

Galactoglucomannan fibres promote a beneficial porcine gut microbiome

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1 MOTIVATION

Most mammals and their microbiomes are codependent, forming a functional unit known as a **holobiont**. Exchanging metabolites, regulating gene expression, and combating pathogens are vital to the **health** and **performance** of the holobiont. By understanding the interactions occurring within this system, we can more effectively improve **animal** and **feed production**, favouring both animal welfare, production efficiency, and the needs of the World's **growing human population**.

Mannan fibres made from spruce can be broken down into **host-accessible compounds** by microbes with carbohydrate-active **enzymes**. These microbes also ease piglets' **transition** from milk to **solid feed**. Can we thus **jump-start the porcine microbiome by mannan fibre supplementation?**

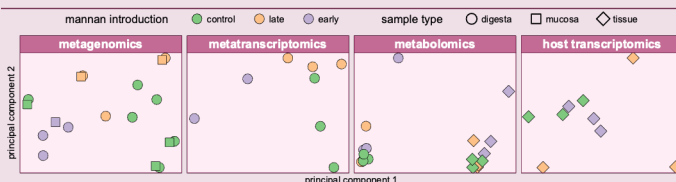
2 THE TRIAL

We used **three groups** of 10-day old piglets and gave fibres - in addition to the basal feed - to two groups; starting either **before** or **after weaning**.

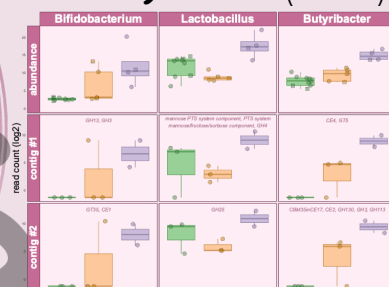


After one month, we sampled their caeca and generated **four omic data layers**: metagenomics, meta-transcriptomics, metabolomics, and host transcriptomics. The resulting data were analysed both as **individual omics** layers and jointly through a **holo-omic** approach.

3 SELECTIVE PROMOTION



Individual principal component analyses show **gradients** corresponding to **mannan exposure** duration. Among the populations of different abundance in control- and mannan-supplemented piglets, we find ***Bifidobacterium longum*** (LFC 8.3), ***Lactobacillus johnsonii*** (LFC 5.9), and ***Butyribacter*** (LFC 5.7).

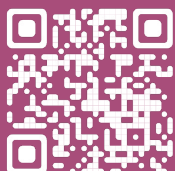


Many of their differentially expressed genes yield enzymes involved in mannan degradation: **glycoside hydrolases** and **transferases** and **carbohydrate esterases**.

4 HOLO-OMICS TITLE

Holo-omic model, shared and private dimensions through MCFAs...

REFERENCES 1 ... 2 ... 3 ... 4 ... 5 ... 6 ...



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