

URLs

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PMMV

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genome&cmd=Retrieve&dopt=Overview&list_uids=16125



 MICROBIAL DIVERSITY

Gutsy results...

Although the human gastrointestinal tract is the natural habitat for a large microbial community, very little is known about the microfloral composition of this unique ecosystem. Two recent studies now shed new light on the enormous diversity of microbial life in the human stomach.

The first, published in *PloS Biology*, was a comparative metagenomic analysis of the RNA virus community in the human gut, analysed using faecal samples. A total of 36,769 sequences were obtained, with 25,779 virus-like sequences. Surprisingly, almost all of the virus-like sequences (97.1%) were homologous to plant viruses, many of which are pathogens of food crops. The most abundant virus was pepper mild mottle virus (PMMV), a common pathogen of members of the *Capsicum* genus. The faecal RNA virus community was shown to be dynamic and variable, changing both between individuals and in the same individual over time. Foodstuffs are thought to be the main source of these viruses, and it was shown that faecally borne PPMV remained infectious to host plants. The second study, published in *PNAS*, characterized the diversity of the bacterial microflora in the stomach using 16S rDNA clone libraries generated from gastric biopsy samples. Given the hostile environment of the stomach, the diversity of bacterial phylotypes detected was surprisingly high — 128 phylotypes were identified, across eight bacterial phyla. 10% of phylotypes were previously uncharacterized, and included the first *Deinococcus*-related sequence to be identified in humans. The described rDNA data set differs from that characterized from the mouth and oesophagus and suggests that, like the intestine, the human stomach might contain a distinct microbial ecosystem.

As well as demonstrating the power of the metagenomic approach for analysing ecosystem composition, both studies also provide yet more evidence of the remarkable ability of microbial life to survive and thrive in the most challenging of environments.

David O'Connell

ORIGINAL RESEARCH PAPERS Zhang, T. et al. RNA viral community in human feces: Prevalence of plant pathogenic viruses. *PLoS Biol.* 4, e3 (2006) | Bik, E. M. et al. Molecular analysis of the bacterial microbiota in the human stomach. *Proc. Natl Acad. Sci. USA* 103, 732–737 (2006)