



SELECTION PARAMETERS AGAINST LEAF BLIGHT SCREENING FOR ENHANCING GRAIN YIELD UNDER SALINE SOILS IN BREAD WHEAT (*TRITICUM AESTIVUM* L. EMHELL.)

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Abstract

Analysis of variance, genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance (GA) in 143 genotypes of bread wheat including three checks KRL-210, NW-2036, NW-1067 were evaluated during 2010-11. The mean sums of squares due to checks were greatly significant for all the eleven traits excluding peduncle length and plant height while mean squares due to blocks were non-significant for all the traits excluding plant height and grain yield. GCV were close to PCV for every trait. Maximum appraisals of heritability and genetic advance were indicated through plant height follow by flag leaf area, test weight and biological yield per plant respectively. High heritability and high genetic advance indicated that the heritability is due to additive nature of gene action and reliability of these characters in subsequent generation through selection for developing high yielding cultivar resistant against Leaf blight.

Key words : Variability, selection, genetic advance, salt.

Introduction

Human management practices can increase the salinity of soils by adding salts by use of irrigation water. Saline and saline-sodic soils are caused by surplus accumulation of salts Na^+ , K^+ , Ca^{2+} , Mg^{2+} and Cl^- at the soil surface. These soils condition are categorized into two types- sodic (alkali) and saline. Saline soils contain sodium cations with electrical conductivity (EC) more than 4 dSm^{-1} , but the dominant ions are usually soluble chloride and sulphate. Exchangeable Sodium Percentage (ESP < 15) and pH values of these soils are much lower than in sodic soils. It can either be natural or primary or secondary or main made salinity. Prime salinity of soil and ground water is owing to the weathering of naturally saline rocks or by deposition of organic salt passed by the wind and rain. Minor salinity is owing to human-activities like unreliable irrigated schemes and source of water. Successive salinity in the soil has the devastating effect on plant growth reducing crop yields that leads complete crop failure in worst affected areas. Many number of strategies available for managing saline soils, one of these involves in the various use of crops with a

moderate or high level of salt tolerance. Significant amounts of salt in the soil solution can affect plant growth through a number of mechanisms which can be described as osmotic, ion-imbalance or specific ion-toxicities. The facts of variability present in a crop species for the traits under improvement is of most prominence for the accomplishment of any crop improvement programme. The availability of variability is the basic requirement for genetic improvement through efficient breeding programme. Heritability and genetic advance are important selection parameters which clear-cut indicates that selection can be practiced to improve desirable character. Heritability estimates along with genetic advance are normally more helpful in predicting the grain yield under selection.

Materials and Methods

Augmented Block Design is basically Randomized Block Design with a provision in ABD only checks are replicated in each block. In this article some modifications are also presented as GCV, PCV, heritability and genetic advance are considered only for the checks. A total of 143 wheat lines along with three checks KRL-210, NW-2036 and NW-1067 were evaluated in Augmented Block

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Design at Main Experiment Station Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad during *rabi* (2010-11). The entire experimental field was divided into 7 blocks of equal size and each block having 23 plots. Out of 23 plots in a block, 20 plots were used for accommodating the test genotypes which were not replicated while remaining 3 checks i.e. KRL-210, NW-2036, NW-1067, which were replicated in three rows plot having 3 m long and contain with inter and intra-row spacing with 25 cm and 15 cm, in that order. Experimental site was salt affected and soil having EC =0.39; pH = >8.5; ESP = <15 and rich in potash and low in organic carbon, nitrogen and phosphorus. Recommended dosage of fertilizers N:P:K @ 150:60:60 and cultural packages were applied to raise a good and healthy crop. The observation were subjected to five randomly competitive plants for all the quantitative characters Plant height (cm), number of tillers per plant, Spike length (cm), Peduncle length (cm), Grains per spike, Test weight (g), Biological yield per plant (g), Grain yield per plant (g), Harvest index (%), Flag leaf angle, Flag leaf area(cm²), Leaf blight [Double digit system (Asif *et al.*, 2004)], except days to maturity, which was recorded on the plot basis. The angular position of the flag leaf of the plant was visually observed. The data recorded on above characters were subjected to analysis of variance (ANOVA) (Chaitali and Bini, 2007) and genotypic and phenotypic coefficients of variation (GCV & PCV) (Federer, 1956), estimate of broad sense heritability (h^2_b) (Gupta *et al.*, 2004), genetic advance as

percent of the mean, was computed by the method suggested by Hanson *et al.* (1956) only for the checks.

Results and Discussion

The analysis of variance of Augmented Block Design for eleven traits showed extremely significant difference among the genotypes under study, showed presence of significant amount of variability in the germplasm (table 1).

The variation due to checks was significant for all the traits apart from peduncle length and plant height while mean squares due to blocks were non-significant for all the traits except plant height and grain yield per plant, which indicated that the experimental site was heterogeneous. The high order of least significant difference between two checks mean (LSD_1) were recorded in case of plant height (3.42) followed by peduncle length (2.11) indicated, high variation was present in the metric measurement of both the character. Slightest significant variation between adjusted mean of two genotypes in same (LSD_2) and different block (LSD_3) was observed in case of plant height (9.05), peduncle length (5.58) biological yield plant⁻¹ (4.79) and plant height (10.44), peduncle length (6.45). Plant height (8.06), peduncle length (4.97) and biological yield plant⁻¹ (4.27) showed highest least significant difference between adjusted means of genotype and check mean (LSD_4) (Hanson *et al.*, 1956; Johnson *et al.*, 1955; Khan *et al.*, 2004). The most desirable genotypes identified for different eleven characters on the basis of their mean

Table 1 : Analysis of variance of augmented design for 11 characters and least significant differences in wheat germplasm.

S. no.	Characters	Source of variation			Range of parameters			
		Blocks	Checks	Error	LSD_1	LSD_2	LSD_3	LSD_4
		d. f. (6)	d. f. (2)	d. f. (12)	5 % ¹	5 % ²	5 % ³	5 % ⁴
1	Flag leaf area (cm ²)	2.45	17.62**	1.44	1.39	3.69	4.26	3.29
2	Days to maturity	1.72	80.62**	1.28	1.32	3.492	4.03	3.11
3	Peduncle length (cm)	2.76	5.67	3.29	2.12	5.58	6.45	4.98
4	Plant height (cm)	43.10**	4.51	8.63	3.42	9.04	10.44	8.06
5	Spike length (cm)	0.04	2.25**	0.03	0.19	0.50	0.58	0.45
6	Grains ⁻¹ spike	2.61	12.56**	1.34	1.35	3.56	4.12	3.18
7	Productive tillers plant ⁻¹	0.06	2.31**	0.07	0.32	0.83	0.96	0.7
8	1000-grain weight (g)	2.32	14.38**	1.14	1.24	3.28	3.79	2.93
9	Biological yield plant ⁻¹ (g)	4.09	40.73**	2.42	1.81	4.79	5.53	4.27
10	Grain yield plant ⁻¹ (g)	2.14*	5.40**	0.52	0.84	2.25	2.55	1.97
11	Harvest index (%)	0.65	17.35*	0.34	0.68	1.79	2.07	1.60

* significant at 5% and ** significant at 1% level of probability

LSD_1 =Least significant difference between two check means.

LSD_2 =Least significant difference between adjusted mean of two genotypes in same block.

LSD_3 =Least significant difference between adjusted mean of two genotypes in different block.

LSD_4 =Least significant difference between adjusted mean of genotype and check mean.

Table 2 : Range, mean, CV, heritability, GA and GA in % of mean for 11 traits of wheat genotypes.

Characters	Range (Min-Max)	Mean value	PCV(%)	GCV(%)	h ² (b)(%)	GA(%)	GA in (%) of Mean
Flag leaf area (cm ²)	12.00-36.04	20.29	19.76	18.85	91.00	7.52	37.05
Days to maturity	118.38-130.71	124.68	1.53	1.23	64.70	2.54	3.04
Peduncle length (cm)	23.13-45.47	29.84	11.50	9.78	72.20	5.12	17.11
Plant height (cm)	65.77-111.01	82.46	8.69	7.94	83.30	12.31	14.91
Spike length (cm)	6.52-13.63	10.10	9.99	9.86	97.30	2.03	20.05
Grains per spike	30.44-48.60	39.57	7.22	6.60	83.60	4.92	12.44
Productive tillers plant ⁻¹	3.77-6.78	4.85	11.99	10.59	78.10	0.93	19.29
1000-grain weight (g)	30.60-47.90	39.74	7.82	7.35	88.20	5.65	14.22
Biological yield plant ⁻¹ (g)	12.48-28.38	19.95	16.37	14.38	77.20	5.18	26.03
Grain yield plant ⁻¹ (g)	4.04-12.25	7.65	17.06	14.22	69.50	1.86	24.41
Harvest index (%)	34.33-42.90	38.33	4.58	4.32	89.00	3.22	8.40

Table 3 : The most desirable genotypes identified for 11 different characters.

S.no.	Characters	Genotypes
1.	Flag leaf area	GW 2007-80, ESWYT-110, KRL-315, GW 2008-153, 1CSISADRYT-5217, RWP2009-12, IBWSN-175, 1SATYN-53, IBWSN-34, IC-524284
2.	Days to maturity (Early) type	IC-546933, GW 2008-157, GW 2008-156, EC-634300-99, GW 2007-92, KRL-315, EC-634300-64, IC-549914, IC-524288, EC-664236, EC-634300-110
3.	Peduncle length	IBWSN-103, IBWSN-63, EC-634300-63, 43IBWSN-1107, EC-664199, EC-664189, EC-634300-133, EC-634300-95., ESWYT-110, IBWSN-137, IBWSN-112
4.	Plant height (Dwarf)	EC-634300-133, EC-634300-94, IBWSN-103, IBWSN-63, GW 2006-17, RWP2009-12, KRL-324, GW 2008-159, GW 2007-96., LBP 2009-24, EC-634300-63
5.	Spike length	10EGPYT-11, EC-664236, GW 2008-153, 10DSBWYT-420, 27SAWSN-3027, ESRN-51, 27SAWSN-3069, EC-663954, EC-634300-110, EC-664244, EC-664215
6.	Grains per spike	27SAWSN-3027, 27SAWSN-3069, ESRN-51, EC-664236, EC-634300-63, EC-664196, 10DSBWYT-420, GW 2008-153
7.	Reproductive tillers per plant	IC-524282, GW 2008-157, 29ESWYT-130, IC-524284, 43IBWSN-1107, EC-664236, 29ESWYT-136, IC-553917, EC-634300-110, EW-EC-664215, NW-5029
8.	Test weight	45IBWSN-1175, 1CSISADRYT-5218, IBWSN-152, ESRN-51, 27SAWSN-3107, 30ESWYT-131, KRL-323, 43IBWSN-1107, 29ESWYT-130
9.	Biological yield per plant	EC-664236, EC-634300-110, 29ESWYT-130, IC-524282, IBWSN-158, 27SAWSN-3107, 1CSISADRYT-5217, EC-664244, EC-663946, EC-664215
10.	Harvest index	KRL-306, EC-663961, 1SATYN-46, GW 2007-80, 1SATYN-60, 29ESWYT-130, 1SATYN-26 EC-634300-94, NW-5029, EC-634300-76
11.	Grain yield per plant	29ESWYT-130, IBWSN-158, 27SAWSN-3107, EC-664236, EC-634300-110, IC-524282, 19HRWSN-2026, 1CSISADRYT-5217, 43 IBWSN-1107, 27 SAWSN-3027

- Bold figure indicated highly significant group of genotypes.

performance which are shows in table 3.

The PCV and GCV (table 2) were calculated only in the case of checks for 11 different character, exhibited that phenotypic and genotypic variances were near to each other but significantly different for the majority of all the traits. The degree of environmental variance was comparatively lower which showed that no considerable

effect of environment was observed on the total phenotypic expression of the character. Highest magnitude of phenotypic as well as genotypic coefficient of variation was observed for flag leaf area (19.76 & 18.85), grain yield plant⁻¹ (17.06 & 14.22), biological yield plant⁻¹(16.37 & 14.38), productive tillers plant⁻¹ (11.99 & 10.59) and peduncle length (11.50 & 9.78) and remaining

Table 4 : Response of 140 Wheat genotype of flag leaf angle.

S no.	Character	Genotypes	No. of genotypes
1.	Erect	42 nd IBWSN-1038-I, 42 nd IBWSN-1063, 42 nd IBWSN-1103, 42 nd IBWSN-1146, 42 nd IBWSN-1164, 42 nd IBWSN-1169, IBWSN-1170, 12 th EGPSN-51, 4 th EBWYT-511, 19 th HRWSN-2026, 27 th SAWSN-3004, 27 th SAWSN-3082, 42 nd IBWSN-1021, 42 nd IBWSN-1038-II, 1 st CSISADRYT-5217, 1 st CSISADRYT-5218, EC-664199, EC-664208, IC-546933, 10 th DSBWYT-407, KRL-299, KRL-300, KRL-302, KRL-303, KRL-305, KRL-309, KRL-312, KRL-316, KRL-324, WH-1083, NW-5029, GW-2007-96, GW-2008-159.	33
2.	Semi erect	42 nd IBWSN-1039, 42 nd IBWSN-1112, 42 nd IBWSN-1113, 42 nd IBWSN-1119, 42 nd IBWSN-1121, 42 nd IBWSN-1150, 42 nd IBWSN-1152, 42 nd IBWSN-1158, 42 nd IBWSN-1166, 42 nd IBWSN-1167, 42 nd IBWSN-1173, 42 nd IBWSN-1175-I, 42 nd IBWSN-1151, 10 th EGPYT-7, 10 th EGPYT-11, 4 th EBWYT-509, 29 th ESWYT-110, 29 th ESWYT-130, 29 th ESWYT-136, 16 th HRWYT-206, 4 th SAMNYT-411, 27 th SAWSN-3011, 27 th SAWSN-3027, 27 th SAWSN-3052, 27 th SAWSN-3069, 27 th SAWSN-3097, 27 th SAWSN-3107, 30 th ESWYT-118, 30 th ESWYT-119, 30 th ESWYT-131, 42 nd IBWSN-1057, 42 nd IBWSN-1065, 42 nd IBWSN-1087, 42 th IBWSN-1175-II, 1 st CSISADRYT-5212, 1 st CSISADRYT-6764, 1 st CSISADRYT-6767, EC-634300-64, EC-634300-69, EC-634300-76, EC-634300-81, EC-664196, EC-664215, 42 nd IBWSN-1034, EC-664236, EC-664244, EC-663954, EC-663961, IC-524282, IC-524284, IC-524288, IC-553917, IC-549914, EC-414149, 1 st SATYN-23, 1 st SATYN-26, 1 st SATYN-35, 1 st SATYN-37, 1 st SATYN-38, 1 st SATYN-45, 1 st SATYN-46, 1 st SATYN-53, 1 st SATYN-60, ESRN-3, ESRN-11, ESRN-15, 10 th DSBWYT-420, 10 th DSBWYT-422, KRL-301, KRL-304, KRL-306, KRL-307, KRL-315, KRL-322, KRL-323, WH-1097, LBP-2009-24, RAJ-4211, RWP-2009-12, GW-2006-17, GW-2007-87, GW-2007-92, GW-2008-156.	83
3.	Drooping	42 nd IBWSN-1023, 42 nd IBWSN-1137, 42 nd IBWSN-1107, EC-634300-63, EC-634300-82, EC-634300-88, EC-634300-94, EC-634300-95, EC-634300-99, EC-634300-103, EC-634300-106, EC-634300-110, EC-634300-133, EC-664189, EC-664193, EC-664200, EC-664227, EC-664229, EC-663946, EC-664009, ESRN-51, GW-2007-80, GW-2008-153, GW-2008-157.	24

All checks namely KRL210, NW-2036, NW-1067 were drooping, semi-erect and erect, respectively.

Table 5 : Screening of 140 wheat genotypes against foliar blight (leaf blight) under natural disease pressure during 2010-11.

S. no.	Disease Response	Double Digit Scale	Genotypes	No. of genotypes
1.	Immune (I)	00-01	Nil	
2.	Resistant (R)	12-24	10 th EGPYT-7, 4 th EBWYT-509, 30 th ESWYT-118, 42 nd IBWSN-1023, 42 nd IBWSN-1038-I, 42 nd IBWSN-1063, 42 nd IBWSN-1103, 42 nd IBWSN-1112, 42 nd IBWSN-1113, 42 nd IBWSN-1119, 42 nd IBWSN-1121, 42 nd IBWSN-1152, 42 nd IBWSN-1164, 42 nd IBWSN-1166, 42 nd IBWSN-1167, 42 nd IBWSN-1170, 42 nd IBWSN-1173, 42 nd IBWSN-1175-I, 42 nd IBWSN-1151, 10 th EGPYT-11, 12 th EGPSN-51, 27 th SAWSN-3097, 30 th ESWYT-119, 27 th SAWSN-3107, 4 th EBWYT-511, 27 th SAWSN-3069, 29 th ESWYT-110, 27 th SAWSN-3011, 27 th SAWSN-3027, 27 th SAWSN-3027, 29 th ESWYT-130, 29 th ESWYT-136, 4 th SAMNYT-411, 16 th HRWYT-206, 42 nd IBWSN-1021, 42 nd IBWSN-1038-II, 42 nd IBWSN-1057, 42 nd IBWSN-1065, 42 nd IBWSN-1107, 1 st CSISADRYT-5218, 1 st CSISADRYT-6764, EC-634300-69, EC-634300-81, EC-634300-82, EC-634300-88, EC-634300-94, EC-634300-99, EC-634300-103, EC-634300-110, EC-634300-76, EC-664189, EC-664193, EC-664196, EC-664199, EC-664200, 1 st CSISADRYT-6767, EC-634300-64, EC-664215, EC-664227, EC-664236, EC-663946, EC-663954, EC-663961, EC-664009, IC-524284, IC-546933, IC-553917, KRL-316, KRL-322, KRL-323, KRL-324, WH-1083, WH-1097, LBP-2009-24, RAJ-4211, NW-5029, RWP-2009-12, GW-2006-17, GW-2007-80, GW-2007-96, GW-2008-153, GW-2008-156, GW-2008-157, GW-2008-159, EC-414149, 1 st SATYN-23, IC-549914, 1 st SATYN-35, 1 st SATYN-37, 1 st SATYN-45, 1 st SATYN-53, 1 st SATYN-60, ESRN-51, 10 th DSBWYT-407, 10 th DSBWYT-422, KRL-300, KRL-303, KRL-304, KRL-305, KRL-306, KRL-309.	100

Table 5 continued...

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3.	Moderately resistant	34-46	42 nd IBWSN-1034, 42 nd IBWSN-1169, 42 nd IBWSN-1039, 42 nd IBWSN-1137, 27 th SAWSN-3052, 27 th SAWSN-3082, 42 nd IBWSN-1146, 42 nd IBWSN1158, 42 nd IBWSN1150, 19 th HRWSN-2026, 27 th SAWSN-3004, 30 th ESWYT-131, 42 nd IBWSN-1087, 42 nd IBWSN1175II, 1 st CSISADRYT5212, 1 st CSISADRYT-5217, EC-634300-63, EC-664208, EC-634300-95, EC-634300-106, EC-634300-133, EC-664229, EC-664244, IC-524282, IC-524288, 1 st SATYN-38, 1 st SATYN-26, 1 st SATYN-46, ESRN-3, ESRN-11, ESRN-15, 10 th DSBWYT-420, KRL-299, KRL-301, KRL-302, KRL-312, KRL-315, KRL-307, GW-2007-87, GW-2007-92.	40
4.	Moderately susceptible	56-68	Nil	
5.	Susceptible	78-89	Nil	
6.	Highly susceptible	99	Nil	

characters have moderate to very low genotypic and phenotypic variation (Kumar *et al.*, 1998, 2008; Lal *et al.*, 2009; Lush, 1940; Pal *et al.*, 2009; Panwar and Singh, 2000; Paul *et al.*, 2006; Sachan and Singh, 2003).

The coefficient of variation (CV) indicates only the amount of variability present in different traits and does not indicate the heritable part. This can be ascertained from the heritability estimates in broad sense, which comprise both additive and non-additive gene effects (Sidharthan and Malik, 2007). Topmost heritability and genetic advance was exerted by plant height (83.30% & 12.31) followed by flag leaf area (91.00% & 7.52), test weight (88.20% & 5.65), biological yield plant⁻¹ (72.20% & 5.65), peduncle length (72.20% & 5.12), grains per spike (83.60% & 4.92) respectively and remaining characters have moderate to very low heritability and genetic advance (Surya and Kerketta, 2000), which indicated the prevalence of additive gene action in controlling those traits. Hence, assortment might be rewarding for the improvement of characters like plant height, grains spike⁻¹, Peduncle length, 1000 seed weight and biological yield per plant. Both heritability and genetic advance showed that the additive nature of gene action was consistent for selection and emerged the same as ideal traits for hybridization programme to develop desirable high yielding cultivar.

The screening result of 140 wheat genotypes for flag leaf angle and response of foliar blight (leaf blight) under natural disease pressure condition are presented in the tables 4 and 5, respectively.

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