SL311

A REGULATORY SWITCH GOVERNING TWO ALTERNATIVE DEVELOPMENTAL PATHWAYS IN *BACILLUS SUBTILIS*

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Genetic competence in *B. subtilis* requires the expression of the late competence operons that function in the uptake of DNA. These operons are transcriptionally activated by the ComK protein, the activity of which is controlled by the ComS, MecA, and ClpC regulatory factors. The *comS* gene is expressed in response to high cell density and nutritional stress. The small ComS peptide then interacts with the MecA/ClpC/ComK complex, thereby releasing active ComK and stimulating late com operon expression. We have found by chemical cross-linking and affinity chromatography that ComS peptide interacts directly with MecA protein. Random PCR and Alanine-scanning mutagenesis have identified two regions within the ComS peptide that are essential for in vivo activity, although some of these mutations do not affect MecA binding in vitro. This suggests that ComS may perform another function apart from contacting MecA protein. Mutations in *comS* and *comK* eliminate competence development but cause the derepression of genes that function in the development of motility and are transcribed by the σ^D form of RNA polymerase. The negative control exerted by ComK is due to the ComK-dependent transcription of the *flgM* gene encoding a σ^D-specific anti-sigma factor. The *flgM* operon is located immediately downstream of the late com operon, *comF*, the transcription of which requires ComK. Insertion mutations at the *comF-flgM* junction that exert polarity on the flgM operon result in the derepression of hag, a gene encoding the major flagellar protein, flagellin, and transcribed by the σ^D-form of RNA polymerase. The regulatory factors ComS, ClpC, MecA and ComK constitute a regulatory switch that mediates the cell's decision to embark on a specific developmental pathway.