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ARMOr project : genome-wide association analysis of ruminal microbiota in ovis

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HAL Authorization

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The microbiota of herbivorous animals plays a central role in the nutrition of its host: it directly affects his health and his ability to produce both products of interest to the human diet as undesirable products such as methane. Studies on ruminal microbiota and its activity point out a significant effect of the "host" factor, but no publications reported results concerning the impact of host genetics on the composition of ruminal microbiota.

The **ARMOr** project consist in a **genome-wide association analysis** (GWAS) **between the sheep genome** (with a 54 kSNP genotyping) and **its ruminal microbiota**, in connection with milk quality and udder health.

Material and Methods

- Studied animals are **700 adult Lacaune ewes**, reared in similar feeding conditions at the INRA Experimental Unit of La Fage.



These animals belong to 4 different lines:

- 2 lines selected divergently on somatic cells count (CCS+ vs CCS-) highly different for mastitis resistance,
- 2 lines selected on milk persistency (PERS+ vs PERS-),

- Sampling of rumen fluid and blood samples done from 2015 to 2018,

- Sequencing the **ruminal metagenome using 16s rRNA gene** with Illumina Miseq technology at the Genomic and Transcriptomic Platform (INRA, Toulouse, France),

- Bioinformatic analysis of the microbiota sequences with FROGS pipeline to obtain relative abundance of phylum, class, order, family or genre of bacteria,

- **Genotyping** of the 700 sheep carried out with the ovine 54 kSNP chip,

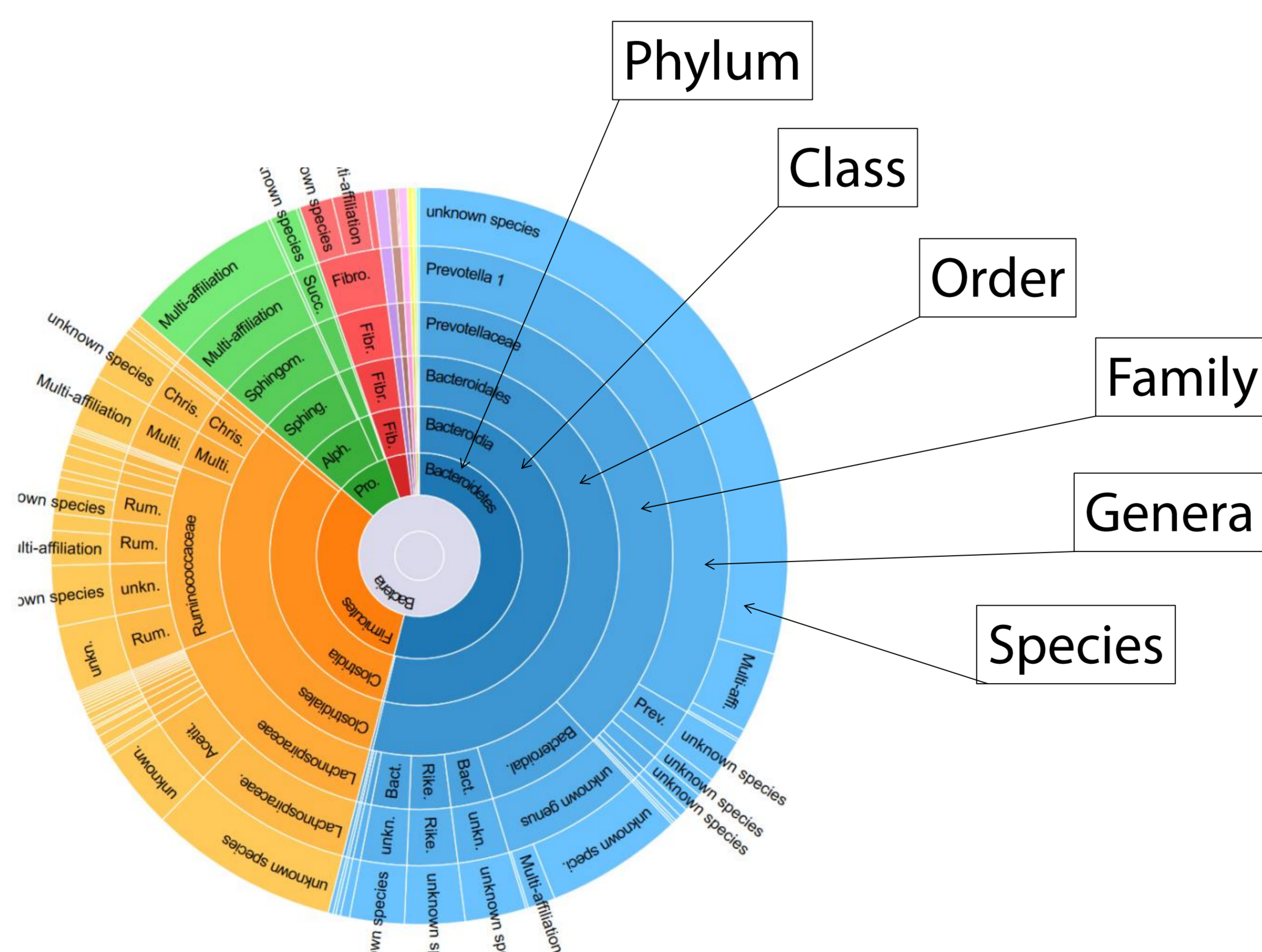
- Recording of the milk quality phenotypes (milk fat and protein contents, milk quantity, milk fatty acids prediction by mid-infrared), the udder health (SCS), the udder morphology and milk emission traits.

- Genetic analysis of the global design will be achieved by linking ruminal microbiota with the sheep genome.

Work in progress

In 2015, 120 ewes had their ruminal microbiota sampling and profiling twice with a gap of 1 week, allowing :

A first description of the bacteria relative abundance of Lacaune ewes



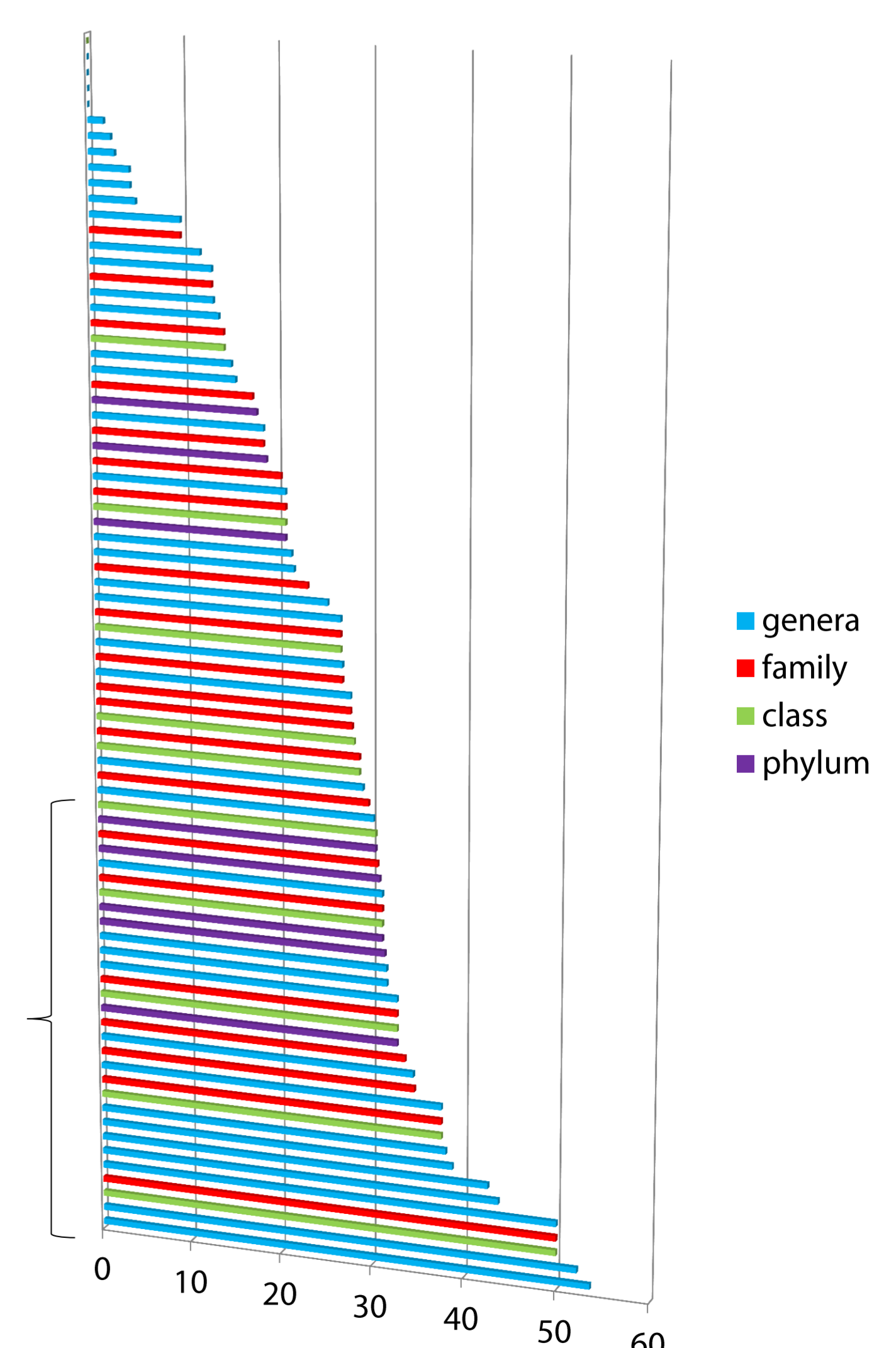
Identified bacteria were aggregated in 8 phylum, 11 classes, 12 orders, 22 families and 39 genera; species are mostly not identified.

The main representative bacteria phylum are « Bacteroidetes » (59%) and « Firmicutes » (32%),

A repeatability (*) estimation of the bacteria relative abundance

Repeatability of bacteria relative abundance vary from 0% to 53%.

14 genera, 7 families, 6 classes and 5 phylum have repeatabilities higher than 30%



(*) correlation between to successive bacteria abundance