

# Influence of yeasts supplementation on microbiome composition in liquid fraction of rumen content of lactating cows

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## Introduction

A greater understanding of rumen microbiome genetic traits and its metabolic potential allows to improve feed efficiency reducing GHG emissions and related ecological footprint.

## Aim

Use a gene centric molecular approach and next generation sequencing for investigate rumen microbiome compositions associated to VFA production in lactating cows after supplementation with 2 types of *Saccharomyces cerevisiae* yeast or placebo (50g/d).

## Material and methods

12 cows feed corn silage based diet housed in the same barn

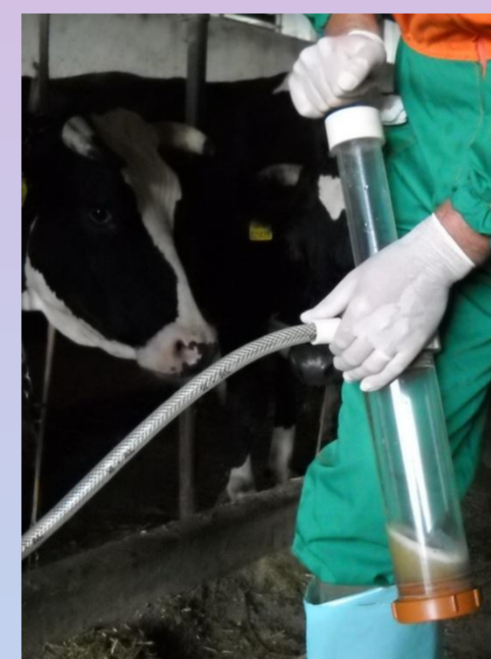
4 SV group  
Type 1 yeast

4 LV group  
Type 2 yeast

4 CTRL group  
Potato protein

Day 0  
Beginning of  
Experimental period

Day 15 Rumen  
content sampling



Separation of  
liquid phase

VFA's  
determination

Individual  
pyrosequencing  
(454 Roche)

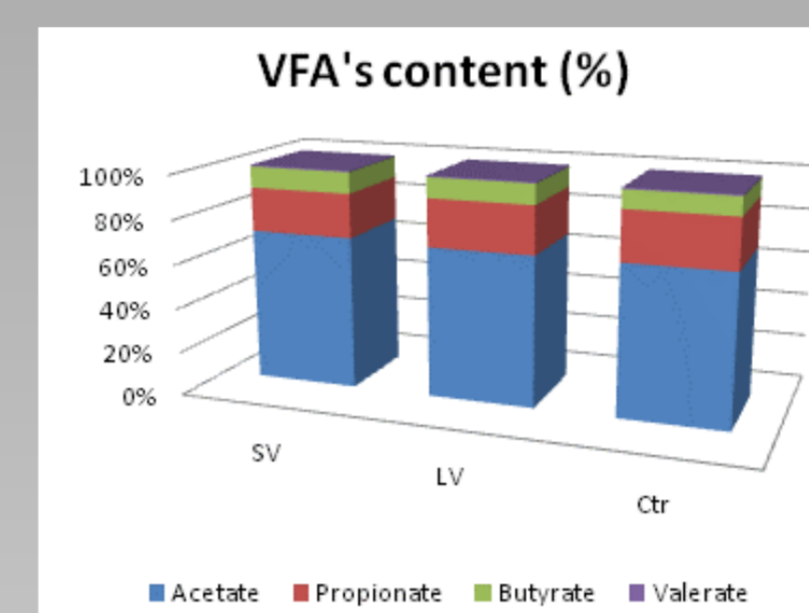
Rumen genomic  
DNA amplification  
16S rRNA V1-V3  
regions

*Eubacteria* universal primers  
E8F (AGAGTTTGATCCTGGCTCAG)  
E534R (ATTACCGCGGCTGCTGGC)

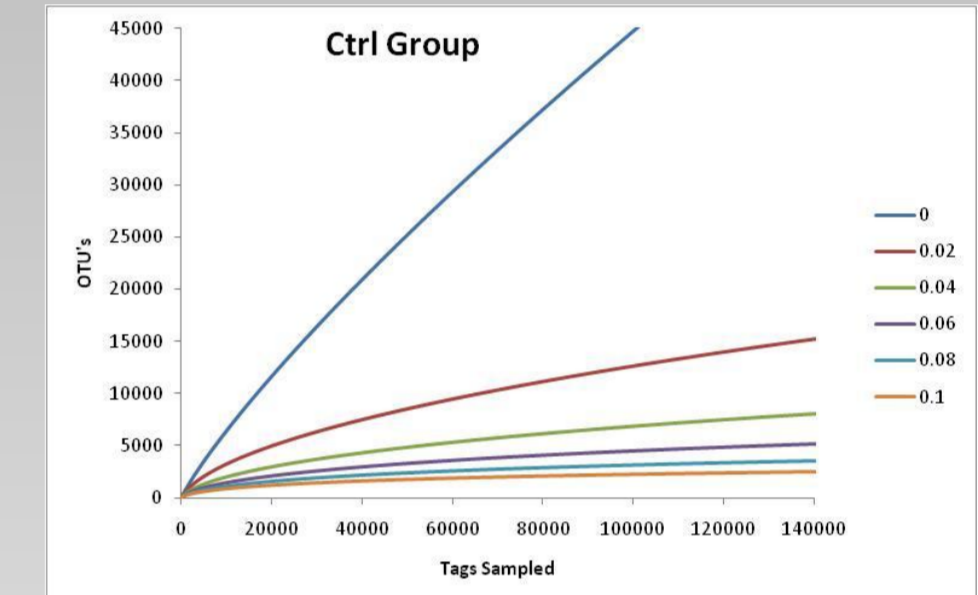
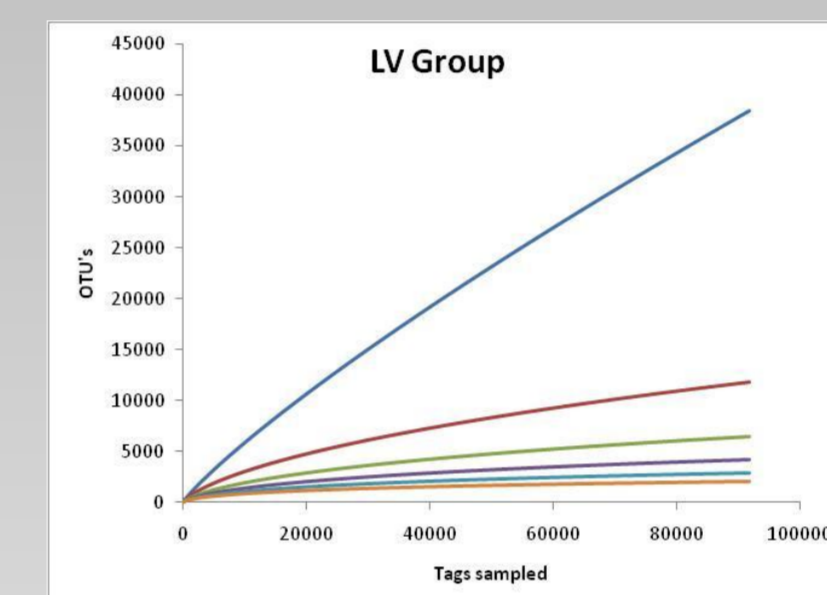
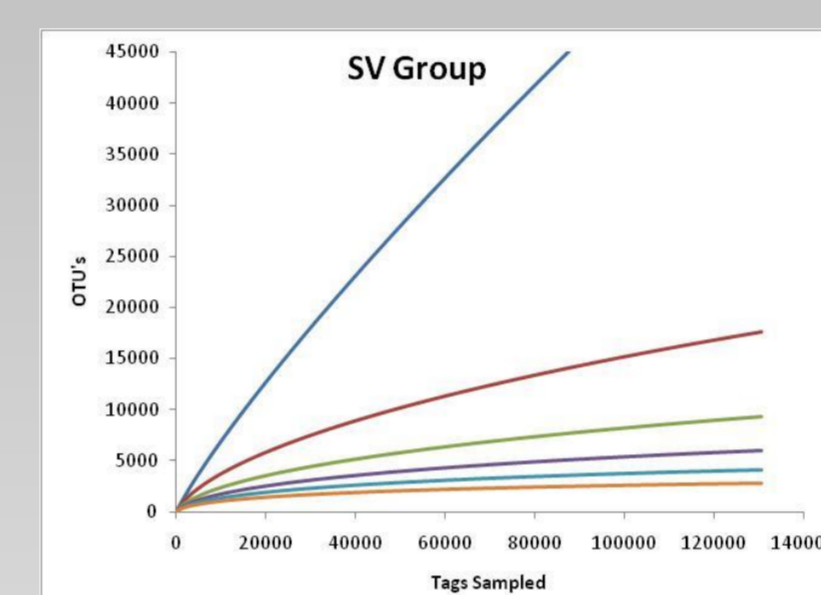
Assignment to  
OTU's with RDP  
tools (groups)

Annotation for  
phylogenetic  
composition with  
RDP Classifier  
(groups)

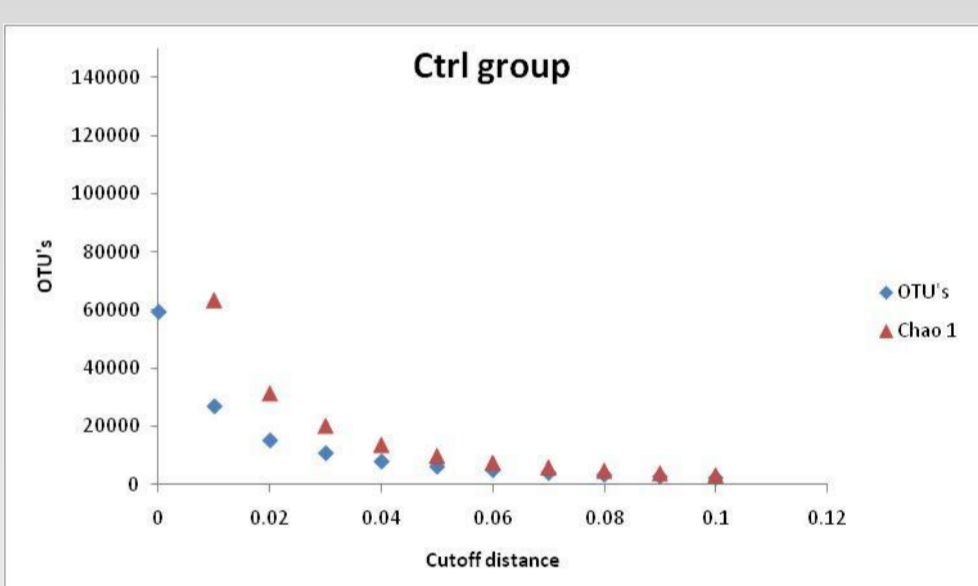
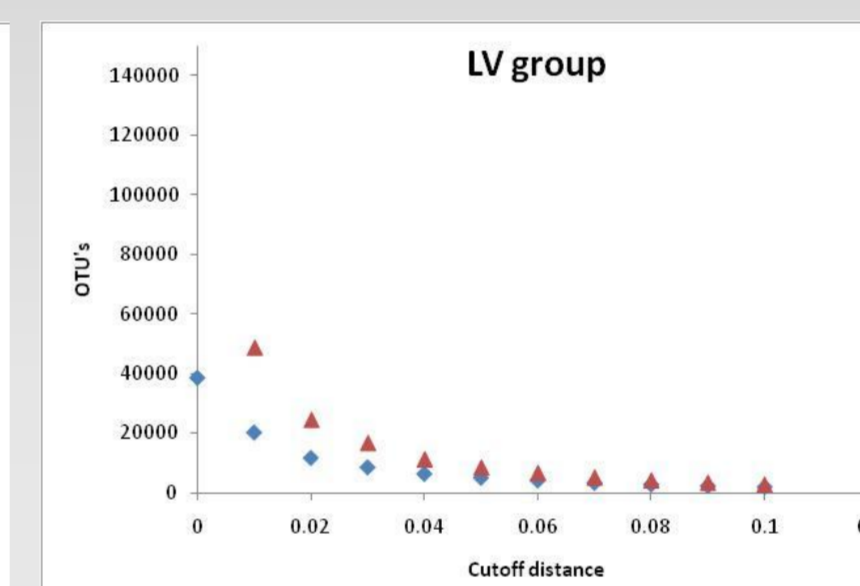
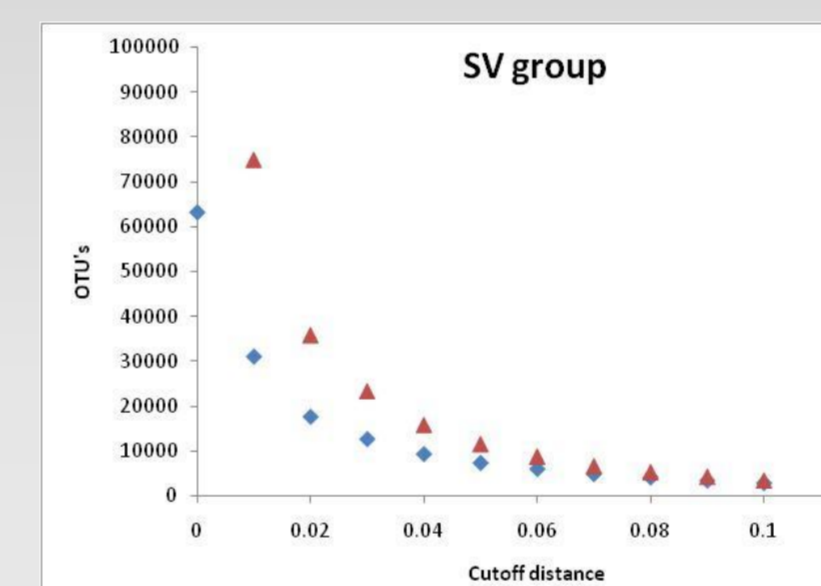
## Results and discussion



No significant differences for VFA's in rumen liquid between groups



Rarefaction curves at increasing cutoffs of phylotypes (0, 0.02, 0.04, 0.06, 0.08, 0.1)

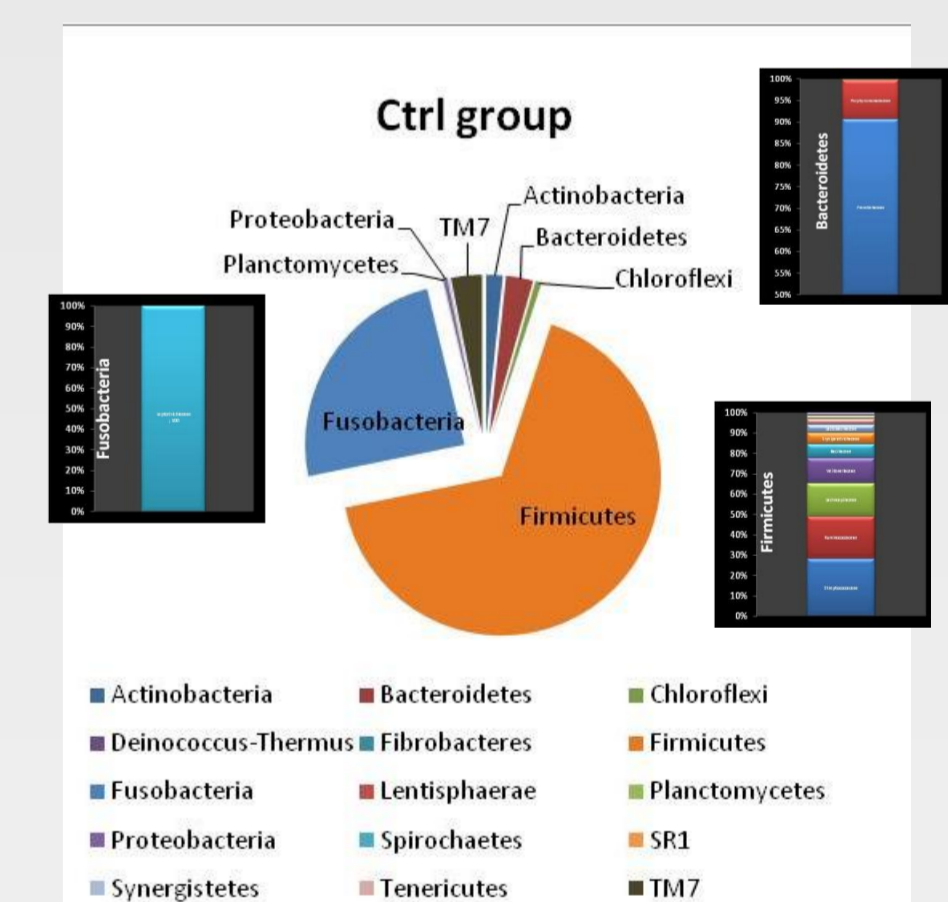
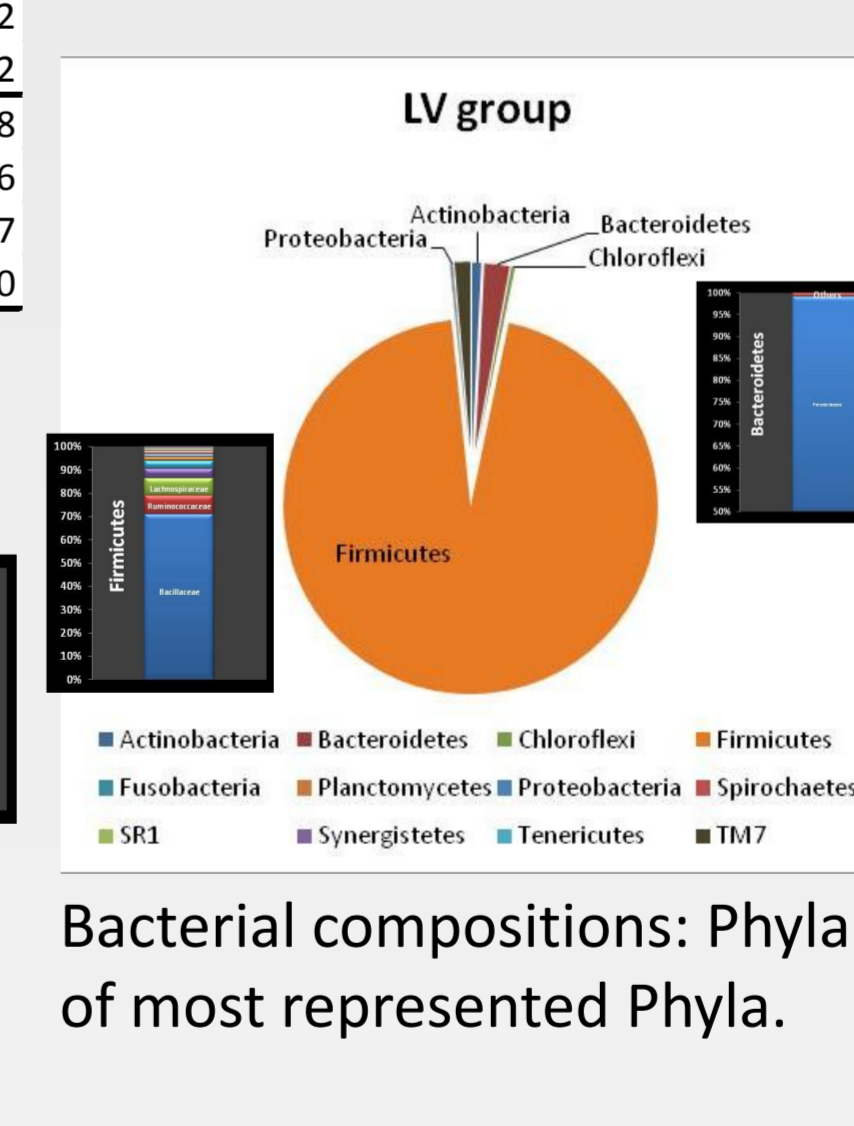
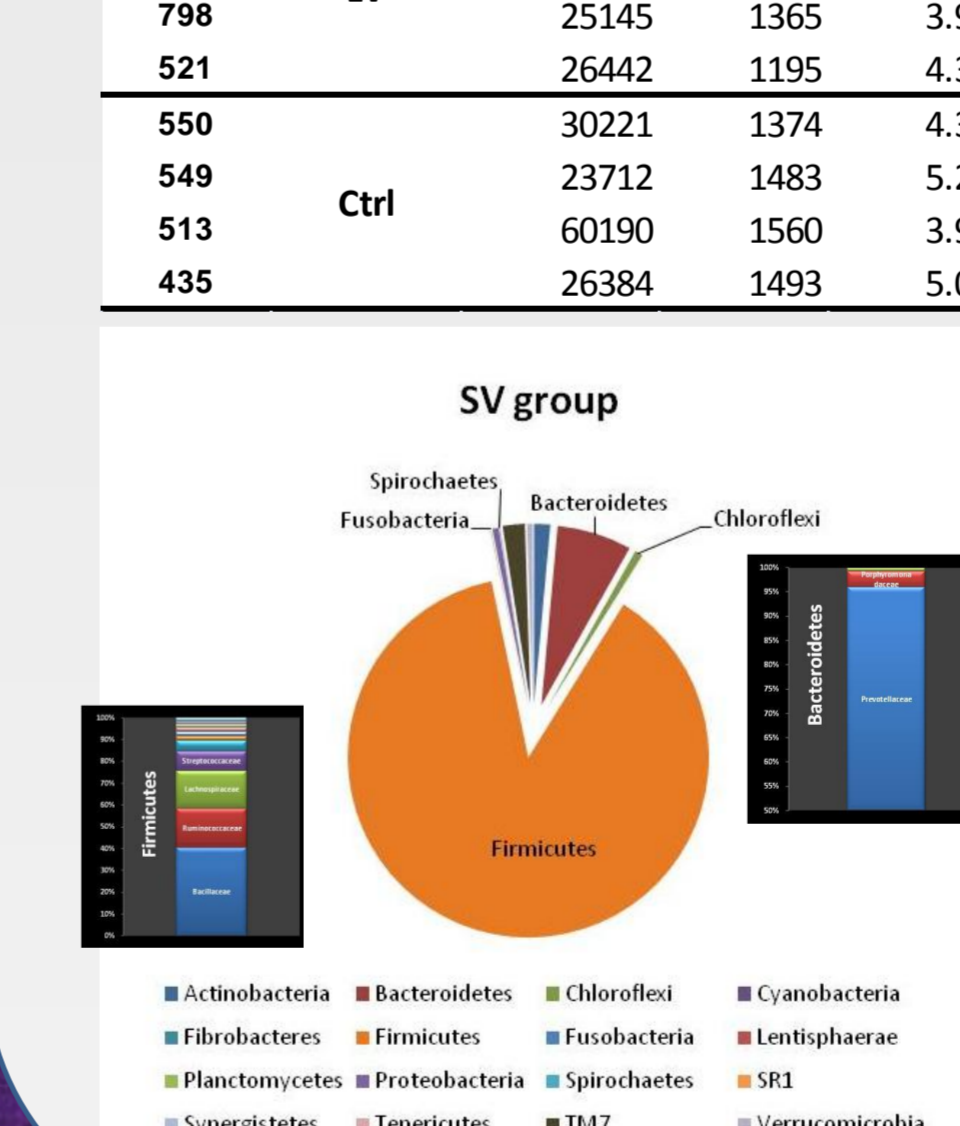


OTU's observed Vs minimum numbers of OTU's estimated (Chao 1 Index)

Sample	Group	N° of reads	0.06 <sup>n</sup> OTU's	H'
420	SV	24258	1288	4.04
424		55330	2469	5.87
428		22802	2093	5.52
516		28213	687	3.24
517	LV	22601	1024	3.67
430		17652	821	3.02
798		25145	1365	3.92
521		26442	1195	4.32
550	Ctrl	30221	1374	4.38
549		23712	1483	5.26
513		60190	1560	3.97
435		26384	1493	5.00

Summary of Pyrosequence data and comparison of Shannon diversity Index.

<sup>n</sup> OTU's cutoff in distance units.  
Avg. quality score (Phred Value)  
was > 26,8



Bacterial compositions: Phyla (P < 0.1) and Families (P < 0.2) of most represented Phyla.

## Conclusions

- Limited information for sequence annotation is still available in repository databases for rumen microorganisms
- High individual variability require to be further investigated (farm ? – diet ? – breed ? – genotype ?)
- Firmicutes most representative rumen bacteria in liquid phase of rumen content but large fluctation for other Phyla
- Hydrolized Yeast affect rumen microbiome composition, with a reduction of biodiversity either at Phyla and Family level
- Understanding of the factors affecting rumen microbiome can contribute to control rumen fermentation, feed efficiency and GHG emissions