

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

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## BACKGROUND

The signal transduction pathway leading to the activation of  $\sigma^B$  is well-characterized in *Bacillus subtilis*, and a divergently evolved  $\sigma^B$  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.

## RESULT

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

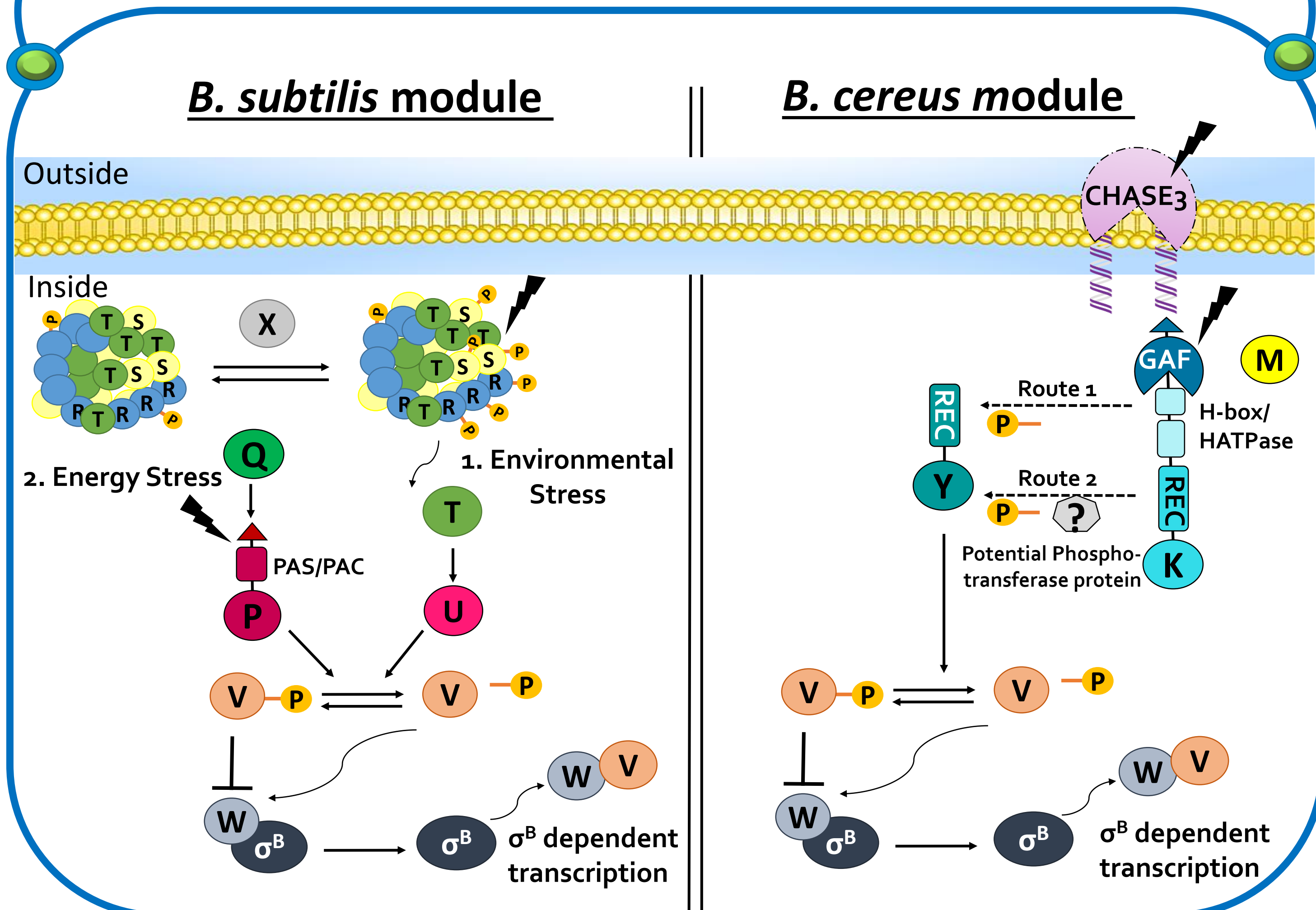


Figure 1:  $\sigma^B$  signal sensing routes in *B. subtilis* and *B. cereus* group members

## AIM

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

## METHOD

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

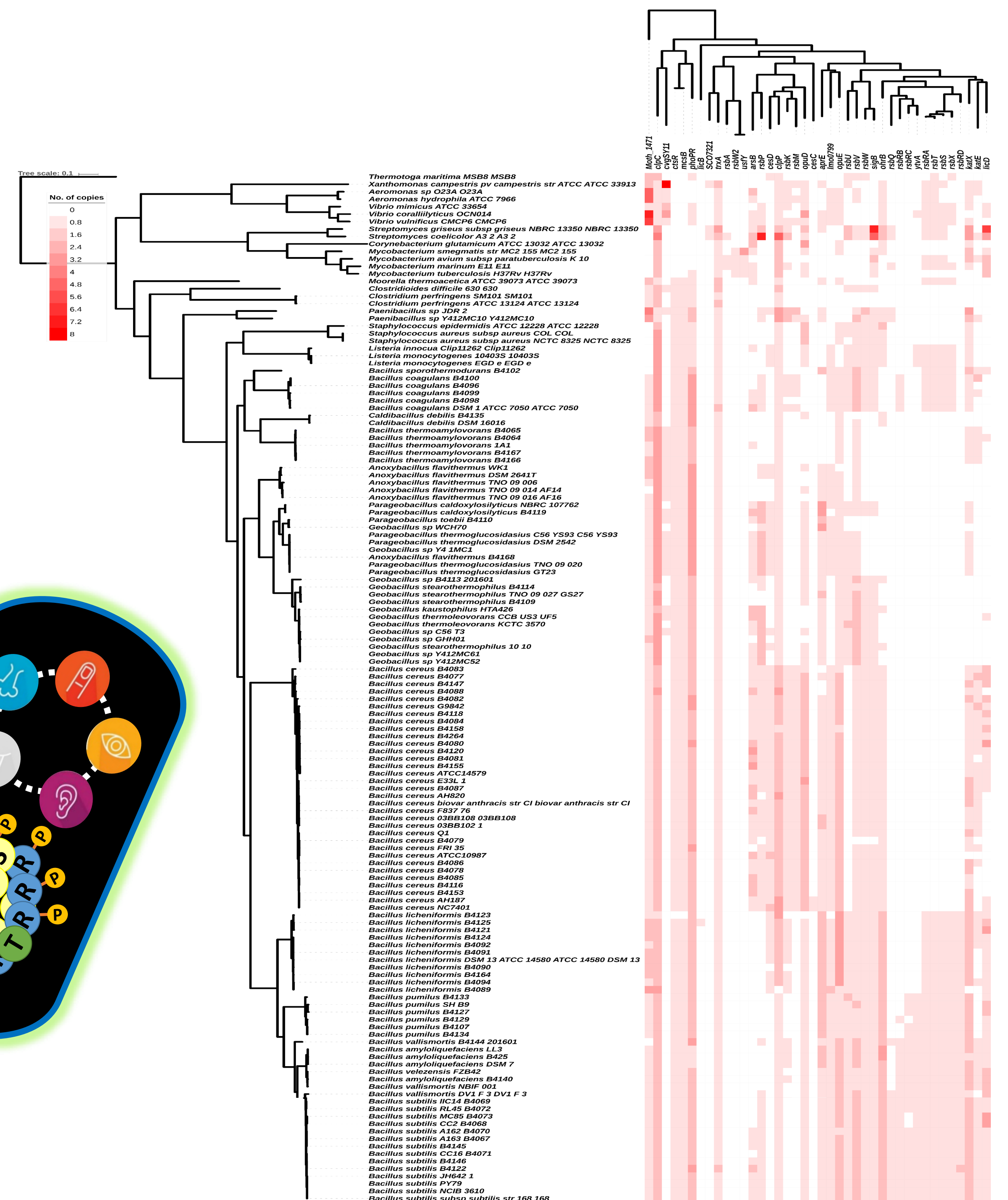
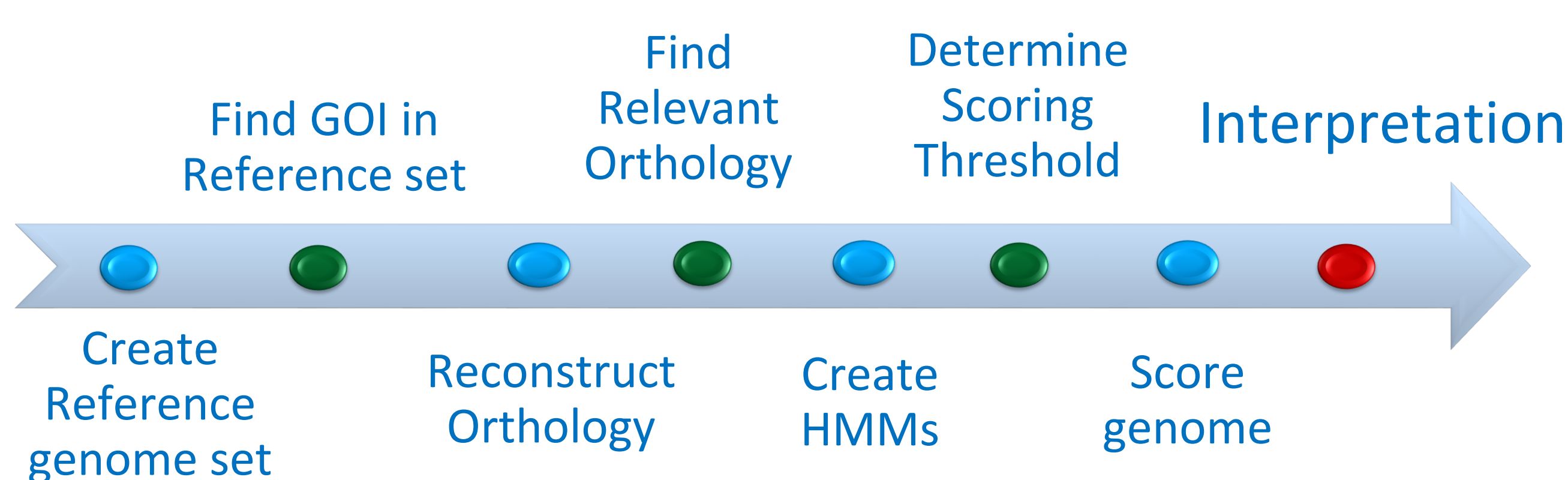


Figure 2: Genome tree heat map of *Bacillus* and other bacterial species

## CONCLUSION

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

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