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Transcriptional analysis of major chaperone genes in salt-tolerant and salt-sensitive mesorhizobia.

Author(s): [Brigido, Clarisse](#); [Alexandre, Ana](#); [Oliveira, Solange](#)

Source: Microbiological research **Volume:** 167 **Issue:** 10 **Pages:** 623-9 **DOI:** 10.1016/j.micres.2012.01.006 **Published:** 2012-Dec-20 (Epub 2012 Feb 23)

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Abstract: Salinity is an important abiotic stress that limits rhizobia-legume symbiosis, affecting plant growth, thus reducing crop productivity. Our aims were to evaluate the tolerance to salinity of native chickpea rhizobia as well as to investigate the expression of chaperone genes *groEL*, *dnaKJ* and *clpB* in both tolerant and sensitive isolates. One hundred and six native chickpea mesorhizobia were screened for salinity tolerance by measuring their growth with 1.5% and 3% NaCl. Most isolates were salt-sensitive, showing a growth below 20% compared to control. An association between salt tolerance and province of origin of the isolates was found. The transcriptional analysis by northern hybridization of chaperone genes was performed using tolerant and sensitive isolates belonging to different *Mesorhizobium* species. Upon salt shock, most isolates revealed a slight increase in the expression of the *dnaK* gene, whereas the *groESL* and *clpB* expression was unchanged or slightly repressed. No clear relationship was found between the chaperone genes induction and the level of salt tolerance of the isolates. This is the first report on transcriptional analysis of the major chaperones genes in chickpea mesorhizobia under salinity, which may contribute to a better understanding of the mechanisms that influence rhizobia salt tolerance. Copyright 2012 Elsevier GmbH. All rights reserved.

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