

In previous studies I have presented the hierarchy in terms of *Proteus mirabilis* territoriality. The genome sequences of *P. mirabilis* strains K1609 and K670, which shown remarkably differences in their territoriality, were annotated and announced as well. I have proposed this strains as a model organisms for territoriality examination. My hypothesis assumed that strain K1609, exhibiting stronger territoriality, start migration earlier which allows to colonize the larger area than it is possible for weak competitors at the same time. The mechanisms of this observation remains unknown. I postulate the hypothesis that *P. mirabilis* K1609 and K670 differ in the gene expression profile and/or transcriptome kinetics during initiation of swarming motility, which causes them to start their migration at different time. Obviously understanding this mechanism is important when consider the swarming motility as one of the the most important virulence factor of *P. mirabilis* strains. Therefore, the presented proposal aims to investigate the quality and/or quantity differences in transcriptome of *P. mirabilis* K1609 and K670 strains at the different stages of swarming motility initiation. The main goal of the proposed research is to establish the molecular factor(s) or regulatory pathway(s) that trigger the earlier initiation of swarming motility in strongly territorial *P. mirabilis* strain K1609. The proposed research based on the use of a modern method of RNA-seq to determine the kinetics of the transcriptome in *P. mirabilis* cells during swarming motility initiation. The rich dataset obtained through the RNA-seq will enables the visualization of dynamics of the entire transcriptome over swarming initiation period. The importance of the observed differences in the studied phenomenon, will be evaluated using combination of *in silico* and statistic methods together with genetic manipulation.