

504f Coregulation Patterns in *Clostridium Acetobutylicum*

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The obligate anaerobe *C. acetobutylicum* sporulates as a way of survival and defense against a chemically hostile environment created by itself. It what can be described as a bid to gain some time until its spores are created and liberated into the environment, *C. acetobutylicum* starts its solvent production programs to convert the toxic organic toxic acids produced earlier. The new environment is also a threat for the cells as it creates new problems: membrane composition must change in order to withstand the increasing solvent concentration, proteins must be kept in working order, and hence properly folded, while non essential transcriptional programs should to be shut down in an orderly fashion. All this should be made simultaneously and involves the activation of sporulation, stress response, solvent production mechanisms, fatty acid and branched amino acid synthesis and the downregulation of the motility and chemotaxis programs and sugar uptake pathways among others.

The intricacy and inter-relationship of so many transcriptional programs requires a step-by-step procedure to its deconvolution and the use of high quality full genome transcriptional data. The present talk will present our first co-regulation map for *C. acetobutylicum* based on the microarray studies carried in our laboratory using our recently described high quality full-genome *C. acetobutylicum* microarray.