

Global Transcriptional Response to Heat Shock of the Legume Symbiont *Mesorhizobium loti* MAFF303099 Comprises Extensive Gene Downregulation

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Abstract

Rhizobia, the bacterial legume symbionts able to fix atmospheric nitrogen inside root nodules, have to survive in varied environmental conditions. The aim of this study was to analyse the transcriptional response to heat shock of *Mesorhizobium loti* MAFF303099, a rhizobium with a large multipartite genome of 7.6 Mb that nodulates the model legume *Lotus japonicus*. Using microarray analysis, extensive transcriptomic changes were detected in response to heat shock: 30% of the protein-coding genes were differentially expressed (2067 genes in the chromosome, 62 in pMLa and 57 in pMLb). The highest-induced genes are in the same operon and code for two sHSP. Only one of the five *groEL* genes in MAFF303099 genome was induced by heat shock. Unlike other prokaryotes, the transcriptional response of this *Mesorhizobium* included the underexpression of an unusually large number of genes (72% of the differentially expressed genes). This extensive downregulation of gene expression may be an important part of the heat shock response, as a way of reducing energetic costs under stress. To our knowledge, this study reports the heat shock response of the largest prokaryote genome analysed so far, representing an important contribution to understand the response of plant-interacting bacteria to challenging environmental conditions.

Key words stress • rhizobia • microarrays • chaperone • sHSP