

- High frequency of digestive trouble in rabbit rearing units leads to important antimicrobial agent use
- Microbiota plays important key roles in the development of the gastrointestinal tract, angiogenesis, maturation of the immune system and acts in health as a barrier against pathogens



- The maternal excretion of hard faeces in the nest, and their ingestion by pups is involved in the microbiota implantation
- The hard faeces would be an efficient tool to modulate microbiota establishment and health of the young rabbit

Objectives

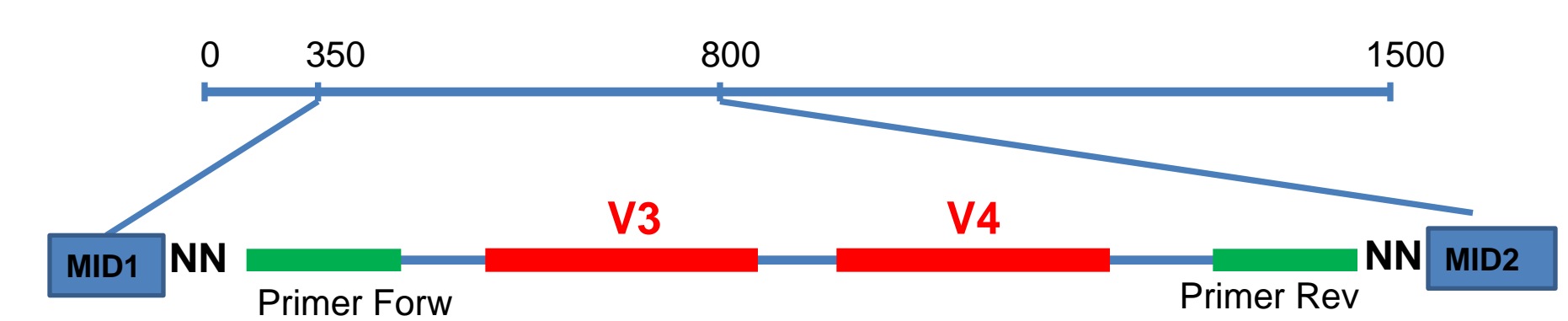
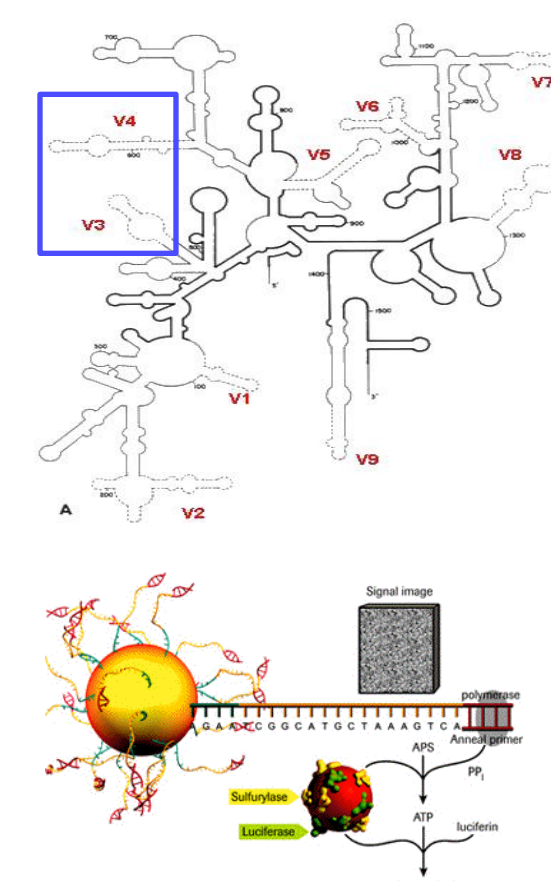
- to quantify both behaviors maternal hard faeces excretion and pups' hard faeces ingestion
- to evaluate the effect of hard faeces ingestion on caecal microbiota implantation process and rabbit health
- to modulate the caecal microbiota implantation process using hard faeces from foreign does



Material and Methods

FM group = Natural behaviour 24 litters	NF group = No faeces ingestion 28 litters	FF group = Ingestion of foreign faeces 28 litters
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Nursing was controlled
Maternal excretion and pups' ingestion of faeces in the nest were measured daily from 2 to 20 d
Mortality was measured daily from 1 – 80 d



Bacterial composition was assessed by 454 pyrosequencing of the V3-V4 region of 16S RNA genes at 14, 35, 49 and 80 d

Results and discussion

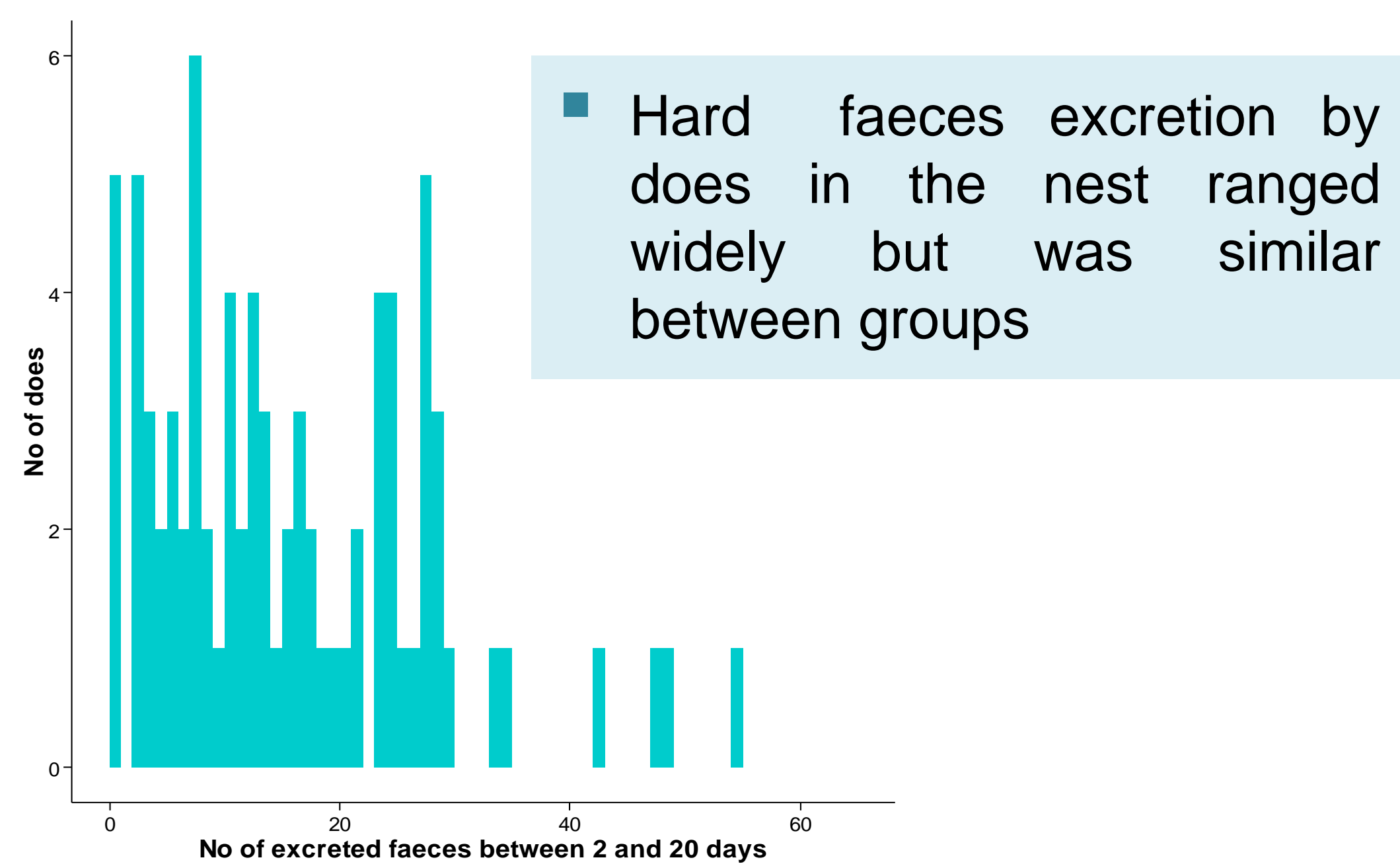


Table 1. Hard faeces excretion of does in the nest, faeces ingestion and mortality of pups

	NF	FF	FM	P value
No of faeces excreted by does (2 - 20d)	15.4	18.8	11.8	0.20
No of faeces ingested by pups (2 - 20d)	-	35.6	9.9	<0.001
Mortality % (1 – 80d)	22.8	9.3	15.5	0.03

- Ingestion of faeces by pups was 3 times greater in FF than in FM group, and could be thus modulated
- Pup mortality was lower (9.3%) in FF group and higher (22.8%) in NF group compared to FM group (15.5 %)

■ At age 14 d the caecal bacterial community was dominated by Bacteroidaceae family (63%). At 80 d Lachnospiraceae and Ruminococcaceae families became the dominant taxa (44% and 37%, resp.)

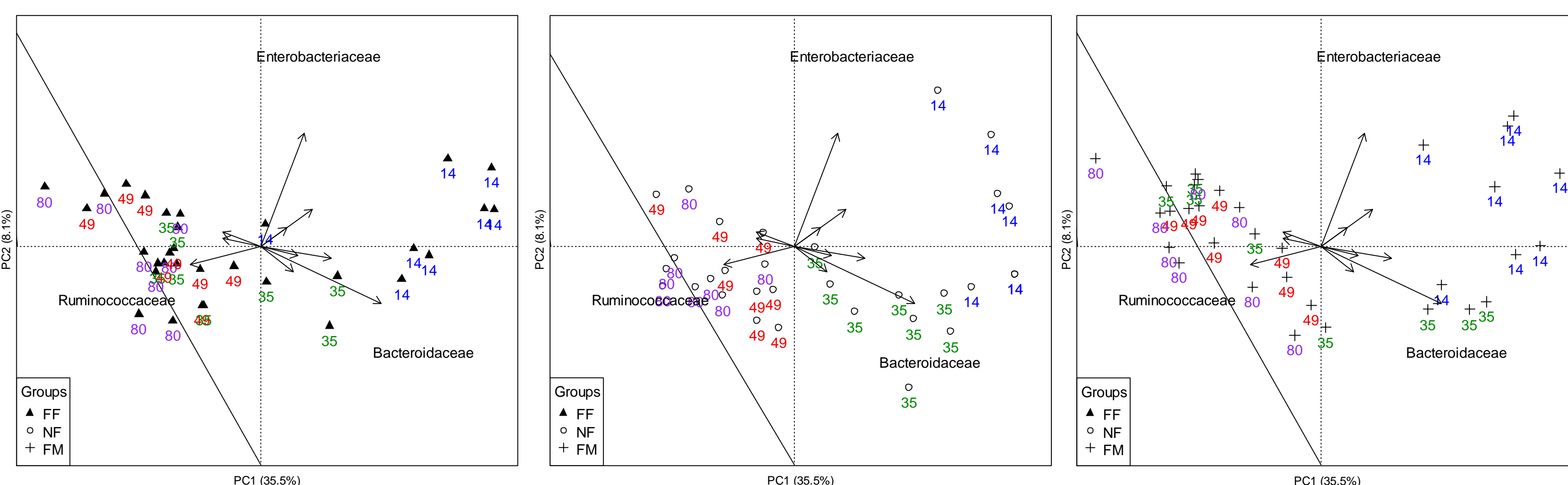
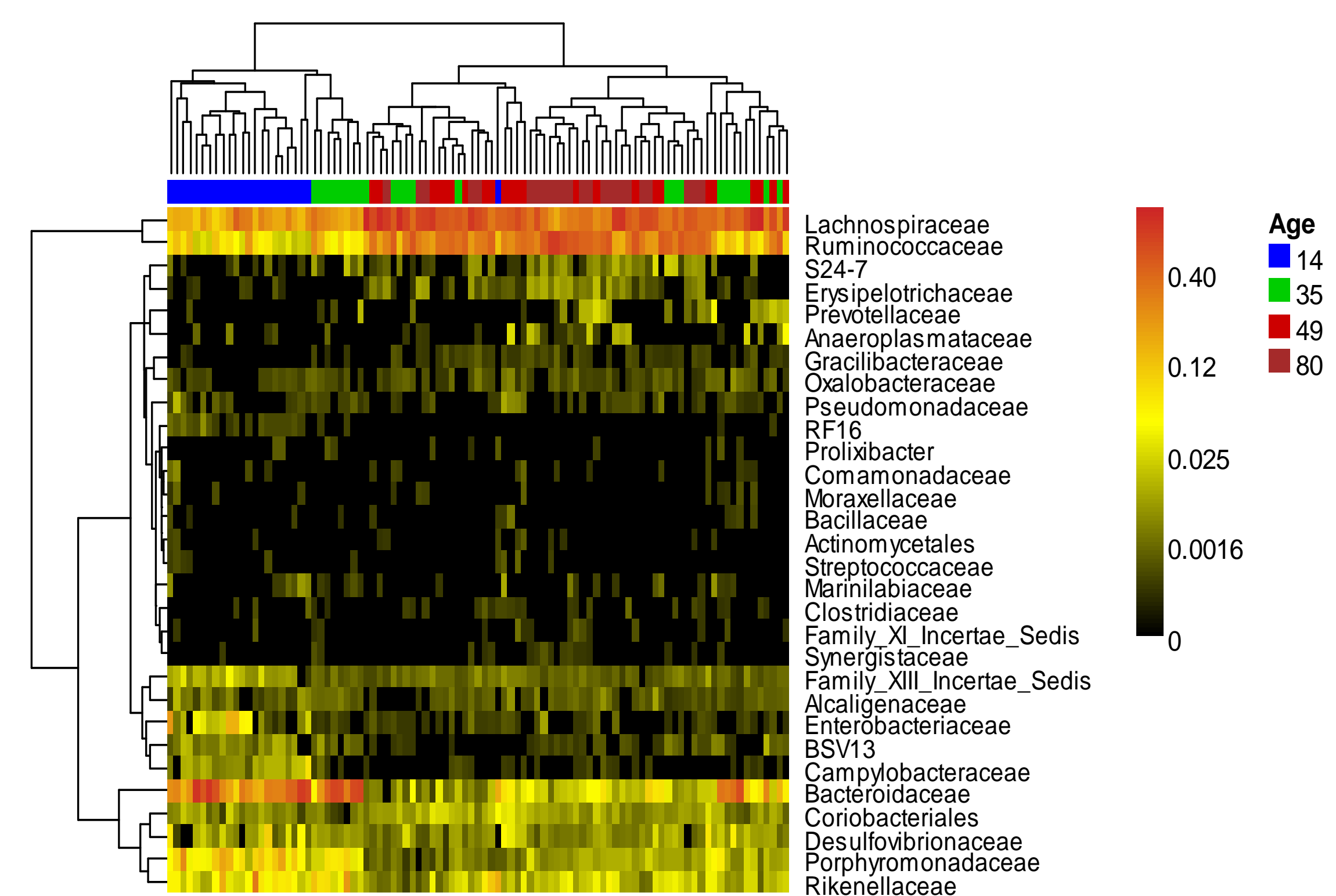


Figure 1. Principal component analysis of bacterial community taxonomic profile at the family level from 16S rDNA 454 pyrosequencing in caecal samples.



■ Impairment of faeces ingestion delayed the ecological succession, with greater and lower relative abundance of Bacteroidaceae and Ruminococcaceae respectively in NF than in the two other groups at age 35 d ($p < 0.05$).

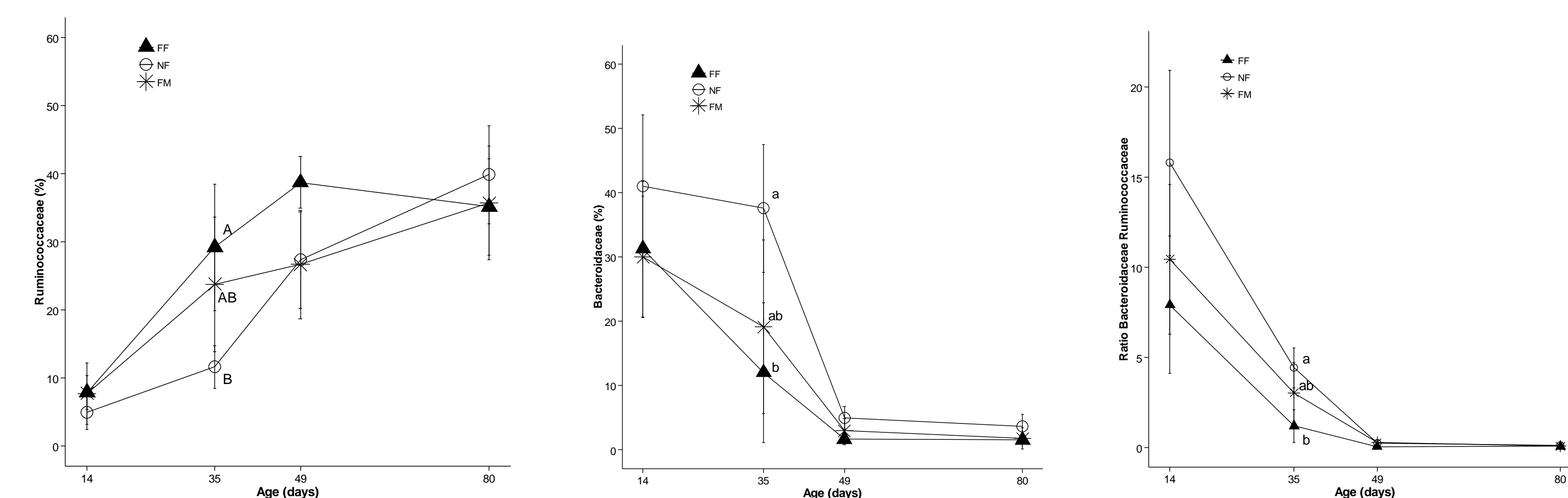


Figure 2. Relative abundance of Ruminococcaceae (A), Bacteroidaceae (B) and Bacteroidaceae / Ruminococcaceae ratio (C) in bacterial caecal community of rabbits from FF, NF and FM groups at 14, 35, 49 and 80 d of age.

The coprophagous behavior of suckling rabbits is implicated in the maturation of caecal bacterial microbiota. Stimulation of this natural behavior improved the health status of animals and could be used to limit the use of antibiotics