

Analysis of bacterial communities in feces of selected groups of consumers with different diets using combined DGGE and quantitative Taqman- PCR

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The microbiome of the human GI tract has been shown to be rather stable and resilient to external influences, but certain differences in the distribution of populations have been reported in specific situations, such as antibiotic treatment or aging. Therefore, strategies to investigate consequences of environmental and nutritional effects on specific bacterial groups in individuals or small groups of consumers are desirable. We explore a strategy combining group specific DGGE analysis and quantitative Realtime PCR (RTQ-PCR) for the assessment of *Bacteroides* and *Bifidobacteria* in small groups of consumers at different ages adhering to different diets.

200 mg of faeces from groups of 20-30 geriatric patients and young volunteers following a vegetarian or typical middle European diet have been analyzed. PCR-DGGE, cloning and sequencing, as well as RTQ-PCR using universal, *Bifidobacteria*- and *Bacteroides*- specific 16S rDNA primers and corresponding 6-FAM labeled Taqman probes were used. Specificity of primers and probes was tested using FASTA and type strains.

Individual differences in the qualitative diversity of the analyzed groups can be seen. Whereas dominant bands seem to be very similar additional bands in individual samples can be observed frequently. The efficiency of the RTQ-PCR assay was 0,99 and no cross reaction of group specific primers and probes could be observed. Calculating the amount of bacterial groups as percentage of the bacterial total DNA (using universal primers), minimizes possible problems with extraction and inhibitors. Experiences of the combination of RTQ-PCR and DGGE analysis for the analysis of *Bacteroides* and *Bifidobacteria* in faeces will be discussed.

