

Effects of pH Shock on the Transcription of Regulatory Genes in *Streptomyces Coelicolor*

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In our previous study, it was observed that an artificial acidic pH shock enhanced the production and/or secretion of actinorhodin in *S. coelicolor* as much as over 10 folds. In this study a transcriptional analysis was performed by RT-PCR for various regulatory genes. Twenty different genes were considered: 3 pathway specific regulatory genes (*actII-orf4*, *redD*, *cdaR*); 8 positive regulatory genes (*relA*, *metK*, *afsR*, *afsQ1*, *afsS*, *absR1*, *absR2*, *redZ*); 7 negative regulatory genes(*ppk*, *orf10*, *cutR*, *phoP*, *scbA*, *kbpA*, *orfB*) and 2 response-related genes(*afsK*, *pkaG*). It was observed that the pH shock promoted cell growth and caused a phase shift in cell growth. The pH shock inhibited the transcription of most of the negative pleiotropic regulatory genes (*orf10*, *cutR*, *phoP*, *kbpA*, *orfB*) in the stationary phase, i.e., secondary metabolite production phase. It is considered that the turning-off of these negative regulatory genes would have been the main factor enhancing actinorhodin production. The transcription of positive regulatory genes were not significantly affected by the pH shock. No clear conclusions could be made for the specific regulatory genes since the analysis of their transcription patterns was very difficult.