

GUT MICROBIOTA

Growing up together — gut microbiota assembly and IgA

New research has characterized the assembly of the gut microbiota in humans over the first 2 years of life, as well as the associated changing gut mucosal IgA responses.

Development and maturation of the human gut microbiota is a complex process that begins at birth and continues over the next few years. Despite the known importance of mucosal IgA in regulating gut barrier function, little is known about how gut mucosal IgA responses evolve during early life. “We designed the current study to determine how IgA responses to the microbiota normally develop in healthy infants and children, as well as how they are impacted by human genetics, environmental factors, and diet history,” explains author Jeffrey Gordon.

Using a cohort of 40 healthy twin pairs, the investigators characterized the bacterial composition of 1,670 faecal

samples taken monthly throughout the first 2–3 years of life by 16S ribosomal RNA (rRNA) sequencing. They identified a series of bacterial taxa defining a programme of gut microbial community assembly; this programme was shared across twin pairs, and varied by family membership and whether the child was fed breast or formula milk.

Next, the researchers investigated how IgA responses co-developed with the gut microbiota. For each stool sample, fluorescence-activated cell sorting employing anti-IgA labelling was used to separate microbiota that had elicited an IgA response. This technique generated IgA⁺ and IgA⁻ gut microbiota fractions for each individual at

each time point; 16S rRNA sequencing was then used to determine composition and abundance of present bacterial species. This analysis identified specific microbiota members that were consistently targeted, or not targeted, by IgA responses. These mucosal IgA responses, although varying between twin pairs early in life, converged to a common pattern of targeting by the second postnatal year. Lastly, the researchers transplanted faecal samples obtained at 6 and 18 months of age from two twin pairs into germ-free mice. “We find that age-associated IgA responses observed in the human population are largely recapitulated in these mice,” explains first author Joseph Planer.

The authors next plan to assess how IgA responses to microbiota assembly vary depending on environmental influences. “Our group is performing these analyses now,” says Planer.

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ORIGINAL ARTICLE Planer, J. D. *et al.*
Development of the gut microbiota and mucosal IgA responses in twins and gnotobiotic mice.
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