## P-08.01.4-043
## Transcription regulation in *Mycoplasma gallisepticum* under different types of conditions

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*Mycoplasma gallisepticum* is a convenient model object for studying the regulation of transcription because it has a reduced genome, lack of cell wall and many metabolic pathways and also easy to culture and non-pathogenic to humans. Due to the nature of the genomic organization and the loss of many of the known regulators, the effect of disrupting the function of some proteins may be a useful tool for studying the regulation of transcription.

The gene expression study was performed on Agilent one-color microarray with custom design and random-T7 polymerase primer for cDNA synthesis. Microarray represents 3366 probes for 678 ORF including genes and ncRNA.

In this work, we have investigated the effect of changes in the level of gene expression of *M. gallisepticum* for two different types of conditions: a genetic knock-out mutants and the cell response to treatment with sub-lethal concentrations of antibiotics. We characterized transcription of *M. gallisepticum* when the cell responses to dysfunction of proteins with metabolic potential, possible regulators of expression, in violation of permeability of membrane by CCCP, inhibition of ribosomal synthesis by tetracycline, DNA gyrase by novobiocin and ATP synthase by oligomycin.

The data obtained allow to characterize the transcriptional response under different conditions and to identify groups of genes that change expression together. Major transcriptional changes were observed in the response of cells under CCCP treatment due to uncoupling of the proton gradient and further reducing the membrane potential, as well as under novobiocin treatment due to changing the topology of DNA.

## P-08.01.4-045
## Proteogenomic profile of the new alkane-oxidizing strain Tsukamurella tyrosinosolvens PS2 in relation to the emulsification activity

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Global problem of oil pollution forces scientists to search for a new safe remediation technologies constantly. Careful attention is paid to bacteria, some of which possess additional biotechnologically valuable properties, such as utilization of hydrocarbons and production of biofurfactants. In this regard, we carried out proteogenomic characterization of *Tsukamurella tyrosinosolvens* strain PS2, which was isolated from chemical sludge and capable for alkane degradation and biosurfactant production.

Whole genome of the strain was sequenced on the MiSeq (Illumina) platform, assembled and annotated. Proteome on mineral medium with glucose, sucrose and hexadecane as a sole carbon and energy source was studied. Shotgun proteomics approach was performed on hybrid chromatography-mass spectrometry machine (maXis Impact).

Alkane oxidation genes (alkane-1-monooxygenase, rubredoxin and rubredoxin-reductase) under genome sequence, as well as two pathways of trehalose synthesis and genes for mycolic acids production were found. Emulsification activity of cell-free culture liquid was about four times higher on hexadecane in comparison with sugars. Proteomic profile was different at various culture conditions. All glycolysis genes, beginning with glucose-6-phosphate isomerase to pyruvate kinase, were found on the media with sugar. The medium with hexadecane helped to reveal enzymes involved in the beta-oxidation of fatty acids, for example 2,4-dienoyl-CoA reductase, 3-ketoacyl-CoA thiolase and enzymes of the initial mycolic acid synthesis pathways.

Thus we have established that the strain *T. tyrosinosolvens* PS2 utilizes sugar by glycolysis. Also, the bacterium is capable for alkane oxidation followed by beta-oxidation of fatty acids. Based on the proteogenomic data, we assume that the bacterium is able to synthesize trehalose lipids, namely, trehalose mycolates. Obtained results could be useful to create conditions for increased biosurfactants production.

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## Personalized medicine

## P-08.02.5-001
## Serum adiponectin and resistin levels in gestational diabetes

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Gestational diabetes mellitus (GDM) is a glucose intolerance firstly diagnosed during pregnancy. In this study, we aimed to investigate the association between serum adiponectin, resistin levels and insulin resistance in gestational diabetic patients.

A total of 80 patients; 40 healthy pregnant women (control group) and 40 pregnant women diagnosed with GDM (GDM group) were included in this study. Serum adiponectin, resistin, glucose, insulin, HbA1c levels and lipid parameters were measured. Insulin resistance index HOMA-IR values were calculated.

In this study, serum glucose, insulin, HbA1c levels and HOMA-IR were significantly higher in GDM group compared to the control group ($p = 0.038$, $p = 0.011$, $p = 0.001$, $p = 0.008$, respectively). Serum adiponectin levels were significantly lower ($p < 0.001$); whereas serum resistin levels were significantly higher ($p = 0.004$) in GDM group than in the control group.

It can be concluded that resistin contributes to the formation of insulin resistance, adiponectin plays an important role in the regulation of this resistance and they also have effects on GDM pathophysiology.

Key words:*Gestational diabetes mellitus, adiponectin, resistin, HOMA-IR.*

## P-08.02.5-002
## Determination of chemoterapoetic drug sensitivity subgroups of acute leukemia

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Hematological cancers including Acute myeloblastic leukemia (AML) and Acute lymphoblastic leukemia (ALL) in terms of incidence and mortality, are the second most important cancer type in Turkey. Numerous studies show that cancer patients