sowing with 8 second- to third-instar nymphs/seedling. Damage is rated when TN1 dies and rating is done twice at 2- to 3-d intervals. The final rating is used for evaluation. If only TN1 dies, the colony is biotype 1. If TN1, IR26, and Mudgo die, it is biotype 2; and if TN1, ASD7, and IR36 die, the population is biotype 3.

Mixtures of biotypes in a colony originating from a single pair may still exist in the third generation. They are detected when 10-20% of the seedlings of the resistant test varieties are killed. When this occurs we separately cage 20 individual pair of 3d-generation adults and repeat steps 2 to 6 (see figure). This cycle is repeated until a colony that exhibits the typical reaction of the desired biotype is selected.

Population growth study. A population growth study confirms the reaction of the colony selected from the seedling bulk tests. We place two pair of 3d-generation adults on 30-d-old potted TN1, Mudgo, and ASD7 plants in a mylar cage. The progenies in each cage are counted 30 d after infestation. If population is high only on TN1, the colony is biotype 1 ; on TN1 and Mudgo, it is biotype 2; and on TN1 and ASD7, it is biotype 3. When we get those results, we culture those insects for the screening program. □

A comparative study of some bionomic parameters of three species of green rice leafhopper (GLH)

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We studied the bionomics of two tropical GLH species (*Nephotettix nigropictus* and *N. virescens*) and a temperate species (*N. cincticeps*) in a 25+1°C room with 16-h photoperiod using a susceptible japonica variety (see table).

Some bionomic parameters of 3 species of green rice leafhopper, *Nephotettix* spp.[a]

		N. nigropictus	*N. virescens*	*N. cincticeps*
Incubation period (d)		7.81 ± 0.32 c	9.42 ± 0.11 a	8.31 ± 0.23 b
Developmental period (d) of nymphs	female	21.50 ± 0.18 a	19.11 ± 0.21 b	17.83 ± 0.10 c
	male	19.60 ± 0.16 a	18.43 ± 0.19 b	16.94 ± 0.11 c
Preovipositional period (d)		4.91 ± 1.25 a	5.43 ± 1.75 a	5.25 ± 1.11 a
Longevity (d)	female	19.35 ± 0.60 b	21.72 ± 0.65 a	16.82 ± 0.55 c
	male	13.85 ± 0.55 c	22.68 ± 0.50 a	15.55 ± 0.71 b
Fecundity (d)		198.0 ± 10.33 a	165.55 ± 8.74 b	140.19 ± 10.70 b

[a] In a row, means with the same letter are not significantly different at the 5% level (Duncan's multiple range test).

The three species significantly differed in mean incubation period. *N. virescens* had the longest, followed by *N. nigropictus* and *N. cincticeps.* Mean nymphal development for males and females of the three species was longest for *N. nigropictus* and shortest for *N. cincticeps.*

There was no significant difference in the mean preovipositional period of the three species.

Female *N. nigropictus* and *N. cincticeps* lived longer than males, but there was no significant difference in longevity between male and female *N. virescens.* Among females, those of *N. virescens* lived longest.

The mean number of eggs laid per female was highest for *N. nigropictus.* The difference between *N. virescens* and *N. cincticeps* was not significant. □

Intraspecific hybridization between rice- and grass-infesting brown planthopper (BPH) biotypes

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We conducted several studies to determine the taxonomic and biological status of a BPH *Nilaparvata lugens* (Stål) population that thrives on the common weed grass *Leersia hexandra* (L.) Swartz along irrigation canals on the IRRI farm.

The BPH population was strongly specific to *Leersia* and individuals died when caged on rice plants. Morphological evaluation of the grass-infesting (BL) BPH showed the population was heterogeneous but distinct from the rice-specific BPH biotype 1 (Bl), biotype 2 (B2), and biotype 3 (B3). There were also cytological differences.

Successful matings, oviposition, and egg hatchability in crosses between and within *N. lugens* biotype 1 (B1) and the grass-infesting biotype (BL), IRRI.[a]

Cross (female × male)	Successful mating (no.)	Eggs laid (no.)	Nymphs that emerged (no.)	Hatchability (%)
B1 × B1	10	558 a	520 a	94 a
BL × BL	10	160 b	154 a	95 a
B1 × BL	9	506 a	436 a	81 a
BL × B1	4	108 b	56 b	27 b
	x^2 = 17.14			

[a] Av of 10 replications. In a column, means followed by a common letter are not significantly different at 5% level.

We hybridized grass-infesting and rice-infesting BPH to determine the biological and evolutionary relationships and the way host specificity or virulence is inherited.

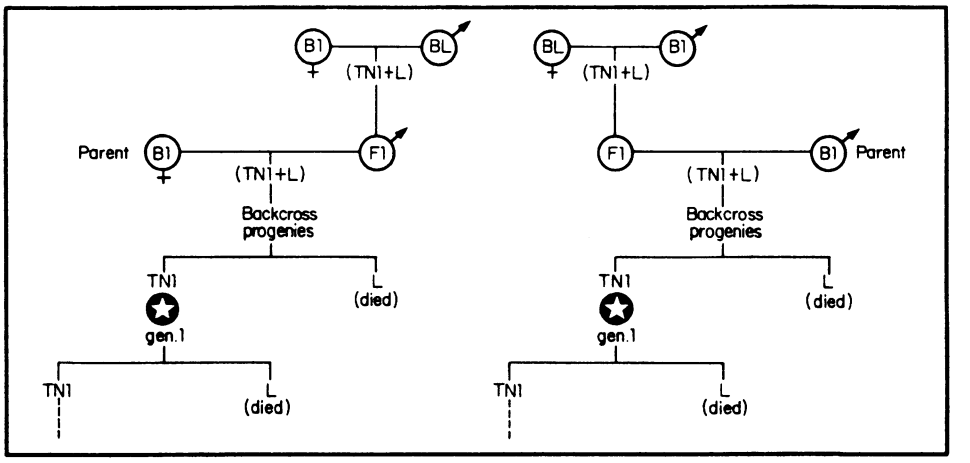
Genetic crosses of individual pairs of grass- and rice-specific populations were made on the grass host and on TN1 for B1, Mudgo for B2, and ASD7 for B3 enclosed together in mylar cages. Three generations of offspring and backcross progenies were produced from the Bl and BL cross. The cross of a female BL with a male B1 showed low successful mating

frequency and low egg hatchability percentage (see table). In the reciprocal cross, female B1 × male BL, there was a high mating frequency and egg hatchability, but survival of F_1 hybrids remained low. These results show there are pre- and post-mating barriers between the two populations.

Host specificity tests showed the ability of the F_1 progenies to feed and survive on rice (TN1) plants was dominant over that on the grass. Dominance was observed to the 3d generation of the genetic cross and the 1st generation of the backcross progenies (see figure), indicating that host specificity was controlled by a single major autosomal gene.

Preliminary cytological examinations of F_1 hybrids showed that the B1 parent contributed more to the total genome of the progenies. Chromosomal aberrations were also observed, which further confirmed the existence of some degree of reproductive isolation between the BPH populations.

Intraspecific matings were also possible between B1 and B2 or B3. However, mating frequency and egg hatchability were significantly higher in conbiotic crosses than in interbiotypic pairs. These discrepancies indicate the presence of some restrictions to the normal gene flow between those biotype populations. □



Scheme of direct crosses, reciprocal crosses, and backcrosses involving *N. lugens* biotype 1 (Bl) and the grass-infesting biotype (BL), IRRI.

Enzyme polymorphism in rice brown planthopper (BPH)

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Using horizontal starch gel electrophoresis, we analyzed enzyme polymorphism in BPH biotype 1 and 3 populations. Polymorphism was noted in 6 of 11 enzymes: catalase (CAT), esterase (EST), isocitrate dehydrogenase (IDH), malate dehydrogenase (MDH), malic enzyme (ME), and phosphoglucose isomerase (PGI). We carefully evaluated PGI, IDH, and MDH.

For each of those three enzymes, the variability of the main bands was explained by the polymorphism of one gene coding for dimeric enzymes. This was established by using two indirect lines of evidence: 1) the inferred heterozygous genotypes for a particular locus displayed an additional intermediate band more intense than both parental bands, and 2) the inferred genotype distributions observed in the two populations did not deviate significantly from the distributions predicted by the Hardy-Weinberg expectation (Table 1).

Table 1. Observed frequencies of genotypes in 3 protein loci of BPH biotype 1 and biotype 3. IRRI, 1983.

Locus	Genotype	Biotype 1			Biotype 3		
		Observed	Expected[a]	c^2	Observed	Expected	c^2
Pgi	105/105	30	22	9.01[b]	5	2	6.75[b]
	100/105	50	64	(df = 4)	16	23	(df = 4)
	100/100	54	47		80	77	
	95/105	0	2		0	0	
	95/100	3	3		1	1	
	95/95	1	0		0	0	
	Total[c]	138			102		
Idh	100/100	149	149	0[b]	154	154	0[b]
	93/100	12	12	(df = 1)	1	1	(df = 1)
	93/93	0	0		0	0	
	Total[c]	161			155		
Mdh	100/100	147	148	0.084[b]	153	153	0[b]
	100/109	14	13	(df = 1)	1	1	(df = 1)
	109/109	0	0				
	Total[c]	161			154		

[a]Compared with Hardy-Weinberg expectation. [b]Not significant at the 5% probability level. [c] Sample size.

Table 2. Allele frequencies in 3 protein loci of BPH biotype 1 and biotype 3. IRRI, 1983.

Locus		Allele frequency			Heterozygosity[a] (H)
		1	2	3	
Pgi	Biotype 1	0.018	0.583	0.398	0.38
	Biotype 3	0.005	0.868	0.128	0.17
Idh	Biotype 1	0.037	0.963	–	0.07
	Biotype 3	0.003	0.997	–	0.01
Mdh	Biotype 1	–	0.957	0.043	0.09
	Biotype 3	–	0.997	0.003	0.01
					$\overline{H}1 = 0.07$
					$\overline{H}3 = 0.02$

[a] The 5 other invariant loci were included in the calculation of $\overline{H}$.