Introduction
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Rice is the major food grain crop of India. It is the staple food for more than 65% of its population. Accounting for 35.5% (42 million hectares) and 42% (84.5 million tonnes of milled rice) of food grain area and production respectively, steady advances in rice production is vital for the country to sustain self-sufficiency in food grains. It is estimated that rice production level should go up by 15-18 million tonnes by 2010 to ensure the current level of food grain and rice supply. The target achievement requires a growth rate around 1.8% per annum. Given the growth trend of the 90’s that is far below the minimum required level especially in the absence of many of the favourable growth factors of the 70’s and 80’s, achieving the target would be an uphill task. Among the possible yield maximization avenues contemplated, consolidation of yield is important. A recent yield gap analysis suggests that the still untapped yield potential in the currently available high yielding varieties is around 55% (Siddiq et al. 2000). Among the factors that contribute to the gap across ecologies, the major is pest-disease incidence, which brings down yields by 30%. In the management of the pests, use of host plant resistance has played a major role. Yet, there is no respite from pest caused crop losses either because of lack of strong sources of resistance or lack of efficient screening techniques against some of them.

Unlike brown planthopper, which assumed serious pest proportion on rice following the introduction of dwarf high yielding varieties, green leafhopper (GLH), *Nephotettix virescens* (Distant) was initially more a
vector for the dreaded viral disease, rice tungro virus (RTV) than a pest. Over the years it has become a pest-cum-vector and attention given to breeding for resistance to this pest has been indeed meagre.

Molecular markers have become quite handy to geneticists for developing high density linkage maps in a variety of crop plants. Rice is one wherein a nearly saturated molecular map with 2275 markers is available (Harushima et al. 1998). The molecular map is a potential tool for both basic and applied investigations. Its uses include study of the phylogeny of crop plants, mapping and cloning of genes of interest and marker assisted selection (Kole and Gupta 2001). The mapping and marker assisted selection have been of practical value to breeders especially in breeding for traits of complex inheritance and those selection of which on the basis of phenotype is not reliable. In rice, several genes of agronomic value have been mapped and they include resistance to blast, bacterial leaf blight, rice tungro virus, planthoppers, gall midge, early flowering, fragrance, fertility restoration, wide compatibility, photoperiod sensitivity, semi-dwarfism, thermosensitive male sterility and submergence tolerance (Khush et al. 1999).

Among the various factors that destabilize productivity in rice, biotic stress is the foremost. Host plant resistance has been extensively used in managing most of the pests. Nevertheless, crop losses due to pests continue to be considerable. More than lack of sources of resistance, pest incidence dependent screening approach has constrained the breeding for pest resistance especially when various gene deployment strategies are contemplated. This situation prompted rice

A major hurdle in combating biotic stresses is the prevalence of the pest in several biotype forms and resistance genes against each of them, most often are available in different genotypes. Development of broad-spectrum resistance, a lasting solution to multiracial pests requires mapping of all the genes before assembling them into a single genetic background. As for green leafhopper though biotype variation is known, it is not as precisely distinguished as in brown planthopper. Broadly they have been designated as Bangladesh biotype (Bb), Philippines biotype (Pb), and Indian biotype (Ib). Genes conferring resistance to them are also known. As regards to their mapping hardly anything has been done except detection of the restriction fragment length polymorphism (RFLP) marker RZ 262 linked to a dominant gene on chromosome 4 (Sebastian et al. 1996). Even then information is incomplete. There is no information with regard to the biotype they studied or the identity of the gene and its allelic relationship with already identified genes as well as the biotypes. Recently, Yasui and Yoshimura (1999) have detected two QTLs controlling antibiosis to both green leafhopper and green rice
Yield is genetically the most complex character which has several component traits (Nickell and Grafius 1969). It is the product of direct and indirect interactions of its component characters. In rice number of effective tillers, grain number and test grain weight primarily contribute to yield. These traits are quantitative in nature and are controlled by polygenes, each of which is of small individual effect. They are highly docile to environmental fluctuations as well. The continuous variation and absence of discrete segregation in these traits have been the serious hurdle for their mapping and accurate tracking. Biometrical approaches are the conventional means to determine the nature of gene action governing these traits.

The possibility of detecting markers associated with quantitative trait loci (QTL) has opened up new vistas in defining and handling quantitatively inherited traits at molecular level. It enables detection and location of gene blocks relating to yield and its major components on different chromosomes. Precise knowledge on yield related QTLs would be of immense value in the ongoing research pursuit for raising the ceiling of genetic yield in crop plants (Tanksley et al. 1989, Li 1999, Zhang and Yu 2000). QTLs controlling yield as well as many other traits have been detected in rice. They include plant height, tiller number, panicle number and 1000-grain weight (Wu et al. 1996), heading date and plant height (Li et al. 1995b, Yano et al. 1997), seed dormancy (Lin et al. 1998), 100 grain weight, grain number/panicle and grain

Random amplified polymorphic DNA (RAPD) marker (Williams et al. 1990) has emerged as a potential tool for construction of genetic linkage maps, mapping and tagging of economic genes and for elucidation of phylogenetic relationship (Kole and Gupta 2001). Linkage maps based on RAPDs have been developed in pine (Chaparro et al. 1992), Arabidopsis (Reiter et al. 1992), faba bean (Torres et al. 1993) rice (Hong et al. 1995) and papaya (Sondur et al. 1996). In rice RAPD markers have also been used in mapping or tagging of several economic genes including gall midge resistance (Mohan et al. 1994), photoperiod sensitivity (Maheswaran 1995), blast resistance (Naqvi et al. 1995), bacterial leaf blight resistance (Yoshimura et al. 1995, Zhang et al. 1996), thermosensitive genetic male sterility (Subudhi et al. 1997) and brown planthopper resistance (Jena et al. 1998). Practically, it involves a very simple, safe and relatively cheaper technique for detection and therefore, is very effective in molecular mapping as well as in molecular breeding.

Keeping in view the foregoing, the present investigation was undertaken for molecular mapping of genes controlling resistance to the
Indian biotype of GLH and three major components of yield with the following specific objectives.

1. Study of the mode of inheritance of resistance against green leafhopper (GLH) of the Indian biotype.
2. Construction of a molecular map in rice with RAPD marker loci and qualitative trait locus conferring GLH resistance.
3. Detection of quantitative trait loci (QTL) controlling GLH resistance and three major yield component characters including total tiller number, effective tiller number and 100-grain weight.