Cloning and DNA sequence of *sigB* gene of *Stigmatella aurantiaca*

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Stigmatella aurantiaca belongs to the myxobacteria, which, upon environmental stress, form species-specific fruiting bodies, containing myxospores. As shown in *Bacillus subtilis* (1), a cascade of sigma factors may activate stage-specific genes during development. This communication reports the cloning and sequencing of the *sigB* gene, encoding a sigma-subunit of the DNA dependent RNA polymerase (RNAP). The gene was isolated from a lambda gt11 library of *S.aurantiaca* DNA by using an oligonucleotide (5'-CAC(GC)GCCTTCATCAGGCCG-AT-3') as a hybridization probe, which corresponds to the highly conserved domain 2 (2) of eubacterial sigma factors (amino acids IGLMKAV). This domain is thought to be involved in RNAP core binding (2) and should be present also in minor sigma factors. The DNA sequence of the *sigB* gene was determined by the Sanger dideoxy method. The ORF encodes a polypeptide of 296 amino acids with a predicted molecular weight of 33,297. The alignment with other sigma-sequences shows, that it belongs to the heat shock sigma cluster (3). The homology to SigA polypeptide of *S.aurantiaca* is about 30%, to *Myxococcus xanthus* SigB polypeptide about 92% and to *E.coli* RpoH polypeptide about 48%. The protein shares some features common to other bacterial sigma factors, i.e. a large number of charged amino acids (14% acidic amino acids and 14% basic amino acids in SigB) as well as domains corresponding to conserved regions of various sigma factors. The alignment of SigB with SigA of *S.aurantiaca* (4) and RpoH of *E.coli* shows some highly conserved amino acid motifs. These are in region 2: (core binding) SNLRFVV/DLIQEGNIGLMKAV; (rpoD-box) WWIRA; region 3: AQRKLFF (this motif is present only in heat shock sigma factors), (helix−turn−helix motif) DEIANKLNVAKSEVREM; region 4: (helix−turn−helix motif) MTLKELG—G-SRER-RQLE-RA−KLK.

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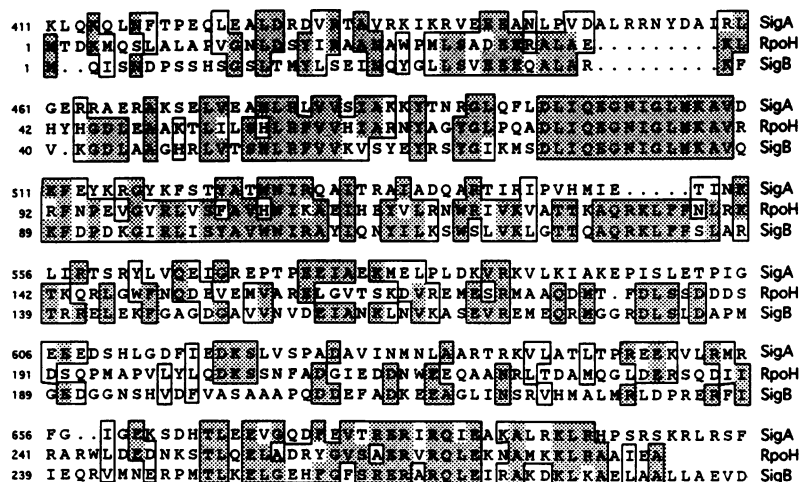

Figure 1. Alignment of SigB protein of *S.aurantiaca* with SigA protein of *S.aurantiaca* and RpoH protein of *E.coli*. Conserved amino acids are boxed (well conserved amino acids in blank boxes and identical amino acids in stippled boxes). The alignment was done with the program Multalign (5).