Allozyme Variation Among Biotypes of the Brown Planthopper *Nilaparvata lugens* in the Philippines

Ramesh C. Saxena, Cesar G. Demayo, and Adelina A. Barrion

Received 11 Sept. 1990—Final 25 Jan. 1991

Allozyme variation was studied in three *Nilaparvata lugens* biotypes infesting specific rice varieties and a biotype infesting a weed grass, *Leersia hexandra*. Of the 20 enzymes in *N. lugens* for which activity was noted, 9 were polymorphic. Eleven enzyme loci were monomorphic for the same allele in all biotype populations; the rest were polymorphic for two or more alleles. The mean number of alleles per polymorphic locus was 2.3, while the mean number of alleles per locus was 1.5; heterozygosity ranged from 0.02 to 0.06 (biotype 1 > biotype 3 > *Leersia*-infesting biotype > biotype 2). Allelic frequency differences were observed in five loci among the four biotypes. However, the coefficient of genetic identity (I) of 0.99+ showed that the four biotype populations were genetically close relatives or merely populations of *N. lugens* undergoing genetic differentiation.

**KEY WORDS:** *Nilaparvata lugens*, allozyme variation, biotypes, brown planthopper

**INTRODUCTION**

The brown planthopper, *Nilaparvata lugens* (Stål), is a major pest of rice in tropical Asia. It causes "hopperburn" and complete wilting and drying of rice plants (Dyck and Thomas, 1979) and also transmits the grassy stunt and ragged stunt viral diseases (Ling, 1977). Large-scale rice crop damage caused by the pest was reported in the 1970s in several South and Southeast Asian countries (Dyck and Thomas, 1979).

This work was partly supported by a financial grant received from the Directorate for Technical Cooperation and Humanitarian Aid, Switzerland.

1 Division of Entomology, International Rice Research Institute (IRRI), P.O. Box 933, Manila, Philippines.

2 Genetics Laboratory, University of the Philippines, Los Baños, College, Laguna, Philippines.
Host plant resistance has played a key role in the management of *N. lugens*. However, the stability of resistant varieties is threatened by the occurrence and evolution of insect pest populations capable of surviving on and damaging the varieties with known genes for resistance. In the case of *N. lugens*, these populations are known as biotypes. Studies conducted at IRRI in the Philippines have demonstrated the existence of three rice-infesting biotypes based on differential varietal reactions. Biotype 1 damages and survives on varieties without any genes for resistance to *N. lugens*, biotype 2 thrives on varieties carrying the *Bph* 1 resistance gene and on those susceptible to biotype 1, and biotype 3 can multiply on varieties having the *bph* 2 resistance gene and on those susceptible to biotype 1 (Seshu and Kaufman, 1980; Saxena and Barrion, 1985). Biotypes 1, 2, and 3 do not attack rice varieties with resistance genes *Bph* 3 and *bph* 4 and *Ptb* 33 carrying two resistance genes. Recently, another *N. lugens* population was found to infest a weed grass, *Leersia hexandra* Swartz, that grows abundantly in canals near irrigated rice fields in Southeast Asia (Domingo et al., 1983; Sogawa et al., 1984). The *Leersia*-infesting *N. lugens* population fails to survive on rice plants. Conversely, rice-infesting *N. lugens* biotypes do not thrive on *Leersia*. The differences in host-plant affinity are presumed to be genetically determined. Studies of hybridization between *N. lugens* biotypes showed differences in crossability (Saxena and Barrion, 1985).

Genetic differences and variability can be assessed precisely by analyzing allozyme variations (Lewontin, 1974; Ayala et al., 1972). We therefore studied the genetic differentiation in *N. lugens* biotypes by allozyme analysis.

**MATERIALS AND METHODS**

Adults of rice-infesting *N. lugens* biotypes 1, 2, and 3 and *Leersia*-feeding *N. lugens* were frozen at −70°C for at least 30 min prior to use. Individual insects were ground and homogenized in wells of a spot plate in 15 μl of a buffer solution (0.0086 M Tris–0.0046 M histidine, pH 8), using a glass rod. Small pieces (4 × 9 mm) of Whatman filter paper No. 3 were used to adsorb the homogenates and were inserted directly into starch gel slots. Horizontal starch gel electrophoresis was conducted at 4°C and 40 mA/gel slab. The starch gel was prepared using 14% starch (Sigma, St. Louis, Missouri) and 0.0086 M Tris–0.0046 M histidine buffer (pH 4.8). After electrophoresis, the gels were sliced and stained, following the procedure of Shaw and Prassad (1970).

Each gene locus was analyzed based on the number of (a) genes sampled, (b) alleles, and (c) bands in the heterozygotes and on whether the locus was polymorphic or monomorphic. Heterozygosity at each locus was estimated by direct counting of heterozygotes (Ho).