

Title: Microbiome and virome analysis in early life

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A wide variety of microorganisms, including bifidobacteria, are known to colonise the human gastrointestinal tract. Bifidobacteria are beneficial bacteria known to be particularly prevalent and abundant in the gut of healthy and breast-fed infants. Together with bacteria also bacteriophages can be vertically transmitted from mother to newborn during vaginal delivery and they are believed to play a role in influencing bacterial levels and microbiota composition in early in life. While there is a significant amount of information on early bacterial colonisers in the infant gut, there is currently very limited knowledge of diversity and prevalence of gut bacteriophages and their impact on the early microbiota composition. The work here presented gives an overview of current methods suitable for the study of metagenomes and viromes in infant fecal samples. By evaluating a range of bioinformatic tools a new analysis pipeline was developed for future application in the analysis and characterisation of phage diversity and host interaction in the early gut microbiota.