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 [1-2]. By understanding the **interactions** occurring within these complex systems, we can more effectively improve **animal** and **feed production**, favouring both animal welfare, production efficiency, and the growing needs of the World's increasing **human population** [3-4].

Mannan fibres made from spruce can be metabolised into **host-accessible compounds** by microbes with carbohydrate-active **enzymes** [5-6]. These microbes also ease piglets' transition from milk to **solid feed** [7]. Hence we ask: can we **jump-start the young porcine microbiome by adding mannan to their pre-weaning diet?** spoiler!

2 THE TRIAL

We used **three groups** of 10-day old piglets and gave fibres to two groups: one starting **before** and one **after weaning**.

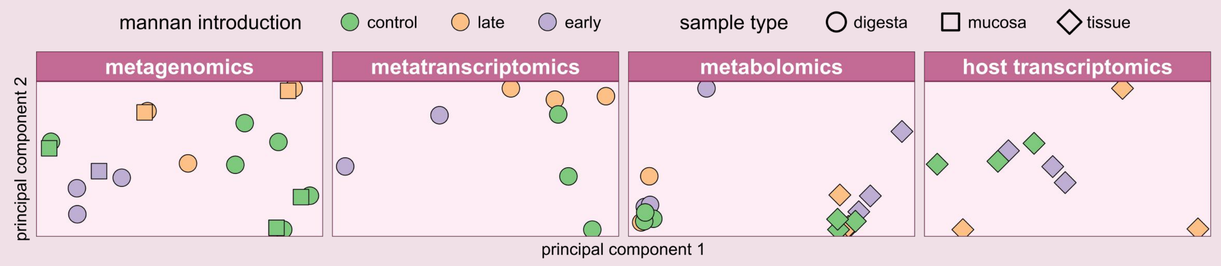
6 x control
no mannan

3 x late
two weeks with mannan

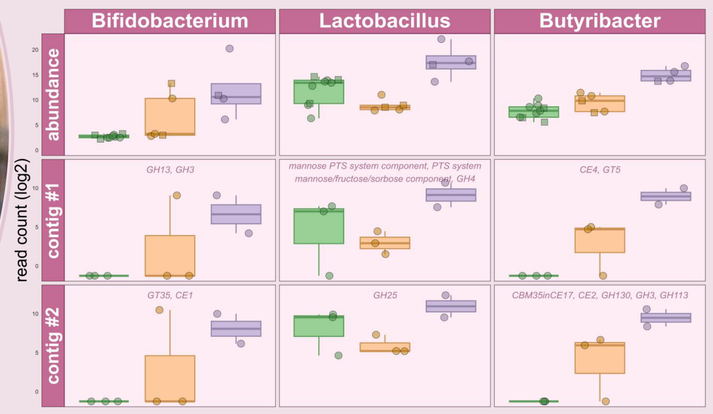
3 x early
two weeks with mannan

After one month, we sampled their caeca and generated **four omic data layers**: metagenomics, metatranscriptomics, metabolomics, and host transcriptomics. The datasets were analysed both as **individual omic** layers, and jointly through a **holo-omic** approach. Utilised methods were R-implemented tools for principal component [8] and differantial abundance [9] analyses, and a Python-based package for holo-omic modelling through multiset correlation and factor analysis (MCFA) [10].

3 SELECTIVE PROMOTION



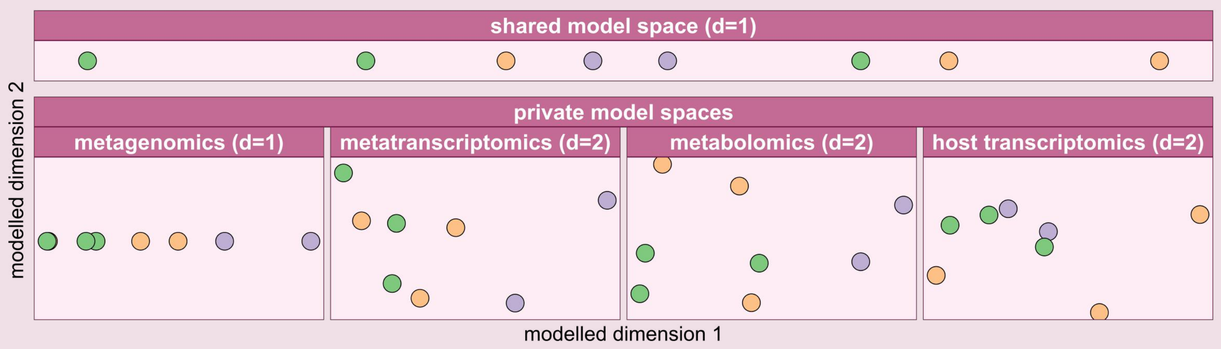
Individual principal component analyses show **gradients** that correspond with duration of **mannan exposure**. Among the differentially abundant populations in control and mannan-fed piglets are **Bifidobacterium** *longum* (log_2 fold change 8.3), **Lactobacillus** *johnsonii* (LFC 5.9), and **Butyribacter** *sp.* (LFC 5.7). Many of their differentially expressed genes yield enzymes for mannan **degradation**, like glycoside **hydrolases** and **transferases**, and carbohydrate **esterases**.



Thus **yes, we can** jump-start their microbiome!

4 HOLO-OMIC MODEL

The fitted MCFA model reconstructs the full dataset as **matrices** across **three feature spaces**: one **shared** by all omic layers; one **private** to each dataset; and an omic-specific **residual**. The inferred features fit well with mannan exposure, hence the model will be used to learn more about the **interactions** across the porcine **holo-omic boundary**.



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