4be Regulon Prediction and Coregulation Patterns in *Clostridium Acetobutylicum*

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C. acetobutylicum is an non-pathogenic, spore-forming, solvent-producing anaerobic microorganism that can be used as a model organism for its pathogenic counterparts, *C. tetani*, *C. perfringens* and *C. botulinum* among others. However, it is by itself an interesting organism to study with a long past as industrial producer of solvents like acetone, butanol and ethanol. Unfortunately solvent production and sporulation form part of the same web of transcriptional programs and their relationship is not completely understood yet.

When entering the stationary phase of growth, *C. acetobutylicum* must sporulate as their only way of survival and defense against a chemically hostile environment created by itself when transforming carbohydrates into organic acids. In what can be described as a bid for gaining time to sporulate and survive, it starts exchanging toxic acids for less toxic solvents. To withstand the increasing solvent concentration while preserving as much as possible the internal micro-environment, the membrane composition must change, proteins must be kept properly folded and non essential transcriptional programs start to be shut down as the mother cell is slowly dying. All this should be made simultaneously and involves the activation of sporulation, stress response, solvent production mechanisms, and also fatty acid and branched amino acid synthesis and the downregulation of the motility and chemotaxis programs and sugar uptake pathways among others.

Using a new and improved version of our computationally predicted transcriptional unit map together with comparative genomic studies between *C. acetobutylicum* and *Bacillus subtilis* and data about sets of co-regulated genes from our recently described full genome *C. acetobutylicum* array, we will present and assess the likelihood of the above mentioned regulons involved in the stationary phase events of *C. acetobutylicum*.