Galactoglucomannan fibres promote a beneficial porcine gut microbiome

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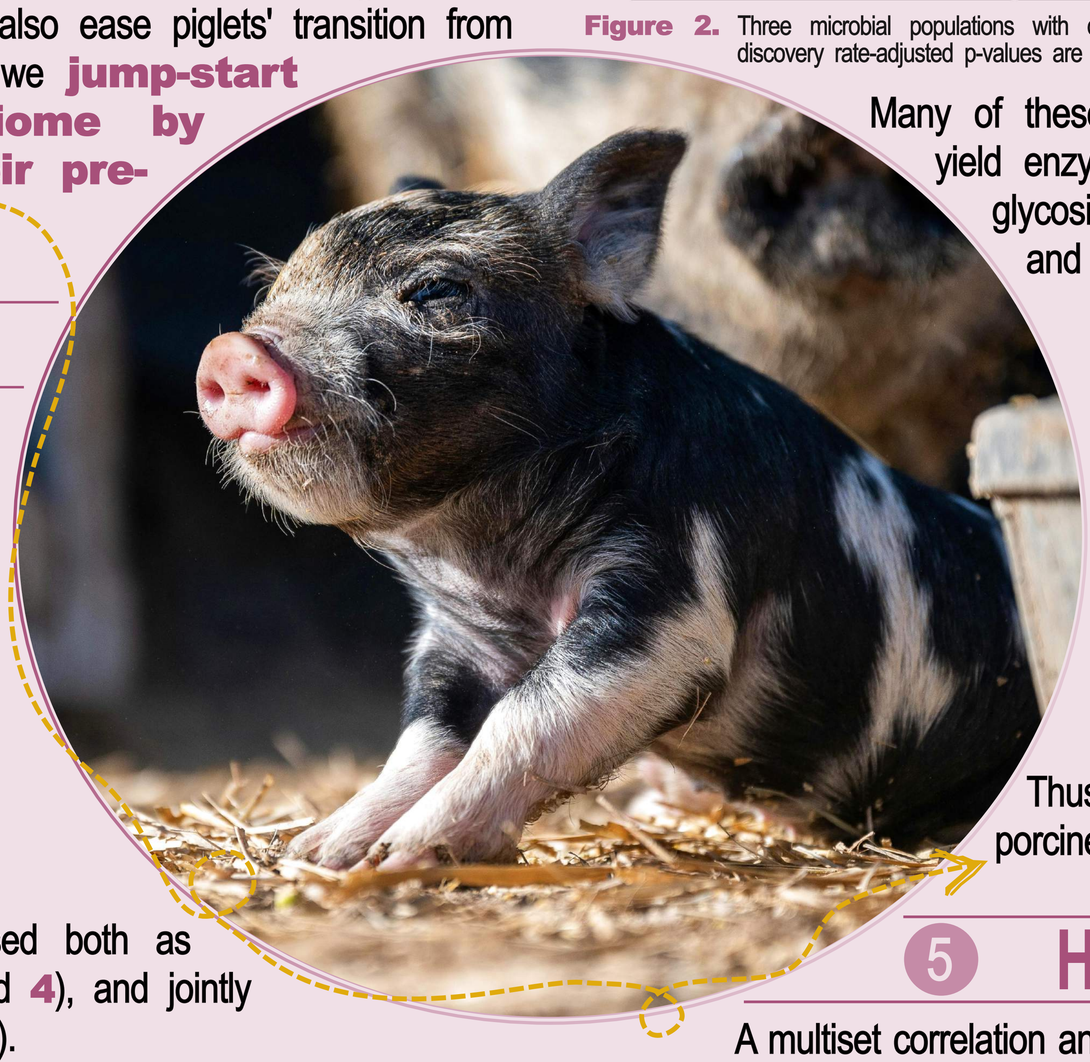
1 MOTIVATION

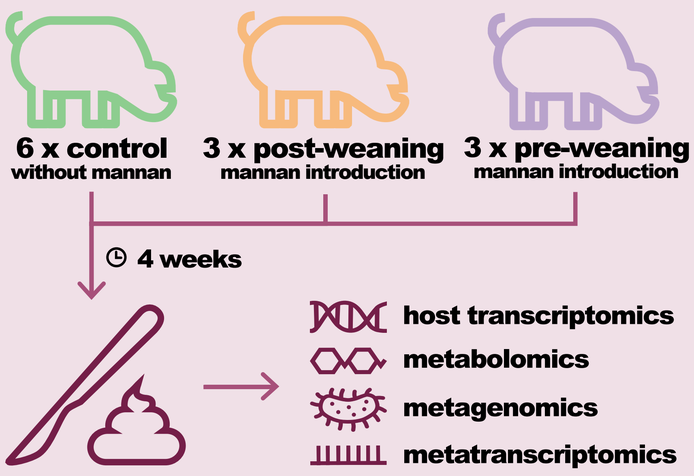
Most mammals and their microbiomes are codependent, forming a functional unit known as a **holobiont**. Exchanging metabolites, regulating gene expression, and combating pathogens are vital to the **health** and **performance** of the holobiont [1-2]. By understanding the **interactions** occurring within these complex systems, we can more effectively improve **animal** and **feed production**, favouring both animal welfare, production efficiency, and the growing needs of the increasing **human population** [3-4].

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

spoiler!



2 THE TRIAL



The four generated datasets were analysed both as **individual omic** layers (**Sec. 3** and **4**), and jointly through a **holo-omic** approach (**Sec. 5**).

3 MICROBIAL GRADIENTS

Principal component (PC) analyses [8] of **individual omic** layers in **Fig. 1** show **gradients** that correspond with **mannan exposure** duration.

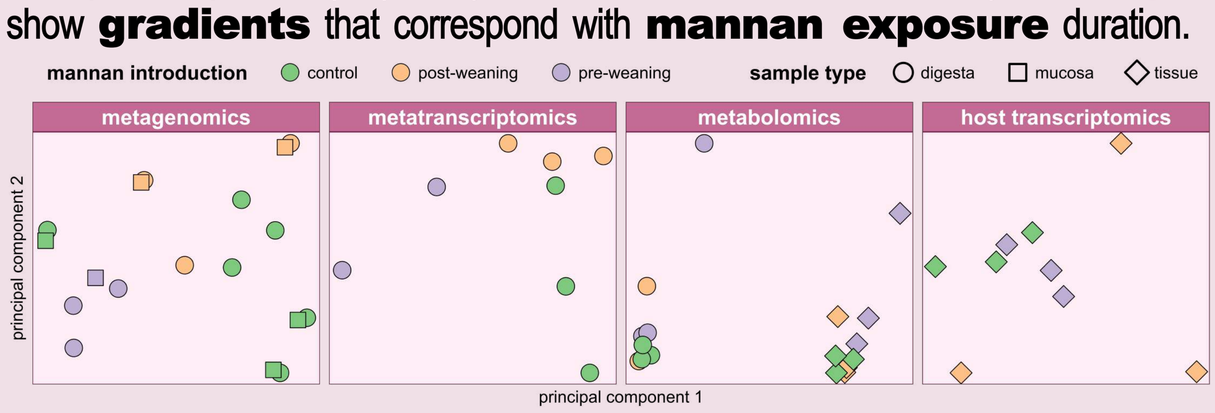


Figure 1. Principal component analyses of each omic layer. Points represent samples from piglets introduced to dietary mannan fibres at different developmental stages. Relative placements indicate similarities between samples' omic profiles.

4 SELECTIVE PROMOTION

Among the **differentially abundant** [9] populations between control and mannan-fed piglets are bacteria often associated with **host health** benefits: *Bifidobacterium longum* (log_2 fold change 8.3), *Lactobacillus johnsonii* (LFC 5.9), and *Butyribacter sp.* (LFC 5.7) (**Fig. 2**).

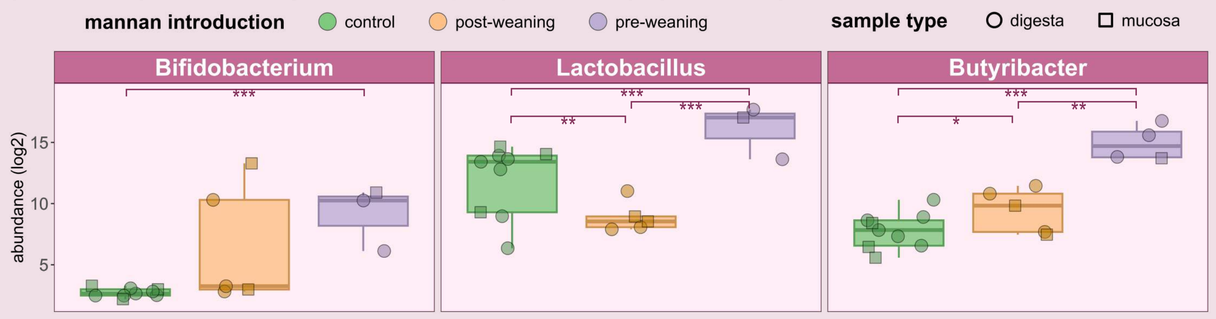


Figure 2. Three microbial populations with differential abundance between piglet groups. Significance by false discovery rate-adjusted p-values are indicated by asterisks: * < 0.05, ** < 0.01, *** < 0.001.

Many of these populations' differentially expressed genes yield enzymes for **mannan degradation**, like glycoside **hydrolases** and **transferases**, and carbohydrate **esterases** (**Fig. 3**).

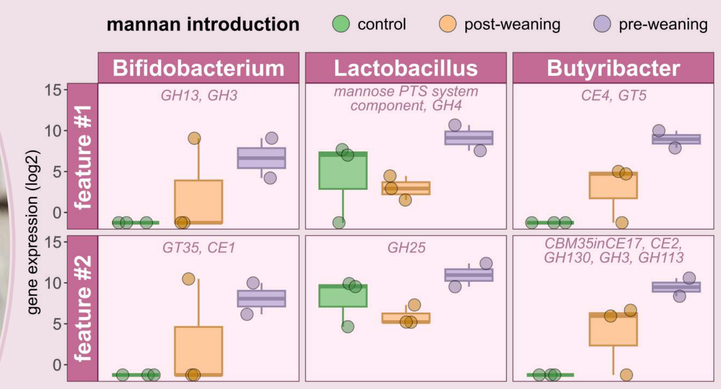


Figure 3. Differentially expressed features in the microbial populations of interest containing genes for mannan degradation.

Thus it seems **yes, we can** jump-start the porcine microbiome by mannan supplementation.

5 HOLO-OMIC MODEL

A multiset correlation and factor analysis (MCFA) [10] model reconstructs the full dataset in three **feature spaces**: one **shared** by all omic layers; one private to each layer; and an omic-specific residual. Inferred shared components are similar to PCs, but comprises features from all omic layers. The model (**Fig. 4**) fits well with mannan exposure, hence it will be used to learn more about the **interactions** across the porcine **holo-omic boundary**.

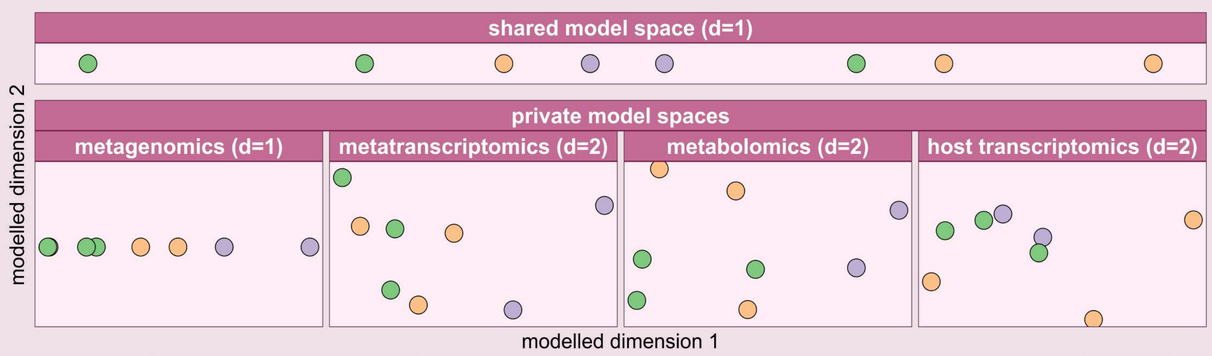


Figure 4. Samples represented by MCFA components in two model spaces. The shared space contains features from all layers. Aspects private to each omic layer add to this shared space, together recontructing the full holo-omic dataset.

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