

EFFECT OF DIETARY FIBER CONTENT ON NUTRIENT DIGESTIBILITY AND FECAL MICROBIOTA COMPOSITION IN GROWING PIGS

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Introduction

Gut microbial population acts in complement with its host on nutrient digestion and health of the gastrointestinal tract. Changes in microbiota composition may have consequences in nutrient digestibility.

The present study aimed at determining the **effects of dietary fiber content** on gut microbiota composition and nutrient digestibility in growing pigs.

Material and methods

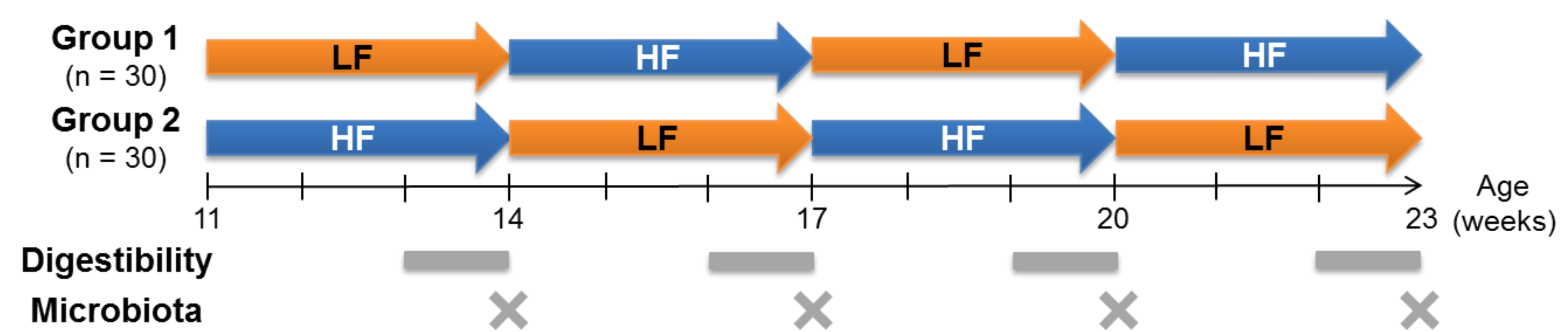


Figure 1: Experimental design of the study

Experimental design and animals

- Large-White, Duroc and Pietrain growing-finishing pigs (n=10 per breed and per group)
- A low-fiber (LF) and a high-fiber (HF) diet during 4 successive 3-week periods

Measurements

- During one week: feed intake and total collection of feces to evaluate the digestibility
- Feces collection for microbiota analyses: one spot sample at the end of the collection period (16S rRNA gene sequencing → Operational Taxonomic Units (OTUs))

Table 1: Diet composition (%)

| | LF diet | HF diet |
|---------------------------------------|---------|---------|
| Cereals ¹ | 70.12 | 53.31 |
| Soybean meal | 15.74 | 9.18 |
| High fiber raw materials ² | 2.50 | 31.97 |
| Crude fiber | 2.8 | 7.7 |
| Neutral Detergent Fiber | 10.0 | 20.0 |
| Digestible Lysine / Net energy (g/MJ) | 0.86 | 0.86 |

¹ corn + barley + wheat

² Wheat bran + rapeseed meal + soybean hulls + sugar beet pulp

Results

Figure 2: sPLS-DA allows discriminating pigs fed high- and low-fiber diets with 31 OTUs

1,641 OTUs over 2,041 were differentially abundant between LF and HF diets using a glm model.

Fecal microbiota of pigs fed 2 diets different in their fiber content have been discriminated using Spare Partial Least Square Discriminant Analysis. The misclassification error-rate was 3.9% using 31 OTUs. These 31 OTUs can be used as fiber diet biomarkers.

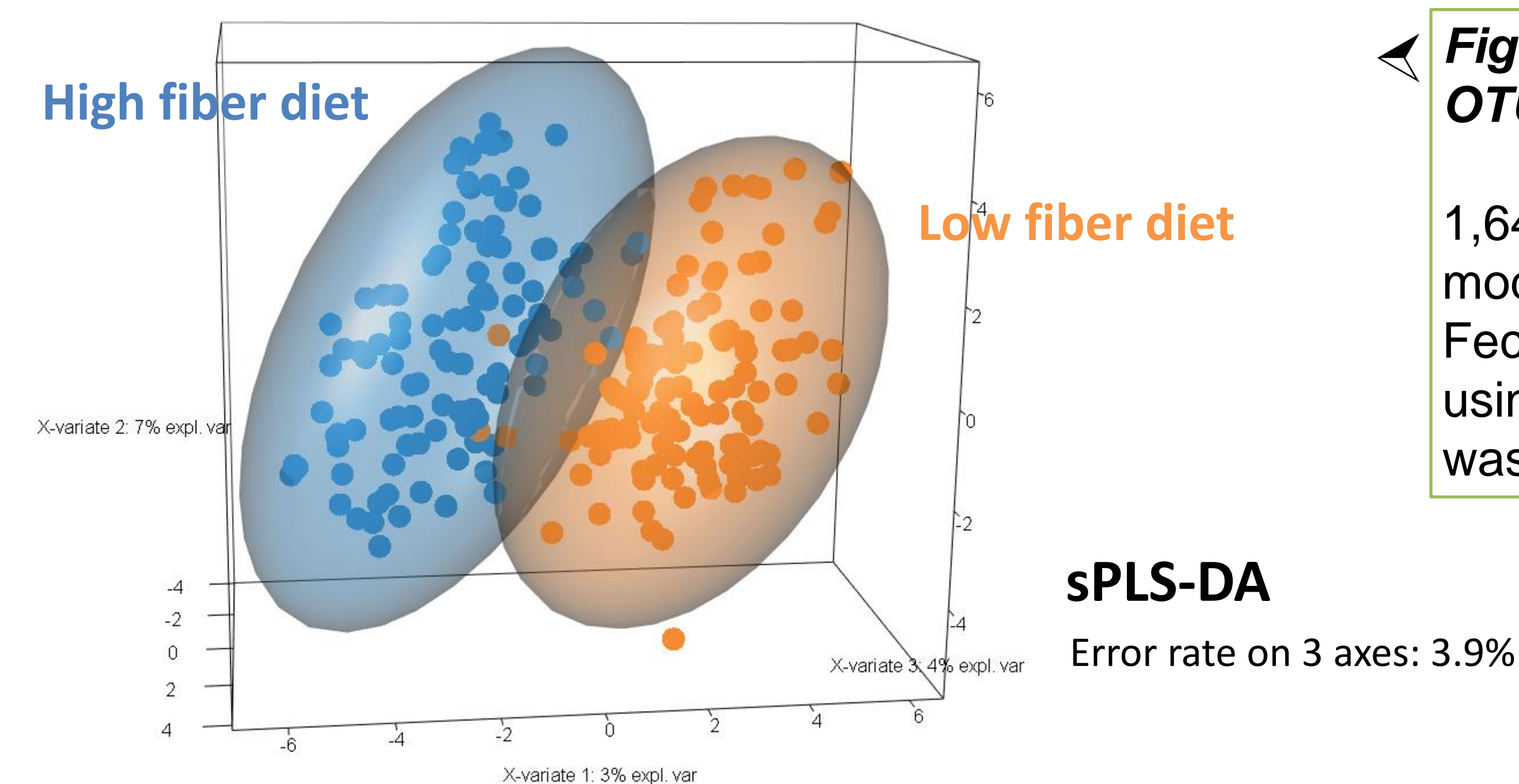
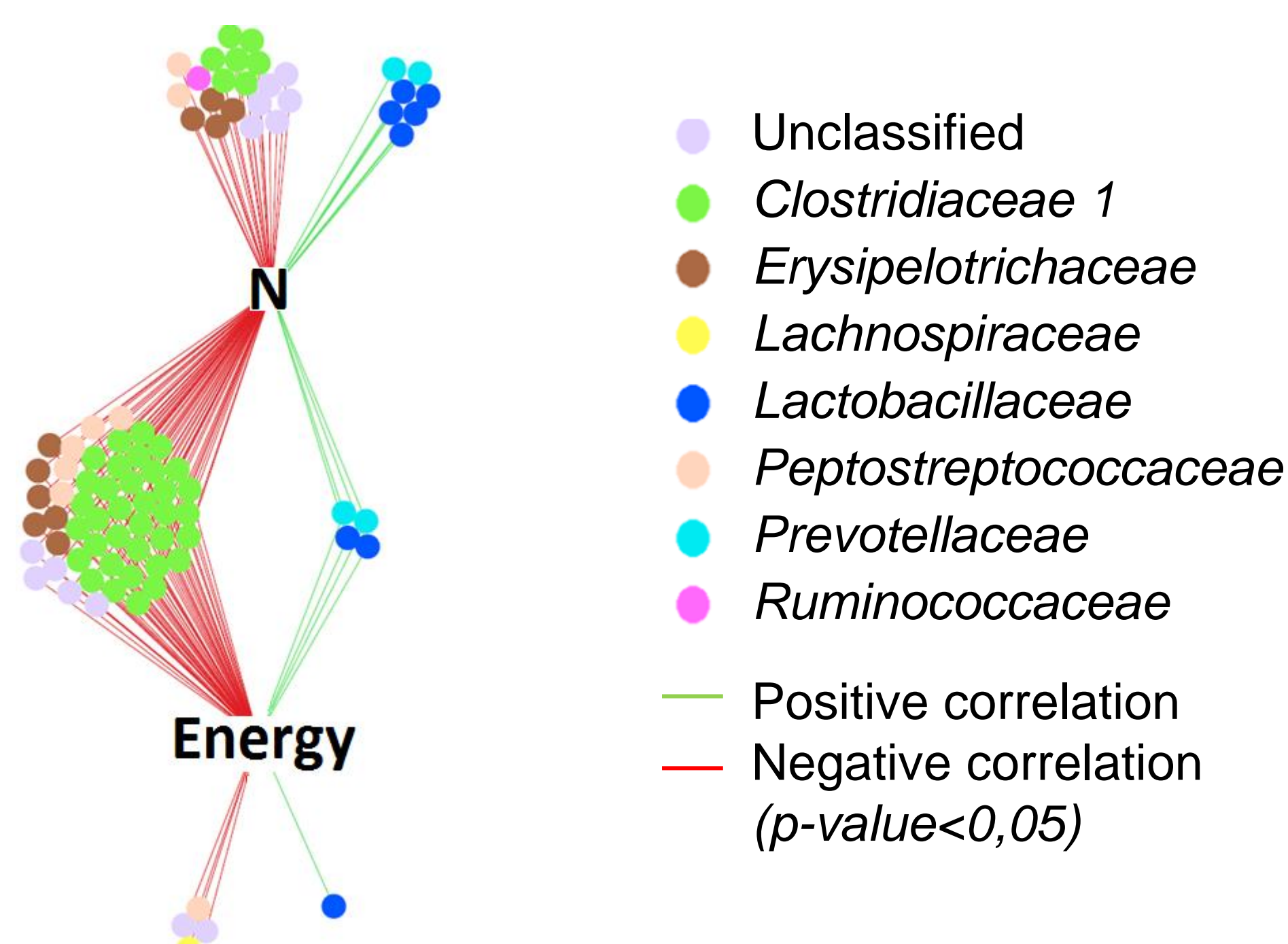


Figure 3: diet bacterial biomarkers are resilient after diet transition (example on 6 OTUs)

The 31 biomarkers of the diet were resilient after each diet transition. These biomarkers belong to *Clostridiaceae*, *Spirochaetaceae*, *Prevotellaceae* and *Peptostreptococcaceae* families.



Mean abundance per sample (%)

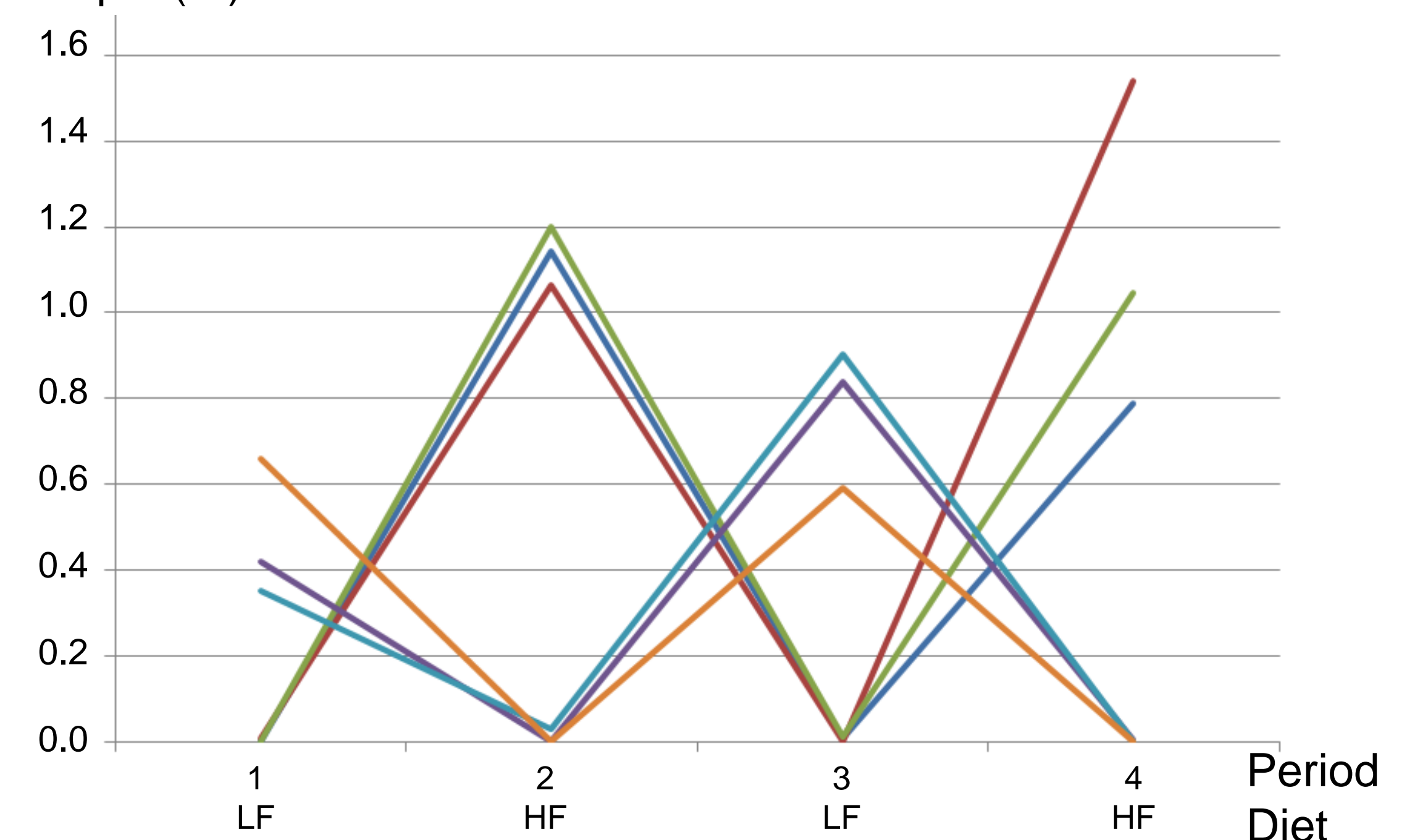


Figure 4: OTUs are correlated with digestibility coefficients of hemicellulose, cellulose, N and energy in LF diet

Pearson correlations associated OTUs belonging to *Lactobacillus* with N and energy digestibility coefficients in a positive correlation. On the contrary, OTUs belonging to *Turicibacter*, *Clostridium sensu stricto* and *Clostridium XI* were negatively correlated with N and energy digestibility. Some OTUs from *Prevotella* and several *Lachnospiraceae* were negatively correlated with the digestibility of cell wall components.

Conclusions

- Fecal microbiota can be used to discriminate pigs according to their diet.
- 3 weeks of adaptation to a new diet seem to be sufficient to observe partial resilience in growing pigs fecal microbiota.
- Bacteria belonging to several bacterial genera and families were correlated with digestibility coefficients.

➔ This study suggests that manipulation of bacterial populations can improve digestibility and feed efficiency.

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