Diversity of the Bifidobacterial Phageome in the Infant Gut

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Extended Abstract

Members of Bifidobacterium play an important role in the development of the immature gut and are associated with positive long-term health outcomes for the host. It has previously been shown that intestinal bacteriophages are detected within hours of birth, and that induced prophages constitute a significant source of such intestinal phages. The gut phageome can be vertically transmitted from mother to newborn and is believed to exert considerable selective pressure on target prokaryotic hosts affecting abundance levels, microbiota composition, and host characteristics.

The objective of the current study was to investigate prophage-like elements and the CRISPR-Cas viral immune system of publicly available, human-associated Bifidobacterium genomes. Analysis of 585 fully sequenced bifidobacterial genomes identified 480 prophage-like elements with an occurrence of 0.82 prophages per genome. Interestingly, we also detected the presence of corresponding bifidobacterial prophages and CRISPR spacers across different strains, and species, thus providing an initial characterisation of the human-associated bifidobacterial phageome in early life. Our analyses show that closely related and likely functional prophages are commonly present across four species of human-associated Bifidobacterium.

Further comparative analysis of the CRISPR-Cas spacer arrays against the predicted prophages provided evidence of historical interactions between prophages and different strains at an intra- and inter-species level. Notably, a spacer representing a putative major capsid head protein was found on different genomes representing multiple strains across B. adolescentis, B. breve, and B. bifidum, suggesting that this gene may be a preferred target for bifidobacterial phage immunity. Overall, our analysis showed clear evidence of CRISPR-Cas acquired immunity to bifidobacterial prophages across several bifidobacterial strains and species.

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