

Assessment of inter-specific diversity of the *Hedysarum* genus in Tunisia

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Introduction In Tunisia, many grassland and pasture species were menaced by genetic erosion. Thus, we were interested in the *Hedysarum* species which constitute a very important phylogenetic patrimony able to produce forage and restore destroyed pasture land especially in arid and semi-arid areas. In order to facilitate fodder improvement, we investigated the phenetic relationships among *Hedysarum* species using rDNA intergenic spacer (IGS) polymorphism.

Materials and methods Appropriate conserved oligonucleotides flanking the rDNA IGS were used to amplify total cellular DNA extracted from eight *Hedysarum* species. Polymorphic bands were scored for their presence/absence and employed to produce genetic relationships among species based on Nei and Li's distance matrix (Nei & Li, 1979).

Results Our data show that this IGS amplification constituted an efficient tool to examine the genetic diversity between species in this genus and showed a high level of polymorphism in the *Hedysarum* genus.

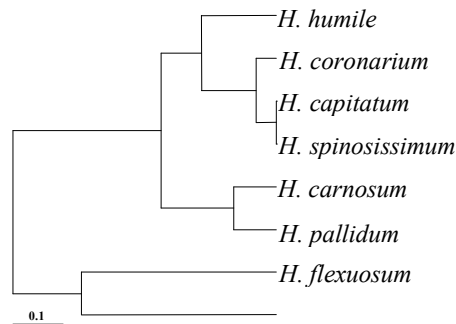


Figure 1 Phylogenetic relationships of *Hedysarum* species based on IGS sequence

The clustering supports two main groups (Figure 1). The first one is represented by two species, *H. flexuosum* and *H. aculeolatum*. All the remaining species are ranged in the second cluster. It seems that the two sub-species *H. capitatum* and *H. spinosissimum* are closely related to each other and characterised by a very similar sequence of rDNA intergenic spacer.

Conclusions There is a high degree of polymorphism at the inter-specific levels and this permitted the establishment of the genetic relationships among species. Our data provide evidence of a nuclear lineage between included species. In spite of their classification as sub-species of *H. spinosissimum* and their distinctiveness by agronomic characters, mating systems and geographical distribution, *H. capitatum* and *H. spinosissimum* are characterised by great similarities of the IGS sequence. Both sub-species, which are closely related to *H. coronarium*, can assist in the selection of genetic materials for improvement programmes.

References

Nei, M., & W.S. Li (1979). Mathematical model for studying genetic variation in terms of restriction endonuclease. *Proceedings of the National Academy of Sciences, USA*, 76, 5269-5273.