1. INTRODUCTION

Wheat is one of the most important cereal crop and serves as a staple food for millions in the world. In India, wheat is the second most important cereal crop after rice occupying 27 million hectares with an annual production of 74 million tons during 1999-2000 (Anonymous, 2000). Wheat belongs to the family Poaceae of the Tribe Triticeae and subtribe Triticinae. The commercially grown wheat includes the common bread wheat (Triticum aestivum L. em. Thell.), macroni wheat (T. durum Desf.) and emmer wheat (T. dicoccum Schrank.).

In early 1960’s, the total wheat production in India was about 12 million tonnes per annum, which increased to around 74 million tonnes in the year 1999-2000. This phenomenal increase of five folds in production was accompanied by the adoption of semi-dwarf wheat varieties, which attributed both to the genetic potential and yielding ability of new varieties and to the more intensive crop husbandry.

As in most other crops, the genetic variation in cultivated wheat has been greatly eroded under modern agricultural systems. In recent years, there has been stagnation in productivity in newly released wheat varieties in comparison to the improvement achieved in earlier released varieties. Wheat yield in India grew at a rate of 3.5% during 1940-82 and declined during the next two decades to 2.9%. This decline can be attributed due to (i) lack of improvement in the genetic yield potential, (ii) susceptibility to diseases. There are twelve important wheat diseases prevailing in India, among which the black (stem) rust (Puccinia graminis Pers. f. sp. tritici Eriks and Henn), brown (leaf) rust (P. recondita Rob ex Desm f. sp. tritici) and yellow (stripe) rust (P. striiformis Westend f. sp. tritici) are ranked the most destructive, causing 10-100% annual loss of wheat production (Sharma et al., 1983a).
Rusts have been historically the most destructive of wheat diseases and cause substantial losses in grain yield worldwide. Stem rust is highly destructive in the temperature range of 15 to 30°C, where as leaf rust rapidly develops and causes considerable destruction in the temperate range of 10 to 30°C. Stripe rust is restricted to cooler regions (1 to 15°C). In the historical records the rust epidemics have occurred from time to time in India (Nagarajan and Joshi, 1975). In 1946-47 rust epidemic caused a loss of nearly 2 million tonnes of wheat (Asthana, 1948). Leaf and stripe rusts appeared in epidemic form in Northwestern region of the country resulted in the loss of 0.8 to 1.5 million tonnes of wheat in 1971-72 and 1972-73 (Joshi, 1975). The epidemic of leaf rust swept over the entire Uttar Pradesh and parts of Bihar in 1980 causing a loss of approximately 1 million tonnes (Joshi et al., 1984).

Several fungicides are reported to control wheat rusts, but they are highly expensive and beyond the means of poor wheat growers in India. Breeding for durable resistance has special significance for developing economy where the frequent replacement of cultivars entails an enormous drain on limited resources. A judicious integration of the genetic studies and breeding efforts is imperative in evolving high yielding disease resistant cultivars and containing the spread of the rusts.

The cultivation of resistant varieties in a given geographical area is followed by changes in the pathogen population enabling the pathogen to overcome the resistance gene(s). This necessitates a continuous search for effective genes and their efficient deployment in a geographic area. With the pathogen displaying a high degree of pathogenic variability, it is important to evaluate the breeding materials against these potential pathotypes. While detailed knowledge of the genetic basis is not essential for an effective resistance breeding (Simmonds, 1985), much can be gained if the genetics of resistance is known.
Development of wheat cultivars carrying diverse rust resistance genes with a broad range of effectiveness and their geographical deployment depending on the race flora may prove as effective barrier to control the spread of rust. The common experience is that new pathogenic races often overcome resistance soon after the extensive cultivation of resistant cultivars. Therefore, breeding rust resistant cultivars is should be looked after as a continuous process.

Desirable characters from any of the 300 or more species within the Triticeae can be transferred to wheat by simple backcrossing and selection. Markers can be used to verify and follow the alien chromosome / chromosomal segment / gene / gene complex introgressed during backcrosses and selection. The usefulness of markers such as morphological, biochemical and genetical markers in the identification and/or confirmation of introgressed gene(s) in wheat breeding need no emphasis.

The Indian wheat cultivars namely, MACS 2496, HD 2687, and PBW 343 are highly popular wheats being cultivated extensively by farmers in various parts of the country despite their susceptibility for leaf and stem rust pathogens. All the three wheat cultivars were completely free from stripe rust because of presence of highly effective stripe rust resistance gene Yr9. In order to improve these wheat cultivars, in the present study, an attempt has been made to transfer genes imparting resistance against leaf and stem rusts to the above three Indian wheat cultivars. The ultimate objective of this exercise was to develop either new cultivars or superior genetic stocks for use in wheat breeding.

The germplasm is the reservoir of genetic diversity, which is often exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for economic traits must exist in the germplasm for profitable exploitation following recombination breeding or selection. Generally a large
number of varieties are available to the breeder in the form of germplasm of a species and it is very difficult to evaluate breeding value of each of them. Many of these varieties might be quite similar to each other with respect to their genetic content. Therefore, the entire germplasm should be classified into various groups of similar or more closely related varieties, so that only one or two varieties from such groups may be picked up for involving then in hybridization programme.

The importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as wheat to recover transgressive segregants has also been repeatedly emphasized. However, the genetic diversity of selected parents is not always based on factors such as geographic diversity or ploidy level. Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as $D^2$ statistic and non-hierarchical Euclidean cluster analysis. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters.

Inter- and intraspecific crosses in wheat often produce different kinds of ‘hybrid weakness’ such as hybrid necrosis, hybrid chlorosis and hybrid dwarfness, among which hybrid necrosis and hybrid chlorosis are more frequently met with. The hybrids in all these cases are lethal or semi-lethal and are often unproductive. The occurrence of these phenomena not only interferes with the choice of parental material but also restricts the productivity of the crosses. Although both hybrid necrosis and hybrid chlorosis are lethal or semi-lethal resulting in progressive death or debility of $F_1$ hybrids, both kinds of weakness are distinguishable phenotypically. Therefore, in order to preclude the problem of these problems in the $F_1$ wheat hybrids, identification of non-carrier lines for necrosis and chlorosis is necessary for their appropriate involvement in hybridization programmes.
Wheat proteins are responsible for the viscoelastic and bread making properties of dough. Glutenin are the seed storage protein of wheat that imparts elasticity to dough, has a high aggregate molecular weight, being built up of subunits. The High Molecular Weight (HMW) subunits of glutenin are coded by genes at three genetically unlinked loci, Glu-A1, Glu-B1 and Glu-D1, which occur on wheat chromosomes 1A, 1B and 1D, respectively (Payne et al., 1984). Each locus exhibits extensive allelic variations and the allelic protein subunits are easily distinguished by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE). HMW subunits of glutenin play important role in determining the functional (bread making) properties of wheat flour. Study of genetic variations in these subunits is being exploited in breeding programme to improve flour properties. Consequently seed storage proteins characterization becomes an important tool in wheat breeding programmes to develop new varieties with improved quality.

In view of the above, the present study is involved with the following objectives.

1. Breeding for rust resistance in hexaploid wheat

(i) Transfer of nine specific rust resistance genes [5 leaf rust (Lr) resistance genes and 4 stem rust (Sr) resistance genes] viz. Lr19, Lr24, Lr28, Lr32, Lr37, Sr24, Sr25, Sr36, Sr38, present either singly or in combination (linked) derived from six hexaploid wheat stocks, to three popular Indian hexaploid wheat cultivars namely MACS 2496, HD 2687, and PBW 343 by simple backcrossing and selection.

(ii) Evaluation of constituted near-isogenic lines for rust resistance and desirable agronomic characters.

(iii) To make rust resistant stocks available in good wheat genetic background.

(iv) Confirmation of transfer of rust resistance gene(s) through morphological, genetical (rust inheritance and monosomic analysis), and biochemical studies.
II. Genetic divergence and character association in hexaploid wheat

i) To determine the magnitude of variability among the germplasm collection for yield and morpho-physiological traits.

ii) To determine the grouping pattern of genotypes in different clusters.

iii) To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme to improve the grain yield.

iv) To study the genetic divergence and character association in different wheat cultivars.

III. Hybrid weakness in hexaploid and tetraploid wheat

(i) Identification of wheat genotypes for hybrid necrosis and hybrid chlorosis in Indian hexaploid (*Triticum aestivum*) and tetraploid (*T. dicoccum* and *T. durum*) wheats by crossing them separately with three hexaploid wheat testers.

(ii) To determine the degree of necrosis and degree of chlorosis in both hexaploid and tetraploid wheat cultivars.

IV. Allelic variation of High Molecular Weight Glutenin subunits in Indian hexaploid wheat

(i) To determine the diversity among the HMW glutenin subunits in 32 Indian hexaploid wheat cultivars.

(ii) To study the allelic variation of HMW glutenin subunits in these wheat cultivars.

(iii) To determine the *Glu-1* quality score of Indian wheat cultivars.