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Fecal (meta) proteomics: A tool to investigate dysbiosis and inflammation in patients with cystic fibrosis

Bart Devreese
Ghent University, Belgium

Cystic fibrosis is a genetic disease caused by mutation of the cystic fibrosis transmembrane conductance regulator (CFTR) protein. The disease is mostly associated with severe lung pathogenesis typically caused by infection by *Pseudomonas aeruginosa*. However, many patients also suffer from intestinal complications. The primary cause is pancreas insufficiency resulting in decreased release of digestive enzymes which is typically cured by enzyme replacement therapy. However, sticky mucus formation and repetitive antibiotic treatment have a severe effect on the gut microbiota. Several microbial studies indeed reported gut microbiota dysbiosis in patients with cystic fibrosis (CF). However, the functional consequences of this phenomenon are poorly understood. We analyzed fecal protein extracts from 15 patients with CF that have pancreatic insufficiency and from their unaffected siblings by shotgun proteomics. Novel computational and statistical tools, among which, the novel Unipept tool, were introduced to evaluate changes in taxonomic composition and protein abundance. Fecal protein extracts from patients with CF were dominated by host proteins involved in inflammation and mucus formation. Taxonomic analysis of the microbial proteins confirmed the strong reduction of butyrate reducers such as *Faecalibacterium prausnitzii* and increase of *Enterobacteriaceae*, *Ruminococcus gnavus* and Clostridia species. Our work showed that fecal meta-proteomics provides insights in intestinal dysbiosis, inflammation in patients with CF and can be used to monitor different disease markers in parallel.

Biography

Bart Devreese has completed his PhD in 1997 at Ghent University. He continued Post-doctoral studies with a Fellowship of the FWO-Flanders. In 2002, he was appointed as Professor in General and Analytical Biochemistry. He was the first in Belgium to use mass spectrometry to study biomacromolecules and developed methods for nanoLCMS and CE-MS. His major research area is in proteomics of micro-organisms known to infect cystic fibrosis patients.

Bart.Devreese@UGent.be

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