

48a The Transcriptional Program of Early Sporulation and Stationary Phase Events in *Clostridium Acetobutylicum*

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DNA-microarray analysis of *Clostridium acetobutylicum* was used to examine the genomic-scale gene expression changes during the shift from exponential growth and acidogenesis to stationary phase and solventogenesis. Self-organizing maps were used to identify novel expression patterns of functional gene classes including aromatic and branched-chain amino acid-synthesis, ribosomal proteins, cobalt and iron transporters, cobalamin biosynthesis, and lipid biosynthesis. The majority of pSOL1 megaplasmid genes (in addition to the solventogenic genes *aad-ctfA-ctfB* and *adc*) had increased expression at the onset of solventogenesis, suggesting other megaplasmid genes play a significant role in stationary phase phenomena. Analysis of sporulation genes and comparison with published *Bacillus subtilis* results indicated conserved expression patterns of early sporulation genes including *spo0A*, the *sigF* operon, and putative canonical genes of the SigH and SigF regulons. However, *sigE* expression could not be detected within 7.5 hours of initial *spo0A* expression, consistent with the observed extended time between appearance of clostridial forms and endospore formation. The results were compared with microarray comparisons of the wildtype and nonsolventogenic, asporogenous M5 strain which lacks the pSOL1 megaplasmid. While some results were similar, expression of primary metabolism genes and heat shock proteins were higher in M5, suggesting a difference in metabolic regulation or a butyrate-stress response in M5. The results of this microarray platform and analysis were further validated by comparing gene expression patterns to previously published Northern analyses, reporter assays, and two-dimensional protein electrophoresis data of metabolic genes (including all major solventogenesis genes), sporulation genes, heat shock proteins, and other solventogenesis-induced gene expression.