

## van Overbeek

### Human pathogens in plant microbiomes

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Food-borne disease outbreaks resulting from consumption of plant-derived fresh produce have been reported world-wide such as from spinach in the USA, from mung bean sprouts in Japan and most recently also in Europe from fenugreek sprouts (Hamburg, 2011). It is clear that particular groups of human pathogenic micro-organisms (HPMO) can be found in plant microbiomes. Basic resources for agro-production, such as soil, water and fertilizers can play a role in contamination of plants. Contamination routes of HPMO to plants are poorly understood, and further it is not always easy to make a distinction between microbial contaminants (i.e. HPMO invading plants from other environments) and HPMO that are indigenously present in plant microbiomes. Because many taxonomic groups of HPMO are ecologically competent in plants, these groups must therefore be considered as integral components of the plant microbiome. Potential human pathogens typically associated with plants are species belonging to the genera of *Fusarium*, *Aspergillus*, *Pseudomonas*, *Serratia*, *Enterobacter*, *Bacillus*, *Burkholderia* and *Stenotrophomonas*. Recently we gained circumstantial evidence that even particular strains of *Escherichia coli* may be indigenous to plant microbiomes. Many microbial species supportive to plant growth are taxonomically related to potential human pathogenic groups. For biological control purposes it is relevant to make better distinction between potential pathogenic and plant-beneficial groups. It is the intention of the new EU COST Action HUPLANTcontrol (16110) to coordinate research on potential negative aspects of plant microbiomes on human health and to integrate novel scientific insight into sanitary measures and agricultural management practices.