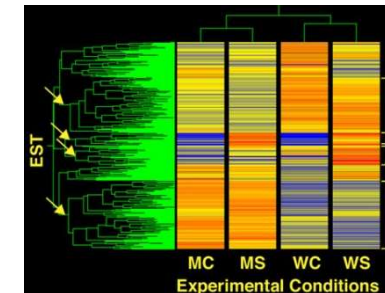
- Impact on safety
- Impact on ripening
- Impact on quality

# Sequencing technologies lead to a new discipline: Agrifood Ecology

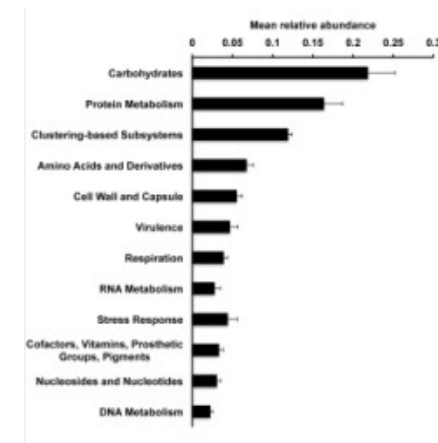
1.) **Microbiome** – „Who“ is there



2.) **Metatranscriptome**- „What do they all there?



3.) **Transcriptome**- „What does a bug there?





# Majority of microbial diversity non-culturable

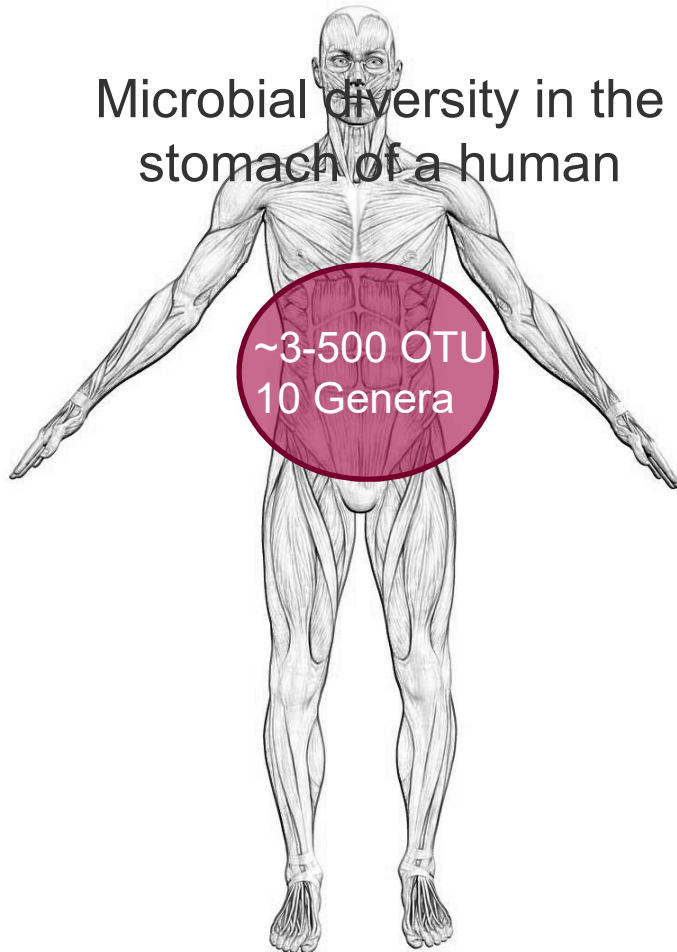
Habitat	Culturable (%)
Sea Water	0.001-0.1
Potable Water	0.25
Lakes	0.1-1
Sewage	0.1-3
Sludge	1-15
Sediments	0.25
Soil	0.3



Numbers based on direct cell counts.  
Amann *et al.*, MMBR, 1995

# The „Who is there“ can lead to unexpected findings

Microbial diversity in the stomach of a human



Bik et al, 2006, PNAS

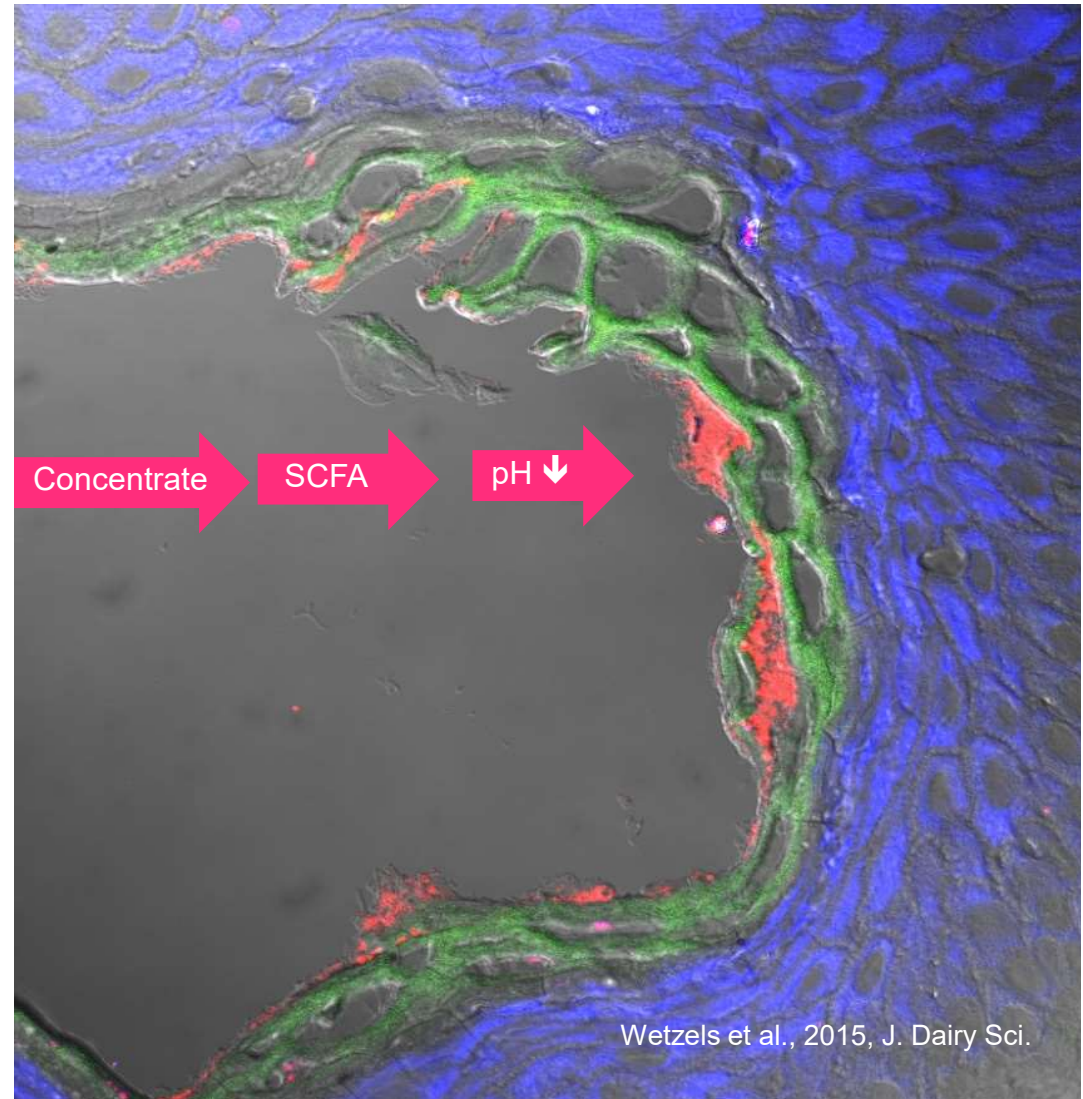
Microbial diversity in the stomach of a vulture



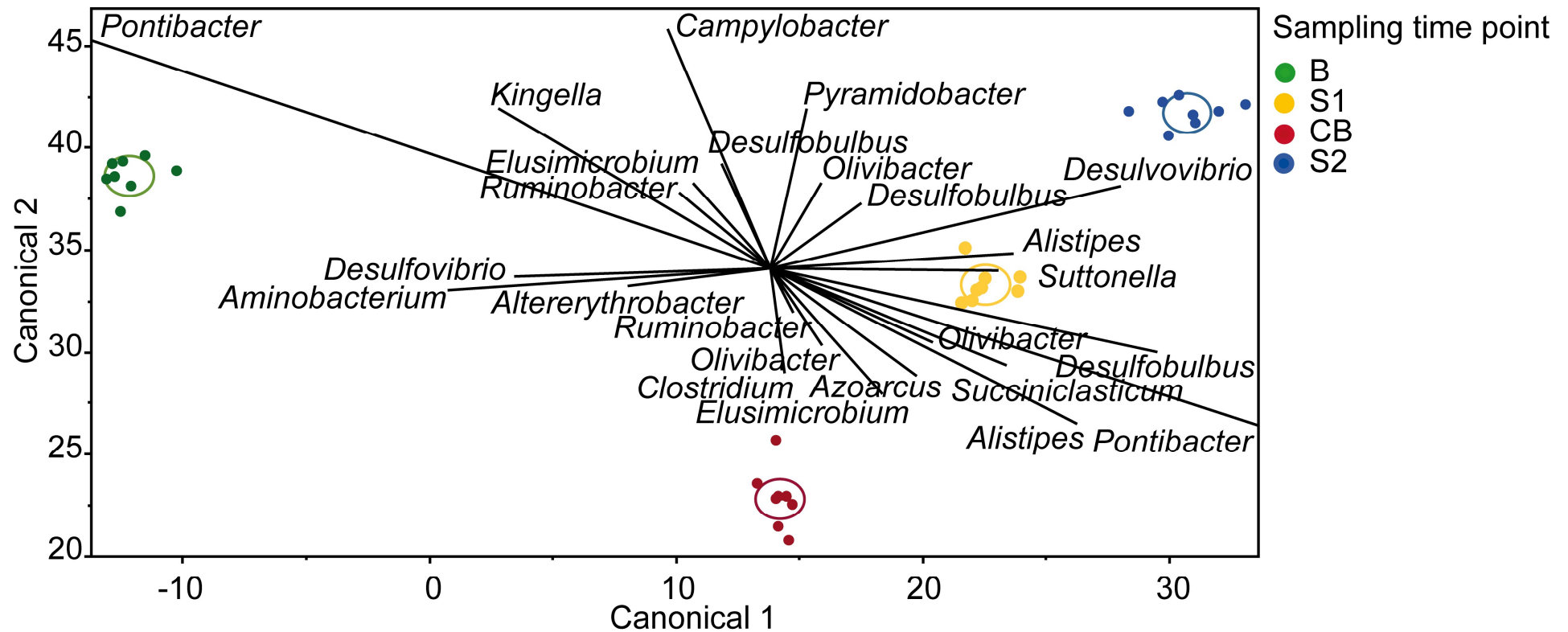
Rogenbuck et al, 2014 Nature Comm.

## Example: Microbiota of the rumen wall

- $10^{13}$  bacteria/g
- 1% of ruminal bacteria attached to rumen wall (Mueller 1984)
- Multilayered keratinized epithelium
- Form protective biofilm (McCowan 1978)
- Possibly involved in the hydrolysis of urea and scavenging of oxygen (Wallace 1979), tissue recycling (McCowan et al., 1978), amino acid metabolism (Mao et al., 2015)



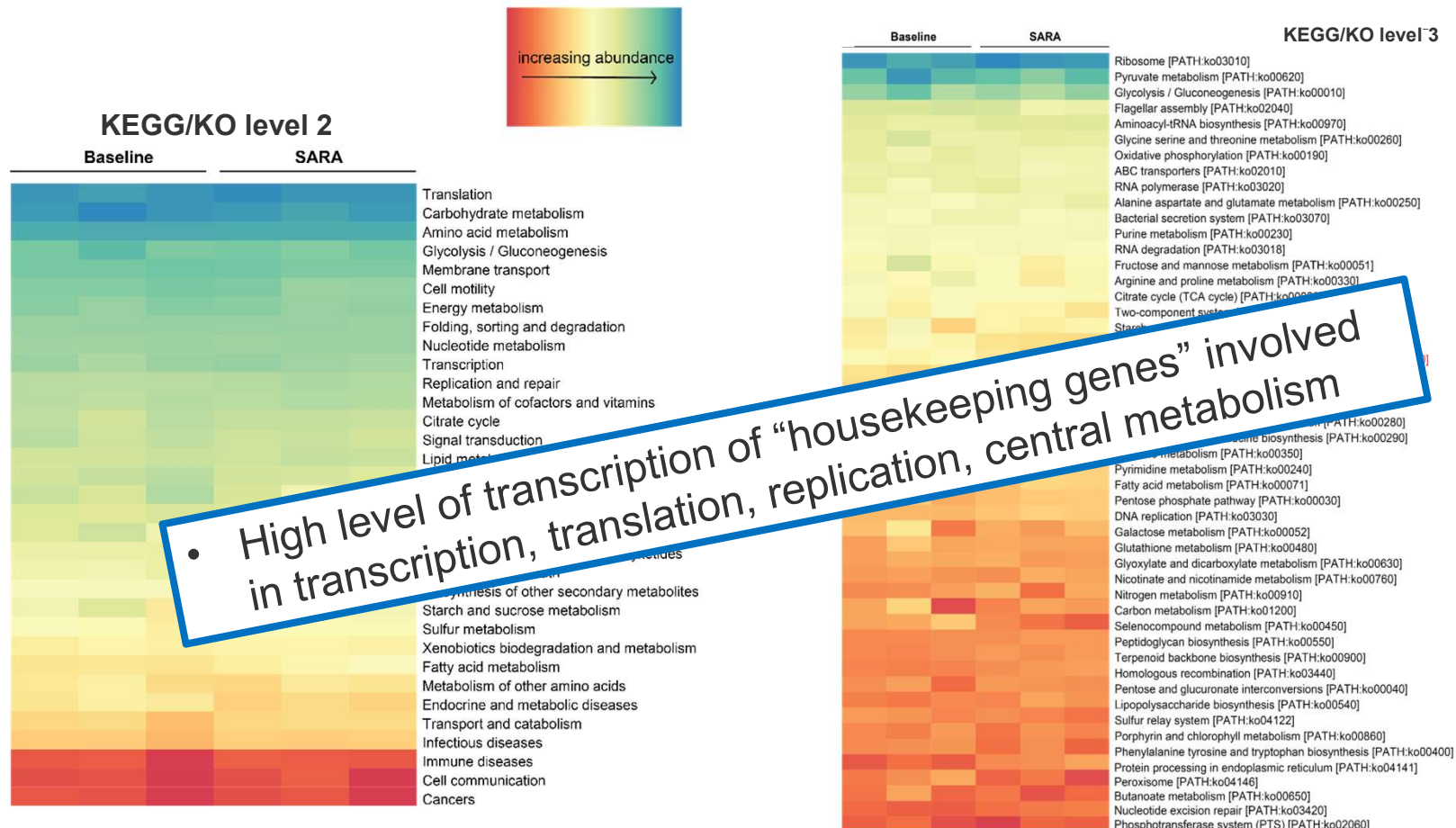
## Microbiomes shift from baseline feeding to SARA periods (S1 and S2)



Neubauer et al, 2018 J Dairy Sci.



# How active are epimural bacteria on a transcriptional level?



Significantly decreased in SARA compared to baseline

# Functional studies allow to speculate about biological pathways

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## Transcriptomics revealed first insights into the gene expression of the rumen wall bacteria

- Housekeeping genes were among the highest expressed genes
- Nitrogen metabolism (Urease activity)
- Oxidative stress response
- Starch and cellulose/cellobiose degradation
- Butyrate and propionate production

## We found only few statistically significant differences between baseline and SARA in the metatranscriptome

- Community composition and functional level
- **Functional guilds** – different strains/species within a genus may fulfil similar functions



# ...what can OMICS technologies help us to achieve?

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## ...in general

- They describe biological (host and/or pathogen) responses in comprehensiveness
- They are usually hypothesis-generating approaches
- They allow an investigative look to hidden biological niches (have eg. overcome the limit of non-culturability in microbiology)

## ...in D4Dairy

- We will use microbiome analysis to study impacts of mycotoxins on rumen microbiota
- We expect to find microbial subpopulation that better adapt to mycotoxin induced stress



# Acknowledgements



## ■ Institute of Animal Nutrition and Functional Plant Compounds

Prof. Qendrim Zebeli

Doz. Dr. Barbara Metzler-Zebeli

## ■ Institute for Milk Hygiene, Milk Technology and Food Science

Evelyne Mann, PhD

Stefanie Wetzels, PhD

## ■ Iowa State University

Prof. Dr. Stephan Schmitz-Esser

## ■ LFG Kremesberg

## ■ Clinic for Ruminants



Ein Fonds der Stadt Wien



VIENNA SCIENCE  
AND TECHNOLOGY FUND