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Paper Poster Session

Microbial pathogenesis and virulence

The *Burkholderia contaminans* operon participates in switching on the biofilm formation

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Background: *Burkholderia cepacia* complex (Bcc) bacteria - opportunistic pathogens causing nosocomial infections, are especially dangerous for cystic fibrosis patients. Biofilm formation (BF) helps Bcc to escape the antimicrobial agents' effect and complicates the Bcc eradication. The two component signal (TCS) transduction systems are in charge of the BF. The purpose of our investigation was the most important TCS determination.

Material/methods: High biofilm producer (HBP) clinical strain *B. contaminans* GIMC4509:Bct370 and lacking biofilm production (LBP) *B. contaminans* strain GIMC4587:Bct370-19 were used. Last one was obtained Romanova et al. by insertion modification of clinical strain with plasmid pTnMod-RKm. The strains were analyzed by Whole-genome sequencing and Liquid Chromatography Mass Spectrometry (LC-MC). 454 Sequencing System Software V 2.7 (Roche), RAST, BioCyc Database Collection, InterPro, MaxQuant were used for genome assembling, annotation, operons prediction, proteins' domains detection and proteins after MC identification. Operons sequences were deposited in GenBank under the accession numbers KP288491, KP288492.

Results: There are 37 two component transcriptional regulators (TCTR) genes in *B. contaminans* or *B. lata* genomes. Most of them are located with sensor signal transduction histidine kinase genes in operon one after the other. We found out four components operon, in which gene of peptidoglycan binding protein with FecR domain was embedded between the TCTR and kinase genes. Fourth component of operon downstream the histidine kinase was uncharacterized protein of DUF4136 superfamily, putative lipoprotein. The extracellular location of peptidoglycan binding protein and lipoprotein was predicted. The multi domain kinase also demonstrated extracellular domain. According genome analysis LBP strain had TCTR gene interrupted by pTnMod-RKm. This insertion switched off all operon frames' translation. LC-MC proteome of LBP strain investigation did not identify discussed operon proteins. The searching of genes orthologs revealed that such operon is common for *Burkholderia* genus. Other representatives of the order Burkholderiales: *Achromobacter*, *Bordetella* and *Ralstonia*, lost lipoprotein gene; *Lautropia* and *Alcaligenes* changed lipoprotein gene by glutamyl-tRNA reductase or AraC family transcriptional regulator, respectively. *Pandora* lost TCTR gene too. All operon is absent in *Pandora* genome. Two components operon (kinase and peptidoglycan binding protein) of *Pseudomonas aeruginosa*, as gamma-Proteobacteria, has low similarity with *Burkholderia*.

Conclusions: Switching off the BF by insertion the plasmid in four component operon demonstrated the importance of this part of genome in BF regulation. Similarity of operon structure between *Burkholderia* and some Burkholderiales will allow to elaborate common drug for all these causative agents.