2. REVIEW OF LITERATURE

Genetic improvement of the crops is very essential for enhancing their productivity. As germplasm is the major source of genes for crop improvement, characterization of the accessions, genetic studies of the population and selection of a core collection are essential for effective utilization. The classical methods of diversity studies are based on morphological characters which are influenced by various environmental factors. However, the molecular markers, which are unrestricted in number and not influenced by the environment, have the ability of sampling diversity directly at the genome level. Biotechnological approaches involving isozyme as well as DNA markers are increasingly being used for diversity studies. Different types of DNA markers have been used for genetic studies in crop plants including restriction fragment length polymorphisms (RFLPs), random amplification of polymorphic DNAs (RAPDs), amplified fragment length polymorphisms (AFLPs) and microsatellites or simple sequence repeats (SSRs). Among different classes of molecular markers, SSR markers are useful in variety of applications like plant genetics and breeding because of their reproducibility, multiallelic nature, co-dominant inheritance, relative abundance and good genome coverage. SSR markers have proved to be an efficient tool to link phenotypic and genotypic variation. The relevant literature pertaining to various aspects of the present study are reviewed in order to obtain a thorough understanding of the subject and have been described under the following headings: 2.1 Genetic Variability 2.2 Correlation coefficient analysis 2.3 Path coefficient analysis 2.4 Mahalanobis D2 analysis 2.5 Principle Component analysis 2.6 Molecular analysis 2.7 In vitro screening of wheat cultivars for drought 2.8 Screening for rust and powdery mildew 5
2.1 Genetic Variability Sheoran et al. (1986) studied 29 genotypes of bread wheat and reported significant differences in spike length, 1000 grain weight, grains per spike and plant height. Singh (1989) reported high phenotypic coefficient of variation (PCV) for tillers per meter (13.11%), followed by grains per ear (12.89%) and low for characters like plant height (4.85%) and days to maturity (1.31%) however, moderate coefficient of variation was reported for spikelets per spike, biological yield, 1000 grain weight, harvest index and economic yield. High genotypic (GCV) and phenotypic coefficient of variability (PCV) for tillers per plant and moderate for spike length, spikelets per spike and grain yield was reported by Singh et al. (1997). Krishnawat and Sharma (1998) studied 98 genotypes of wheat for 11 yield and agronomic characters and reported high GCV and PCV for blade area, weight of grains per spike, whereas moderate for spike length, grain yield per plant, peduncle length, harvest index and biological yield per plant. High estimates of heritability and genetic gain were recorded for flag leaf blade area, weight of grains per spike, grain protein content, grain yield per plant, biological yield per plant and harvest index. High variability for grain yield, tiller number, grain weight per spike; moderate for 1000 grain weight and low for plant height and harvest index was reported by Sharma et al. (1998). Thakur et al. (1999) analyzed 21 F₂ populations and reported high genetic coefficient of variation, heritability and high genetic advance for plant height, ear length, number of tillers per plant and grain yield. Selection for number of tillers per plant and ear length was recommended for improving grain yield. Shukla et al. (2000) studied 25 cross combinations of bread wheat and reported high GCV for grain yield per plant, 1000 grain weight and harvest index. Prasad and Pandey (2001) assessed genetic diversity in 42 genetic stocks of Triticum species and observed high heritability for plant height, productive tillers per plants, 1000-grains weight and protein content. 6
Pawar et al. (2002) observed genetic variability for number of days to 50% flowering, plant height, number of productive tillers per plant, length of spike, number of spikelets, grains per ear, 1000-grain weight and grain yield. They recorded highest GCV and PCV for plant height. Heritability for all the characters examined ranged from 84.13-99.75%. Genetic advance and genetic gain were highest for plant height and lowest for number of productive tillers per plant. Dwivedi et al. (2002) reported the highest genotypic and phenotypic coefficient of variation for total biomass followed by grain yield per plant, grain weight per ear and tiller number per plant. Similarly, high variability and genetic advance were also observed for these traits along with plant height. Kumar et al. (2003) evaluated 24 wheat cultivars for study of genetic variation for yield and yield components. They reported wide range of variation for plant height, number of grains per ear and 1000-grain weight. The estimates of GCV and PCV were low for number of days to heading and number of days to maturity. The remaining traits recorded moderate PCV and GCV estimates. Mahak et al. (2003) in their studies on the yield and its contributing characters reported significant genetic variation for all traits. Harvest index and number of grains per spike exhibited the highest GCV (18.71 and 18.05) and PCV (21.78 and 20.35). Mondal and Kaur (2004) studied bread wheat cultivars for root weight per plant, root length, number of effective tillers per m², number of grains per ear, 1000-grain weight and grain yield per plot. The estimation of heritability and genetic advance was substantially moderate to high for number of tillers per m² and grain yield per plot. Grain yield per plot was positively and significantly correlated with root weight per plant and number of effective tillers per m². Kumar and Mishra (2004) evaluated 30 diverse wheat cultivars for genetic variation. The highest genotypic coefficient of variation was observed for number of tillers per plant and kernel yield. Shukla and Singh (2004) in their studies on bread wheat reported that number of grains per spike, grain yield per plant, total biomass per plant, straw weight per plant and spike weight per plant had high heritability coupled with high genetic advance. 7
Malik et al. (2005) studied 210 genotypes of bread wheat including indigenous and exotic collection for yield and its attributing characters and the results expressed that the variance showed significance for the characters, such as number of tillers per plant, ear length, 100-grain weight, biological yield, grain yield and harvest index. High PCV was obtained for number of tillers per plant, grain yield, biological yield and harvest index. High to moderate heritability coupled with high to moderate genetic advance was exhibited for characters viz., plant height, spike length, grains per spike, spikelets per spike, sedimentation value and 1000-grain weight in bread wheat as reported by Porwal et al. (2005). Rafat and Malik (2005) showed that genetic diversity and variability in the parental material was obtained for number of tillers per plant, grain yield, biological yield and harvest index. Among the other traits plant height, number of spikelets per ear, 1000-grain weight and ear length showed moderate variability, while days to heading and days to maturity showed relatively low variability. Cheema et al. (2006) evaluated various wheat genotypes for genetic variability and results revealed that genotypes and their cross combinations exhibited genetic variability for all the plant traits studied. Singh and Chaudhary (2006) in their studies on the phenotypic and genotypic variance, heritability, genetic advance, correlation coefficients for yield and yield contributing traits observed that harvest index and biological yield per meter had direct positive effect both at genotypic and phenotypic level across the entire environment. Higher heritability was observed for plant height and its components. However, the heritability was in general found to lower under moisture stress conditions. Plant height, peduncle length and seedling dry weight showed positive correlation with grain yield at genotypic level. Khan and Muhammad (2007) observed that phenotypic and genotypic coefficients of variability ranged from higher to moderate for grain yield, 1000-grain weight, grains per spike, spikes per m² and plant height in both normal and stress conditions.
Ali et al. (2008) studied 70 local and exotic wheat genotypes for eight metric traits viz., plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility per cent, 1000 grain weight and yield per plant. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of GCV and PCV were high for yield per plant, number of productive tillers per plant and number of grains per spike. The remaining traits recorded moderate to low PCV and GCV estimates. Moderate heritability was observed for number of productive tillers per plant and fertility per cent. High heritability estimates were recorded for plant height, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant. These traits also indicated high genetic advance (except fertility per cent). Bakshi et al. (2008) revealed that the characters, panicle length, 1000 grain weight and days to maturity showed low heritability coupled with low genetic advance, whereas, number of spikelets per panicle and grain yield per plant showed high heritability coupled with high genetic advance. Mohammad et al. (2008) investigated the association among yield components and their direct and indirect influence on the grain yield of bread wheat in 144 advance lines tested in partially balanced lattice design during 2002-03. Analysis of variance for individual plant characters revealed the existence of genetic variability among the genotypes for all the characters studied. Genotypic correlation of plant height, biological yield, harvest index, 1000 kernel weight, and number of spikes per m² were positive and significantly correlated with grain yield. Pireivatloo and Yazdansepas (2008) evaluated yield and yield components of 24 advanced bread wheat genotypes to pre and post-anthesis drought stress conditions and observed that genotypes produced significantly lower spikes number per m², seeds number per spike and grain yield under pre- than in post-anthesis drought stress conditions. However, an average of 1,000 kernel weight of genotypes under pre-anthesis was higher than under non-stress and post-anthesis drought stress conditions.
Manal (2009) observed that mean for plant height, spike length, number of spikes per plant, number of grains per spike, 50% heading date and 1000 grain-weight revealed highly significant differences among genotypes and crosses under both sowing conditions. Low, medium and high heritability was recorded in different yield traits under study. High heritability accompanied by high genetic advance was observed for spike length and 1000 grain-weight. Low heritability coupled with low genetic advance was for plant height and number of grains per spike. Riaz et al. (2010) observed considerable amount of variation among genotypes for each character and results indicated high GCV and PCV for grains per spike, 1000-grain weight and grain yield per plot. Zecevic et al. (2010) noticed variability, heritability and components of variance for number of grains per spike and grain weight per spike in his studies on winter wheat varieties. Statistical analysis of variance established highly significant differences in mean values for number of grains per spike and grain weight per spike. Phenotypic analysis of variance indicated that ecological factor had higher impact on the expression of number of grains per spike and grain weight per spike than genetic factors. Heritability value in broad sense for number of grains per spike was about 60% and for grain weight per spike about 40%. Tripathi et al. (2011) observed higher PCV and GCV by harvest index, biological yield per plant, number of productive tillers per plant, test weight and grain yield per plant. The role of additive gene action was observed in the expression of characters like plant height, grain yield per plant, biological yield, harvest index and test weight.

Singh et al. (2012) evaluated 64 genotypes of wheat in randomized block design with three replications for variability, heritability and genetic advance for yield and related characters. Moderate PCV, GCV and ECV were recorded for biological yield per plant, harvest index, effective tiller per plant, ear length, total number of tillers per plant, number of grain per spikes and grain yield per plant. High heritability along with high genetic advance was observed for biological yield per plant, harvest index and number of grain per spikes emphasizing the scope for the improvement in these traits through simple selection for seed yield in wheat. 10
Tsegaye et al. (2012) reported high heritability coupled with high genetic advance as percent of mean for 1000 grain weight, spike length and number of spikelets per spike. Ahmad et al. (2016) studied 19 genotypes including 7 parents and their 12 F3 segregating populations of wheat and analyzed data revealed significant genotypic variability among the genotypes for the studied parameters. High heritability value was observed for grains per spike (0.95), grain yield per plant (0.99), fertile tillers per plant (0.98), plant height (0.89), and leaf area (0.88). High genetic advance was observed for grain yield (14.16), flag leaf area (3.12) and grains per spike (2.49).

Kumar et al. (2017) carried out genetic analysis in 55 genotypes (10 parents and 45 F1S) through half-diallel mating design in bread wheat. The highest values of PCV and GCV were found for biological yield, flag leaf area, productive tillers and grain yield. Highest heritability along with highest genetic advance was estimated for flag leaf area, biological yield and grain yield, therefore selection will be effective based on these traits.

2.2 Correlation coefficient analysis

Wang et al. (1998) reported that highly significant positive correlation was found between biomass production before heading and number of grains per ear and between biomass transported to grain after heading and grain weight. Positive significant correlation for tillers per plant, spike length, grain per spike, 1000 grain weight with grain yield was observed by Narwal et al. (1999) Prasad and Pandey (2001) reported low correlation of 1000 grain weight with yield and a low negative correlation of yield with protein content. Budak and Yildirim (2002) reported that grain yield had significant and positive correlation with days to heading and plant height. Protein content had negative significant correlation with heading date, plant height and grain yield.

Dwivedi et al. (2002) in their studies observed positive and significant correlation of grain yield with total biomass, tiller number per plant, grain weight per ear and 1000-grain weight while days to heading showed negative and significant association with 1000-grain weight.
Patel and Jain (2002) studied winter wheat lines and reported that kernel yield had a highly significant and positive correlation with number of tillers per plant and number of kernel per spike, where as it showed a non-significant and negative correlation with days to heading, days to maturity, plant height and 1000 grain weight. Phadnawis (2003) studied 10 agronomic characters of 18 durum wheat genotypes. Number of seed per ear and number of ear head showed positive and significant correlation, whereas number of days to 50% flowering and maturity recorded significant negative association with grain yield per plot both at the genotypic and phenotypic level. Rafat and Malik (2005) studied correlation indicating the nature of relationship between yield and yield attributing traits in order to assess the role of quantitative characters in crop improvement. Phenotypic correlation indicates that plant height, biological yield and 1000- grain weight were positively and significantly associated with grain yield. On the basis of character association it is suggested that grain yield may be improved with improvement in number of tillers per plant, ear length, biological yield, 1000 grain weight and harvest index. Shukla et al. (2005) conducted studies on 25 bread wheat varieties and observed that yield per plant has positive correlation with spike weight per plant, kernel weight per spike, number of kernel per spike, biological yield and harvest index in rainfed condition where as yield per plant had positive correlation with number of tillers per plant, kernel weight per spike, number of kernel per spike and biological yield under partially irrigated condition. Akram et al. (2008) evaluated winter wheat under rainfed conditions and the results revealed positive correlation in case of number of spikelet per spike, number of grains per spike and 1000 grain weight with grain yield at both genotypic and phenotypic levels. Grain yield per plant showed highly significant positive correlation with number of productive tillers per plant, number of spikelet per spike and number of grains per spike and significant positive correlation with spike length in their studies by Ali et al. (2008).
Chander and Singh (2008) observed positive correlation of grain yield with biological yield and harvest index under moisture stress environment, negative correlation of grain yield with "Drought susceptibility index" under moisture stress and significant positive correlation of grains per spike and grain weight with grain weight per spike under both moisture stress and non stress environments revealed that selection must be exercised for high biomass, grain weight per spike and harvest index for yield improvement under dry land conditions. While negative association of index of drought resistance with drought susceptibility index was observed. Khan and Dar (2010) studied that grain yield per plant had a positive and significant association with number of seeds per spikelets, days to maturity and 100 grain weight and number of grains per spike, number of spikelets per plant and 100 seed weight had a positive direct effect on grain yield per plant but number of seeds per spikelets showed a negative direct effect on grain yield per plant. High heritability for characters like tillers per plant, plant height and spike length was observed by Kumar et al. (2010) and also reported that grain yield per plant had a positive and significant correlation with number of seeds per plant, plant height and number of tillers per plant. Sahu (2011) reported high heritability estimates coupled with high genetic advance for characters like number of grains per spike, biological yields and harvest index and observed that yield per plant had significant correlation with number of effective tillers per plant, number of grains per spike and 1000 grain weight. Harvest index showed significant positive correlation with yield per plant and number of grains per spike. Tripathi et al. (2011) showed that grain yield is positively and significantly associated with plant height, spike length, number of grains per spike, 1000 grain weight and biological yield. Karimizadeh et al. (2012) revealed that grain yield positively and significantly correlated with test weight, 1000 kernel weight and plant height. The correlation coefficient between test weight and kernel number per spike and grain yield is nearly equal to its direct effect. 13
Khan and Naqvi (2012) reported that the selection on the basis of number of spikes, number of spikelets per spike and number of grains would be effective for increasing grain yield as they directly contribute to grain yield under irrigated condition. Nafde (2012) observed that the grain yield per plant had a positive and significant association with biological yield per plant, harvest index, number of grains per spikes, number of spikelets per spike, 1000 grain weight and plant height. Kumar et al. (2016) studied that plant height, number of tillers per plant and biological yield had significant and positive correlation to the grain yield per plant at phenotypic and genotypic level Mohanty et al. (2016) found significant positive correlation of yield per plant with plant height, number of tillers per plant, number of spikes per plant, spike length, number of spikelets per spike, number of florets per spike, number of grains per spike, floret fertility and grain weight per spike both at genotypic and phenotypic levels. Ramesh et al. (2016) in their correlation studies indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for all the traits which indicated that association among these characters was under genetic control and indicating the preponderance of genetic variance in expression of characters. Grain yield per plant had high, significant and positive association with number of grains per spike, spike weight, spike length, canopy temperature depression, tillers per plant, grain filling period and chlorophyll content both at genotypic and phenotypic levels indicating that these traits were main yield attributing traits. Phougat et al. (2017) recorded positive and significant correlation of grain yield per plant with harvest index (%), biological yield per plant (g) and tiller number per plant. Biological yield per plant (g) showed the highest direct effect on grain yield which was followed by harvest index (%). 14
2.3 Path coefficient analysis Path coefficient measures the magnitude of direct and indirect contribution of the independent component characters to cause on yield character and it has been defined as a standardized, partial regression coefficient which splits the correlation coefficient into direct and indirect effects. The review of literature on contribution of different traits on yield is illustrated below: Chaturvedi and Gupta (1995) studied path coefficient for 44 strains of spring wheat and found positive direct effect of number of tillers per meter and grains per spike on grain yield. Halloli (1997) recorded positive direct effect of number of tillers per meter, grains per spike and 1000 grain weight on grain yield in F3 and F4 genotypes of tetraploid wheat. Mondal et al. (1997) revealed that grains per ear, 100 grain weight and tillers per plant had a positive direct effect on grain yield while plant height and maturity had a negative direct effect on yield. Uddin et al. (1997) suggested that grain yield per plant was significantly and positively correlated with spikelets per spike and 1000 grain weight. Path coefficient analysis had revealed high direct effect for harvest index and biological yield per plant. Kumar and Hynshal (1998) reported that harvest index, number of effective tillers, grains per ear were the most important components of grain yield of durum wheat and indirect effect of other characters on grain yield through harvest index was higher. Simane et al. (1998) reported that the direct effect of number of spikes per square meter on grain yield, whereas grain per spike showed highest direct effect on grain yield. Narwal et al. (1999) expressed that number of tillers per meter, spike length, grains per spike had positive and large direct effect on grain yield in advanced wheat lines. 15
Dencic et al. (2000) showed that number of grains per spike and grain weight per spike had a sufficient positive direct effect on yield under drought condition. Naik (2000) in his studies on 200 genotypes of durum and dicoccum wheat found that plant height and grains per spike had maximum indirect positive effect on yield via total biomass and harvest index. Pochaba and Wegrzyn (2000) revealed the direct positive effect of grain number per ear, 1000 kernel weight and plant height on yield and negative effect of early heading on yield. Shah and Deora (2002) concluded that grain yield primarily depend on harvest index, biological yield and plant height and had direct effect on yield, however these traits had contributed substantially through harvest index. Singh and Dwivedi (2002) in their studies on correlation and path coefficient in wheat showed that all characters except biological yield and harvest index per plant had small positive or negative effect on grain yield per plant but biological yield per plant had maximum direct effect on grain yield per plant followed by harvest index. Patel and Jain (2002) expressed that the number of kernels per spike, had highest positive effect on kernel yield while a negative direct effect on yield was observed for number of spikelet per spike. Singh et al. (2003) reported that biological yield per plant, grains per ear, 1000 grain weight and effective tillers per plant had positive and higher direct effect on grain yield per plant. Productive tillers per plant had the highest positive direct effect followed by grains per spike, grain weight per spike and length of spike on grain yield as observed by Lad et al. (2003). Mohammad et al. (2005) studied yield and yield contributing traits in bread wheat lines and reported the positive direct effect of days to heading, days to maturity and biological yield on grain yield. Harvest index showed positive and highest direct effect on grain yield.

16
Aycicek and Yildirim (2006) in their studies on path analysis between grain yield and yield components of 20 bread wheat genotypes found positive direct effect of plant height and grain weight per spike and negative direct effect of time to heading on grain yield. Gupta et al. (2007) studied genetic diversity and found highest positive direct effect of biological yield on the grain yield was reported followed by harvest index, specific leaf weight, stomata number, stomata size, 1000-grain weight, spikelets per spike and days to heading. Path coefficient analysis studies done by Chander and Singh (2008) in 20 spring wheat genotypes under moisture stress and non stress environments analysis revealed that biological yield and harvest index exhibited high positive direct effects on grain yield under both the environments. Tillers per plant and grain weight per spike had mainly indirect effects on grain yield via biological yield under moisture stress. Nafde (2012) reported the positive direct effects on grain yield per plant through biological yield per plant, harvest index, plant height, number of spikelets per spike and days to maturity. Singh et al. (2012) revealed that the grain yield per plant had positive and significant correlation with days to maturity, plant height, 1000 grain weight and biological yield per plant. He also observed that days to maturity, plant height, spike length, number of seeds per spike, biological yield per plant and harvest index showed positive direct effect on grain yield per plant. Tsegaye et al. (2012) reported that biological yield, number of tillers per plant and 1000 grain weight had high degree of positive association with grain yield. Phenotypic path analysis described that biological yield and harvest index have direct contribution towards grain yield. Kumar et al. (2016) studied path coefficient and revealed positive direct effect on seed yield of all the traits except plant height, peduncle length, number of grains per spike and 1000 seed weight. 17
Mohanty et al. (2016) studied path coefficient and mentioned number of tillers per plant, spike length, number of florets per spike and floret fertility as selection criteria under late heat stress. Ramesh et al. (2016) revealed that grains per spike, tillers per plant, spike length had the highest positive direct effect on grain yield followed by flag leaf length, flag leaf width, days 50% heading, plant height, grain filling period, membrane stability and days to maturity at genotypic level. The selection of characters such as grains per spike, tillers per plant, spike length and spike weight would be helpful for further improvement. Kumar et al. (2017) estimated path coefficient analysis and observed high positive direct effects of biological yield, flag leaf area and productive tillers on grain yield indicating that these traits may be used as an index for selection to high yield in bread wheat genotypes. 2.4 Mahalanobis D₂ analysis Singhal and Upadhyay (1977) reported that 35 stocks of diverse parentage from 15 geographical regions were grouped into five clusters on the basis of eight characters using Mahalanobis' D₂ statistics and Tocher's method. Plant height, grain number per ear head and growth habit contributed to most of the divergence between clusters and varieties. The clustering pattern was also determined to a considerable extent by parentage. Westerlund et al. (1991) studied 23 variables describing the chemical composition and baking properties of 100 samples of spring and winter wheat. Sixteen of these samples were selected with the aid of principal component analysis (PCA) in such a manner that much of the variation in all the parameters was retained. The selection procedure preserved a larger part of the variation in the original material than selection by random sampling. Mehta and Dhagat (1992) evaluated 60 T. aestivum populations representing a broad spectrum of variation from various agroclimatic regions for nine plant characters. All populations were grouped into 20 genetically distant clusters according to Mahalanobis D₂ and Tocher's analysis. Number of tillers per plant, days to 75% 18
flowering, plant height and number of grains per ear made the maximum contribution to genetic diversity. Cluster 15 (comprising of 3 genotypes) was observed having the highest 100-seed weight (5.66 g) and yield per plant (15.64 g). Singh (1992) studied 33 T. aestivum and two T. durum cultivars originating from different Indian States and from Mexico. Data recorded for nine quantitative traits was analysed for genetic diversity using the Mahalanobis D² statistic. The clustering pattern showed that geographical diversity was not associated with genetic diversity and also T. durum cultivars did not form a separate cluster, suggesting that they were ancestrally related to T. aestivum types. Reddy (2001) studied 52 strains of hexaploid Triticale including two wheat genotypes for genetic diversity analysis. These were grouped into four clusters to determine genetic divergence. Cluster III was the largest group consisting of 36 genotypes followed by the cluster IV with eight; cluster II with six and cluster I with two genotypes. Cluster I and III was the most diverse among the groups and the inter-cluster distance between them was the highest. Singh et al. (2002) reported that 24 genotypes of wheat were grouped into six clusters using Mahalanobis' D² analysis. Cluster I had nineteen genotypes, while clusters II-VI each had single genotype. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied. Maximum and minimum generalized distances were observed between clusters II and IV and between I and V, respectively. Sangwan et al. (2004) evaluated 200 genotypes of durum wheat for genetic divergence in yield and quality characters (number of days to 75% flowering, plant height, peduncle length, number of tillers per plant, number of grains per ear, 1000 grain weight, grain yield per plant, biological yield per plant and harvest index), following the non-hierarchical euclidean cluster analysis, the 200 genotypes were grouped in to 7 cluster with variable number of genotypes, based on data on genetic divergence and mean performance of yield and other traits, 7 diverse and superior genotypes (CBD-212, IDYN-573, HNP-79, P5459, P-5460 and WH-902) were identified, these genotypes may be used in crossing programmes to obtain transgressive segregates for enhancing the yield and quality of durum wheat. 19
Dwivedi and Pawar (2005) studied the genetic divergence among 72 lines of bread wheat, for 12 yield and other quality-attributing traits (number of days to heading, number of days to maturity, plant height, number of tillers per plant, number of grains per spike, grain weight per ear, 1000-grain weight, total biomass, grain yield per plant, protein content, sedimentation value and hectolitre weight) was evaluated using Mahalanobis’ $D_2$ analysis. Based on $D_2$ values, the genotypes were grouped into eight clusters, with cluster I having the highest number of genotypes and cluster VIII with the lowest number of genotypes. The distribution pattern of genotypes in different clusters was random, and the genetic divergence was only slightly associated with the agro-ecological distribution of the genotypes. However, the genotypes of the same agro-ecological origin showed some tendency to cluster together. The genotypes of clusters I, III and IV were identified as diverse and had higher mean values for most of the important yield component traits. Thus, hybridization involving genotypes of clusters I and IV and clusters I and III is advocated to obtain high-yielding segregants. Sharma and Suri (2005) reported 16 clusters using Mahalanobis $D_2$ analysis based on eight morphological characters (days to flowering, number of tillers, plant height, 1000-grain weight, grains per ear, grain yield, biological yield and harvest index). Based on genetic divergence and mean performance of the genotypes, it was recommended that the crosses namely Anza xWG138, Anza x Chris, WH291 x Parula 'S', WH291 x Veranopolis, WH291 x Torim and WH291 x NP846 can be used in hybridization programmes for yield improvement in wheat. Singh and Diwivedi (2005) assessed genetic divergence for 12 characters (days to 50% flowering, days to maturity, number of effective tillers per plant, plant height, ear length, spikelets per ear, number of grains per ear, grain weight per ear, 1000-grain weight, biological yield per plant, grain yield per plant and harvest index) in 24 wheat genotypes. The genotypes were grouped into six clusters. The following cluster I comprised of 19 genotypes and the other clusters were having one genotype each. Maximum generalized distance was observed between clusters II and IV, whereas the minimum generalized distance was observed between clusters I and V. 20
Yashpal et al. (2005) conducted genetic variability study in 60 genotypes. High magnitude of variability was observed for productive tillers per plant, grains per spike, grain weight per spike and grain yield per plant. High to moderate heritability coupled with high to moderate genetic advance was found for characters viz., plant height, spike length, grains per spike, spikelets per spike, sedimentation value and 1000-grain weight, which indicated predominance of additive gene action and chance of improving these traits through simple selection. More et al. (2006) studied 45 diverse genotypes of forage wheat for genetic diversity and to identify the suitable genotypes for hybridization programmes based on clustering pattern. The genotypes were grouped into seven clusters using Mahalanobis $D^2$ statistics. Cluster II was the largest with 25 genotypes followed by cluster III with 11 genotypes and cluster I with five genotypes. Yadav et al. (2006) studied genetic diversity among 90 germplasm lines of bread wheat for yield, its components and quality traits using Mahalanobis $D^2$ analysis. Based on $D^2$ values, the 90 wheat genotypes were grouped into 11 clusters. The distribution pattern of genotypes in different clusters was random and there was little association of genetic divergence with agro-ecological distributions of genotypes. Rawashdeh et al. (2007) evaluated genetic diversity in durum wheat landraces. The collected material was grown under rainfed conditions using an augmented design with five blocks and four repeated check cultivars. Data were collected for 14 morphological and agronomic traits. Phenotypic diversity index was estimated and the relationships among accessions were measured using cluster analysis and dendrogram similarity matrix. The results revealed the presence of a wide range of variability among landraces, which possess high levels of variability for biological yield, fertile tillers, number of seeds per spike, seed weight per spike and weight of 1000 seeds. These landraces must be considered as a reservoir of genes that plant breeders need in their wheat improvement programs and should be conserved both ex-situ and in-situ.

Routray et al. (2007) studied 27 landraces of wheat collected from farmers' fields of hilly areas of Himalaya in Uttarakhand state of India during April 2004. Genetic diversity among 41 genotypes (cultivars and landraces of wheat) was studied 21
using morphological traits, microsatellite markers and SDS-PAGE of HMW-GS. The dendrogram and PCA (Principal Component Analysis) based on morphological data clearly separated landraces of wheat from cultivars. Sharma and Pawar (2007) reported the genetic divergence among 75 genotypes of bread wheat for 11 traits, which include yield, its components and quality traits. Based on $D_2$ values, the genotypes were grouped into 11 clusters with cluster II having the highest number of genotypes, i.e. 27 and clusters X and XI with the lowest number, i.e. one genotype each. The distribution pattern of genotypes in different clusters was random and there was little relationship of genetic divergence with agro-ecological distribution of genotypes. However, the genotypes of the same agro-ecological origin had shown some tendency to come together in same cluster. Chapla et al. (2008) reported genetic diversity among 110 lines of bread wheat for yield and its component traits using Mahalanobis $D_2$ analysis. Based on $D_2$ values, the 110 genotypes of wheat were grouped into 15 clusters. The distribution pattern of genotypes in different clusters was random. The geographic origin was not associated with genetic diversity. Kumar et al. (2009) studied genetic divergence in 30 genotypes of bread wheat ($T. aestivum$ L.) for yield and other related characters. All the 30 genotypes were grouped into six clusters using Mahalanobis $D_2$ analysis. On the basis of the data on genetic divergence and mean performance of yield and other traits, diverse and superior genotypes were found and used in multiple crossing programme to recover transgressive segregants. Kumar et al. (2009) studied genetic divergence using Mahalanobis $D_2$ statistics in a set of 100 wheat genotypes using 12 quantitative traits. On the basis of which, these genotypes were grouped into 11 clusters. Inter-cluster distances ranged from 22.82 (cluster III and IV) to 63.48 (cluster VI and XI) and intra-cluster distances ranged from 0 (cluster VII and XI) to 21.61 (cluster VI). The study indicated that the genotypes included in these clusters have wide genetic diversity and could be used in hybridization programme which may be aimed at either combination breeding or at exploitation of heterosis. 22
Santos et al. (2009) evaluated 52 wheat populations representing Madeira's *Triticum* diversity and a wide range of ecological conditions on the basis of 46 biometrical and cytometrical traits related to plant morphology, cytological and grain characteristics. Taxonomic identification of the collected materials revealed the presence of 3 species, 2 subspecies and 16 botanical varieties among the madeiran wheat germplasm. The obtained results were confirmed by the multivariate analysis since all accessions were grouped in clusters corresponding to different taxonomic levels. The study indicated that detailed description of the Madeiran wheat landraces may contribute to the protection of the existing *Triticum* diversity as well as to support efforts of conservation of landraces, proper germplasm preservation and utilization. Jaiswal et al. (2010) studied genetic diversity for yield, yield contributing traits and quality traits in 300 indigenous germplasm of bread wheat. On the basis of dissimilarity coefficient, these genotypes were grouped into 23 clusters. The genotypes bearing desired value from different clusters can be used in breeding program for improvement of yield as well as quality characters. Habibpor et al. (2011) reported that genetic variation among northwest wheat land races regarding agronomy and morphological traits. With calculating correlation coefficient, the relation between under investigation traits examined and identified the traits such as biological yield, harvest index and fertile tillers per plant in plant tolerance to drought can be effective. WARD cluster analysis was used based on standardized data in order to classify the under investigated genotypes which were grouped into three clusters. Yared et al. (2011) studied genetic variability of Ethiopian mustard genotypes. The cumulative effects of individual traits were responsible for differential grouping of genotypes. Univariate analysis of variance has shown that there was significant variation among genotypes in all traits. Multivariate analysis has resulted in the formation of seven clusters and it shows the presence of substantial genetic diversity for further selection and breeding.
Aharizad et al. (2012) studied various traits viz., days to heading, flag leaf area, peduncle length, spike length, plant height, number of spikelet per spike, number of spikes, number of grain per spike, 1000 grain weight, grain yield, shoot biomass, percent of grain protein, straw yield and harvest index of wheat. Analysis of variance revealed significant differences among the lines for all the traits. The level of genetic variation was higher for peduncle length, flag leaf area, number of spikes, grain yield, straw yield and shoot biomass. Cluster analysis based on all the traits using Ward’s algorithm and squared Euclidean distances assigned the lines into three groups. Mollasadeghi et al. (2012) studied genetic diversity to investigate genetic variation of 12 bread wheat genotypes based on phenological and morphological traits. It was shown by estimating the phenotypic and genotypic coefficient of variation for various traits that the studied genotypes were of more genetic variation in terms of traits such as plant height, spike length, grain number per spike and grain weight per spike, 1000 grain weight and days to heading than of other traits. Studied genotypes fell into two categories using cluster analysis. Mean of square between the categories was significant for all traits except grain yield, spike length and date of heading. Mishra et al. (2013) assessed genetic diversity by cluster analysis for yield and its nine contributing characters in 24 bread wheat genotypes during rabi 2010-11. The cluster analysis grouped all the 24 wheat genotypes into four major clusters. Extreme divergence was observed among clusters. Second cluster with two genotypes (WH 542 and ATTILA) had better yield potential as compared with fourth cluster which had also two genotypes (WL 711 and MALAVIYA 206) indicating their scope for use in crop improvement programmes. Singh and Upadhyay (2013) studied genetic divergence in 27 genotypes of wheat (T. aestivum L.) using D2 statistics considerable diversity was revealed. The genotypes were grouped into six clusters. The cluster I was the largest containing seven genotypes followed by cluster II with six genotypes, cluster V with five genotypes, cluster III and IV had four genotypes each and cluster VI had only one genotype. The inter cluster distance emphasized for improvement of wheat by hybridization and selection. 24
Kolakar et al. (2014) studied D$_2$ analysis for yield and its component characters in 169 wheat genotypes. The genotypes were grouped into 12 clusters, with the variable number of genotypes in each cluster. The inter cluster distance was found to be highest between cluster VIII and XI indicating that accessions from these clusters can be further used for crop improvement programmes. Days to 50 per cent flowering, number of spikelets per spike, grain yield per plot and productive tillers per meter length were the most important characters contributing to total divergence. Uddin et al. (2014) studied variations among 45 wheat genotypes on multivariate scale through Mahalanobis' D$_2$ statistics at saline and non-saline environments. In the both environment, the genotypes were grouped into five different clusters. Number of genotypes in each cluster varied with the environments. In non-saline environment, cluster II was the largest having 13 genotypes while under saline condition, the cluster II also had the highest number of genotypes (16). The distance within cluster was always less than the distances between clusters. The cluster III and IV, I and V and II and V exhibited wide distance between them in non saline, and were distinctly different from others. Cluster mean for yield and its components indicated that 12 genotypes in the cluster V had good performance under non-saline and five genotypes under saline in the cluster IV had good performance. Number of spikes per plant and days to maturity in non-saline environment and number of grains per spike and days to heading in saline environment contributed maximum towards divergence among 45 genotypes. Ramakrishnan et al. (2016) evaluated the genetic divergence among 35 elite wheat genotypes using Mahalanobis D$_2$ statistics for eleven different morphological and physiological traits. D$_2$-clustering grouped the genotypes into six clusters, in which photosynthetic rate (35.63%), leaf senescence rate (17.98%) and plant height (17.98%) contributed significantly for the genetic divergence observed among genotypes. Maximum inter cluster distance was observed between clusters III and VI followed by cluster III and cluster IV, while maximum intra cluster distance was observed in cluster IV followed by cluster II. Cluster mean data indicated that cluster III genotypes viz., CHIRYA7 and HW2041 were stay green with high photosynthetic rate and grain yield among all the clusters and can probably be used in further hybridization programmes. 25
Parveen et al. (2016) studied genetic diversity in exotic germplasm of wheat (*T. aestivum* L.) based on cluster analysis and principle component analysis (PCA). Cluster analysis expressed high level of diversity because two main groups were observed one with 14 and the other with 16 genotypes thereby indicating sufficient variation in the germplasm evaluated to be used in future breeding programmes. **2.5 Principle Component analysis** Pankovic et al. (1997) studied for spike length, grains per spike and 1000-grain weight and measured yield parameters which were analysed by principal component (PCA) and cluster analysis, and phenotypic distances between cultivated wheat and related wild species and found highly significant differences between wild wheat species. Between *Triticum* species highly significant differences were detected only in the 1000-grain weight. According to the PCA, *T. vulgare* and *T. monococcum* are similar to *A. comosa*. According to cluster analysis, *A. ovata* can be classified as a separate group of relatives. Skrbic et al. (2005) in his studies on microelements found that four principal components accounted for 87.2 % of the total variance in the data. The component scores indicated the similarities among the Serbian wheat growing regions. It is enough to measure one variable per group. Naturally, this conclusion is valid only within the limits of the present study of wheat grain samples from different parts of Serbia. Osella et al. (2008) assessed the association between physical properties and baking performance of dough. Sixty-six Argentine wheat breeding lines were milled using an experimental mill. Wet gluten content and physical dough properties were determined in flours; while breads, cookies and crackers were made to evaluate baking performance. Principal component analysis (PCA) was utilized to observe variations among flour samples studied. Lima et al. (2010) studied the development of homogeneity during the preparation of a wheat flour laboratory reference material for use in the quantification of metals and metalloids. Furthermore an alternative multivariate analysis for homogeneity was proposed by performing ANOVA of principal component scores and by inspection of principal component score graphs and hierarchical cluster analysis dendrograms. 26
Mishra et al. (2013) in their PCA studies revealed that all the four principal components (PC1, PC2, PC3 and PC 4) contributed 89.68% of the total variability and accounted with values of 45.38, 20.69, 12.43 and 11.17, respectively. The third principal component had high positive component loading for all variables except spike length and grains per spike. Parveen et al. (2016) assessed genetic diversity in exotic germplasm using cluster analysis and PCA and observed that out of seven, three PCA's axes inhibited more than one Eigen value but the level of dissimilarity was high which indicated that the germplasm was with broad genetic base. 2.6 Molecular analysis Plaschke et al. (1995) studied the genetic diversity among 40 wheat cultivars and suggested the use of relatively small number of microsatellites for estimation of genetic diversity and cultivar identification. Gupta et al. (1999) reviewed various genetic markers used in plant breeding programmes with emphasis on bread wheat and revealed the prominence of SSRs over others and laid stress on further development of these markers. Using 20 microsatellite markers, Prasad et al. (2000) analysed the genetic diversity among 55 elite wheat genotypes and demonstrated the utility of such markers for detecting polymorphism leading to genotype identification. Gupta and Varshney (2000) reported a variety of molecular markers, based on microsatellites or simple sequence repeats (SSRs) thus, necessitating their development and use in a variety of plant systems. The basic principles underlying different hybridization based (oligonucleotide fingerprinting) and PCR-based approaches, making use of microsatellites, have been outlined. Different methods for enrichment of genomic libraries for microsatellites are also outlined. The review also includes a discussion on literature, which deals with the use of microsatellites in genome mapping, gene tagging, DNA finger printing, characterization of germplasm and cytogenetics research. 27
Huang et al. (2002) studied genetic diversity in 998 accessions of hexaploid bread wheat and using microsatellite markers for molecular work results indicated that microsatellite markers permit the fast and high throughput fingerprinting of large numbers of accessions from a germplasm collection in order to assess genetic diversity. Dong et al. (2003) studied and suggested use of microsatellites for studying genetic diversity as they are simple, co-dominant and detect high level of genetic diversity and are easily assayed by the polymerase chain reaction (PCR). In wheat, SSR markers have been applied to genetic mapping, detection of genetic diversity, identification of varieties and genotypes, gene tagging, QTL analysis, and marker-assisted selection. XinMin et al. (2003) reported a set of 59 wheat SSR primers located on 21 wheat chromosomes which were used to investigate the genetic diversity of 48 winter wheat cultivars and lines conferring good quality during winter. A total of 209 allelic loci were detected, the number of alleles per primer pair ranged from 2 to 9 with a 3.5 average. The value of allelic polymorphism information content ranged from 0.16 to 0.87, on an average and 0.56 per primer. The 48 wheat cultivars could be identified with eight combined primers. Cluster analysis showed that all cultivars could be clustered into five groups, which agrees generally with pedigree analysis. SSR markers play an important role in cultivar identification and in the study of genetic diversity. Zhong Fu et al. (2003) studied SSR markers to evaluate the genetic diversity of the D-genome in 23 wheat cultivars or lines (17 winter and six spring wheat) and indicated that the genetic variation among winter wheat cultivars was relatively abundant compared with spring wheat cultivars. The genetic base of the D-genome, especially in chromosome 1D, was very narrow. Kuleung et al. (2004) examined the transferability of SSR markers among wheat (T. aestivum L.), rye (Secale cereale L.) and Triticale (Triticosecale wittmack) by using 148 wheat and 28 rye SSR markers and found that transferability of wheat SSR markers to rye was 17 per cent, whereas 25 per cent of rye markers were amplified into wheat, whereas in triticale they achieved transferability of 58 per cent and 39 per cent for wheat and rye markers, respectively and the results revealed a high degree of collinearity between closely related species by comparative mapping. 28
Mahmood et al. (2004) carried out a study to examine the genetic similarity among wheat cultivars based on the variation in chromosome 3A. Forty-eight cultivars, two promising lines and four substitution lines (induplicate) were included in the study. Thirty-six chromosome 3A specific and 12 group-3 barley SSR primer pairs were used. A total of 106 polymorphic bands were scored. Transferability of barley microsatellite markers to wheat was 70%. The coefficient of genetic distance (D) among the genotypes ranged from 0.40 to 0.91 and averaged $D = 0.66$. The cultivars were separated into three main clusters by using three SSR markers that identify known agronomically important quantitative trait loci (QTL) regions. Naghavi et al. (2004) studied genetic diversity using 17 RAPD and 35 SSR markers. The level of polymorphism was 88% with RAPDs compared to 100% with SSRs. Mean genetic similarity was 0.88 based on RAPDs and 0.85 using SSRs. The wide range of genetic similarity was obtained by SSR than RAPD, reflecting the hyper variability of SSR markers and their high resolution power. Matrix correlation analyses suggested that a good representation of the relationships among the bread wheat cultivars per lines can be obtained by using RAPDs alone or in combination with SSRs, but SSRs alone cannot be used for this purpose. Both techniques discriminated the genotypes very effectively. You et al. (2004) reported genetic relationships among common wheat varieties from the 10 wheat growing regions of China using SSR markers. The wheat varieties included 33 modern wheat varieties and 63 landraces selected from the national gene bank collection of China. SSR data was analyzed using NTSYS-pc software. The separated simulations from six subsamples revealed that 550 alleles were the minimum number required to confidently determine the genetic relationships. It was shown that the number of alleles (loci) needed do not have a strong association with the number of wheat lines in the sample size. This indicated that genetic diversity of Chinese common wheat has a close association with their geographic distribution and ecological environment.

Medini et al. (2005) studied 34 durum wheat cultivars representing the Tunisian durum ($T.\, durum$ Desf.) wheat collection and seven wild species of wheat relatives ($T.\, turgidum$ L., $T\, dicoccon$ Schrank., $T\, dicoccoides$ (Korn) Schweinf., $T\, 29$)
araraticum Jakubz., T monococcum L., Aegilops geniculata Roth, and Aegilops ventricosa Tausch) were analysed with AFLP and SSR markers. Both marker systems used were able to differentiate durum wheat cultivars from the wild relatives and to specifically fingerprint each of the genotypes. Stodart et al. (2005) genetic diversity of 44 bread wheat land races was estimated using 16 Amplified Fragment Length Polymorphism (AFLP) primers and 63 wheat SSR markers in identifying polymorphisms between accessions. Principle coordinate analysis suggested that the AFLP and SSR loci could be used to discriminate among accessions collected from North Africa and Southern Europe from those collected from the Middle East. The results indicated the usefulness of the molecular markers to assess genetic diversity present within germplasm collections. Costa et al. (2007) estimated the molecular diversity of 54 genotypes of triticale using 42 wheat genomic microsatellites and indicated the possibility of exploiting transferable markers in the genetic and breeding studies of triticale. Jian Cheng et al. (2007) used 24 wheat SSR markers determining 25 loci on 14 different chromosomes to evaluate the gene pool. In total, 115 alleles were detected in gene pool with an average of 4.6, ranging from 2 to 9 alleles per locus. Statistical test showed that genetic diversities had no significant difference between the gene pool and the 30 parents. The results suggested that the gene pool is improved after several cycles of selection, while genetic variation is still maintained. Therefore, the gene pool is suitable for further breeding programme. An agronomic gene pool of wheat (T. aestivum L.) was constructed through recurrent selection.

Malik et al. (2008) studied genetic diversity in 31 wheat genotypes of main sowing zones and major wheat series of India was assessed using 22 microsatellite markers. The 22 Gatersleben wheat microsatellites (GWM) representing 15 chromosomes of genomes A, B and D of wheat, revealed a total of 161 alleles, with an average of 7.31 alleles per GWM marker (range:3-14). The UPGMA based cluster analysis discriminated all genotypes and grouped separately all three types of wheat (diploid, tetraploid and hexaploid) as expected. The major cluster of bread wheat varieties revealed distinct groups for indigenous and exotic material based on their pedigrees. Over all, this study confirmed the existence of high amount of genetic diversity in Indian wheat and showed that SSR markers can be useful for varietal analysis and a more detailed diversity evaluation.
Salem et al. (2008) evaluated genetic diversity of seven wheat varieties using 48 SSRs and 9 morphological characters and showed that microsatellite markers distinguished all genotypes. Iqbal et al. (2009) reported genetic diversity of 48 Pakistani wheat varieties and 12 landraces, loss of genetic diversity in bread wheat during the change from traditional landraces to modern breeding varieties was examined and recent trends of national wheat breeding programmes were identified. A total of 29 SSR markers, representing at least one marker from each chromosome of wheat, were used to analyze the genetic diversity. Ahmed et al. (2010) assessed the genetic diversity among 32 advanced wheat breeding lines using molecular & biochemical markers and observed that the genetic base in wheat lines of the rainfed area was narrow, suggesting the use of DNA fingerprinting in future endeavors. Yildirim et al. (2011) studied genetic diversity of 20 durum wheat landraces collected from different regions of Turkey using 12 SSR markers. Polymorphic bands ranged 4 to 9 per each SSR locus and the most polymorphic SSR loci were Wms 18, Wms 155, Xgwm 166 and Stm 578. The results showed that durum wheat landraces have high genetic variability and microsatellite DNA markers could be successfully employed for revealing the variability. Islam et al. (2012) examined genetic diversity of 12 wheat genotypes using four SSR markers and found positive correlations between genetic diversity, number of alleles, allele size range and types of repeat motifs of microsatellite markers. Investigation of 20 wheat genotypes using 34 polymorphic SSRs was carried out by Sehgal et al. (2012) who observed that SSRs could distinguish and characterize all of genotypes. He recommended the use of more screened primers for such studies. Sonmezoglu et al. (2012) analysed 20 bread wheat land races using SSRs and morphological markers and concluded that SSR markers and morphological characters can be efficiently utilized in such studies. 31
Genetic diversity of 30 wheat genotypes using 24 simple SSR markers was evaluated by Spanic et al. (2012). They observed average number of 8.44 alleles per locus and suggested that genetic diversity can be used as an effective tool for selecting genotypes in breeding programmes. Malik et al. (2013) analysed 48 elite wheat genotypes using 56 SSR and 12 STS markers and recommended the use of discriminative SSR and STS markers in varietal characterization. Siddig et al. (2013) studied genetic relationship of 12 Sudanese wheat cultivars using 184 SSRs and 23 ISSR primer sets and based on SSRs and ISSRs grouped cultivars into three and four clusters, respectively and revealed existence of significant variation among cultivars based on markers. Niaz et al. (2014) analysed the genetic diversity in 175 durum wheat accessions using morphological markers, seed storage proteins and DNA markers and observed sufficient diversity. Drikvand et al. (2015) assessed the genetic diversity of 40 wheat genotypes using 30 SSR primers. A total of 71 alleles (ranged between 2 to 4 alleles per each locus) were distinguished. According to similarity matrix, genetic similarity value ranged from 0.18 to 0.95 with an average of 0.48. The lowest and the highest genetic diversity was observed between the Sistan and Arg (Bread wheat, No 27 and 28), Karkheh and Behrang (Durum wheat no 35 and 38) genotype respectively. Unweighted pair group method of the arithmetic average (UPGMA), based on jaccard similarity clustering formed a dendrogram with three genotype group. Clustering somewhat distinguished durum and bread wheat‟s principle co- ordinate analysis (PCA). 2D plot confirmed the results of cluster analysis. Cophenetic correlation showed that molecular data and cluster corresponded. It was concluded that SSR marker was suitable for evaluation of genetic diversity in wheat genotypes and this genetic diversity can be used in wheat breeding programs.

Kumar et al. (2016) evaluated molecular diversity of the seven wheat (T. aestivum L.) genotypes using 50 SSR primers. Genetic distances were calculated using UPGMA procedure. A high degree of genetic polymorphism was observed among the wheat varieties with average genetic polymorphism 70%. SSR diversity 32
data was generated using above primers and a total of 114 alleles were detected with an average of 2.71 alleles per locus. The number of alleles per locus ranged from 2 to 6 and the percent of polymorphism ranged from 20% for the Xwmc 254 to 100% for the Xbarc 26. The average genetic diversity based on SSR markers was 0.465 with a range of 0.037-0.892, indicating that microsatellite markers permit the fast and high throughout fingerprinting of accessions from a varieties collection in order to assess genetic diversity. Kumar et al. (2016) characterized 54 wheat genotypes comprising of 41 Indian origin and 13 exotic genotypes using 39 polymorphic SSR markers for DNA fingerprint and extent of genetic diversity. A total of 112 alleles ranging from 1 (Barc 1, Barc 26, Barc 147) to 7 alleles (Barc 77) were generated with an average of 2.87 per SSR marker. Similarity values ranged from 22.8% (between MP-4161 and K-424) to 78.7% (between GP-350 and GP-365) with an average of 51.33%. UPGMA based cluster analysis, broadly grouped 54 genotype into 4 clusters represented as A, B, C and D. Cluster D include maximum number of genotypes (43) which was further divided into seven sub cluster. Out of 13 exotic genotypes used in the present study, six were included in sub cluster D4. However, two exotic genotypes each were sub clustered with Indian genotypes into three sub-clustered, D-2, D-6 and D-7 revealing their genetic similarity with genotypes of Indian origin. Genotypes from same origin were usually clustered together, e.g. K-65 and K-68 belong to Kanpur origin were clustered into “cluster B”. Similarly, MP-4115, MP-4131, MP-4136 and MP-4010 released for Madhya Pradesh were clustered into “D-3” sub cluster. 2.7 In vitro screening of wheat cultivars for drought The use of polyethylene glycol (PEG) of high molecular weight (4000 or more) for in vitro screening of drought tolerance was proposed by Manohar and Hevdecker (1964) as it posseses osmotic properties with no evidence of toxicity. Blum et al. (1980) concluded that tolerance to water stress in growing seedlings can be screened by using PEG containing nutrient solutions. Seed germination and seedling growth under osmoticum-induced water stress has been reported to be good screening technique for the identification of drought tolerant genotypes under laboratory conditions (Blum 1988; Corbellini et al. 1988).
Tyankova et al. (2004) analyzed the response of various wheat cultivars, stabilized wheat-wheatgrass lines and intergeneric wheat amphidiploids to in-vitro cultivation on the nutrient media containing 5 and 10% PEG solution, observed that the best rooting occurred on the control medium, while PEG medium suppressed rooting with different regeneration frequencies for the different genotypes. Ghanifathi et al. (2011) conducted a study involving 12 bread wheat genotypes and reported that germination indices reduced significantly in all the genotypes with the reduction in the water potential. Mirbahar et al. (2013) studied germination of 25 wheat genotypes under different osmotic potentials of PEG-6000 and observed that germination percentage decreased with the decrease in the water potential of the medium and water uptake reached at its peak within 48 hours in all the genotypes under all the water stress conditions. Khayatnezhad and Gholamin (2011) conducted an investigation to study the tolerance levels of two Durum wheats under different levels of PEG-6000 and NaCl and found that germination rate was delayed by both the solutions in both varieties and conclusively proved the adverse effect of PEG on germination and early seedling growth rate. Ahadzadeh et al. (2014) observed that stress applied by PEG-6000 had impact on traits such as coleoptile length, shoot length, shoot weight, germination percentage and germination index at 1% probability level. Chachar et al. (2014) evaluated six wheat genotypes for drought tolerance using 0, -0.5, -0.7 MPa of PEG 6000 solution and found that seedling traits showed a decreasing trend in response to increased concentrations of PEG 6000. More et al. (2014) studied 25 wheat genotypes studied for the response to water stress at three different levels of PEG 6000 solution revealed a decrease in the germination stress index, plant height stress index, root length stress index, shoot length stress index and dry matter stress index corresponding to the increase in the water stress levels. 34
Sial et al. (2016) studied germination percentage, root length and shoot length of the 25 wheat genotypes under different PEG concentrations and control solution and found significant variation among the genotypic means regarding the observed traits and they significantly decreased with the increasing osmotic potential. **2.8 Screening for rust and powdery mildew**

Pathan et al. (2008) screened 105 European wheat cultivars for seedling and adult plant resistance to stripe rust under greenhouse and field conditions and reported that 12 cultivars were susceptible to all type of pathogens, 43 cultivars expressed seedling resistance but the genes could not be characterized and 24 cultivars lacked seedling resistance but exhibited high levels of APR though uncharacterized thus leaving scope for further exploration and usage. Park et al. (2011) have emphasized on The Global Cereal Rust Monitoring System for surveillance on a global scale to overcome the shortcomings of surveillance at the regional and national levels. The system consists of an elaborative information platform comprising of standardized protocols of surveys, preliminary virulence testing, data, sample transmission, management at the field, national and global levels plus two web based visualization tools. Wei et al. (2011) evaluated 48 accessions of wheat for rust resistance against eight races of *P. graminis* f. *sp. tritici* under field conditions and observed that 26 accessions expressed high adult-plant resistance to stripe rust, 16 were screened as sources with broad spectrum stripe rust resistance and some land races also exhibited desirable stripe rust resistance. Safavi and Afshari (2012) assessed 36 wheat lines along with susceptible checks for seedling and adult plant resistance to yellow rust and observed that lines M-89-5, M-89-4 and M-88-18 along with the check had the highest value of final rust severity (FRS) and coefficient of infection (CI) thus identified as moderate to susceptible type whereas M-88-3, M-88-6, M-88-14, M-89-8, M-89-10 and M-89-11 expressed durable resistance based on low values of FRS and CI. 35
Yahong (2012) reported that genes Pm12, Pm16, Pm21, Pm18, Pm2, Pm23, Pm30, Pm4a can be used in mildew resistance breeding programmes as Pm8, Pm1, Pm3a etc. have reached virulence frequencies 90% and above thus breakdown of the resistance. Bhardwaj et al. (2012) in their survey studies on stem rust in Leh-Ladakh area recommended the replacement of wheat land races with cultivars like Sinchen, HS365 and HS375 for an effective disease resistance. Ming et al. (2013) demonstrated that real-time PCR assay was a useful tool to rapidly and accurately quantify the latent infection levels of wheat powdery mildew and to efficiently estimate the initial inoculum potentials of epidemics in the fields. Ping et al. (2014) proposed a forecasting method for wheat powdery mildew prevailing trend based on group analytic hierarchy process (GAHP) to deal with the effects of single factor and false on the predicted results. Bender et al. (2016) in their studies on rust screening under greenhouse conditions using Kareiga x Avocet S doubled haploid populations and two races of P. graminis f. sp. triticii reported that phenotyping and genetic analysis of especially major effect stem rust resistance in adult wheat plants is possible and reproducible under controlled conditions in a greenhouse. Gupta et al. (2016) evaluated 370 Indian bread wheat, durum, dicoccum and triticale varieties using mixture of natural occurring patho types from four locations Out of 370, only 23 varieties exhibited immune reaction (0) whereas 150, 83 and 114 varieties expressed resistance (1-3), moderately susceptible (4-6) and highly susceptible (>6) response, respectively against powdery mildew, thus highlighting the urgent need to broaden the genetic base of wheat by identifying and introgressing new sources of powdery mildew resistance. Menardo (2016) in their studies on the diversification of pathogen species upon the triticale species concluded that hybridization between mildews specialized on different species is a mechanism of adaptation to new crops introduced to agriculture.
Wei et al. (2016) used ground based remote sensing technology for the estimation of powdery mildew severity in winter wheat at different levels of disease incidence and different crop growth stages and revealed the precision of monitoring based on the different wavelengths.