1. INTRODUCTION
Rice is the staple food for more than one half of the world's population and is cultivated worldwide under diverse agroclimatic conditions. Over 90 percent of the world's rice is produced and consumed in Asia. Most of the consumers, whose staple is rice, live in less developed countries. The United Nations' recent publications indicate that the world population would increase by 35% from 5.69 billion in 1995 to 7.67 billion by 2020. The increase will be more than 95% in the developing countries, whose share of the global population is projected to be around 84% in 2020. Over the period absolute population increase would be highest in Asia, where rice has to meet largely its food needs (Pinstrup-Anderson et al., 1996). Thanks to the plant type based high yielding varieties' introduction and extensive adoption of them since mid 1960s enabled many countries in the continent including India attain and remain till now self sufficient in food and rice. To sustain the current level of sufficiency, rice production has to grow by more than 40% by 2020. On the basis of modest income growth of 5 percent and the current consumption pattern, demand projection of milled rice for India has been estimated at 125 million tonnes by 2020 which amounts to an additional 40 million tonnes. With practically no scope for expansion of net area under rice and limited opportunities for bringing more area under irrigated crop, lack of high yielding varieties as yet to cater to the needs of the vast rainfed ecosystem and plateauing of productivity growth in high productivity areas, achieving of the projected target would be a challenging task (Siddiq, 1999). Consolidation of sizeable yield potential still remaining untapped in the currently available high yielding varieties and maximization of
yield levels of relatively favourable rainfed ecologies would help sustain the
growth for a couple of decades maximum. Such opportunities cannot sustain the
population growing indefinitely warranting need for technologies with new yield
thresholds. Four major strategies are being contemplated world over to raise the
ceiling to genetic yield. They are (i) exploitation of hybrid vigour (ii) tailoring of
new plant type with more efficient physio-morphological frame (iii) unlocking and
use of hitherto untapped yield genes hidden in the land races and wild species
of rice and (iv) engineering of biosynthetic pathway of starch biosynthesis. While
exploitation of hybrid vigor and development of new plant type varieties are now
distinct possibilities for commercialization, given the progress made in China, IRRI
and IARI (Khush, 1995). Sustenance of these strategies would depend on
availability and rational deployment of new variability for yield related traits.

Traits of economic importance such as yield and its components are of
complex inheritance governed by a number of genes with small effect. The yield
breakthrough achieved through plant type based varieties in the sixties has been
by exploiting a simply inherited non-lodging dwarf trait accessed from a single
source Dee-Geo-Wugen. Since then keeping high yields as the common
objective, breeding research has been to improve accessory characteristics like
resistance to biotic stresses, improved cooking quality etc., rather than for more
focused research to raise the genetic yield level. On so generated material
representing a very narrow genetic variation breeders continue to depend on for
progressive yield improvement. It is the notion among breeders that the
improved cultivar gene pool now in use possessed the required level of
variability (allelic variation) for achieving higher yield thresholds that continues to
dissuade them from going in search of additional yield genes from the least used
primitive land races and wild/weedy progenitor species of *O. sativa*. In fact, the
germplasm breeders depend on today represents not more than 15% of the total
variability available and over 85% of the genetic variation remains untapped in
the wild/weedy relatives (Wang *et al*, 1992). The importance of the wild/weedy
gene pool representing such a large variability is not however know beyond
finding it as a source of a few rare and valuable major genes. But for stray
reports, hardly there is any systematic study to the effect that wild germplasm as
well could be a source of variability for quantitatively inherited traits like yield.
Characteristic to quantitative traits, yield is conditioned by several genes having
predominantly either trait-enhancing "positive" or trait-depressing "negative"
alleles. Desirable positive alleles present at very low frequencies in the
wild/weedy species are invariably masked by the effects of the deleterious
negative alleles occurring at high frequencies. As a result the phenotype of the
wild/weedy species looks agronomically inferior leading to the wrong notion
among breeders that wild/weedy species component of the germplasm is of low
breeding value for yield enhancement. It is increasingly evident that largely due
to lack of techniques, potential variability for yield available in the wild
ergermplasm could not be assessed and utilized for long.

Rapid advances in cellular and molecular biology during the last two
decades have provided, among several, two innovative tools for genetic
manipulation of plant genomes viz., recombinant DNA technology for moving
genes across sexual barriers and molecular marker technology for achieving precision in selection. While genetic transformation is dependent on availability of candidate genes, tissue specific promoters and efficient transformation protocols, marker-assisted selection depends on availability of high-density map. The advent of DNA based markers such as Restriction Fragment Length Polymorphism (Helentjaris, 1987), Random Amplified Polymorphic DNA (Williams et al, 1990), Simple Sequence Repeats or Microsatellites (Jeffereys et al, 1985a), Amplified Fragment Length Polymorphism (Zabeau and Vos, 1993) and Inter Simple Sequence Repeats (Zeitkiewicz, 1994) have led to the development of high-density molecular maps for plant species. The maps have enabled mapping and tagging of several traits of economic significance. Using Restriction Fragment Length Polymorphism (RFLP) markers, the first ever genome map in plants was reported in maize (Helentjaris et al, 1986; Stuber et al, 1987) closely followed by tomato ( Tanksley and Hewitt, 1988), rice (McCouch et al, 1988) and Arabidopsis (Cheng et al, 1988; Nam et al, 1989). Mapping of microsatellite markers in plants was initiated by Zhao and Kochert (1992) in rice using tri-nucleotide repeat (GGC)\textsubscript{n}, followed by mapping of di-nucleotide repeats by Panaud et al (1995). The first report on gene tagging was in tomato (Paterson et al, 1988) followed by a series of reports on successful linking of characters of economic importance with molecular markers (Schachermayr et al, 1994). These pioneering efforts have led to better understanding of the genetics of quantitative variations and served as models for subsequent work to exploit the tool in breeding for complexly inherited traits.
like yield etc. Like Mendelian traits polygenic traits have also been mapped using marker association in a variety of crop plants including rice (Paterson et al. 1988). In rice, using highly saturated molecular map several gene blocks governing genetically complex polygenic traits like yield and its components could be tagged (Xiao et al., 1996b, c; Hayes et al., 1993).

The range of genetic variation for a trait is often believed to be much greater in exotic (wild) germplasm than among the cultivated types as the latter are usually derived from a small number of ancestral species and have been selected over centuries (Vaughan, 1994). Rice is one such crop endowed with rich genetic diversity but least exploited. The genus *Oryza* comprises 21 wild and 2 cultivated species representing nine different genomes. *Oryza rufipogon* and *O. nivara* closely related to and progenitors of the world over cultivated Asian cultivar *O.sativa* and *O.barthii* and *O. longistaminata* corresponding wild relatives of the African cultivar *O.glaberrima* sharing the AA genome along with cultivars account for the maximum variability. Utilization of these wild relatives, especially *O. rufipogon* and *O. nivara* is critical to future improvement of Asian cultivated rice considering their compatibility with the latter and the fact that sizeable allelic variation of genes related to traits of complex inheritance still remains in them uncaptured in the course of origin and domestication of cultivars (Tanksley and McCouch, 1997). As experienced in other crop species the genetic potential of the progenitor species growing sympatrically with *O. sativa* has been evident so far from a few valuable Mendelian genes accessed from them and utilized in the improvement of cultivated rice. Whereas *O. rufipogon*
provided the widely used WA (wild abortive) source of cytoplasmic male sterility for hybrid rice production (Yuan, 1997). *O. nivara* proved a valuable source for the rare genes for resistance to grassy stunt virus, sheath blight, bacterial leaf blight and abiotic stresses such as acidic soils (Vaughan, 1994; Brar and Khush, 1997; Khush *et al*, 1999; Dalmacio *et al*, 1996). As against the foregoing reports on the utility of the wild species limited to simply inherited traits, the recent investigations using high-density molecular markers have shown wild species of rice to possess a rich reservoir of genes that directly or indirectly influence grain yield (Xiao *et al*, 1998). The pioneering report has aroused interest all over to search for new allelic variations of yield genes in rice and explore the possibility of using them (Xu, 1997).

During the last five years as many as 70 yield related unique QTLs have been identified in rice by various workers (Zhang and Yu, 2001). Significantly the two unique yield influencing QTLs *yld1.1* and *yld2.1* identified in an accession of *O. rufipogon* by Xiao *et al* (1998) have been exploited by conventional breeding by Chinese breeders to raise further the yield ceiling (Yuan, 2001). Keeping in view the unlimited potential of wild/weedy species of rice for yield genes as evident from the foregoing and the high density molecular map now available to identify and tag new yield related QTLs, the present study has been undertaken with the following two specific objectives:

(i) Identification of prospective *Oryza rufipogon* accession for use as donor having unexploited genetic potential for yield.
(ii) Mapping of unique molecular marker-associated yield QTLs identified in the wild species.

The salient findings therefrom have been presented in this thesis.