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## Multilocus sequence analysis reveals multiple symbiovars within *Mesorhizobium* species.

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### Abstract

The genus *Mesorhizobium* includes species nodulating several legumes, such as chickpea, which has a high agronomic importance. Chickpea rhizobia were originally described as either *Mesorhizobium ciceri* or *M. mediterraneum*. However, rhizobia able to nodulate chickpea have been shown to belong to several different species within the genus *Mesorhizobium*. The present study used a multilocus sequence analysis approach to infer a high resolution phylogeny of the genus *Mesorhizobium* and to confirm the existence of a new chickpea nodulating genospecies. The phylogenetic structure of the *Mesorhizobium* clade was evaluated by sequence analysis of the 16S rRNA gene, ITS region and the five core genes *atpD*, *dnaJ*, *glnA*, *gyrB*, and *recA*. Phylogenies obtained with the different genes are in overall good agreement and a well-supported, almost fully resolved, phylogenetic tree was obtained using the combined data. Our phylogenetic analyses of core genes sequences and their comparison with the symbiosis gene *nodC*, corroborate the existence of one new chickpea *Mesorhizobium* genospecies and one new symbiovar, *M. opportunistum* sv. *ciceri*. Furthermore, our results show that symbiovar *ciceri* spreads over six species of mesorhizobia. To our knowledge this study shows the most complete *Mesorhizobium* multilocus phylogeny to date and contributes to the understanding of how a symbiovar may be present in different species.

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