Clinical Study of Microbial Markers by Mass Spectrometry Method

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ABSTRACT: Determination of semi-pathological bacteria is considered an important tool at disease diagnostics, selection of appropriate treatment methods and verification of the correct choice. Wide spread methods include biota sampling and bacterial incubation. The method is hardly quantitative and takes several days. No need to say that in some cases it is too slow to treat the disease timely.

This review presents a novel express method of quantitative and reliable measurement of wide variety of semi-pathogenic bacteria - Mass Spectral measurement of Microbial Markers (MSMM). The method allows simultaneous determination of more than one hundred microbial fatty acids *in situ* for clinical, biotechnological or environmental samples. The method is quantitative and express, since the measurements are made without prolonged incubation (precultivation) and without using of biochemical test-materials and primers.

The proposed MSMM method has been applied for clinical studies. Unprecedented information on the quantity of anaerobes and uncultivated aerobes, as well as actinobacteria, yeasts, viruses and microscopic fungi provides full understanding of microbial etiology, and such information may be obtained quick in critical cases in clinical practice. In one particular study of intestine dysbiosis, the tested mass spectral method has confirmed the hypothesis about the nosological specificity of changes in the intestinal microbiota. It has been proven that infectious processes are polymicrobial. Measurements have shown that anaerobes dominate by number and by functional activities at inflammations. The division of microbes into pathogenic and non-pathogenic is artificial – most of microbes in a human body exist in both forms simultaneously. Lactobacilli and bifidobacteria appear as agents of septic conditions and endocarditis. MSMM data confirm that anaerobes of *Clostridium*, *Eubacterium*, *Propionibacterium*, as well as actinobacteria of *Streptomyces*, *Nocardia*, *Rhodococcus* are infection dominants and usually act in groups. The data testify translocation of

these microbes in inflammation loci from the intestine. Relative markers concentration stay consistent between different biota samples, thus, any clinically convenient sample may be used for determining microbes within the inflamed organ or at any specific locus. Quantification using GC-MS reveals that the influence of antibiotics on the normal intestine's microbiota are not as dramatic as believed. Growth-promoting effects are the most important benefits of probiotic applications. The probiotic essence is not the microbial biomass itself, but growth factors, alarm molecules, and other factors of intestinal microbes. There are new possibilities in improving probiotics by using microbial "consortia"