

7<sup>th</sup> International Conference and Expo on

# Metabolomics

November 14-16, 2016 Orlando, Florida, USA

## System proteometabolomic profiling of bacterial vesicles

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**B**acteroides represent a major constituent of the human gut microbiota. However pathogenic strain *Bacteroides fragilis* BOB25 stimulates human intestinal epithelial degeneration and cause necrosis associated with inflammation and colorectal neoplasia of colon epithelial cells. An important feature of *B. fragilis* is an intense release of outer membrane vesicles. These vesicles could be easily absorbed by the colon epithelium. We showed the vesicles include numerous biochemical compounds, including proteins and metabolites. Considering vesicles as delivery system, the question is: what components of the vesicles can affect the intestinal epithelium. To identify qualitative and quantitative biochemistry composition of the *B. fragilis* vesicles, we performed its proteomic and metabolomic analysis. Proteomic analysis of the vesicles was performed by mass spectrometer tripleTOF 5600 (ABSciex), combined with the HPLC system using IDA method. Metabolomic analysis of the BF vesicles was performed using HPLC-QQQ 8030 (Shimadzu) in the MRM analysis mode. We detected more than 200 different vesicles proteins representing membranaric, periplasmic and cytosolic fractions of *B. fragilis* cells. It is important that among the identified proteins, we identified a number of proteases, hydrolases and oxidoreductases and patatin that potentially cause significant changes in physiology of colon epithelium cells. Metabolome analysis allowed revealing differences in vesicles composition of non-toxigenic and toxigenic *B. fragilis* components of amino acids, nucleosides, nitrogen bases and cofactors metabolic pathways. These findings open huge perspectives for studying of cell-host interactions mechanism and therapy development for inflammatory bowel diseases with high colon cancer risk caused by *B. fragilis*.

### Biography

Anna Vanyushkina has completed her PhD in Biochemistry from FRCC PCM Russia. She is a Junior Researcher studying "Bacterial and human metabolomics using HPLC-MS/MS approach in laboratory proteomic analysis". She has published five papers in reputed journals.

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