



RAPD analysis of the genetic diversity among accessions of Fabaceous forages (*Poincianella* spp) from the Caatinga

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ABSTRACT. Among members of the Fabaceae family, native to the Brazilian Caatinga, the species *Poincianella pyramidalis* and *P. bracteosa* exhibit particular potential as forage for cattle, sheep and goats. With the aim of establishing genetic relationships within *Poincianella*, random amplified polymorphic DNA analysis was performed on eight accessions of *P. pyramidalis* and two accessions of *P. bracteosa*, originating from the semiarid zone of the state of Piauí, northeastern Brazil, and present in the germplasm bank of Embrapa Meio Norte (Teresina, Piauí, Brazil). Amplification reactions using 11 selected arbitrary sequence primers generated 167 fragments with an overall polymorphism of 70.38%. Five monomorphic loci were generated exclusively in *P. pyramidalis* accessions, while three unique monomorphic loci were associated with *P. bracteosa*, and these represented potential species-specific markers. The similarity coefficients between *Poincianella* accessions were low (mean value 0.59) but with a wide variation (range 0.443 to 0.748). The similarity

matrix and the dendrogram constructed using the unweighted pair group method allowed the separation of *Poincianella* accessions into two major clusters represented by the two distinct species, while the accessions of *P. pyramidalis* could be separated further into three subgroups. The high level of genetic diversity detected in the genus *Poincianella* could be used in future breeding programs to produce enhanced cultivars, although the variability could be better exploited if more specimens were collected from other locations within the semiarid region of northeastern Brazil.

Key words: Forage; Genetic diversity; Species-specific markers; RAPD; Plant improvement