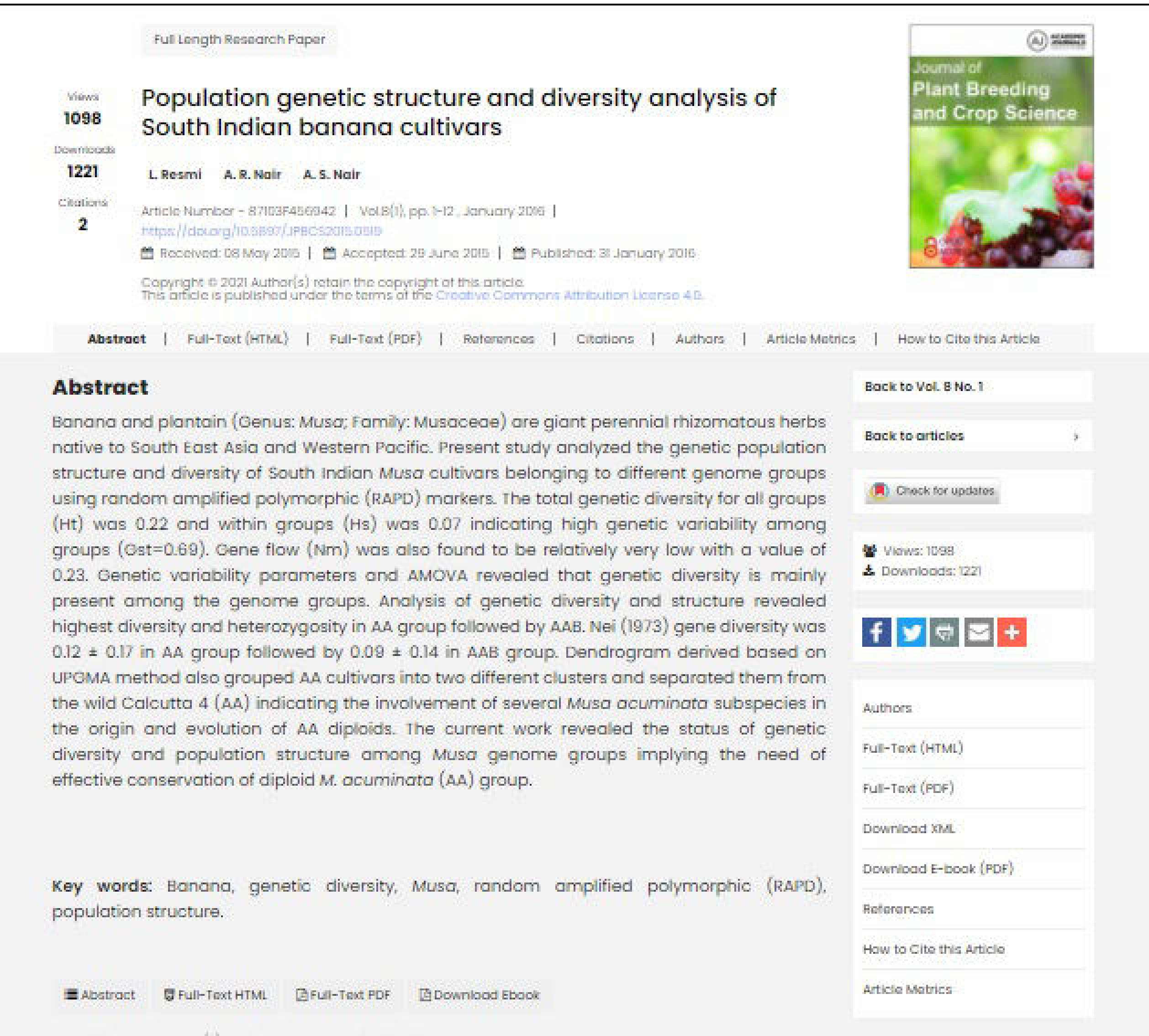

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# Population genetic structure and diversity analysis of South Indian banana cultivars

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## Abstract

Banana and plantain (Genus: *Musa*; Family: Musaceae) are giant perennial rhizomatous herbs native to South East Asia and Western Pacific. Present study analyzed the genetic population structure and diversity of South Indian *Musa* cultivars belonging to different genome groups using random amplified polymorphic (RAPD) markers. The total genetic diversity for all groups (Ht) was 0.22 and within groups (Hs) was 0.07 indicating high genetic variability among groups (Gst=0.69). Gene flow (Nm) was also found to be relatively very low with a value of 0.23. Genetic variability parameters and AMOVA revealed that genetic diversity is mainly present among the genome groups. Analysis of genetic diversity and structure revealed highest diversity and heterozygosity in AA group followed by AAB. Nei (1973) gene diversity was 0.12 ± 0.17 in AA group followed by 0.09 ± 0.14 in AAB group. Dendrogram derived based on UPGMA method also grouped AA cultivars into two different clusters and separated them from the wild Calcutta 4 (AA) indicating the involvement of several *Musa acuminata* subspecies in the origin and evolution of AA diploids. The current work revealed the status of genetic diversity and population structure among *Musa* genome groups implying the need of effective conservation of diploid *M. acuminata* (AA) group.

**Key words:** Banana, genetic diversity, *Musa*, random amplified polymorphic (RAPD), population structure.

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