208b Sporulation Regulons and Their Prediction in Clostridia

Carlos J. Paredes, Keith V. Alsaker, and Eleftherios T. Papoutsakis

The availability of complete genomes from related microorganisms confers us with the capability of conducing computational studies among those organisms. Such kind of studies when coupled with experimental evidence help us to advance the genome annotation past the gene level into the transcriptional unit and regulon annotation. Recent experimental studies have mapped the sporulation cascade in *B. subtilis*. Such a cascade is mainly controlled by the expression of several sigma factors and other transcriptional factors that have also been identified in clostridia. However, at the regulon level, the conservation seems to be low. Despite having genomes of comparable size, only around 250 of the more than 800 genes belonging to *B. subtilis* sporulation regulons have an ortholog in the sporulating *C. acetobutylicum*, and around 190 and 150 putative orthologs in the cases of *C. perfringens* and *C. tetani* respectively.

In this talk we will present the combination of newly developed transcriptional maps for all three clostridia together with promoter predictions using Hidden Markov Models using a new scoring procedure to predict the putative regulons involved in the sporulation cascade of *C. acetobutylicum*, *C. perfringens* and *C. tetani*. The differences and similarities between them and when compared to the reference sporulating organism *B. subtilis* will be presented.