5. SUMMARY AND CONCLUSIONS

The investigation on “Assessment of genetic diversity amongst winter × spring wheat and triticale × wheat derived wheat doubled haploids using molecular and morpho-physiological markers” was undertaken to characterize the wheat genotypes at the morpho-physiological and molecular level.

The experimental material comprised of 196 wheat genotypes, which were evaluated in Simple Lattice Design with two replications during rabi 2014-15 at the Experimental Farm of the Department of Crop Improvement CSK HPKV, Palampur. The molecular work was carried out in the Molecular Cytogenetics and Tissue Culture Laboratory, Department of Crop Improvement, COA, CSK HPKV, Palampur. The data were recorded for various morpho-physiological traits viz., days to 50% flowering, days to 75% maturity, plant height, tillers per plant, spikelets per spike, biological yield per plant, grains per spike, seed yield per plant, harvest index and 1000-seed weight. Statistical analysis was done as per Federer (1963), character association between yield and yield components through correlation and path analysis given by Al-Jibouri et al. (1958), Dewey and Lu (1959) and Mahalanobis $D^2$ statistics (1936). Molecular analysis was also done for diversity studies using SSR markers.

Analysis of variance revealed significant differences among wheat genotypes for all the morpho-physiological traits studied, suggesting prevalence of wide range of genetic variability and scope of selection for these traits.

On the basis of mean performance for seed yield, four genotypes viz., TWDH-6, HPW-236, HPW-147 and HS490 were superior, whereas DH-6, DH-7, DH-30, DH-106, DH-109, DH-110, DH-128D, DH-137, DH-157, DH-192, DH-193, DH-776, TWDH-2, HPW-349, DBW-17, DBW-621-50, HS507, VL907 and PBW-550 were statistically at par with the best check Him Palam Gehun-1. So, these genotypes need to be further evaluated in multilocational trials over the years or can also be utilized in future hybridization programme.
High PCV and GCV observed for seed yield per plant and harvest index indicated scope for effective selection. High heritability coupled with high genetic advance observed for seed yield per plant and harvest index indicated additive genetic control in the inheritance of these traits suggesting that selection would be effective for these traits.

In general, genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients, indicating the inherent association among the various traits. Seed yield per plant showed significant and positive correlation with plant height, tillers per plant, grains per spike, 1000 grain weight, biological yield and harvest index indicating that selection for higher seed yield per plant through these traits would be effective. Path analysis revealed positive and high direct effects on seed yield per plant by harvest index followed by biological yield per plant. Highest indirect effects on seed yield per plant through harvest index was exhibited by 1000 grain weight followed by grains per spike and tillers per plant.

Genetic diversity analysis on the basis of D^2-statistics, grouped 196 wheat genotypes into 6 clusters. Maximum genotypes were placed in cluster I. The highest inter-cluster distance was observed between cluster II and III. The highest intra-cluster distance observed for cluster VI revealed that genotypes within the same cluster were quite diverse; hence selection of parents within cluster would also be effective. Cluster mean for different traits showed that the cluster II and VI exhibited maximum divergence for majority of traits viz., days to 50% flowering, spikelets per spike, grains per spike, plant height, seed yield per plant and harvest index. Days to 50% flowering followed by days to 75% maturity and seed yield per plant contributed maximum towards genetic divergence.

Principal component analysis revealed 65.33 per cent variation which was elaborated by the first four significant principal components. The first principal component (PC1) was the most important and explained 25.49 per cent variation followed by PC2 (16.1 per cent), PC3 (13.5 per cent) and PC4 (10.1 per cent). In all the principle components, harvest index resulted in highest positive value followed by days to maturity and plant height. So these traits should be maximum contributors towards genetic divergence. Hence, selection on the basis of these characters would be effective for yield improvement in wheat.
Molecular markers (SSR) were effective in the gene pool characterization. Dendrogram based on DARwin helped in grouping different genotypes into three major clusters and cluster I and II were further divided into 5 subclusters. Principal Coordinate Analysis successfully delineated genotypes into 4 subclusters, first principal component explained 14.95 per cent of the total variation, whereas the second component explained 8.11 per cent variation and the third one explained 4.36 per cent variation of the data. STRUCTURE also divided the genetic stock into three major gene pools. It further confirmed the grouping of genotypes found in the principal component analysis and DARwin analysis. Very little introgression between the genotypes was observed. Analysis of molecular variance, (AMOVA) depicts high proportion of variability among individuals, that is, 81 per cent of total variation, whereas 19 per cent genetic variation among population.

Based upon the rust and powdery mildew screening studies, DH-47, DH-52, DH-85 and DH-87 expressed very strong resistance to both the diseases but need critical evaluation for further use in the breeding endeavours. The drought screening studies revealed that there was a significant reduction in the seedling characteristics with increase in stress levels. Based upon the screening studies DH-40 and DH-100 appear to be promising for drought.

CONCLUSIONS

- Sufficient genetic diversity was observed among all the genotypes using analysis of variance, $D^2$-statistics and molecular markers.
- On the basis of mean performance for seed yield, four genotypes viz., TWDH-6, HPW-236, HPW-147 and HS490 were superior to the best check Him Palam Gehun-1.
- The magnitude of PCV was higher than GCV for all the traits studied indicated the influence of environment on these traits. High heritability coupled with high genetic advance was observed for seed yield per plant and harvest index.
- Seed yield per plant was positively correlated with plant height, tillers per plant, grains per spike, 1000-grain weight, biological yield and harvest index.
Harvest index followed by biological yield per plant were observed to be best selection indices for increasing seed yield per plant. Highest indirect effects on seed yield per plant through harvest index was exhibited by 1000-grain weight followed by grains per spike and tillers per plant.

- Days to 50% flowering followed by days to 75% maturity and seed yield per plant contributed maximum towards genetic divergence.
- $D^2$ statistical analysis grouped genotypes into six clusters. Maximum genotypes, that is, 157 genotypes were placed in cluster I.
- Principal component analysis revealed 65.33 per cent variation which was elaborated by the first four significant principal components.
- The SSR markers characterized the genetic stock into three major clusters, out of which, cluster I and cluster II exhibited sub clustering with each of them having five sub clusters.
- Further grouping of genotypes based on DARwin analysis was confirmed by principal component analysis and population structure.
- A total of 114 genotypes were found common while comparing molecular and morphological clusters, thereby exhibiting the congruence between morphological and SSR data.
- DH-47, DH-52, DH-85 and DH-87 expressed very strong resistance against rust and powdery mildew diseases, whereas DH-40 and DH-100 appear to be promising for drought.
- The present study on panel of diverse wheat genotypes revealed that the population structure was mainly based on genetic origin along with moderate to high gene flow. The entire genetic stock has been clearly delineated both by morphological as well as SSR marker analysis. This study also paved the way for rational use of diverse wheat genotypes in the future breeding programmes.