**BACKGROUND**

The signal transduction pathway leading to the activation of σ^B is well-characterized in *Bacillus subtilis*, and a divergently evolved σ^B signaling pathway that involves the hybrid kinase RsbK has been observed in *Bacillus cereus* group members. However, the molecular mechanisms involved in signal sensing and signal integration into the stressosome are unknown.

**AIM**

In this study, we investigated the presence/absence of σ^B signal sensing and integration modules in *Bacillus* species and other bacteria.

**METHOD**

1. We performed genome mining and phylogenetic reconstruction of members involved in σ^B signal sensing modules and transduction pathways in about 125 *Bacillus* wild isolates.
2. We compared the stressosome members, σ^B regulon genes and additional genes encoding regulators involved in the activation of the σ^B regulon.

**RESULT**

1. The generated genome tree heat map of 144 genomes shows that most *B. subtilis* and *B. cereus* strains have the σ^B signalling RsbRSTU and RsbKY pathways, respectively.
2. The heat map revealed that some strains contain both RsbRSTU and RsbKY pathways.
3. Putative σ^B operon and regulon members are also found in other microorganisms, other than *Bacillus*, *Staphylococcus* and *Listeria*.

**CONCLUSION**

An overview of the presence or absence of the σ^B transduction pathways, σ^B operon genes, σ^B regulon genes and potential σ^B regulators across *Bacillus* species and other bacteria was created. Based on these findings, the function of putative σ^B sensory and signal integration genes in selected *Bacillus* strains will be studied.

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**Figure 1:** σ^B signal sensing routes in *B. subtilis* and *B. cereus* group members

**Figure 2:** Genome tree heat map of *Bacillus* and other bacterial species

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**Sigma B stress response in the genus *Bacillus* – Stressosome proteins, RsbK Signalling Pathways and Predicted Regulons**

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