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GENETIC DIVERSITY IN *HELICONIA* - A TROPICAL FLOWER AND RELATED GENERA USING DNA MARKERS

Heliconia varieties/types along with related genera were subjected to RAPD analysis for genetic diversity and to construct phylogenetic tree based on RAPD data. Twenty primers were selected from the initial of 120 RAPD primers. The selected primers produced a high degree of polymorphism, where, of a total of 156 amplified bands, 154 were polymorphic, with each primer giving an average of 7.7 polymorphic bands and accounting for 99.05 % polymorphism. Number of bands per primer varied from 2 (OPN-17) to 13 (OPB-17). Polymorphic Information Content ranged from 0.06 in OPN-17 to 0.50 in OPY-19 with an average of 0.31. The highest resolving power of 9.58 was calculated for OPQ-03 which was closely followed by 9.52 for OPY-19. The lowest resolving power (*Rp*) of 0.12 was calculated for OPN-17. Average *Rp* for 20 primers was found to be 4.29. In the dendrogram, the genotypes which belong to related genera, *viz. Canna indica* (Red), *Canna indica* (Orange), *Musa* spp. (Grand Naine), *Maranta arundinacea*, *Alpinia purpurata*, *Zingiber officinale*, and *Curcuma longa* are all out groups, while all the 26 genotypes of Heliconia grouped in the Cluster E and Cluster F at coefficient value of 0.19. Thus it proves that Heliconia forms a distinct genus in order Zingiberales.