International Journal of Bio-resource and Stress Management 2013, 4(2):224-229

Genetic Variability Studies in Wheat (*T. aestivum* L.) under Waterlogged Sodic Soils

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Article History

Manuscript No. c161
Received in 5th September, 2012
Received in revised form 15th May, 2013
Accepted in final form 5th June, 2013

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Keywords

Wheat, water logging, sodic soils, genetic variability

Abstract

Genetic diversity analysis helps in selecting genetically diverse parents. Water logging-prone environments are highly diverse and complex and the mechanisms of tolerance to water logging include a large range of traits. This is further evaluated with the aim of prioritizing traits required for waterlogging tolerance of wheat in the field condition. A field experiment was conducted during 2010-11 with 108 bread wheat genotypes to study genetic variability and interrelationship estimates for 11 attributes in wheat under waterlogged sodic soils. The whole experiment was conducted in 2 sets; the first set was irrigated and drained after 24 hr. (control) while second set was grown under waterlogged condition for 10 days after 27 days of sowing. The entries Kharchiya-65 and Perenjori were to be found highest grain yielder under drained and waterlogged condition, respectively. Significant correlation between grain yield and biological yield plant^{-1}, spike weight plant^{-1}, productive tillers plant^{-1}, harvest index, grains spike^{-1} and 1000-grain weight under both conditions indicated scope for improving grain yield through simultaneous selection. Path analysis further supported and highlighted the importance of biological yield plant^{-1} and harvest index under drained and waterlogged condition. The cluster analysis grouped the 108 bread wheat genotypes into 11 different clusters under both drained and waterlogged conditions. Hybridization among the genotypes separated by high inter-cluster distance is recommended for getting high heterosis as well as for getting transgressive segregants in F_2 generation.

1. Introduction

Wheat (*Triticum aestivum* L.), a self-pollinated crop of the *Graminae* family, is the world's largest famous energy rich cereal crop. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. It is a C_3 plant grown from temperate, irrigated to dry and high-rain-fall areas and from warm, humid to dry, cold environments. Undoubtedly, this wide adaptation has been possible due to the complex nature of the plant's genome, which provides great plasticity to the crop. Waterlogging has been shown to limit wheat yields in many regions of the world; an area estimated at 10 million ha is waterlogged each year in developing countries (Sayre et al., 1994). Waterlogging occurs when rainfall or irrigation water collects on the soil surface for prolonged periods without infiltrating the soil. In the northern Indo-Gangetic Plains of India alone, 2.5 million ha of wheat are affected by irregular waterlogging (Sharma and Swarup, 1988). The present investigation has its direct relevance considering the problem of water logging in eastern Uttar Pradesh, India. Rice-wheat cropping system is one of the most important cropping systems contributing in sustaining the food production in India. Identification of diverse genotypes with good yielding ability *per se* as well as for important yield components in waterlogged conditions will help in having transgressive segregants and that would help in the development of high yielding varieties of wheat suited to sodic soils.

2. Materials and Methods

A field experiment was conducted during *Rabi* season 2010-11 at the Main Experimental Station (MES) of NDUA&T Kumarganj, Faizabad (UP) India. The experimental material consisted of 108 diverse genotypes including 4-checks (DBW-14, DBW-17, HD2009 and KRL3-4) of wheat from Australia and India. These genotypes were grown under sodic soils condition (pH>8.5, Redox potential 415.8 mV) in an Augmented Block Design comprising of 4 blocks, where each block contains 26 test entries and 4 checks (randomly allocated). The whole experiment was conducted in 2 sets; the first set was irrigated and drained after 24 hr. (control) while second set was grown under waterlogged condition with 8.5 cm water depth for 10 days after 27 days of sowing. The waterlogged condition was remaining for 10 days only. Each genotype was grown in 4 rows of 2.5 m long plot with 23 cm distance between rows. The recommended cultural practices were adopted to raise good crop. Ten random plants from middle rows per plot were selected to record observations on yield and yield contributing characters. Analysis of variance was done from the mean data obtained in each character (Federere, 1956). Correlation coefficients for all pairs of eleven characters were estimated (Searle, 1961) and path coefficient analysis was carried out as described by Dewey and Lu (1959). The cluster analysis was done on the basis of Beale (1969) and Spark (1973). Coefficient of variations, heritability, genetic advance and cluster analysis was done as per available software (Windowstat Version 8.6).

3. Results and Discussion

The analysis of variance for 11 quantitative characters evaluated during 2010-11 indicated significant differences for all the traits under drained and waterlogged sodic soils conditions. The estimates of genetic parameters *viz;* mean, range, heritability (h^2) (broad sense), genetic advance (GA% of mean), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are presented in Table 1.

3.1. Genetic variability

The result revealed that genotypic variability was high and that promoted us to go for further analysis. The performance under waterlogged condition for eleven metric traits revealed that most of the genotypes were adversely affected by water logging (Table 1). The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits under both environments. Higher PCV and GCV indicated that there was high variability existing among the genotypes. The magnitude of phenotypic and genotypic coefficient of variability (PCV and GCV) for different parameters except days to 50% flowering and grains spike^{-1} under stress condition (waterlogged) were higher than their counterparts under normal i.e. non-waterlogged condition, which indicated that wide variability is manifested under waterlogged stress for exercising

Table 1: Range, mean, heritability (h^2 broad sense), genetic advance (GA), genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and standard deviation (SD) for 11 traits in wheat

Characters		Range	Mean	Heritability	GA % mean	GCV	PCV	SD
Days to 50% flowering	D	73-94	80	82.98	6.41	3.41	3.75	3.23
	WL	74-94	83	78.85	5.56	3.05	3.44	3.10
Days to maturity	D	114-126	120	78.08	3.01	1.65	1.87	2.37
	WL	116-131	122	78.29	3.19	1.75	1.98	2.57
Plant height (cm)	D	61-100	77	84.66	17.76	9.37	10.18	8.26
	WL	52-96	72	86.67	20.42	10.65	11.43	9.07
Productive tillers plant^{-1}	D	2-7	4	16.64	7.69	9.16	22.46	1.11
	WL	2-7	4	72.37	39.83	22.72	26.71	1.22
Spike length (cm)	D	6-13	9	57.31	10.73	6.88	9.08	1.10
	WL	5-12	9	75.61	15.56	8.68	9.99	1.14
Spike weight plant^{-1} (g)	D	3-12	7	92.15	48.31	24.37	25.39	2.15
	WL	1-14	6	92.33	65.31	32.99	34.33	2.45
Grains spike^{-1}	D	26-49	39	85.28	22.67	11.92	12.91	5.30
	WL	23-47	35	88.84	21.45	11.04	11.72	4.52
1000-grain weight (g)	D	24-45	36	79.35	19.44	10.59	11.89	4.50
	WL	21-43	34	85.92	22.82	11.95	12.89	4.50
Biological yield plant^{-1} (g)	D	9-24	16	92.28	44.73	22.60	23.53	4.18
	WL	6-24	14	96.70	53.76	26.54	26.99	4.09
Harvest index (%)	D	26-44	36	45.57	10.08	7.25	10.74	4.00
	WL	20-47	34	46.08	12.40	8.86	13.06	5.07
Grain yield plant^{-1} (g)	D	3-10	6	90.69	52.92	26.97	28.32	1.85
	WL	1-11	5	94.32	68.18	32.08	33.03	1.76

the selection. Higher values for genetic coefficient of variability (GCV) are shown for grain yield plant^{-1}, biomass plant^{-1}, grains spike^{-1}, productive tillers plant^{-1} and plant height under both drained and waterlogged environment (Table 1) indicating better opportunity for improvement through selection.

The heritability estimates ranged from 16.64 to 92.28% for productive tillers plant^{-1} and biological yield plant^{-1} respectively in drained treatments and 46.08 to 92.33% for harvest index and spike weight plant^{-1} in waterlogged treatments respectively. High estimates of heritability (broad sense) were obtained for all the characters in both environments except productive tillers plant^{-1} (drained), harvest index and 1000-grain weight (drained & waterlogged). This might be possible owing to low effect of environment on these traits.

High heritability coupled with high genetic advance gives the most effective criteria for selection (Johnson et al.*,* 1955). In the present study, high heritability estimates coupled with high genetic advance were observed for biomass plant^{-1}, grain yield plant^{-1}, spike weight plant^{-1}, 1000-grain weight, grains spike^{-1}, productive tillers plant^{-1} and plant height for both control and water logging conditions. Panse and Shukhatme (1978) have expressed that if a character is governed by additive gene action, heritability and genetic advance both would be high. High to moderate heritability along with low genetic advance were noticed for days to 50% flowering, days to maturity, ear length, and harvest index, indicating that these character might be controlled by non-additive gene action and improvement for these characters through selection would be rather limited.

3.2. Correlation coefficients

The genetic architecture of grain yield in wheat as well as other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another. Under both drained and waterlogged conditions the grain yield plant^{-1} showed positive and highly significant correlation with harvest index, biological yield plant^{-1}, 1000-grain weight, grains spike^{-1}, productive tillers plant^{-1}, spike weight plant^{-1} and plant height while, the grain yield plant^{-1} was significantly and negatively correlated with days to 50% flowering and days to maturity in drained condition (Table 2). If selection is made for one of these

Table 2: Genotypic correlation coefficients between different characters under drained (D) and waterlogged (WL) conditions for 10 days at 27 DAS

Characters		A	B	C	D	E	F	G	H	I	J	K
Days to 50% flowering	D	1.000	0.428**	0.013	-0.137	-0.056	-0.317**	-0.036	-0.094	-0.204*	-0.119	-0.234*
	WL	1.000	0.466**	-0.179	-0.037	-0.230*	-0.136	-0.237	-0.256	-0.105	-0.129	-0.114
Days to maturity	D		1.000	0.039	-0.050	0.047	-0.109	0.001	-0.020	-0.164	-0.223*	-0.206*
	WL		1.000	0.001	0.023	0.037	-0.129	-0.311**	-0.122	-0.175	0.043	-0.117
Plant height	D			1.000	0.171	0.085	0.229*	0.002	0.380**	0.213*	0.143	0.222*
	WL			1.000	0.167	0.244*	0.186	0.190	0.400**	0.114	0.315**	0.204*
Productive tillers plant^{-1}	D				1.000	0.020	0.659**	0.207*	0.017	0.777**	0.183	0.729**
	WL				1.000	0.098	0.778**	0.223*	0.194*	0.794**	0.378**	0.810**
Spike length	D					1.000	0.231*	0.272**	0.327**	0.089	0.129	0.143
	WL					1.000	0.120	0.204*	0.273**	0.107	0.204*	0.146
Spike weight plant^{-1}	D						1.000	0.557**	0.336**	0.801**	0.493**	0.888**
	WL						1.000	0.514**	0.487**	0.896**	0.461**	0.935**
Grains spike^{-1}	D							1.000	0.199*	0.419**	0.464**	0.532**
	WL							1.000	0.248**	0.484**	0.335**	0.525**
1000-grain weight	D								1.000	0.259**	0.204*	0.312**
	WL								1.000	0.358**	0.479**	0.481**
Biological yield plant^{-1}	D									1.000	0.208*	0.925**
	WL									1.000	0.220*	0.906**
Harvest index	D										1.000	0.547**
	WL										1.000	0.598**
Grain yield plant^{-1}	D											1.000
	WL											1.000

A=Days to 50% flowering; B=Days to maturity; C=Plant height; D=Productive tillers plant^{-1}; E=Spike length; F=Spike weight plant^{-1}; G = Grains spike^{-1}; H=1000-grain weight; I=Biological yield plant^{-1}; J=Harvest index; K=Grain yield plant^{-1}

positively correlated traits, simultaneous selection of other traits each achieved that help in improving the grain yield.

There is little information on the genetics and heritability of yield and yield related traits for wheat grown under water logging condition in nutral and sodic soils (Setter and Waters, 2003). However for normal soils, positive association of grain yield with yield related traits was earlier reported by different workers. Khan et al. (2004) also reported significant and positive correlation between grains spike^{-1}, effective tillers plant^{-1} and spike weight with yield plant^{-1}, thus supporting our results. The grain yield was positively and significantly correlated with grain weight, grains spike^{-1}, test weight, plant height, 1000-grain weight and spike length whereas, negatively correlated with days to 50% flowering as reported by Oguz et al., 2011.

3.3. Path coefficient analysis

In order to obtain a clear picture of the inter-relationship between different characters, the direct and indirect effects of the different characters on grain yield plant^{-1} were worked out (Table 3). The direct and indirect effects of different characters under drained and waterlogged conditions indicated that under drained condition biological yield plant^{-1} followed by harvest index emerged as most important direct contributors towards grain yield plant^{-1} while, under waterlogged condition biological yield plant^{-1} followed by harvest index also emerged as most important direct contributors towards grain yield plant^{-1}. Subhani, 2000; Sachan and Singh, 2003; Singh and Sharma, 2007; Khan, et al. 2005; have also identified biological yield plant^{-1} as a character making substantial direct positive contribution towards manifestation of grain yield in wheat. Positive direct effect of spike length and 1000-grain weight on yield was also reported by Dokuyucu and Akkaya (1999). Under drained condition days to 50% flowering, plant height and grains spike^{-1} showed considerable negative direct effects on grain yield plant^{-1} while, under waterlogged condition days to maturity, plant height, spike length and 1000-grain yield showed considerable negative direct effects on grain yield plant^{-1}. The direct effects of remaining five characters were found to be too low to be considered of any consequence. In general indirect effects were either positive or negative and lower in magnitude with low residual effect (0.1015 D & 0.1016 WL).

3.4. Genetic diversity

The cluster analysis grouped the 108 bread wheat genotypes into 11 different clusters under both drained and waterlogged conditions (Table 4). Clustering pattern of genotypes showed no

Table 3: Genotypic path coefficient showing direct (Bold) and indirect effects of various traits on grain yield in wheat under drained (D) and waterlogged (WL) condition

Characters		A	B	C	D	E	F	G	H	I	J	K
Days to 50% flowering	D		0.005	0.000	0.000	0.000	-0.032	0.001	-0.002	-0.160	-0.041	-0.234
	WL	0.023	-0.003	0.003	0.000	0.003	-0.014	0.002	0.003	-0.077	-0.053	-0.114
Days to maturity	D	-0.002	0.012	-0.001	0.000	0.000	-0.011	0.000	0.000	-0.128	-0.076	-0.206
	WL	0.011	-0.006	0.000	0.000	-0.001	-0.014	0.003	0.001	-0.128	0.018	-0.117
Plant height	D	0.000	0.001	-0.023	0.000	0.001	0.023	0.000	0.006	0.166	0.049	0.222
	WL	-0.004	0.000	-0.014	0.000	-0.004	0.020	-0.002	-0.005	0.083	0.128	0.204
Productive tillers plant^{-1}	D	0.001	-0.001	-0.004	-0.001	0.000	0.067	-0.003	0.000	0.606	0.063	0.729
	WL	-0.001	0.000	-0.002	0.000	-0.001	0.082	-0.002	-0.002	0.583	0.154	0.810
Spike length	D	0.000	0.001	-0.002	0.000	0.006	0.024	-0.004	0.005	0.070	0.044	0.143
	WL	-0.005	0.000	-0.003	0.000	-0.015	0.013	-0.002	-0.003	0.079	0.083	0.146
Spike weight plant^{-1}	D	0.002	-0.001	-0.005	-0.001	0.001	0.102	-0.008	0.005	0.624	0.169	0.888
	WL	-0.003	0.001	-0.003	0.000	-0.002	0.106	-0.004	-0.006	0.658	0.188	0.935
Grains spike^{-1}	D	0.000	0.000	0.000	0.000	0.002	0.057	-0.015	0.003	0.327	0.159	0.532
	WL	-0.005	0.002	-0.003	0.000	-0.003	0.054	-0.008	-0.003	0.355	0.136	0.525
1000-grain weight	D	0.001	0.000	-0.009	0.000	0.002	0.034	-0.003	0.015	0.202	0.070	0.312
	WL	-0.006	0.001	-0.006	0.000	-0.004	0.052	-0.002	-0.011	0.263	0.195	0.481
Biological yield plant^{-1}	D	0.001	-0.002	-0.005	-0.001	0.001	0.082	-0.006	0.004	0.780	0.071	0.925
	WL	-0.002	0.001	-0.002	0.000	-0.002	0.095	-0.004	-0.004	0.734	0.089	0.906
Harvest index	D	0.001	-0.003	-0.003	0.000	0.001	0.050	-0.007	0.003	0.163	0.343	0.547
	WL	-0.003	0.000	-0.004	0.000	-0.003	0.049	-0.003	-0.005	0.161	0.406	0.598

A=Days to 50% flowering; B=Days to maturity; C=Plant height; D=Productive tillers plant^{-1}; E=Spike length; F=Spike weight plant^{-1}; G = Grains spike^{-1}; H=1000-grain weight; I=Biological yield plant^{-1}; J=Harvest index; K=Grain yield plant^{-1}

Table 4: Distributing pattern of 108 genotypes of bread wheat into eleven clusters based on Non-hierarchical Euclidean Cluster analysis under drained and waterlogged condition

Cluster No.	No. of genotypes		Name of genotypes	Name of genotypes
	Drained	Waterlogged	Drained	Waterlogged
I	10	4	CHARA, NWL-9-22, WESTONIA, PBW-642, NW-3087, KRL-238, NW-1067, KRL-266, WH-1094, CAMM	K-0807, K-0808, NW-4098, DBW-46
II	7	12	KRL-268, HD-3024, PBW-636, NW-4099, DBW-52, KRL-240, SCHOMBURGK	NW(S)-2-4, KRL-210, RAJ-3765, KRL-19, RAJ-4205, DBW-50, NW-2036, HI-1563, HD-3027, NW-1014, KRICHAUFF, KRL 3-4©
III	12	8	PBW-550, KRL-283, NW-4082, KRL-259, HUW-636, KRL-227, KRL-236, PBW-343, PBW-590, KALANNIE, NW-1076, KRL-261	CHARA, KRL-213, BT-SCHOMBURGK, KRL-227, NW-3069, NW-1076, HD-2997, HUW-636
IV	8	26	RW-3684, DBW-59, SPEAR, UP-2003, DUCULA-4, DBW-50, AMERY, PBW-621	PBW-343, KRL-240, NW-1012, DBW-51, DBW-58, PBW-631, PBW-634, NW(S)-6-5, DBW-55, RSP-561, DBW-39, PBW-621, DBW-52, KRL-1-4, NWL-7-4, KRL-105, HUW-638, NWL-9-24, PBW-635, NW-4082, TINCURRAN, PBW-590, KRL-99, RAJ-4201, WH-1094, PBW-639
V	16	9	PBW-635, HI-1563, HD 2009©, PBW-631, GUTHA, UP-262, HUW-635, DBW-58, DBW-39, DBW-60, PBW-634, RSP-561, NW-4092, KRL-249, HD-3028, CUNDERDIN	BH-1146, HD 2009©, DBW-60, UP-262, CBW-38, CUNDERDIN, RW-3684, NW-4092, KRL-35
VI	16	22	NW-2036, TINCURRAN, NW-4083, KRL-99, RAJ-3765, DBW 14©, PBW-639, KRL-210, NW-3069, HD-2997, KRL-1-4, GAMENYA, BT-SCHOMBURGK, BROOKTON, KRL-229, HD-3027	NW-4099, HD-3024, KRL-266, UP-2003, WESTONIA, GAMENYA, PBW-550, KRL-238, NW-1067, KRL-236, BROOKTON, AMERY, KRL-229, KRL-259, HUW-635, HD-3028, KRL-268, HD-2967, DBW-59, NW-3087, NW-4091, HD-2733
VII	13	4	NW-4035, NWL-7-4, NWL-9-23, NW-4081, DBW-51, DBW 17©, HD-2967, CHIRYA-7, HD-2733, NW-1012, KRL-19, RAJ-4201, KRL-233	NWL-9-22, PBW-642, PBW-636, SCHOMBURGK
VIII	5	1	DBW-55, KRL-213, HD-2985, NW(S)-6-5, NW-4091	CAMM
IX	12	3	RAJ-4205, HUW-638, K-0808, CBW-38, KRL-104, KRL-35, KRL-105, NW-4018, PERENJORI, NWL-9-25, KRICHAUFF, NW-4098	NWL-9-25, DBW 14©, GUTHA

definite relationship between genetic divergence and geographical distribution of genotypes. The highest genetic divergence was observed between clusters I and X under drained while cluster VIII and IX in waterlogged condition. Verma et al. (2006) assessed the nature and magnitude of 225 wheat genotypes and all genotypes grouped in eleven different clusters.

4. Conclusion

Present study revealed that, wide genetic variability was found in investigated agronomic traits. The high and positive correlations will help in improving the grain yield through selection and the high heritability and genetic advance will be useful for population improvement through hybridization. Data presented here can be used to conclude that the characters like biomass plant^{-1}, productive tillers plant^{-1}, plant height, grains spike^{-1} and 1000-grain weight are important while selecting high yielding genotypes in wheat under waterlogged or sodicity stress or both.

5. Acknowledgements

The authors are grateful to Dr Tim L. Setter, ACIAR Project Supervisor and Principal Scientist Crop Improvement Institute, Department of Agriculture South Perth Western Australia for providing necessary guidance and genetic materials.

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