# Xylanase improves performance and alters the microbiome of lactating sows fed low or high fiber diets

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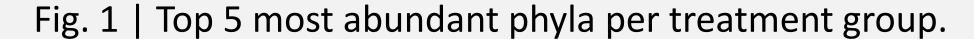
### Introduction

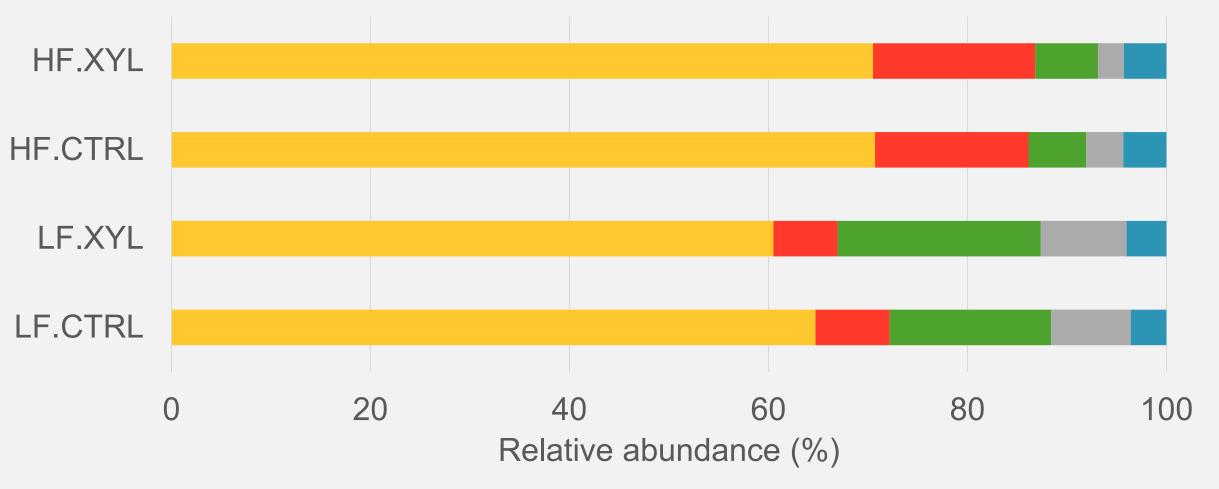
## Material & Methods

High fibre diets for lactating sows can reduce costs and increase gut fill and satiety, but also reduce nutrient digestibility and performance. The present study aimed to assess the impact of a new xylanase from *Thermopolyspora flexuosa*, expressed in *Pichia pastoris*, on the performance and fecal microbiome of lactating sows. At transfer to farrowing crates, 48 sows were assigned to four groups in a 2x2 design: a low fibre control diet (LF), a LF supplemented with 45,000 U/kg xylanase, a high fibre control diet (HF), and a HF supplemented with 45,000 U/kg xylanase. Diets were commercially relevant and fed *ad libitum*. BW was recorded at transfer, d0, d14, d28 of lactation. P2 backfat thickness was recorded at transfer, d14, and d28. Fecal samples were collected from all sows at d14 and sent for 16S rRNA sequencing.

#### **Results** | Microbiome

The biggest determining factor of the fecal microbial composition is dietary fibre level (Fig. 1). Sows receiving HF diets showed numerically more of the *Bacteroidetes*, and *Firmicutes* phyla compared to sows receiving LF diets. Compared to LF diets, HF increased the relative abundance of *Prevotellaceae* and *Rikenellaceae* (*g: Allistipes*) significantly. *Prevotellaceae* are potent dietary fibre degraders and are a so-called keystone taxon, having profound influence on community structure and function of the gut microbiota. *Rikenellaceae* have the rather unique ability to breakdown cellulose. This might explain the significant increase in relative abundance in the *Lachnospiraceae* family (g: *Roseburia*): cross-feeding can feed and stimulate butyrate-producing genera such as *Roseburia* (Fig. 2A).



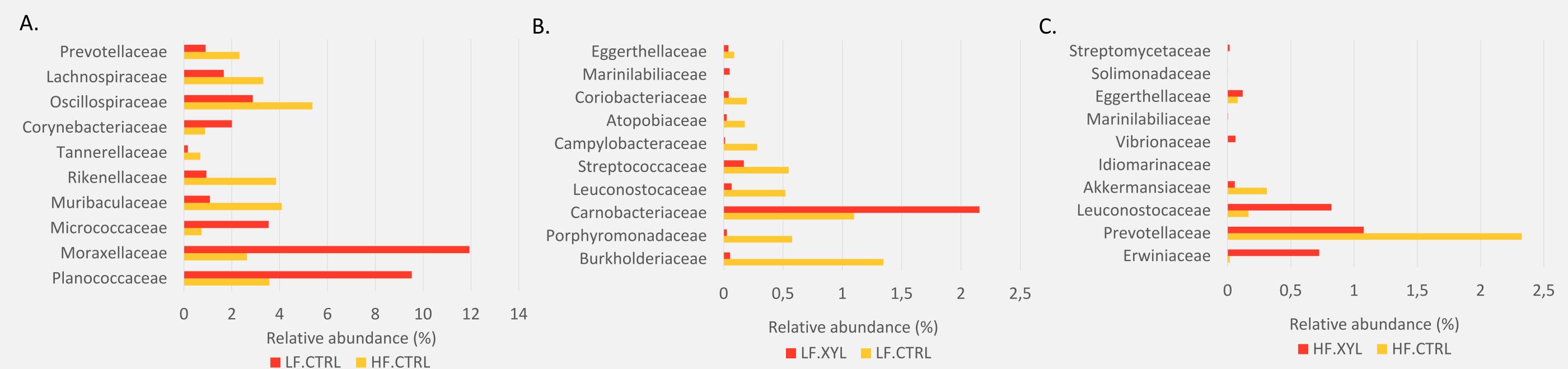


Firmicutes Bacteroidetes Proteobacteria Actinobacteria Other

Xylanase addition to the diet reduces *Prevotellaceae* counts, possibly by degrading the preferred substrate of this family, generating different breakdown products (Fig. 2C).

Fig. 2 | Top 10 differential families (p<0.05)

HF: high fibre, LF: low fibre, CTRL: control, XYL: Xylanase



(A) Low fibre control diet versus High fibre control diet, (B) Low fibre control diet versus Low fibre diet supplemented with Xylanse, and (C) High fibre control diet versus High fibre diet supplemented with Xylanase.

**Results | Performance** 

Across the study, HF and xylanase-supplemented sows consumed significantly more feed (P=0.003 and P=0.002, respectively). The percentage of weight loss was significantly higher in control sows (P=0.002) and tended to be higher in the LF than in the HF group (P=0.056). Xylanase supplemented sows lost less backfat during lactation compared to control sows (P=0.030).

## Conclusions

- Dietary fibre content was the main driver of compositional changes of the fecal microbiome.
- Addition of xylanase resulted in the relative decrease of fibre-consuming *Prevotellaceae*. Increased feed intake
  is known to be associated with *Prevotella* abundance. Addition of xylanase probably reduced the numbers
  of *Prevotellaceae* by degrading the preferred substrate of members of this family.
- Xylanase was expected to increase the energy harvest, and this was confirmed with lower weight and backfat loss
  in xylanse supplemented sows.

Performance data were analyzed as 2x2 factorial in the Fit Model platform of JMP 15; means separation was conducted using Tukey's HSD (P<0.05). Microbiome data was analyzed using Kruskal Wallis pairwise comparison (P<0.05).

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