

**Genetic dissection of sympatric populations of brown planthopper, *Nilaparvata lugens* (Stål), using DALP-PCR molecular markers.**

ABSTRACT

Direct amplified length polymorphism (DALP) combines the advantages of a high-resolution fingerprint method and also characterizing the genetic polymorphisms. This molecular method was also found to be useful in brown planthopper, *Nilaparvata lugens* species complex for the analysis of genetic polymorphisms. A total of 11 populations of *Nilaparvata* spp. were collected from 6 locations from Malaysia. Two sympatric populations of brown planthopper, *N. lugens*, one from rice and the other from a weed grass (*Leersia hexandra*), were collected from each of five locations. *N. bakeri* was used as an out group. Three oligonucleotide primer pairs, DALP231/DALPR'5, DALP234/DALPR'5, and DALP235/DALPR'5 were applied in this study. The unweighted pair group method with arithmetic mean (UPGMA) dendrogram based on genetic distances for the 11 populations of *Nilaparvata* spp. revealed that populations belonging to the same species and the same host type clustered together irrespective of their geographical localities of capture. The populations of *N. lugens* formed into two distinct clusters, one was insects with high esterase activities usually captured from rice and the other was with low esterase activities usually captured from *L. hexandra*. *N. bakeri*, an out group, was the most isolated group. Analyses of principal components, molecular variance, and robustness also supported greatly to the findings of cluster analysis.

**Keyword:** Genetic analysis; DALP; Brown planthopper complex; Rice; Biological species.