Natural Populations of Chickpea Rhizobia Evaluated by Antibiotic Resistance Profiles and Molecular Methods

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Abstract The aims of this study were to investigate the hypothesis that intrinsic antibiotic resistance (IAR) profiles of chickpea rhizobia are correlated with the isolates site of origin, and to compare the discriminating power of IAR profiles with molecular approaches in rhizobial strain identification and differentiation. Rhizobial diversity from five Portuguese soils was assessed by IAR profiles and molecular methods [16S rDNA restriction fragment length polymorphism (RFLP) analysis, direct amplified polymorphic DNA (DAPD) fingerprinting, and SDS–PAGE analysis of protein profiles]. For each analysis, a dendrogram was generated using the software BioNumerics. All three molecular methods generated analogous clustering of the isolates, supporting previous results on 16S rDNA sequence-based phylogeny. Clusters obtained with IAR profile are similar to the species groups generated with the molecular methods used. IAR groups do not correlate significantly with the geographic origin of the isolates. These results may indicate a chromosomal location of antibiotic resistance genes, and suggest that IAR is species related. DAPD and IAR profiles proved to be the most discriminating approaches in strain differentiation and can be used as fast methods to screen diversity in new isolates.