**FIRST GENETIC DIVERSITY ANALYSIS IN GREATER YAM (*DIOSCOREA ALATA* L.) OF A REPRESENTATIVE WORLD GERMPLASM USING MICROSATELLITE MARKERS**

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**Abstract**

Yams (*Dioscorea* sp.) are important food security crops for millions of people in tropical and subtropical regions. *Dioscorea alata,* also known as greater yam, is one of the major cultivated species and most widely distributed throughout the tropics. Despite its economic and cultural importance, very little is known about its origin and genetic diversity, which limits the efficacy of genetic improvement programmes. The objective of this study was to contribute to the understanding of worldwide *D. alata* genetic diversity by genotyping 384 accessions from different geographical regions (South Pacific, Asia, Africa and the Caribbean), using 24 microsatellite markers. Diversity structuration was assessed via Principal Analysis, UPGMA analysis and the Bayesian approach implemented in STRUCTURE. Our results revealed the existence of a wide genetic diversity and a significant structuring associated with geographic origin, ploidy levels and morpho-agronomics characteristics. Seventeen major groups of genetically close cultivars have been identified, including eleven groups of diploids cultivars, four groups of triploids and two groups of tetraploids. STRUCTURE revealed the existence of six populations in the diploid genetic pool and a few admixed cultivars. These results will be very useful for rationalizing *D. alata* genetic resources in breeding programs across different regions and for improving germplasm conservation methods.