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Overexpression of *whiA* in *Mycoplasma gallisepticum*

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Motivation and Aim: Mycoplasma species are bacteria that lack cell wall and have reduced genome. There is a scanty knowledge about proteinaceous regulators of transcription in Mycoplasmas [1]. WhiA is a conserved protein in Gram-positive bacteria, and also is present in the Mycoplasmas. This protein has DNA-binding domain. In *Streptomyces coelicolor* WhiA regulates sporulation [2], but in *Bacillus subtilis* it influences in chromosome segregation [3] and is involved in cell division [4]. The function of this protein in the Mycoplasmas remains unclear. In this work we searched for targets of WhiA in an avian pathogen *Mycoplasma gallisepticum*.
Methods and Algorithms: Transposon-based vector pTn4001opt_whiA were constructed for overexpression *whiA* gene in *Mycoplasma gallisepticum S6.* Transformation of *M. gallisepticum* was done by electroporation. All bacteria strains were cultured in liquid medium for exponential phase and cDNA samples were prepared as previously described [5].
Results and Conclusions: The growth rate of trasformants and wild-type bacteria was the same. We selected two independent clones for all experiments. RT-PCR analysis was done for genes involved in all main biological processes and metabolic pathways. The expression of about 80 genes (10 % of all ORFs) was checked. Expression level of *nei* (*mutM*), *fba* and *glpF* was changed under *whiA* overexpression condition. All these proteins can take part in control of redox homeostasis. Fba is a central enzyme of glycolysis but it also has a moonlight function as transcription regulator of catalase and RNA polymerase subunit [6]. Nei (MutM) is a base excision repair enzyme that identifies and eliminates a large variety of oxidized purines from DNA. GlpF is a transporter of glycerol in a pathway for production peroxide. The exact role of WhiA is still not unclear but our results show a further direction of the study.
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