

[BIO05]

**Genetic structure of glyphosate-resistant (R) and glyphosate-susceptible (S) populations of *Eleusine indica* (L.) Gaertn from peninsular Malaysia**

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A total of 840 accessions representing six populations of glyphosate-resistant and eight populations of glyphosate-susceptible goosegrass (*Eleusine indica*) from Peninsular Malaysia were screened for genetic variation using isozyme markers. 13 enzyme loci from eight enzyme systems were scored in this study. The mean percentage of polymorphic loci ( $P = 23.08\%$ ), mean number of alleles per locus ( $A = 1.2$ ) and effective number of alleles per locus ( $A_e = 1.1$ ) was similar for the R and S populations. Levels of expected heterozygosity ( $H_e$ ) was low and not significantly different ( $P > 0.10$ ) between the R ( $H_e = 0.067$ ) and S ( $H_e = 0.069$ ) biotypes but the levels of observed heterozygosity ( $H_o$ ) was found to be significantly lower ( $P < 0.10$ ) in the R populations ( $H_o = 0.003$ ) than in the S populations ( $H_o = 0.014$ ). The low genetic variation within populations is consistent with the autogamous reproduction in *E. indica*. The reduced level of genetic variation in the R populations may be due to the effects of genetic drift associated with the selection for herbicide resistant individuals and the subsequent build-up of homogenous resistant populations. Overall degree of genetic differentiation for the 14 populations was high ( $F_{ST} = 0.53$ ), indicating high genetic divergence among the populations surveyed. In agreement with the low genetic diversity in the R populations, the  $F_{ST}$  value among the 6 R populations was low (0.240) while the high genetic differentiation among the 14 populations was mainly contributed by the S populations ( $F_{ST} = 0.622$ ). The total gene flow across populations was low ( $N_m = 0.2247$ ), which is consistent with the high  $F_{ST}$  values. The mean genetic distance for the 14 populations was 0.046 with values ranging from 0.00 to 0.169. UPGMA clustering analysis revealed two main clusters; cluster I consisting of all the R populations and the S populations from Bidor, Chaah, Lenggeng and Temerloh, while cluster II consists of the S populations from Kuala Selangor, Melaka, Sungai Tangkas and Pulau Pinang.