

A scanning electron micrograph (SEM) showing a dense population of microorganisms in the rumen. The organisms are mostly rod-shaped and appear to be attached to a fibrous, organic substrate. The background is a complex network of fibers and smaller microbial cells.

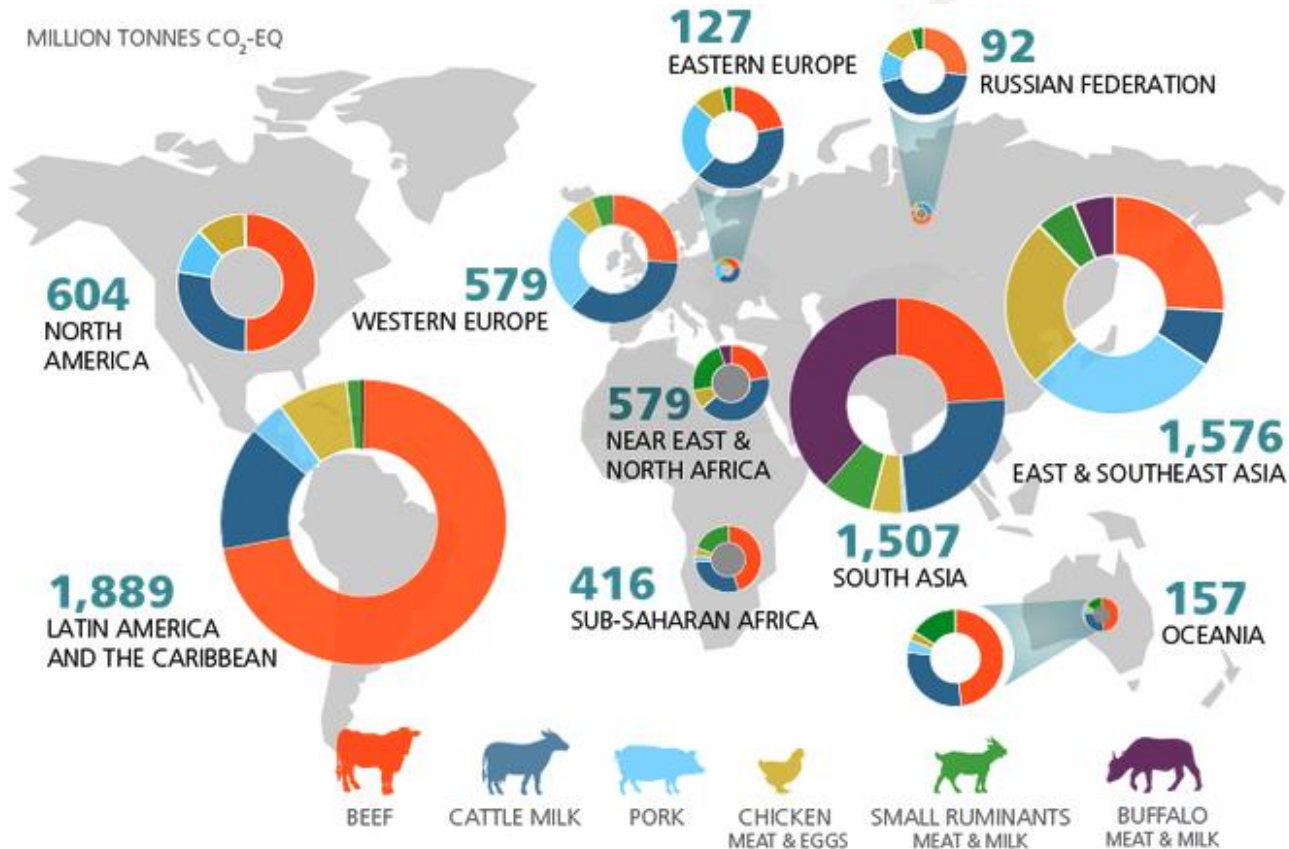
***Biology of Methane production in the rumen***

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Department of Animal Science  
University of Nebraska***



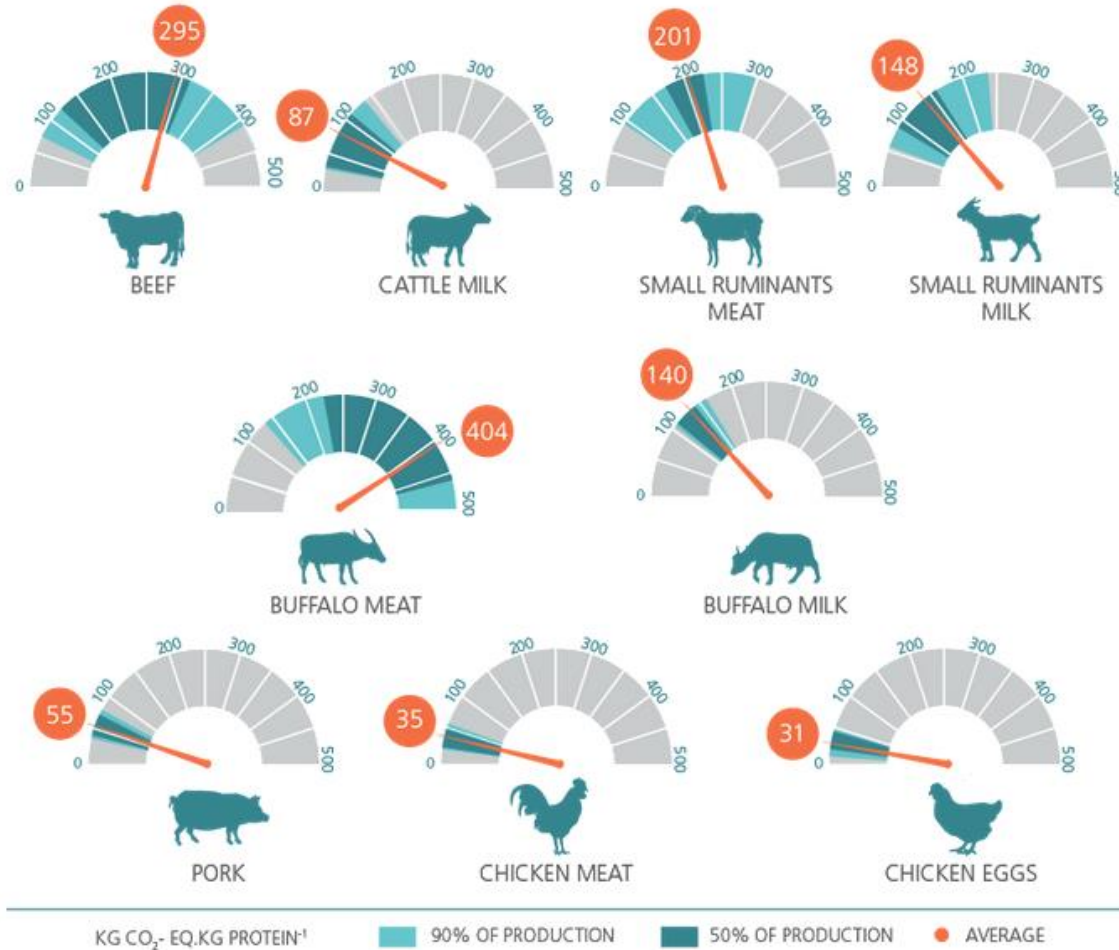
WD20.8mm 25.0kV x3.0k 10um

# Global Livestock Environmental Assessment Model



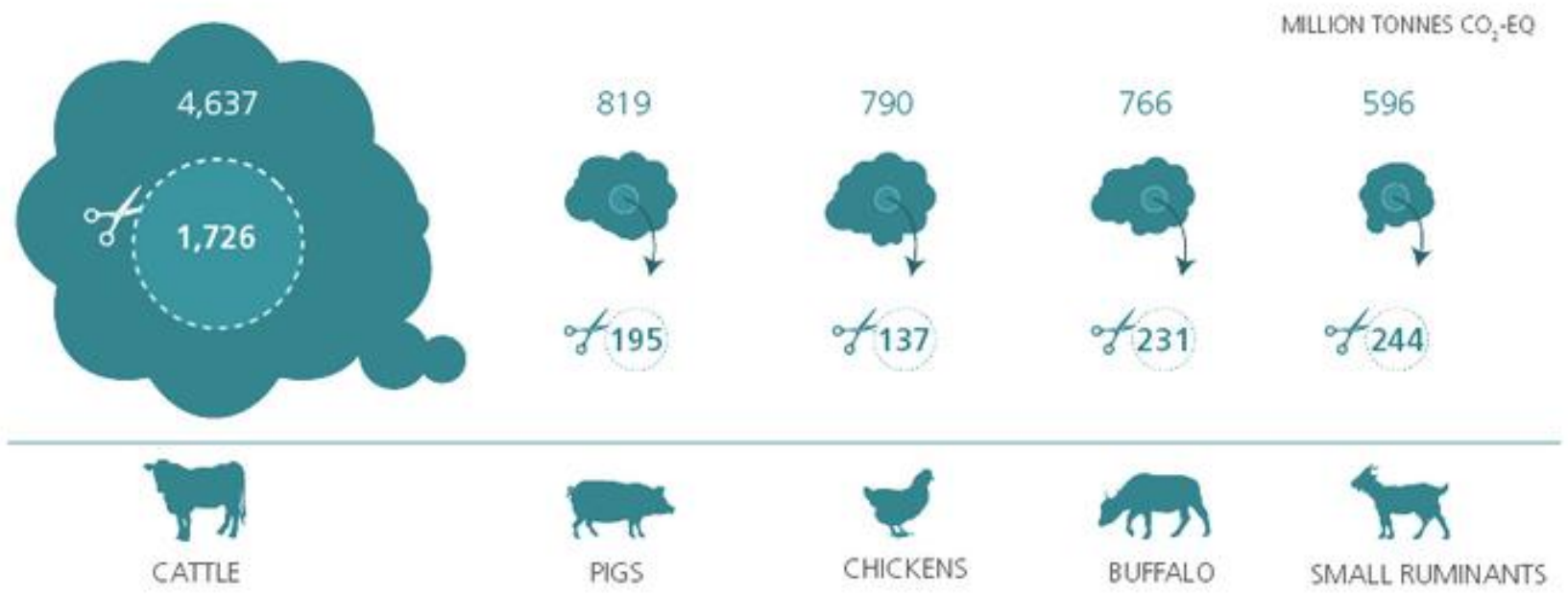
**Regional emissions.** Regional total emissions and their profile by commodity are shown. Results do not include emissions allocated to non-edible products and other services.

# Global Livestock Environmental Assessment Model



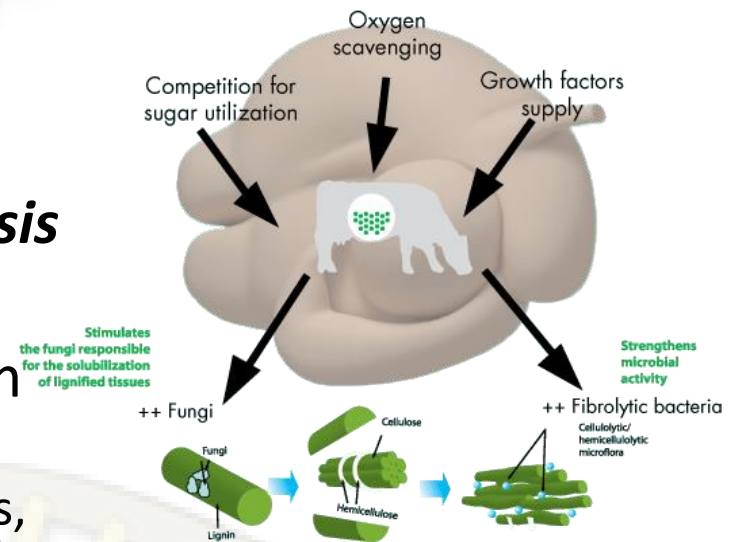
**Global emission intensities by commodity.** All commodities are expressed in a per protein basis. Averages are calculated at global scale and represent an aggregated value across different production systems and agro-ecological zones.

# Global Livestock Environmental Assessment Model



# Methane

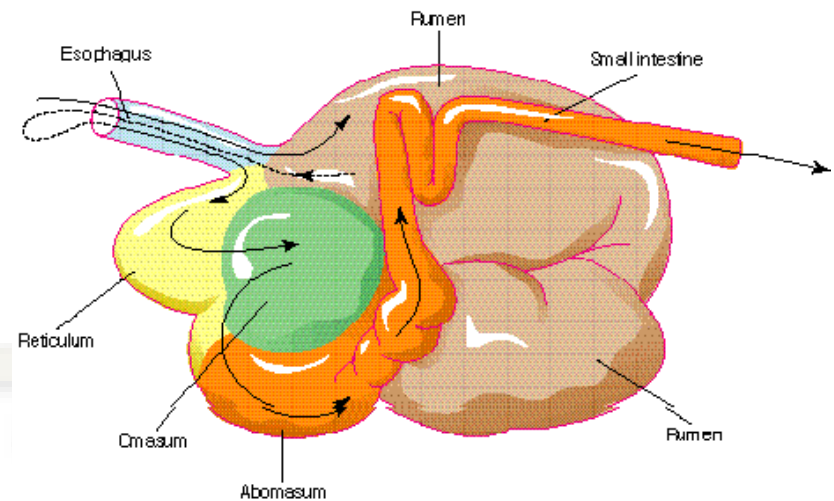
- Many significant sources of methane on a global scale (both natural and anthropogenic)
- ***All sources have one thing in common microbial methanogenesis***
- More than 60 species isolated from anaerobic environments
  - landfills, water-logged soils, peat bogs, thermal environments, salt lakes, and intestinal tracts of animals
- Five species isolated from the rumen



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# What is the Rumen?

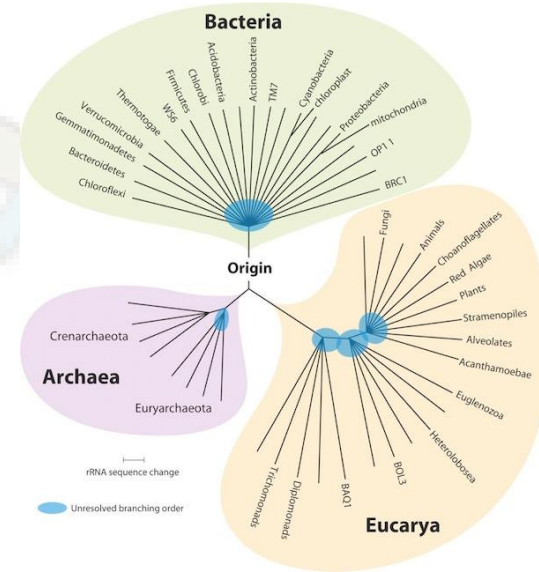
- “Fermentation Vat”
- Anaerobic
- Digestion of a cellulose rich diets
- Provide animal with nutrients as VFA and MCP
- 40 – 60 gal
- ~65% of the GI tract



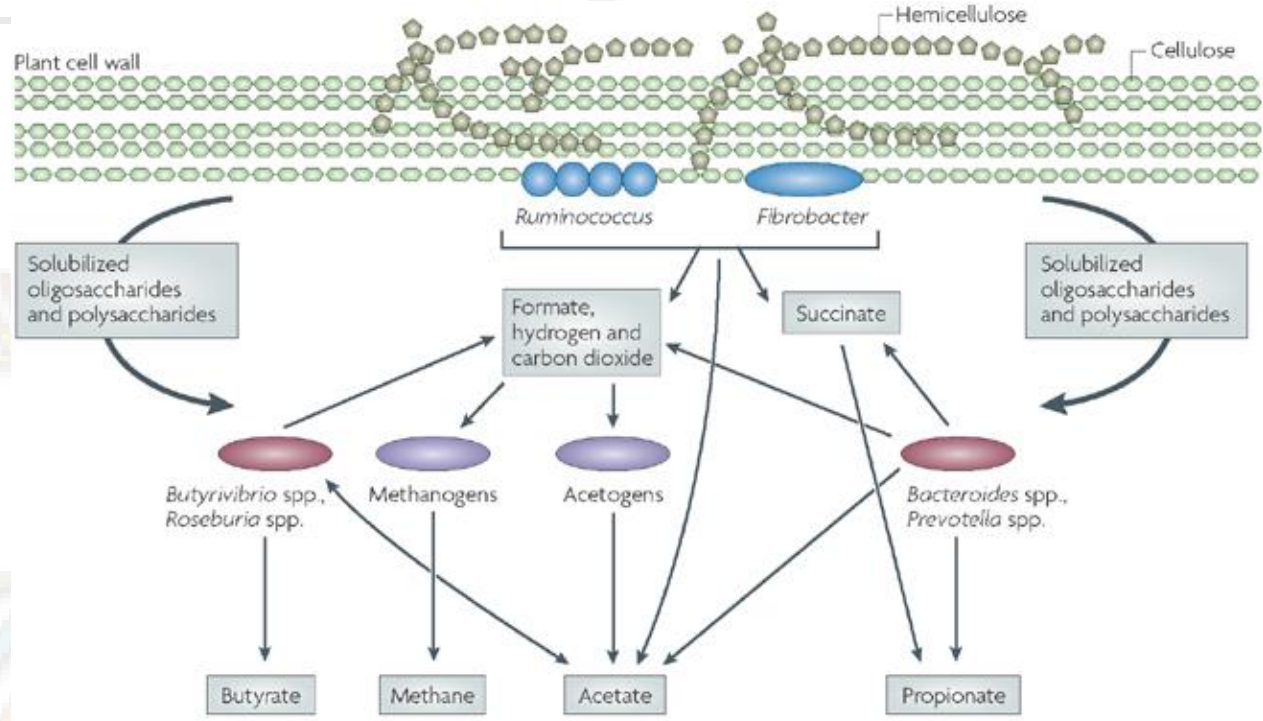
Source: Brock, biology of microorganisms

# Rumen Microbes

- **Bacteria**
  - $10^9 - 10^{11}$ /ml
  - 25% free
  - 75% attached to feed particles
- **Protozoa**
  - $10^4 - 10^7$  /ml
  - Depolymerize pectin
  - Engulf and metabolize starch granules
- **Fungi**
  - $10^3 - 10^5$  /ml
  - 5-10% of the microbes
  - Solublize lignin
  - Only anaerobic fungi known in nature
- **Archaea and viruses**

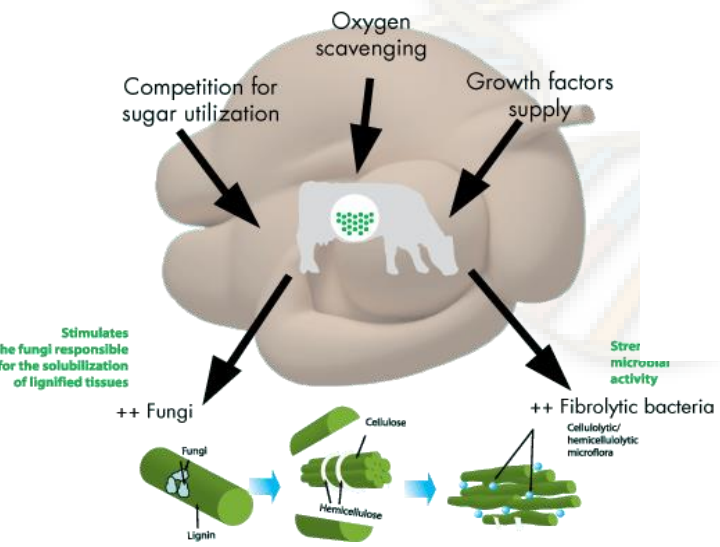


# Microbial role in digestion



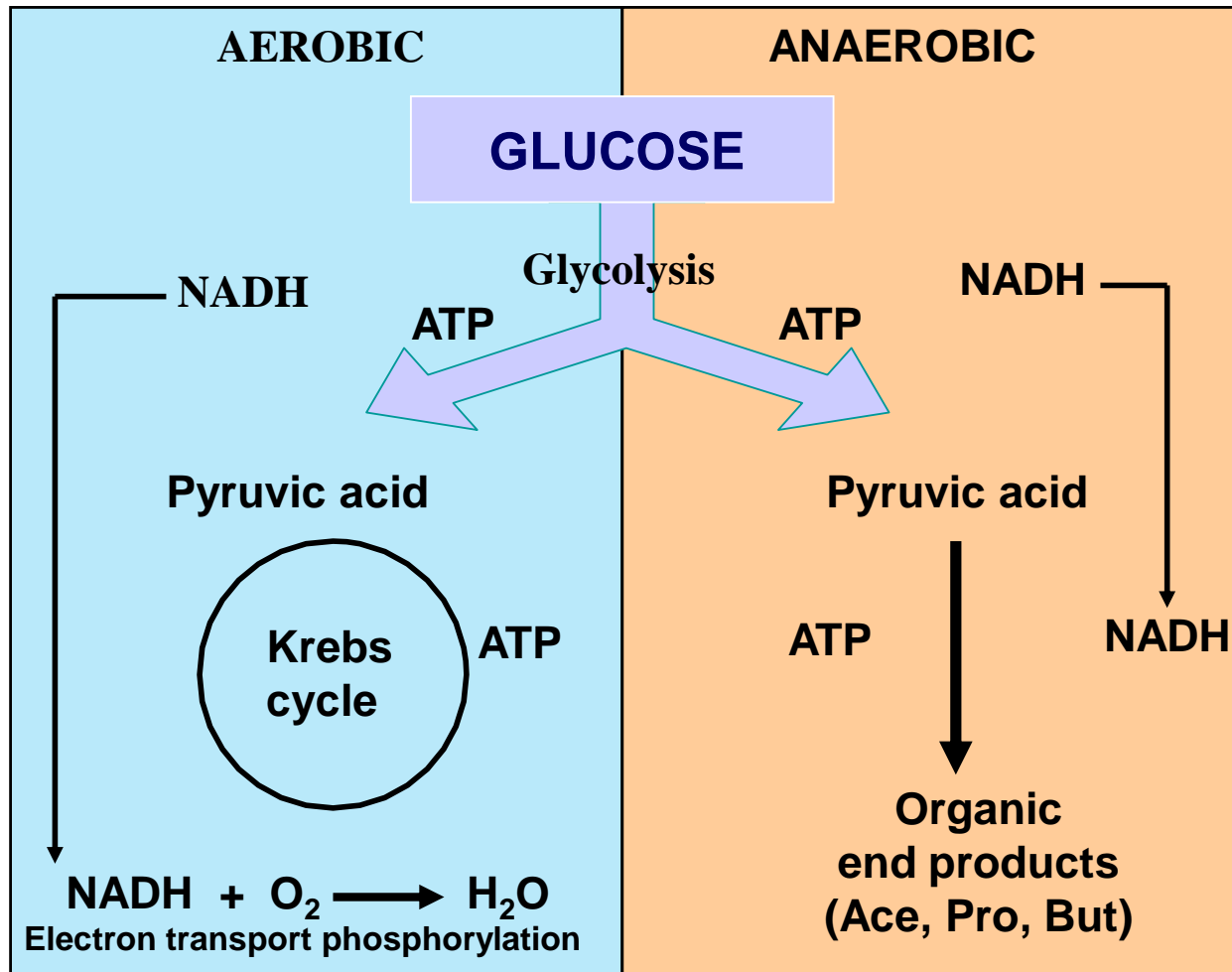
Nature Reviews | Microbiology

Nature Reviews Microbiology 6, 121-131 (February 2008) |

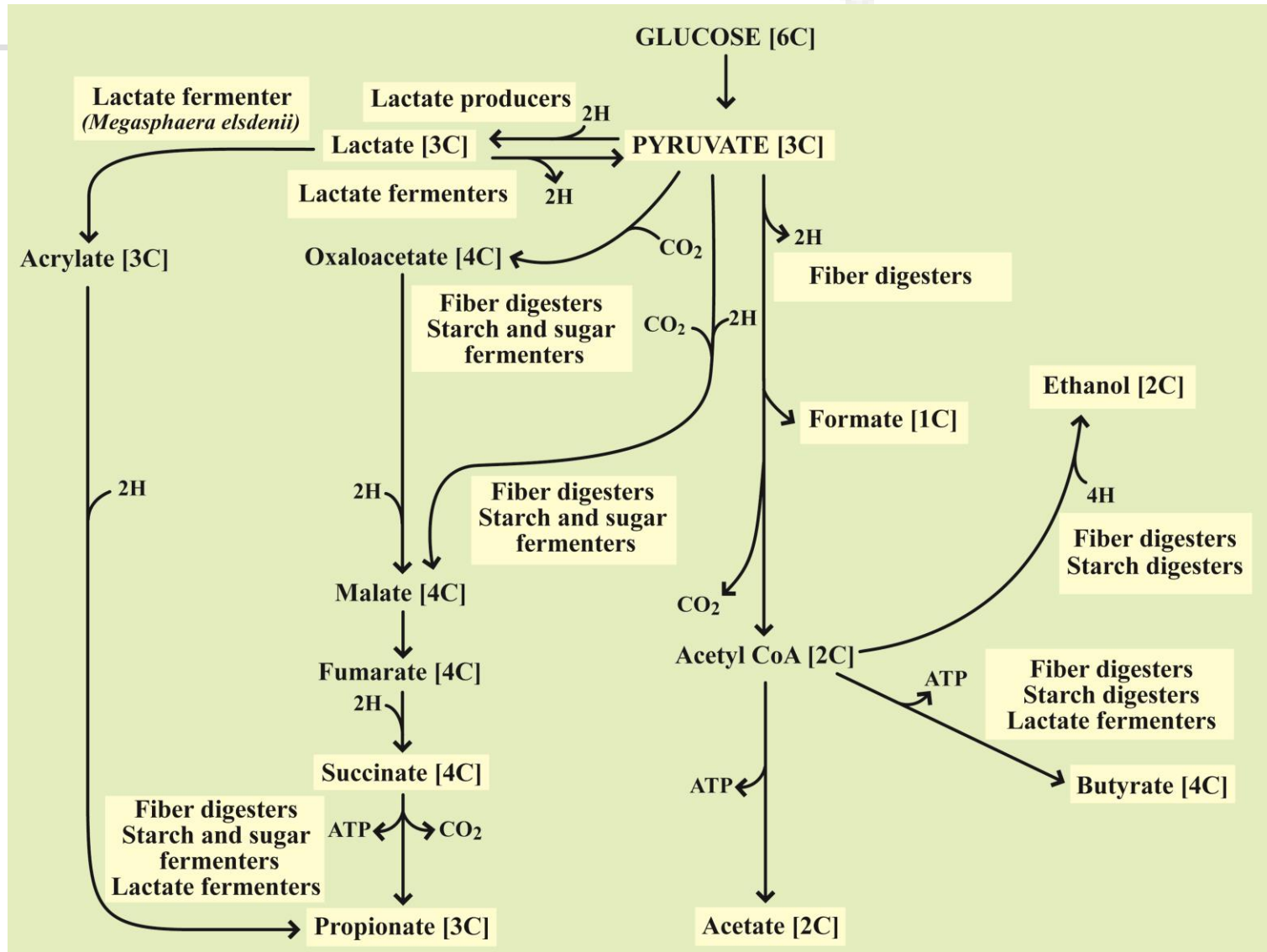




# Aerobic vs. Anaerobic Metabolism



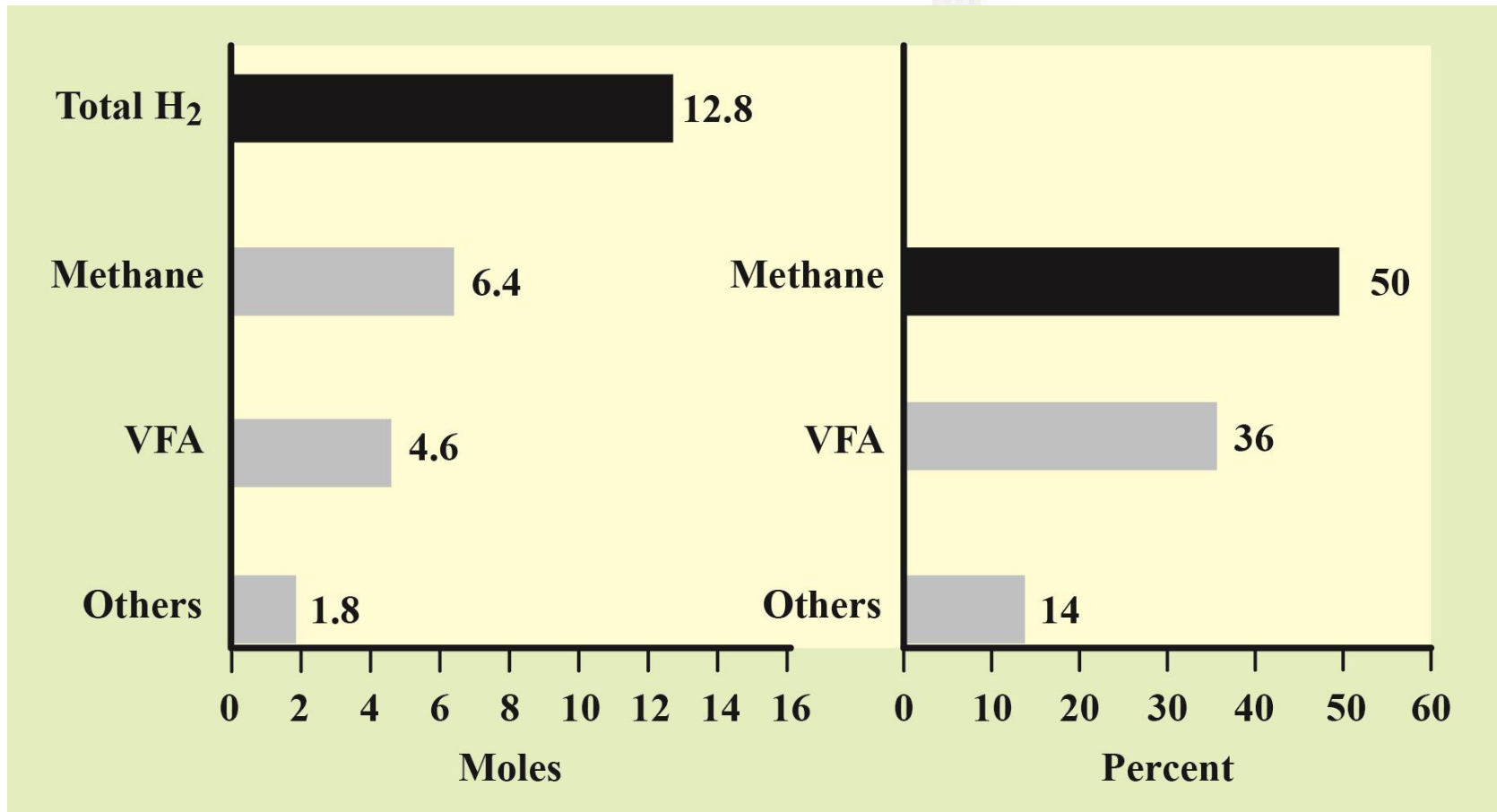
# Pyruvate Metabolism in the Gut



Courtesy of Dr. Nagaraja et al. (Kansas State University)

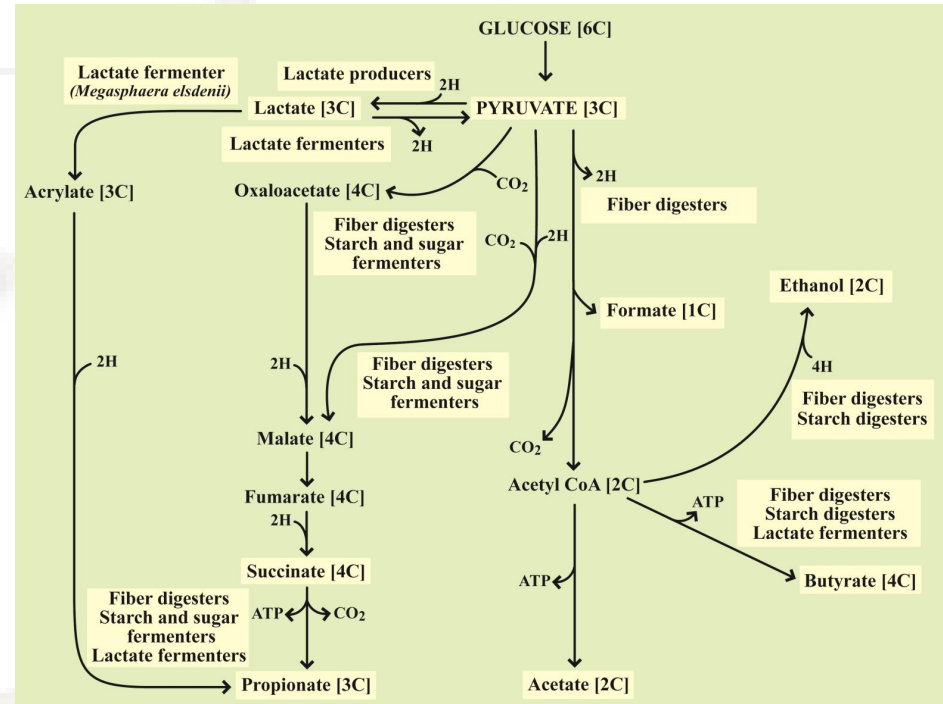
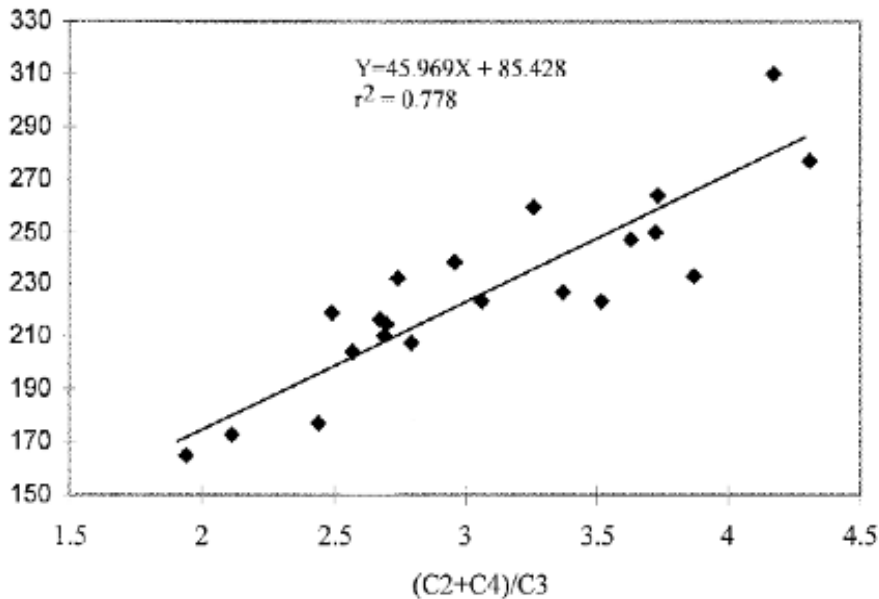
# Hydrogen Production and Utilization in the Rumen

From 1 Kg of DM



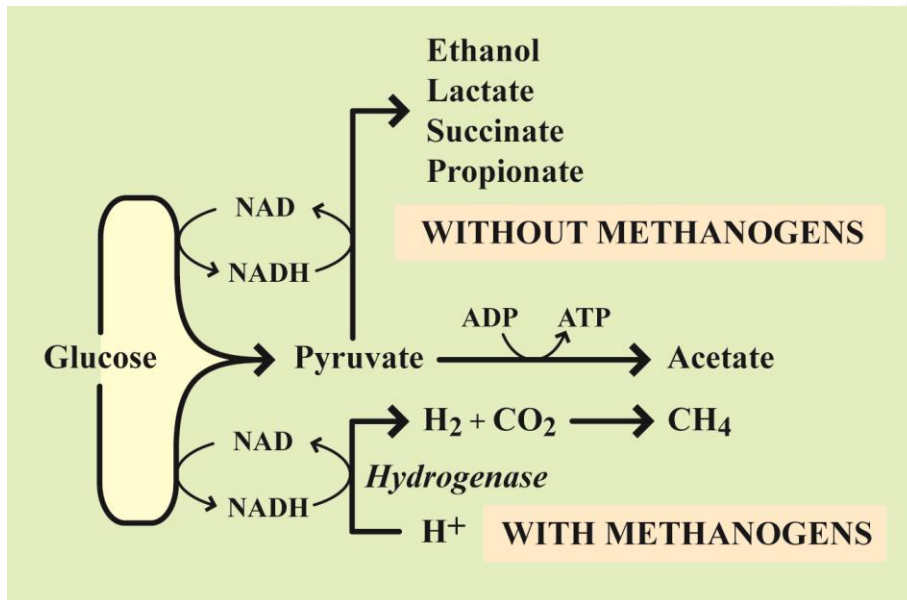
# Methane and VFAs

Methane ( $\mu\text{mol}$ )

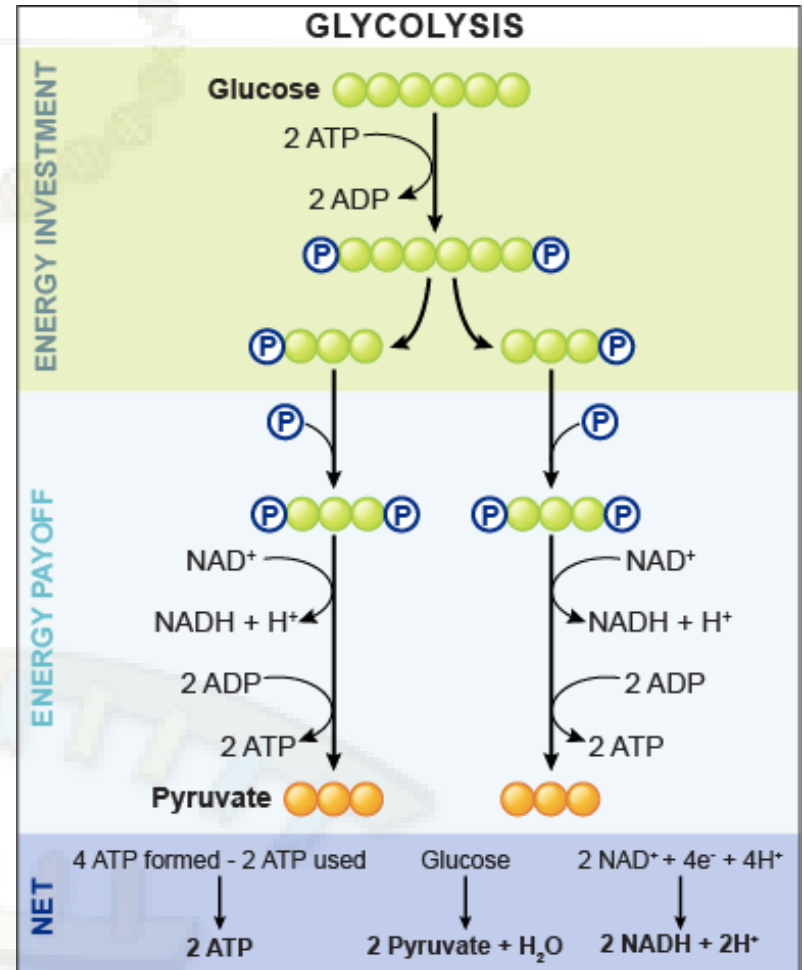


Courtesy of Dr. Nagaraja et al. (Kansas State University)

# Role of Methanogens



Courtesy of Dr. Nagaraja et al. (Kansas State University)



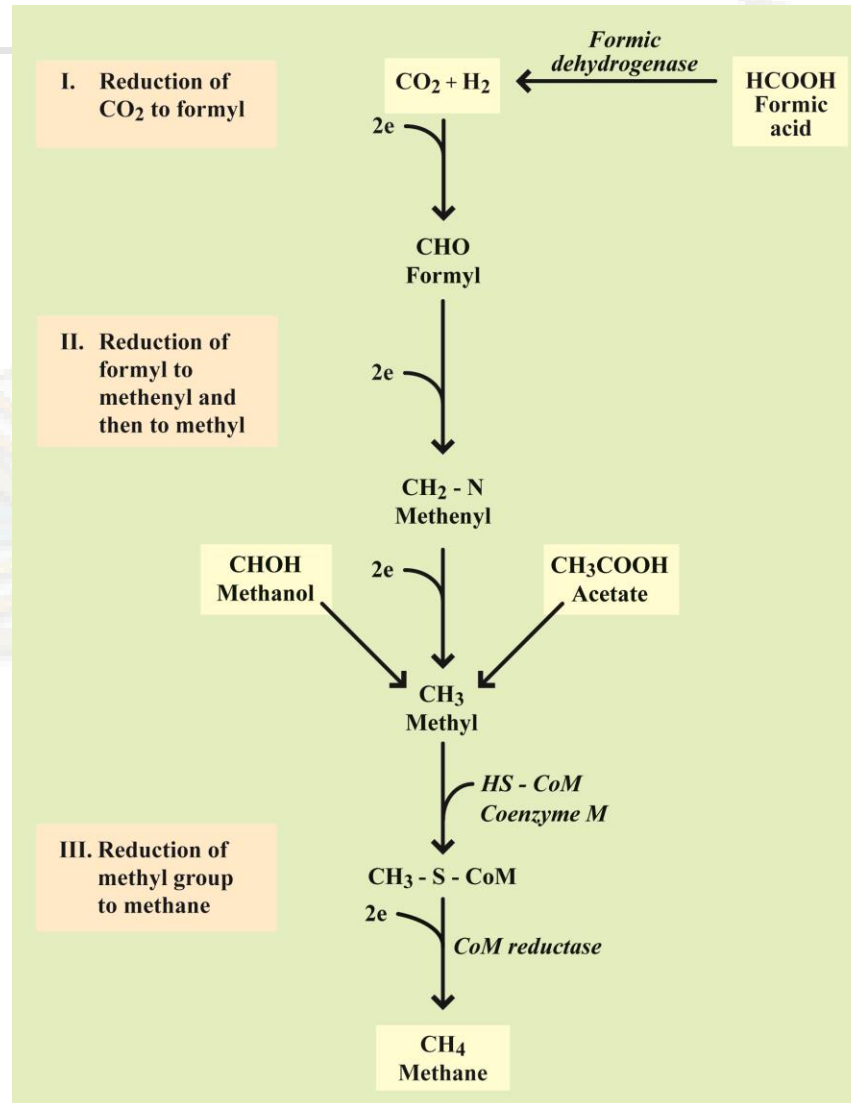
# Inter Species Hydrogen Transfer

Hydrogen Producers	Hydrogen utilizers
<b>Bacteria</b> <i>Lachnospira multiparus</i> <i>Ruminococcus albus</i> <i>Ruminococcus flavefaciens</i> <i>Selenomonas ruminantium</i>	<b>Methanogens</b> <i>Methanobrevibacter ruminantium</i> <i>Methanobacter formici</i> <i>Methanomicrobium mobile</i> <i>Methanosarcina barkeri</i>
<b>Protozoa</b> Holotrichs Entodiniomorphs	<b>Non-methanogens</b> <i>Eubacterium limosum</i> ( $\text{CO}_2 + \text{H}_2 \rightarrow \text{A, P, B}$ ) <i>Wolinella succinogenes</i> ( $\text{Fumarate} + \text{H}_2 \rightarrow \text{Succinate}$ )
<b>Fungi</b> <i>Neocallimastix</i> <i>Piromyces</i> <i>Caecomyces</i> <i>Orpinoomyces</i>	<b>Acetogen</b> <i>Acetitomoculum ruminis</i> <b>Biohydrogenators</b> <b>Nitrate reducers</b> <b>Sulfur reducers</b>

# Substrates for Methane Production in the Rumen

Substrates		Reactions	
<b>MAJOR</b>			
H <sub>2</sub> and CO	4 H <sub>2</sub> + CO <sub>2</sub>	→	CH <sub>4</sub> + 2 H <sub>2</sub> O
Formate	4 HCOOH	→	CH <sub>4</sub> + 3 CO <sub>2</sub> + 2 H <sub>2</sub> O
<b>MINOR</b>			
Methanol	4 CH <sub>3</sub> OH	→	3 CH <sub>4</sub> + CO <sub>2</sub> + 2 H <sub>2</sub> O
<b>Amines</b>			
Methylamine	4 CH <sub>3</sub> NH <sub>2</sub> Cl + 2 H <sub>2</sub> O	→	3 CH <sub>4</sub> + CO <sub>2</sub> + 4 NH <sub>4</sub> Cl
Dimethylamine	2 (CH <sub>3</sub> ) <sub>2</sub> NHCl + 2 H <sub>2</sub> O	→	3 CH <sub>4</sub> + CO <sub>2</sub> + 2 NH <sub>4</sub> Cl
Trimethylamine	4 (CH <sub>3</sub> ) <sub>2</sub> NHCl + 2 H <sub>2</sub> O	→	3 CH <sub>4</sub> + CO <sub>2</sub> + 2 NH <sub>4</sub> Cl
Acetate	CH <sub>3</sub> COOH	→	CH <sub>4</sub> + CO <sub>2</sub>

# Methane production in the Rumen

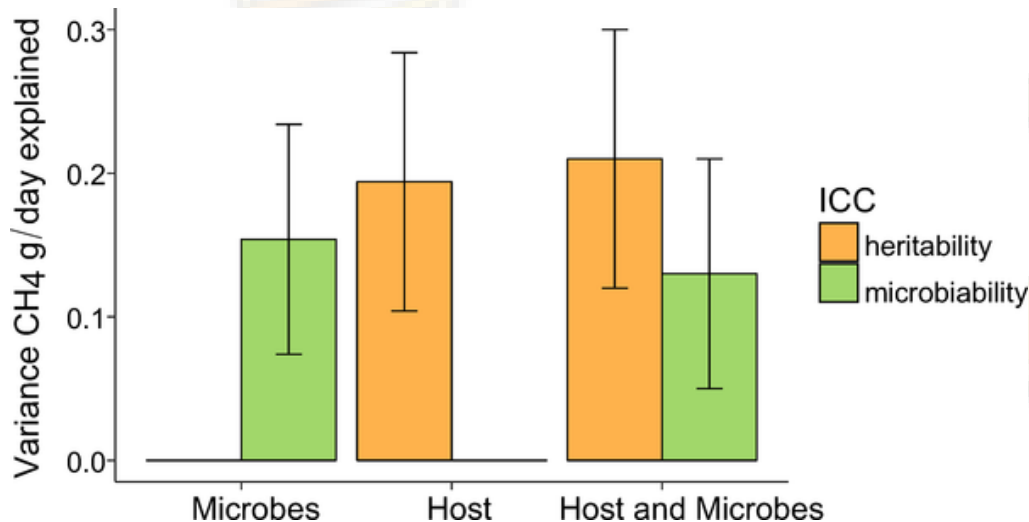


Courtesy of Dr. Nagaraja et al. (Kansas State University)



# Genetic and microbial effect on Methane emission in Ruminants

- Host genetics effect methane production
  - Heritability 21%
- Microbiome
  - Bacteria and Archaea 13%
- Host genetics and microbiome effect is independent of each other



Host genetics and the rumen microbiome jointly associate with methane emissions in dairy cows

Gareth Frank Difford , Damian Rafal Plichta, Peter Lovendahl, Jan Lassen, Samantha Joan Noel, Ole Højberg,

André-Denis G. Wright, Zhigang Zhu, Lise Kristensen, Henrik Bjørn Nielsen, Bernt Gulbrandsen, Goutam Sahana 

# Genetic effect on Methane emission in Ruminants

Article | [Open Access](#) | [Published: 04 May 2020](#)




## Bayesian modeling reveals host genetics associated with rumen microbiota jointly influence methane emission in dairy cows

[Qianqian Zhang](#) , [Gareth Difford](#), [Goutam Sahana](#), [Peter Løvendahl](#), [Jan Lassen](#), [Mogens Sandø Lund](#), [Bernt Gulbrandsen](#) & [Luc Janss](#)

[The ISME Journal](#) **14**, 2019–2033 (2020) | [Cite this article](#)

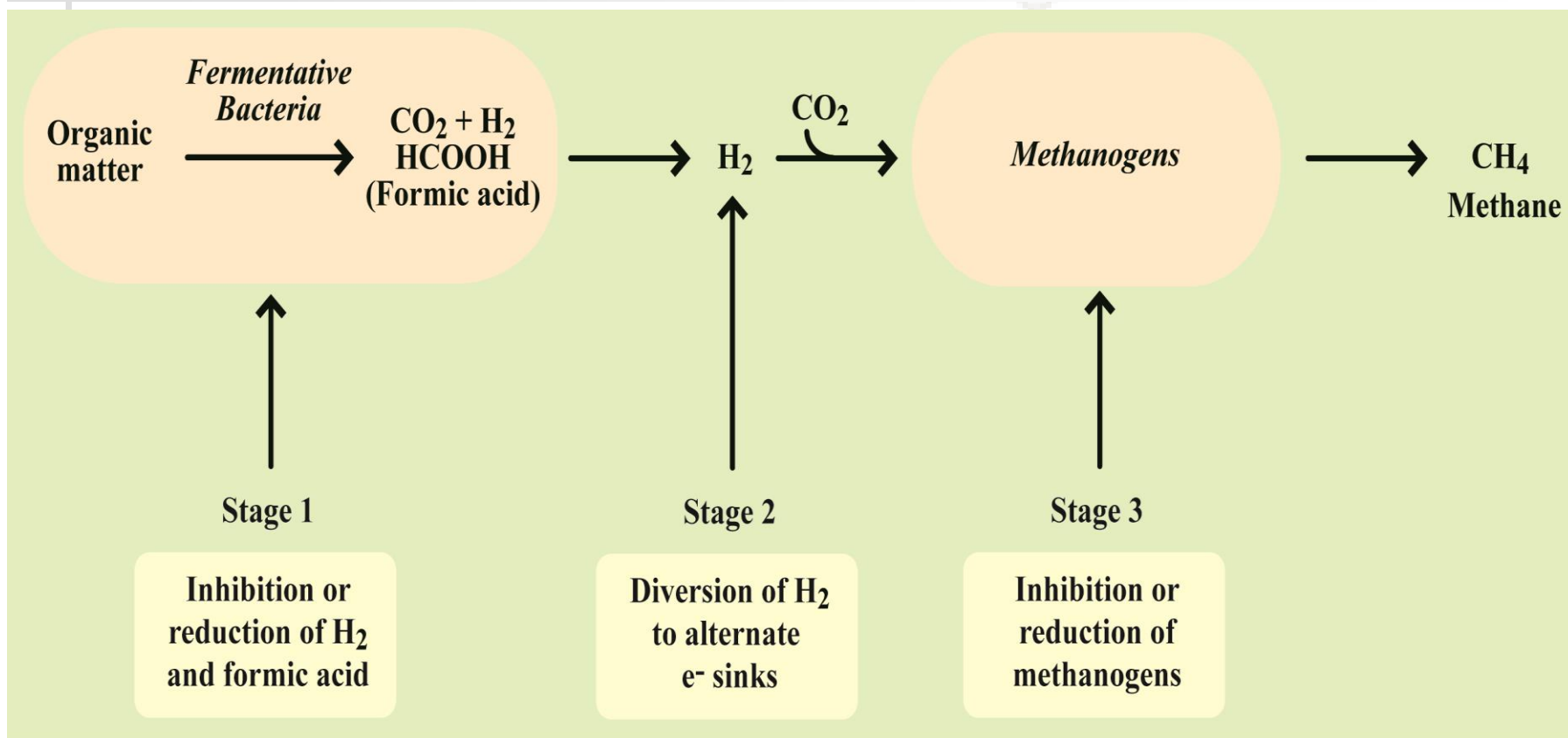
**2869** Accesses | **5** Citations | **18** Altmetric | [Metrics](#)

## Bovine Host Genetic Variation Influences Rumen Microbial Methane Production with Best Selection Criterion for Low Methane Emitting and Efficiently Feed Converting Hosts Based on Metagenomic Gene Abundance

[Rainer Roehe](#) , [Richard J. Dewhurst](#), [Carol-Anne Duthie](#), [John A. Rooke](#), [Nest McKain](#), [Dave W. Ross](#), [Jimmy J. Hyslop](#), [Anthony Waterhouse](#), [Tom C. Freeman](#), [Mick Watson](#) , [R. John Wallace](#) 

Published: February 18, 2016 • <https://doi.org/10.1371/journal.pgen.1005846>

# Inhibition of Methane Production in Ruminants

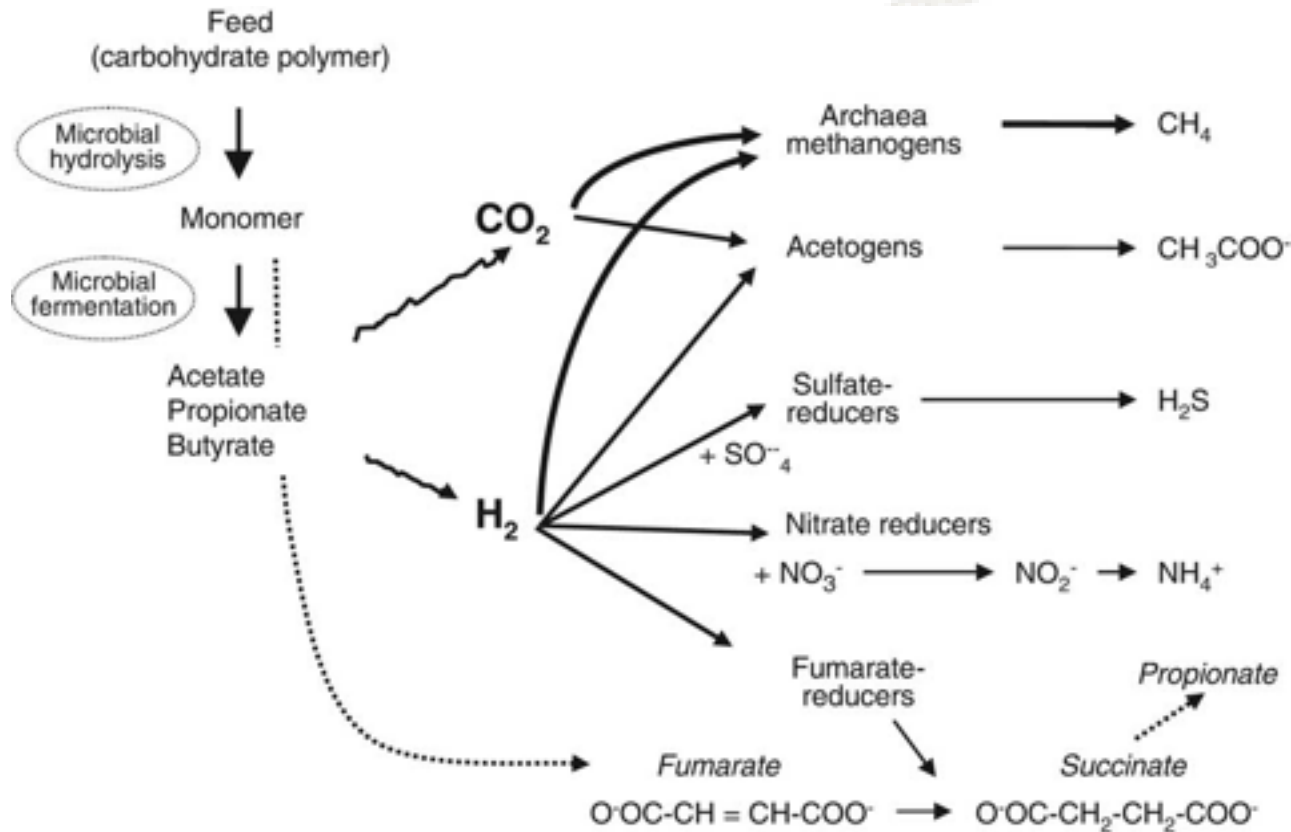


Deaminase Inhibitors  
Grinding, pH,  
Ionophore

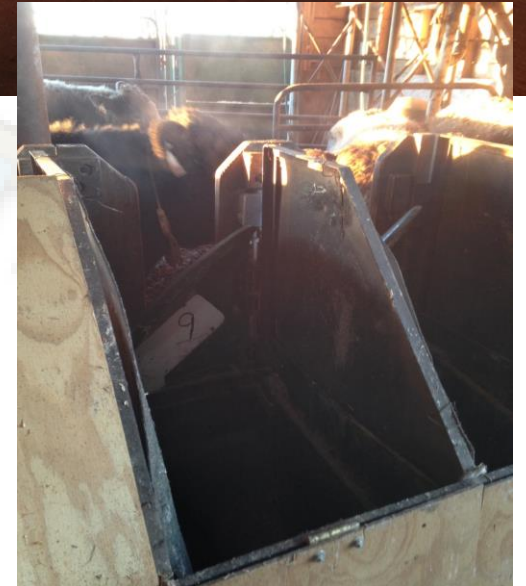
Fat supplementation  
Sulfates, Nitrates, etc.  
Promoting Acetogens

Vaccines,  
Defaunation,  
Halogen compounds

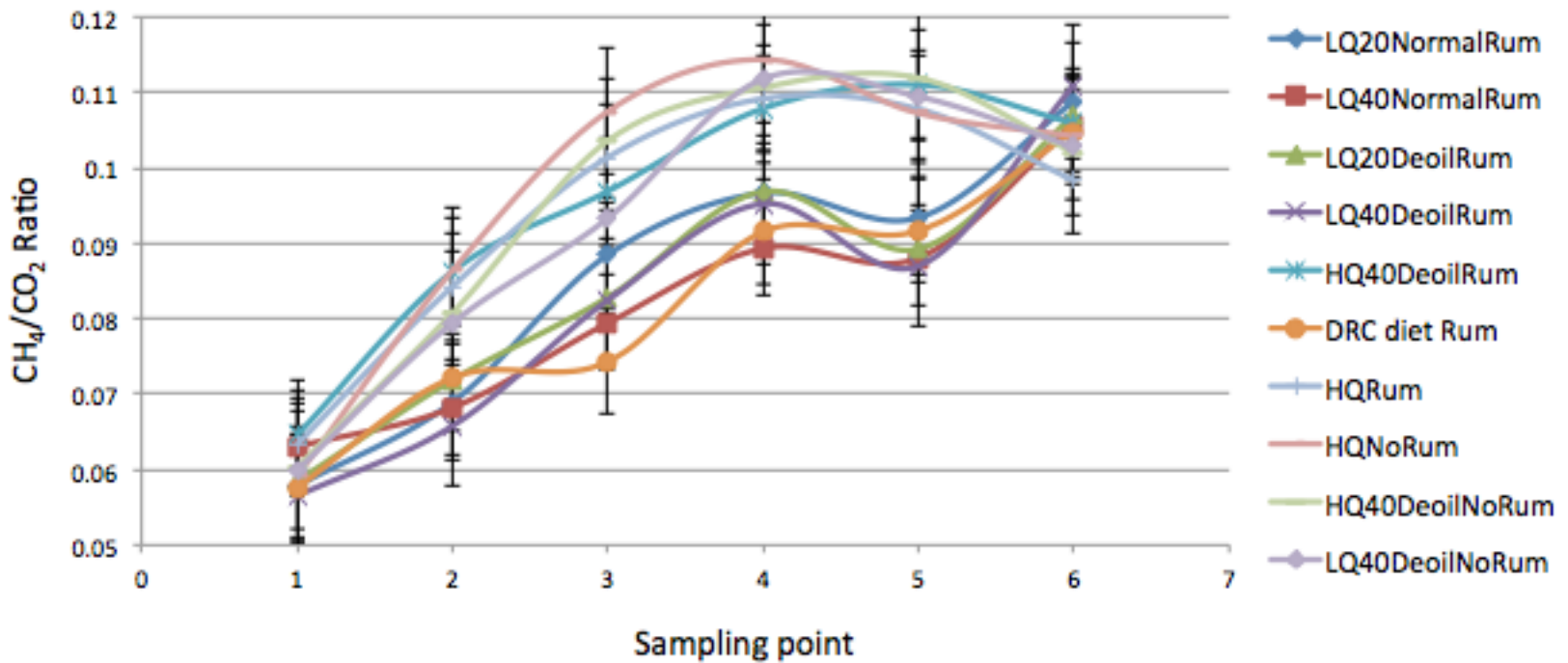
# Hydrogen sinks in the rumen



# Methane Sampling



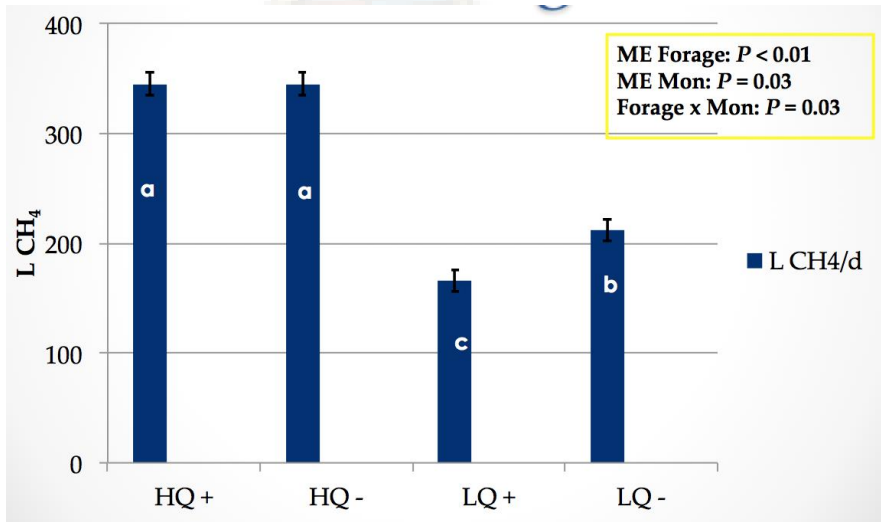
# CH<sub>4</sub>/CO<sub>2</sub> based on Diet



# Emissions: Forage x Mon.

40% De-Oiled MDGS

Monensin	HQ		LQ		SEM	P-value		
	+	-	+	-		Forage	Mon.	Int.
CH <sub>4</sub> :CO <sub>2</sub>	0.101 <sup>a</sup>	0.101 <sup>a</sup>	0.083 <sup>b</sup>	0.101 <sup>a</sup>	0.003	<0.01	<0.01	<0.01



Methane and carbon dioxide ratio in excreted air for quantification of the methane production from ruminants

CO<sub>2</sub> as internal marker  
Relate heat production to CO<sub>2</sub>

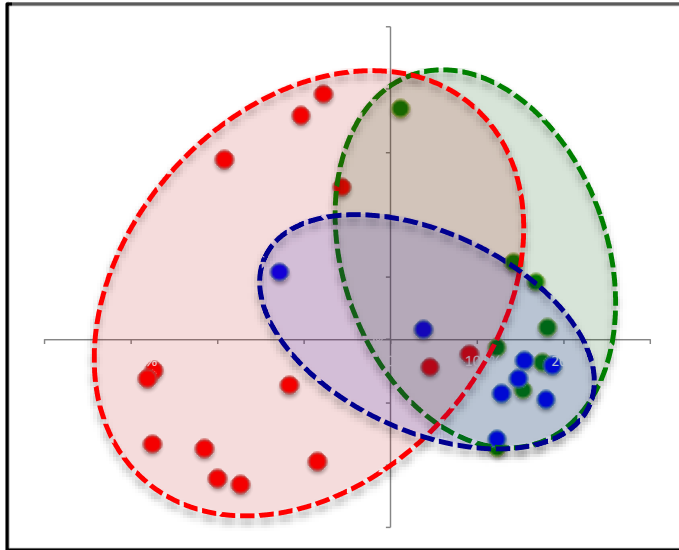
HP = intake of ME – energy in products (gain)

Use:

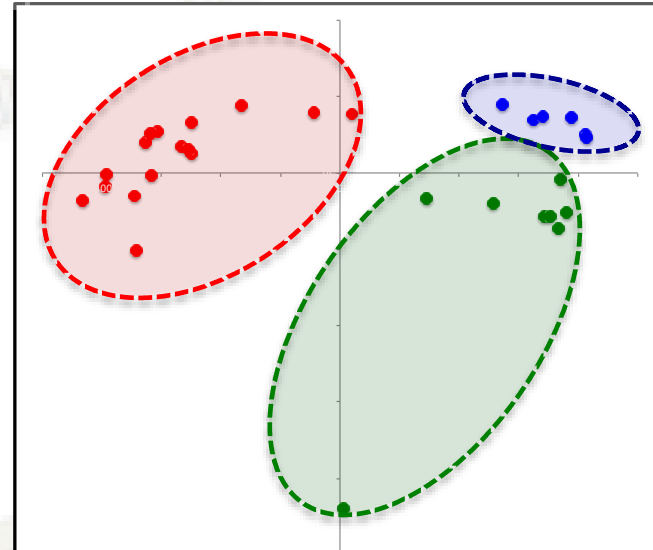
- Calculated TDN
- Actual DMI and ADG
- Actual average CH<sub>4</sub>:CO<sub>2</sub>




# Community to Pathways

Archaeal diversity



Bacterial diversity

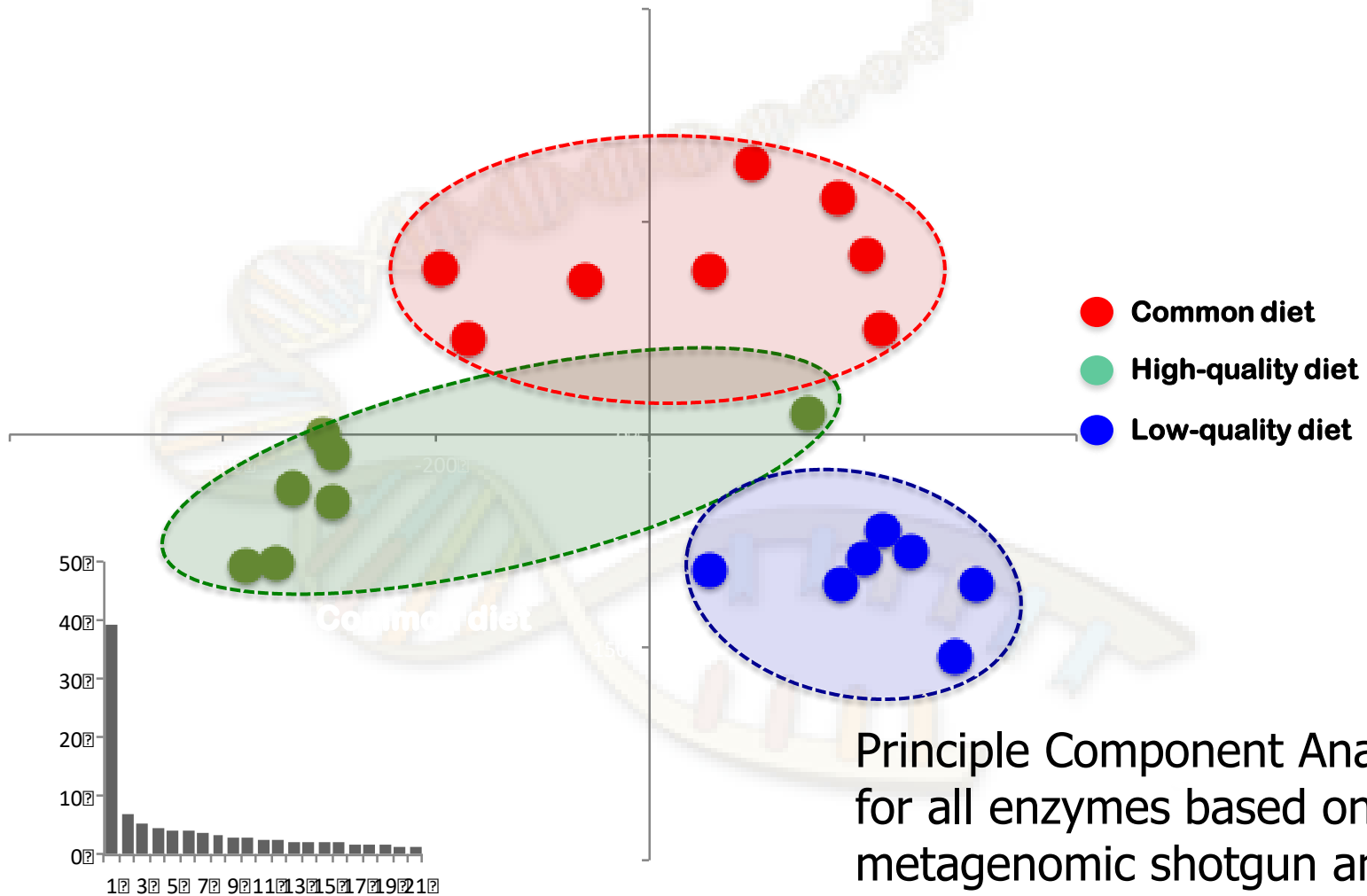


-  **Common base diet**
-  **High quality forage diet**
-  **Low quality forage diet**

Principle Component Analyses  
based on 16S rRNA community  
analyses



# Metagenomic Analysis to Identify Microbial Pathways



Principle Component Analyses for all enzymes based on metagenomic shotgun analyses

Anthony-Babu et al. Unpublished data

# Key Points

- Production of methane within the rumen plays an important role in efficient substrate utilization
- Decreasing methanogenesis needs to be coupled with efficient rumen function
  - Re-cycling NADH using alternative pathways to methanogenesis
- Dietary intervention, microbiome manipulation and genetic selection are viable strategies to reduce methane production through enteric fermentation
- Whole rumen ecosystem needs to be considered



**Thank You!**