Göteborg, 2020

Development and dynamics of the normal gut microbiota

Akademisk avhandling

Som för avläggande av medicine doktorsexamen vid Sahlgrenska akademin, Göteborgs universitet kommer att offentligen försvaras i Arvid Carlsson, Medicinaregatan 3, den 28 maj, klockan 13.00

av Lisa Olsson

Fakultetsopponent:
Docent Anne Salonen
Helsingfors universitet, Finland

Avhandlingen baseras på följande delarbeten

I. Josefine Roswall*, Lisa M Olsson*, Petia Kovatcheva-Datchary, Staffan Nilsson, Rozita Akrami, Valentina Tremaroli, Marie-Christine Simon, Manuela Krämer, Mathias Uhlén, Göran Bergstöm, Karsten Kristiansen, Jovanna Dahlgren, Fredrik Bäckhed. **Developmental trajectory of the healthy human gut microbiota during the first 5 years of life.** *Manuscript*
*contributed equally

II. Lisa M Olsson, Fredrik Boulund, Valentina Tremaroli, Staffan Nilsson, Anders Gummesson, Linn Fagerberg, Lars Engstrand, Mathias Uhlén, Göran Bergström, Fredrik Bäckhed. **Dynamics of the gut microbiota in a normal population: a prospective 1-year study.** *Manuscript*

III. Lisa M Olsson, Christine Poitou, Valentina Tremaroli, Muriel Coupaye, Judith Aron-Wisnewsky, Fredrik Bäckhed, Karine Clément, Robert Caesar. **Gut microbiota of obese subjects with Prader-Willi syndrome is linked to metabolic health.** *Gut (2019), doi:10.1136/gutjnl-2019-319322*

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Abstract

Altered gut microbiota configurations have been linked to human diseases. To identify mechanistic links between altered gut microbiota and disease states, definitions of the healthy gut microbiota need to be established. Therefore, in this thesis, we investigated how the gut microbiota develops in Swedish children up to 5 years of age, and characterized dynamics of the adult gut microbiota in a normal Swedish population. Using a longitudinal design to study the gut microbiota in both the Swedish children and adults, we identified complex sets of bacteria acquired by the children during their development and compared them to the gut microbiota of the adult population. We identified features of the gut microbiota that were associated to richness at different stages of a child's gut microbiota development.

In the adult Swedish population, we analyzed how the composition and functional potential of the gut microbiota fluctuate over the course of a year in normal population aged 50-64 years. We characterized the total variability of the gut microbiota and determined to which extent gut microbiota variability between individuals is due to intra-individual variability over time. We observed large fluctuations in abundance of facultative anaerobes and in potential bacterial functions, identified from metagenomic analysis, linked to these bacteria. Interestingly, large fluctuations of the facultative anaerobes were indicative of highly variable individual gut microbiota composition.

In the third study in this thesis, we investigated the gut microbiota in relation to obesity and insulin resistance. Here we characterized the gut microbiota in morbidly obese individuals with the genetic Prader-Will syndrome and in obese people matched for fat mass composition. Less insulin resistance and healthier blood lipid in the individuals with Prader-Willi were associated with a less heterogeneous gut microbiota composition as well as higher diversity, which are important ecological features of a stable and resilient microbial community. Importantly, these potentially beneficial microbes were also observed to link to community richness in the children and adult Swedish populations. In summary, we identified gut microbes that associate to community stability and community richness in children as well as adults, and that may play a key role for metabolic health.

Keywords: dynamics, ecology, gut microbiome, gut microbiota development, microbiota, richness, Prader-Willi Syndrome, stability, variation

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