

effect. LA influenced the LY via weight of 100 leaves, NPBP and PH. The result obtained by path analysis technique helps in direct and indirect selection of traits for genetic improvement of LY. It allowed us to detect those components which exhibit the highest effect on LY expression. Character *viz.* PH, NPBP, NNML and weight of 100 leaves had positive direct effect on LY which should be paid close attention by breeders and direct selection of these traits will be rewarding for LY improvement. However, TNLP and LA influence the LY indirectly via PH, NPBP and weight of 100 leaves, indirect selection through such traits will be effective. The results obtained in this technique are in agreement with the earlier reports, of Susheelamma *et al.*, (1988).

An understanding of the nature of association of yield with their agronomic traits would give appropriate suggestions in the selection procedure for breeding programme. The component traits which are strongly correlated with leaf yield as the basis of selection would minimise the effect of epistasis, then linkage will not influence the progeny mean for any trait.

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VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND QUALITY PARAMETERS IN *Aestivum* WHEAT

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ABSTRACT

Studies on variability, heritability and genetic advance for yield and quality parameters were carried out in *aestivum* wheat by using 64 entries. The study revealed the existence of wide range of variation for almost all the characters studied, showing a lot of scope for selection. The highest level of variability was found for tryptophan content and lowest for number of days to maturity. High heritability estimates together with high genetic advance were observed for plant height and pelshenke value. Grain yield per plant, tryptophan content and DBC value showed low heritability and low genetic advance, indicating high influence of environment on the expression of these characters.

KEY WORDS : Wheat, variability, heritability, genetic advance, yield, quality

The success in any breeding programme depends on the amount of variability present for different characters in a population and its efficient management and utilisation. In order to exploit different types of gene actions in the population,

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information on the relative magnitude of genetic variability in the population, heritability and genetic advance of important agronomic and quality traits is essential. Though, extensive work has been done to understand the heritability and

genetic advance of the quantitative characters, only a few reports are available on quality parameters. Nutritive value of wheat has a special significance for our country since wheat serves as a staple diet for majority of our people. Heritability with genetic advance is of more value in predicting the effect of selection. If the heritability is mainly due to additive gene effects, the realised genetic gains would be high in comparison to the situation where both additive and nonadditive gene effects are involved. In view of this, the present study was undertaken to derive information on heritability and genetic advance of the important yield components and quality parameters.

MATERIALS AND METHODS

The experimental material consisted of 16 genotypes, selected from advance uniform generations on the basis of their protein content and 48 F1 hybrids derived from these 16 lines. These 16 lines were crossed in a 12 x 4, line x tester mating design. The lines included are, P38-15, P118-2, KLM 26 and P104 of early maturity group, P608, P769, P925 and Pusa 5-3 of medium maturity group and P768, P932, WLR154 and P1035 of late maturity group. The four testers are HD2285, HD 2428, HD2329 and DL153-2.

The hybrids along with their parents were grown in a randomised block design with four replications. Five plants from each entry and per replication were selected together data on number

of days to flower (NDF), number of days to maturity (NDM), plant height (PH), number of tillers per plant (NTP), spike length (SL), number of spikelets per spike (NSS) number of grains per spike (NGS), weight of grains per spike (WGS), 1000 grain weight and grain yield (GY) per plant. Quality analysis was carried out for protein content, pelshenke value, tryptophan content and DBC value following routine methods. The data was subjected to analysis of variance (Panse and Sukhatme, 1967). The genotypic and phenotypic coefficients of variances (PCV, GCV) heritability and expected genetic advance were estimated as per normal procedures. The results of this experiment are applicable to the location and the environment where the experiment was conducted.

RESULTS AND DISCUSSION

The results of the analysis of variance for parents and hybrids are presented in the Table 1. Significant values of variances were observed for all the characters in case of both parents and hybrids while, the values for parents vs hybrids also found to be significant for all the characters except for NGS, single plant yield and pelshenke value. This revealed the existence of significant variation for most of the important characters.

The estimates of population mean and range for the characters (Table 2) have shown a wide range of variation for all the characters, showing a lot of scope for selection in the following

Table 1. Analysis of variance for parents and hybrids

Characters Source of Variation Degrees of freedom	Mean Sum of Squares				
	Replications 3	Parents 15	Hybrids 47	Parents Vs Hybrids 1	Error 189
Plant height	2.134	298.00**	215.40**	53.72**	4.62
No. of tillers/plant	0.263	160.65**	42.97**	1867.73**	5.66
Days to flower	1.482	28.35**	9.24**	75.00**	3.32
No. of days to maturity	1.59	6.34**	4.18**	59.63**	2.51
No. of spikelets/spike	0.173	30.24**	7.79**	2.39**	0.41
Length of spike	0.076	4.00**	2.46**	8.91**	0.13
No. of grains/spike	34.48	391.79**	109.33**	6.05	23.71
Weight of grains/spike	0.048	0.38**	0.31**	3.79**	0.096
1000-grain weight	2.61	139.94**	67.87**	10005.59**	4.03
Single plant yield	3.21	95.37**	80.80**	13.52	12.72
Protein percentage	0.53	7.99**	2.72**	233.97**	0.30
Pelshenke value	29.81	1551.73**	1040.06**	80.73	61.47
Tryptophan content	1.5×10^{-6}	2.6×10^{-5} **	3.1×10^{-1} **	1.2×10^{-2} **	2.9×10^{-4}
DBC value	9.1×10^{-6}	6.4×10^{-5} **	7.8×10^{-5} **	7.0×10^{-4} **	5.9×10^{-5}

*, ** : Significant at 5% and 1% level respectively

Table 2. Estimate of phenotypic and genotypic parameters

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability N.S. (%)	Genetic Advance
Plant height	89.42	74.13 - 104.48	8.78	8.44	85.02	16.07
No. of tillers/plant	20.62	13.47 - 41.88	26.22	23.55	2.53	0.21
Days to flower	87.33	83.00 - 91.25	2.85	1.94	28.28	4.28
No. of days to maturity	130.21	128.25 - 134.00	1.39	0.67	23.44	0.82
No. of spikelets/spike	17.78	11.98 - 22.22	10.62	10.00	11.22	0.32
Length of spike	13.26	11.72 - 14.85	6.88	6.31	60.00	1.07
No. of grains/spike	62.03	41.92 - 74.60	12.64	9.91	6.38	0.84
Weight of grains/spike	2.70	1.97 - 03.25	15.18	9.91	24.10	0.20
1000-grain weight	41.82	30.00 - 54.35	12.65	11.71	62.92	6.46
Single plant yield	35.43	27.42 - 48.81	15.55	11.85	9.45	1.20
Protein percentage	15.88	13.58 - 19.75	9.21	8.53	43.30	0.88
Pelshenke value	149.64	123.25 - 186.75	12.91	11.01	61.39	25.84
Tryptophan content	0.034	0.009 - 0.061	29.25	24.63	0.37	0.002
DBC value	0.18	0.145 - 0.213	9.00	7.90	0.13	0.0013

generations. The variation was almost uniform on both sides of the mean indicating normal distribution of the population.

Estimates of the PCV and GCV showed the presence of different levels of variability for different characters, the highest being for tryptophan content and the lowest for NDM, showing more scope for selection of tryptophan and less scope for NDM. The mean of the characters, PH, days to flower, NDM, length of the spike and DBC value were found to be just in between the population values. The GCV for all these characters was low showing less scope for selection of these characters in the population studied. Other characters like NTP, single plant yield, NGS, and WGS, 1000 grain weight, NSS and pelshenke value were having wide variability showing ample scope for selection of these characters. High heritability estimates together with high genetic advance were observed for PH and pelshenke value showing the predominance of additive gene effects controlling these characters which can be improved by simple selection procedures. Deshmukh and Deshmukh (1987) also observed high expected genetic advance along with higher heritability for plant height. High heritability for pelshenke value was noted by Borghi *et al.* (1975) and Li (1990). High heritability with moderately high genetic advance was observed for 1000 grain weight, supporting the earlier reports by Perwez and Haque (1975). Eventhough the heritability of the characters, NDF, NDM, SL, WGS and protein percent was high to moderately high, their genetic advance was low

indicating that these characters are controlled by both additive and nonadditive gene effects. Breeding methods which can exploit both gene systems like biparental mating and selection for seggregants in advanced generations may be followed.

NTP, NSS, NGS, GYP, tryptophan and DBC values showed low heritability and low genetic advance, indicating high influence of environment on the expression of these characters. So, direct selection for these characters may not be effective. Recurrent selection for *sea* would be a right choice for genetic amelioration. Low heritability and low genetic advance for grain yield was reported by many workers. In contrast, Deshmukh and Deshmukh (1987) and Abid Mahmood (1991) reported high heritability and high genetic advance for grain yield. Other characters showed different levels of heritability and genetic advance by different workers. Such a variation is expected because the estimates of heritability are applicable only to the population under consideration and cannot be extrapolated to other populations.

In conclusion, it can be said that for selecting high yielding lines the possibilities of improvement are more through indirect selection for yield contributing characters like 1000 grain weight, SL, WGS, etc.

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OCCURRENCE OF SILICATE SOLUBILIZING BACTERIA IN RICE ECOSYSTEM

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ABSTRACT

Silicate and phosphate solubilizing bacteria were enumerated from soils, tank sediments, water, agroinputs like super and rock phosphates and commodities of anthropogenic activities. Silicate solubilizers were lesser than the phosphate solubilizing bacteria in these materials. Three out of 17 promising isolates were authenticated by Gram and Spore staining and biochemical characteristics. All of them were *Bacillus* spp. The isolate of *Bacillus* sp. from granite crusher yard exhibited marked silicate solubilization under *in vitro* both in medium and in liquid culture. The presence of silicate solubilizing bacteria in rice ecosystem might contribute to the silicate requirement of rice.

KEY WORDS : Silicate solubilizing bacteria, distribution, rice

Rice like other members of the gramineae, accumulate silica in its culms, leaf blades and husks, which confer rigidity and resistance against pest and diseases. It also plays a role in transport of oxygen to roots (Ponnamperuma, 1964). Silicon nutrition to rice is essential as it acts similar to phosphate and also as a substitute for sulphate, besides its interrelationship with several other nutrients. Further with application of higher and higher levels of nitrogen to boost the yield plant requires more of silicon to prop itself.

Silicon although abundantly available in earth's crust is in an unavailable polymerized form and occurs in the form of silicates (salts of SiO₃) and silicon dioxide (SiO₂). Polymerized silicon is almost insoluble. However dissolved silicon is observed in water in rice fields. Webley *et al.* (1960) reported that certain bacteria can depolymerize crystalline silica to soluble form. The present study was undertaken to assess the occurrence of silicate solubilizing bacteria (SSB) in rice ecosystem.

MATERIALS AND METHODS

The silicate solubilizing bacteria (SSB) present in soils, tank sediments, water and agro-inputs and commodities of anthropogenic activity like cement were enumerated in medium containing insoluble magnesium trisilicate (0.25 %). Simultaneously phosphate solubilizing bacteria (PSB) were also enumerated in Sperber's hydroxy apatitic agar. The samples were serially diluted in sterile water and appropriate dilutions were plated in th respective media. The total bacterial population was enumerated in soil extract agar and the proportion of SSB and PSB to total bacteria was calculated.

The extent of silicate and phosphate solubilization by the isolates were assessed both qualitatively by the clearing zones in plate assay and quantitatively by determining the soluble silicon released during the growth of bacteria. The available phosphorus was estimated by routine method. The pH of the liquid broth after filtration was also recorded. The efficient elite isolates