RESEARCH PAPER:

Effect of environment on clustering pattern in bread wheat (*Triticum aestivum* L.)

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SUMMARY

Genetic divergence was studied in 40 genotypes of bread wheat to assess the nature and extent of diversity over four diverse environments. Analysis of variance (ANOVA) revealed significant genotypic differences for all the environments studied. The genotypes were grouped in eight clusters each in E-I and E-II and six clusters each in E-III and E-IV. The only genotype MP-4010 in E-III was observed most divergent among all. The maximum contribution to the divergence was made for harvest index followed by grain yield. Three genotypes (HD-2643, NIAW-34 and RAJ-3077) were screened most desirable and stable for early heading and early maturing character. Four genotypes (GW-366, HD-2733, PBW-533 and SUJATA) were found most stable for high mean grain yield.

Key words : Genetic divergence, Bread wheat, Inter-and intra-cluster distances, Grain yield

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The germplasm, the reservoir of genetic diversity, is often exploited to most of the changing needs for developing improved crop varieties. The importance of genetic diversity for selecting parents for recombination breeding in wheat to recover transgressive segregants has been emphasized (Jatasara and Paroda, 1983). Use of diverse parents in hybridization programme can serve the purpose of combining diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. Parents be selected on the basis of multivariate D^2 analysis (Mahlanobis, 1936). This technique measurers the forces of differentiation at intra-and inter-cluster levels. The present study is an attempt to classify 40 genotyes of bread wheat into different groups in four diverse environments and to quantify the magnitude of genetic divergence for their further use in recombination breeding with expectation of getting potential transgressive segregants.

MATERIALS AND METHODS

Forty genotypes of bread wheat were evaluated in randomized block design with three replications under four diverse micro-environments for two successive crop seasons (2007-08 and 2008-09) at Agricultural Research Farm, C.C.R. P.G. College, Muzaffarnagar (U.P.), India. In each replication, the genotypes were evaluated in single row plot of 3m length with a distance of 0.3m and 0.1m between rows and plants, respectively at two different dates of sowing (25th November and 20th December) in both the years. All the standard cultural practices and irrigation schedule were followed to raise the good crop. Five competitive plants/genotypes/replications were tagged and observations on 10 yield related characters were recorded in all the environments. Per cent contributions for these characters towards divergence in all four environments were computed using the formula :

$$\textbf{Per cent contribution of pth character } Z \frac{pN}{n(n-1)/2} x\, 100\%$$

where, N is the number of possible genotypic combinations and n(n-1)/2 is the number of total possible genotypic combinations among n number of genotypes. The genetic divergence analysis was conducted on data collected on individual environments and inter-and intra-cluster distances were also analysed in each environment.

RESULTS AND DISCUSSION

The ANOVA suggested adequate genetic variability for yield and other yield related traits *Triticum aestivum* using multivariate analysis (Table 1). A perusal of this table revealed that