survey of the plant wealth be conducted and priority be given to areas which are especially rich in genetic diversity. The survey, however, should not be merely taxonomic, but a dynamic one carried out by multidisciplinary field parties with the objectives of identifying the contributions which the proper exploitation of plant wealth can make to medicine, agriculture, forestry and other allied fields[10]. Stress should also be laid to survey the less-known wild plants, which the tribal people use to supplement their diet, especially during the long winters or in times of stress[11]. Information on distribution and structure of medicinally important plants obtained from interpretations of the IRS 1C/1D images in conjunction with ground data is being used to strengthen the ongoing studies of the economically important plant species.

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Inheritance of protein markers detecting polymorphism among rice genotypes with contrasting host response to green leafhopper

Green leafhopper (GLH) [*Nephotettix virescens* (Distant)] is one of the most destructive insect pests of rice throughout south and south-east Asia. It damages the crop as a pest by direct feeding and as a vector of rice tungro virus causing yield losses even up to 100% during tungro epidemics[1]. Host plant resistance is widely recognized as the reliable strategy to contain this pest, given the fact that diverse sources of resistance are available. Eight genes conferring resistance to GLH have so far been identified[2,3]. An attempt earlier by the authors to relate resistance–susceptibility of rice varieties to GLH with protein markers revealed the presence of the polypeptides of molecular weight 46.8, 42.7 and 33.9 kD together to be associated with susceptibility and their absence with resistance[4]. Although these polymorphic polypeptides could be used for detection of hybridity in GLH resistance breeding programme, understanding the mode of inheritance is necessary for using them as reliable markers in the selection process. Keeping this in view, a cross between the susceptible variety T(N)1 and resistant variety IET 15120, which differs distinctly in the expression of the three polypeptides was made and studied in the F_2 for both phenotypic response to the pest and electrophoretic analysis of seed proteins. Individual F_2 seeds were cut into two halves, of which the one with the embryo was grown into plants for screening against GLH at tillering stage by adopting tiller test method of screening[5], while the other de-embryonated half was used for extraction of seed proteins for electrophoresis.

Total proteins were extracted by suspending seed flour obtained from grinding individual F_2 seeds and the two parents in 50 µl of 0.5 M NaCl (pH 2.4) for 30 min at room temperature with intermittent mixing at an interval of 10 min. The suspension was centrifuged at 12,000 rpm at 10°C for 5 min. An aliquot (25 µl) of the supernatant was uniformly mixed with an equal volume of cracking buffer containing 0.125 M Tris HCl (pH 6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol and 0.01% bromophenol blue followed by denaturation in hot waterbath at 100°C for 1 min. SDS-PAGE of denatured protein samples was carried out[6]. Each sample (25 µl) was loaded in a lane of one-dimensional, 1 mm thick, 12% SDS-polyacrylamide gel and electrophoresed in a buffer containing 0.025 M Tris (pH 8.3), 0.192 M glycine and 0.1% SDS for 9 h at 50 V. The gels were stained in 0.125% Coomassie brilliant blue, destained, photographed and scored.

Phenotypic evaluation of the F_2 population against GLH suggested a single dominant gene to confer susceptibility. The χ^2 test confirmed the segregation ratio of 3S : 1R ($\chi^2 = 2.285$ with $P =$

Table 1. Segregation for GLH reaction in F_2 population

Phenotype	Observed (o)	Expected (e)	χ^2 (3S : 1R)
Resistant	15	21	2.285
Susceptible	69	63	

Table 2. Segregation of polypeptide bands associated with susceptibility/resistance in F_2 seeds

Combined occurrence of 3 polypeptides (46.8, 42.7 and 33.9 kD)	Observed (o)	Expected (e)	χ^2 (3 : 1)
Expression	60 (+)	63	3.1904
Non expression	13 (–)	21	

+, Present (susceptible); –, Absent (resistant).

0.05 and 0.01, non-significant; Table 1). Electrophoregrams of the corresponding 84 F_2 seeds revealed 60 of them to express the polypeptide bands of 46.8, 42.7 and 33.9 kD together, characteristic of the susceptible genotypes, suggesting single dominant gene to control the protein expression ($\chi^2 = 3.1904$ with $P =$ 0.05 and 0.01, non significant; Table 2). Relationship of GLH resistance/susceptibility with expression/non expression of the polypeptide bands showed the polypeptides 46.8, 42.7 and 33.9 kD to be present in 60 of 69 susceptible segregants and absent in 13 of 15 resistant individuals. In fact, all the 69 susceptibles phenotypes should have shown the combined expression of three polypeptides and all the 15 resistant lines should not have shown them. The observed deviation could presumably be due to incomplete or differential penetrance of the gene controlling the combined expression of the three polypeptides. The absence of all the three polypeptides observed consistently in the resistant donor variety IET 15120 and the resistant segregants might be due to either deletion or regulation of the structural gene(s) coding for these polypeptides or mutation in the base sequence of the structural genes/regulatory loci that inhibit their transcription or translation[7].

Monogenic segregation of seed protein expression, with its presence dominant over absence, has been reported earlier in several other crops[8–17]. The interesting part of this study however, is that three polypeptide bands determining together susceptibility/resistance reaction to the pest are under monogenic control. While the donor-specific polypeptide combination can be used as a reliable marker in breeding for GLH resistance, it is still to be ascertained, if the identified polypeptide combination would be the same or different for diverse sources of resistance. Further investigation is underway to determine donor/source-specific protein markers, which would be of great value in various gene deployment strategies, including gene pyramiding against GLH.

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