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THE GENETIC DIVERSITY OF *Monochoria vaginalis* IN SRI LANKA AS DETERMINED BY USING RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) MARKERS

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Monochoria vaginalis (Burm.f.) ex Kunth ('Diyahabarala') is a weed found in rice fields of Sri Lanka. The plant belongs to the family Pontederiaceae. The ability of weeds in adapting to the environment may depend on their high genetic variability. Therefore, it is important to have an idea of the genetic diversity of *M. vaginalis* within and between populations in order to control these weeds successfully. Three phenetic groups with clear morphological differences have been identified within *M. vaginalis*. These morphological traits have been found to be stable across different environments. Molecular data can provide evidence for genetic variations and therefore the present study was conducted to determine the genetic diversity among the three phenetic groups using RAPD markers.

Live plants of *M. vaginalis* were collected from eight populations (Midigama, Aranayaka, Pujapitiya, Matale, Penideniya, Maradankadawala, Thirappane and Mawathagama) in Sri Lanka, representing the three phenetic groups. Four individuals from two populations were selected to determine the genetic diversity within populations. DNA was extracted and subjected to RAPD-PCR amplification with OPC15 primer. To determine genetic variation among populations, one individual from each eight populations was selected and DNA was subjected to RAPD-PCR amplification with eight oligonucleotide primers. Amplified bands were scored as presence/absence of bands for all samples. The resulting presence/absence data matrix was analyzed using Statistical Software Minitab version 15.

According to the cluster analysis, the highest similarity level (77.6%) was observed between Maradankadawala and Thirappane populations. These populations are morphologically similar and located in geographically nearby areas. The lowest similarity level (9.2%) was observed between Penideniya and Midigama populations. These populations are morphologically distinct and located in geographically distant areas. According to these results, there is very high genetic variation among *M. vaginalis* populations in Sri Lanka as explained by its morphology. There were no polymorphic bands observed among individuals within populations. According to these results there is no genetic diversity within *M. vaginalis* populations. Thus, pathogens that can be effectively used for biological control of one population of *M. vaginalis* are likely to be ineffective against another population as they have different genotypes. The cluster analysis resulted in three distinct clusters that corresponded to the three phenetic groups identified based on their morphological differences. Thus, RAPD data analysis confirmed the presence of three phenetic groups within *M. vaginalis* populations in Sri Lanka.