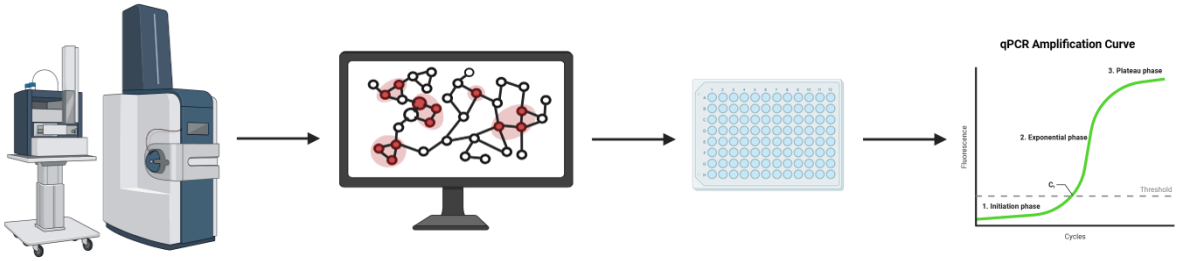
Defining host glycan-microbiome interactions through integrated multi-omics

Background

Host-derived glycans influence gut microbial colonisation, but current evidence linking specific glycan structures to distinct microbial taxa remains largely correlative. While integrated multi-omic profiling can identify potential associations between mucosal glycan motifs and specific bacterial groups, these networks require experimental validation. This project aims to **move beyond prediction to directly validate these host-microbe associations** by **a)** establishing robust correlation networks between specific glycans and the microbiome, and **b)** optimising a SYBR Green-based assay to functionally validate these predicted interactions.

Methodology & Workflow



Multi-Omic profiling
Generating glycomics and proteomics datasets using LC-MS/MS and microbiome datasets using 16S rRNA sequencing

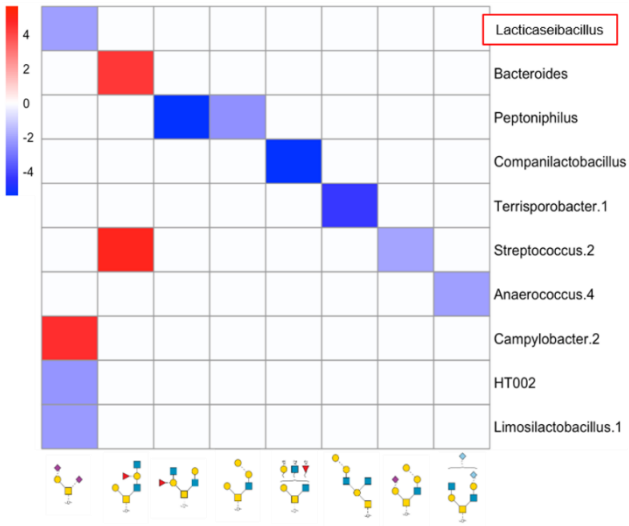
Correlation network mapping
Building correlation networks to identify predictive associations between specific glycans and microbial taxa

Adhesion assay
Immobilising glycan substrates to microplates and washing over bacteria

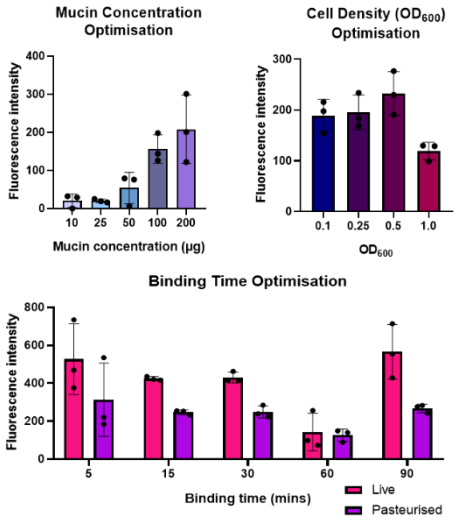
Bacteria quantification
Using either qPCR or fluorescence intensity to quantify bacterial adhesion

Preliminary results

a) Genus ~ O-glycan associations ($\rho > 0.8$, FDR < 0.05)



b) Binding Assay Optimisation using *Lacticaseibacillus rhamnosus*



a) Spearman correlation ($\rho > 0.8, \text{FDR} < 0.05$) mapped distinct bacterial genera against specific mucosal O-glycan motifs.

b) Binding assay validation: *Lacticaseibacillus rhamnosus* demonstrates robust concentration-, cell density-, and time-dependent binding to mucin. Reduced adhesion in pasteurised controls confirms dependence on active, live-cell surface structures.

Conclusions & Next Steps: We have successfully optimised a microplate-based bacterial binding assay framework to validate predicted glycan-microbiome correlation networks. Next steps include multiplexing targeted qPCR assays to investigate structure-specific microbial binding and initiating competitive co-culture experiments.