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Joint Conference

GLOBAL APPLIED MICROBIOLOGY CONFERENCE

&

International Congress on

MICROBIAL & BIOCHEMICAL RESEARCH AND TECHNOLOGIES

October 18-19, 2017 Toronto, Canada

Large-scale molecular detection of microorganisms

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ith the advent of high-throughput molecular techniques in molecular microbiology (Next Generation Sequencing, NGS) it became possible to explore microbiomes of rather complicated niches, such as microbiome of the gut, genitourinary tract, skin, or environmental microbiomes. The NGS technology enables to decipher even the most complex biological samples and analyze the DNA contents thereof. We have developed a large-scale 16S rDNA (panbacterial) and 18S rDNA (panfungal) NGS approach, combined with quantitative Real-Time PCR, to identify the microbiome and fungome in their complexities, in a quantitative way. This technological approach allows us to assess the microbial flora of a given anatomic location in full extent, with direct relevance to the rational selection of antimicrobial agents, if relevant. This high-throughput approach also allowed us to identify novel microbial agents, previously not suspected

to infect humans – e.g. *Candidatus Neoehrlichia mikurensis* in two immunocompromised individuals, or several zoonotic *Chlamydia* and *Mycoplasma species* directly transmissible to humans. The presented data will cover a unifying concept of molecular microbiology, entailing both human and veterinary infections, as the overlap between both is greater than previously anticipated.

Speaker Biography

Sona Pekova has completed her graduation as MD from the Medical Faculty, Charles University in Hradec Kralove, Czech Republic. She continued her PhD studies at the Academy of Sciences of the Czech Republic in Prague and the 1st Medical Faculty, Charles University in Prague, Czech Republic. She has her PhD in Molecular Biology, Virology and Immunology. She has extensive expertise in molecular hematology, molecular hematooncology, molecular microbiology and molecular genetics, both in human and veterinary medicine, with tens of peer reviewed scientific papers documenting her medical and scientific history.

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