BHARATHIAR UNIVERSITY
Cytogenetics Laboratory, Department of Botany, Coimbatore – 641 046, India.

Evaluation of near-isogenic wheat lines carrying various stripe rust-resistance genes.

V.R.K. Reddy.

A total of 28 NILs are available in the genetic background of two Indian wheat cultivars HW 1015 and HD 2408. These lines, which carry one or more rust-resistance genes (leaf rust, stem rust, or stripe rust) present either singly or in combination, were evaluated for rust resistance and yield performance. Fourteen different wheat donor parents contributing a total of 17 stripe rust-resistance genes (*Yr5, Yr8+Yr19, Yr9, Yr10, Yr11, Yr12, Yr13, Yr14, Yr15, Yr3a+Yr4a+Yr16, Yr17, Yr28, Yr29, Yr30*), present either singly or in linked condition with the same stripe rust-resistance genes or other wheat rust-resistance genes, are involved in the NILs. Both the Indian wheat parents are completely susceptible not only to stripe rust but also to stem and leaf rust. The severity of stripe rust in these cultivars ranged from 70S (HW 1015) to 90S (HD 2408). Chemically treated control plants were found completely free from all the three types of wheat rust. Except for *Yr28* in HW 1015 and HD 2408 and *Yr8+Yr19* and *Yr17* in HD 2408, all other stripe rust-resistance genes provided high degree of resistance (F to 10R reaction) in both the Indian wheat cultivars. Near-isogenic lines with *Yr28* showed a 10MS type of moderate susceptibility in both the Indian wheats. Similarly, the stripe rust resistance gene complex *Yr8+Yr19* and stripe rust-resistance gene *Yr17* did not provide adequate resistance in HD 2408. These lines exhibited a 10MS to 20S type of susceptible reaction to stripe rust. Chemically treated control plants exhibited a higher grain yield compared to the untreated control. The grain yield of the NILs with various stripe rust-resistance genes showed a significant increase in grain yield when compared to both the untreated and chemically treated control. The degree of increase in grain yield in the NILs was considerably higher when compared to the untreated control. In some NILs, grain yield was less than that of the chemically treated control.

Confirmation of specific rust-resistance gene Lr19 through use of a molecular marker.

S. Premalatha and V.R.K. Reddy.

In a backcross-breeding program, genes conferring rust resistance were transferred into several Indian hexaploid wheat cultivars. The constituted NILs with leaf rust-resistance gene *Lr19* together with the respective recurrent wheat parents HW 517, HD 2135, HD 2204, and UP 301 and the donor source stocks were screened for polymorphism at the molecular level using RAPD primers. Primer S73 showed polymorphism corresponding to all the resistant NILs including the donor, compared to the recurrent parents. One band of 728 bp was present in the source stock and in all the NILs but was absent in the recurrent parents.

Rheologic and baking performance of composite flours.

V.R.K. Reddy.

Composite flour samples were prepared by blending commercial wheat flour 'resultant atta' (a mixture of part of clear/tail end flour, fine bran, and germ) with various legumes, i.e., sorghum, soya, and maize in different proportion to study their rheologic and baking performance. Sixteen treatments were prepared by blending commercial wheat flour with the above materials in different proportions for the preparation of chapatti and parota. Rheological behaviour of the composite flours showed decrease in water absorption and increase in dough development time. The dough rheological properties of the different flours, including Farinographic and Extensographic properties, also were studied for correlating with their protein compositions. Sensory attributes of chapatti, such as color, flavor, taste, texture, chewing ability, and folding ability, decreased during the storage period. We noticed that soya gives a whiter look and puffiness to the chapaties and parota.

Genetic divergence in bread and durum wheat.

K.Thamayanthi and V.R.K. Reddy.

We evaluated 150 genotypes of bread and durum wheat, including Indian and exotic collections, for various agronomic characters following a nonhierarchical Euclidean cluster analysis. Genotypes were grouped into 13 clusters with a variable number of genotypes. Heterogenous genotypes of original place of release and different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. On the basis of the data on genetic divergence and mean performance of yield and other traits, five diverse and superior genotypes were selected, HI 1077, WH 147, WH 542, HD 2285, and UP 262. These genotypes may be involved in multiple crossing program to recover transgressive segregates.

HMW-glutenin subunit composition in Indian hexaploid wheat cultivars.

V.R.K. Reddy.

Thirty-two cultivars of bread wheat were analyzed for allelic variation in the HMW-glutenin subunits by SDS-PAGE. A total of nine alleles were identified in the 32 cultivars. At the *Glu-A1* locus, the alleles a and b encoded 1, 2-HMW-glutenin subunits. The HMW-glutenin subunits 2* was found in 22 of the 32 cultivars. Ten cultivars had subunit 1 (the a allele). At the *Glu-B1* locus, the alleles a, b, c, and d encoded glutenin subunits 7, 7+8, 7+9, and 6+8, respectively. Eight cultivars had glutenin subunit 7, four had subunit 7+8, 16 had the subunits 7+9, and four had subunits 6+8. At the *Glu-D1* locus, the alleles a, b, c, and d encoded HMW-glutenin subunits 2+12, 3+12, and 5+10, respectively. The *Glu-1* quality score 8 is present in a large number of cultivars.

CH. CHARAN SINGH UNIVERSITY
Molecular Biology Laboratory, Department of Genetics and Plant Breeding, Meerut-250 004, U.P., India.

P.K. Gupta, H.S. Balyan, J. Kumar, A. Mohan, A. Goyal, A. Kumar, R.R. Mir, S. Kumar, R. Kumar, S. Banerjee, and M. Das.

Development and use of molecular markers for wheat genomics and breeding.

Construction of framework linkage maps using trait specific intervarietal RIL populations. Three framework linkage maps using three mapping populations have been prepared in our laboratory for QTL interval mapping of various agronomically important traits. The three mapping populations were originally prepared for the following three traits: (i) grain protein content (GPC); (ii) grain weight (GW), and (iii) preharvest-sprouting tolerance (PHST).

Updating the framework linkage map of the GPC population. We earlier prepared a framework linkage map for the GPC population using 171 SSR markers. The map spanned a genetic distance of 3,272.4 cM and had large gaps in certain regions, which adversely affected the precision of QTL mapping studies. In view of this, the following two exercises were undertaken.

(a) Genotypic data on a set of 39 markers (including ISSR, SSR, and RAPD markers) was procured from the NCL, Pune (India), as a collaborative activity.

(b) An additional set of 124 SSRs was used to study polymorphism between parents of GPC population (WL711 and PH132). Forty-six of the above 124 SSRs showed polymorphism and were used for genotyping of RILs.