

## *Paspalum* L. (Poaceae, Panicoideae, Paniceae) species identification using molecular genetic evaluation

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*Paspalum* (Poaceae) is an important genus of the tribe Paniceae, which includes several species of economic importance for forage, turf and ornamental purposes. Traditional taxonomical identification of many of its species is difficult, particularly within some of its informal groups, as result of the complex evolutionary history of this genus. The complexity derives from several factors, often concomitant. These include extensive hybridization, both ancient and recent; absence of clear differences between many species; polyploidy and apomixis. These factors have played a crucial role in its evolution; thus, this work aimed to use genetic molecular approach as a tool to characterise these species. The cross-species amplification of 19 simple sequence repeat (SSR) markers developed for *P. atratum* and *P. notatum* was evaluated in 34 different *Paspalum* species and other unclassified accessions for the assessment of genetic differences among them to assist in their proper botanical identification. Twelve of these SSR markers were successfully cross-amplified for most species and were used to evaluate 214 accessions comprised the different species, representing 14 informal botanical groups of *Paspalum*. The 12 SSR loci revealed 187 bands scored (15.58 per locus). Variable degrees of polymorphism within species were observed and an important observation in our study was that the proportion of the detected polymorphisms decreased with the increasing genetic distance of taxa for which microsatellite markers were originally developed. This observation is in agreement with other results obtained in plant. Based upon different methods (PCoA, NJ) accessions were grouped into three main groups of species, of which two corresponded respectively to the Plicatula and the Notata informal *Paspalum* groups. The molecular genetic approach was able to distinguishing the different taxa studied, except for the species belonging to the Plicatula group, recognised as a very complex one. For this particular case, use of molecular markers specifically developed to the Plicatula species is probably necessary. This molecular genetic approach as an initial assessment of germplasms may represent a valuable tool for species identification and as well as for the characterization, conservation and successful species hybridization. Financial Support: CNPq and FAPESP.