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GENETICS OF LODGING RESISTANCE RELATED TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

To evaluate the genetic background of lodging traits, six populations of two wheat crosses were sown under different nitrogen levels by using split plot design. Generation mean analysis was used to estimate the gene action for lodging related traits. Results showed genetic variability and significant differences for all traits. Allelic and non-allelic gene actions were operative for different traits with different magnitude under both normal and lodging condition. Duplicate types of espistasis were observed for grain yield per plant, 1000- kernel weight, number of grains per spike and number of tillers. The stem diameter, height of basal nodes and basal inter-nodal distance depicted the additive, additive × dominance and dominance gene action. The aforementioned results showed that plant height, stem diameter, height of basal nodes and basal inter-nodal distance were more prone traits for lodging and selection should be practiced in later generations with increasing homozygosity.

Introduction

Wheat (*Triticum aestivum* L.) is one of the important agricultural crops as well as staple food in the world. In Pakistan, wheat occupies a pivotal position and dominates all other crops in acreage and production, accounts for approximately 9.9% of value added and 2% of GDP in agriculture sector (Anon. 2016). Getting higher yield in both irrigated and water scare environments has been restricted by lodging, about 20 - 40% reduction in final grain weight has been witnessed due to lodging (Stapper and Fischer 1990, Berry *et al.* 2004). Lodging affects the crop net yield by altering the plant standing condition, preventing proper light and air, restricting the assimilation of dry matter and nutrients, respiration and providing favorable conditions for pathogen proliferation (Berry and Spink 2012).

The interaction among the factors like plants, rainfall pattern, wind speed and soil quality, nitrogen fertilizer and inefficient management practices together cause the lodging. To understand the nature and mechanism of lodging in field, nitrogen (N) regulation is the best method for screening and identifying the lodging resistance genotypes as it mainly affects the plant anchor related traits like plant height, number of internodes, length of internodes, stem thickness, stem weight, anatomical ratio of second internode diameter (mm) to stem length (cm) (Zuber *et al.* 1999, Berry *et al.* 2004). The study was initiated to investigate the genetic architecture of lodging resistance traits, their gene actions and lodging resistance in two selected crosses. It could be useful to identify the potential for further breeding programs by identifying parental lines with high rate of desirable segregates.

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Materials and Methods

The experimental material was planted at the research field of the Department of Plant Breeding and Genetics (PB&G), University of Agriculture, Faisalabad, Pakistan during 2012 - 2016. The experiment material consisted of four parents' genotypes named as Aas-2011, Chenab-2000, Saher-2006 and Bhakkar-2001 and their subsequent generations *viz*., first filial generation (F_1), segregating generation (F_2), first backcross (BC_1) generation and second backcross (BC_2) generation. Two lodging resistance varieties (Chenab-2000 and Bhakkar-2001) and two lodging susceptible varieties (Aas-2011 and Saher-2006) were selected upon screening and crosses (Aas-2011 × Chenab-2000 and Saher-2006 × Bhakkar-2001) were made between parents in 2012 - 2103 cropping season.

The F_1 seeds and their parental seeds were harvested separately at maturity. In 2013 -14 cropping season, F_1 were sown along with parents to produce backcrosses by crossing the F_1 with their respective recurrent parents. The seeds from all generations with two replicates were sown in the field by using split plot design under two doses of nitrogen fertilizer application named as normal N (nitrogen @ 120 kg/ha) and lodging L (nitrogen @ 240 kg/ha) in 2014 - 2015 growing season.

Periodically normal agronomic practices were carried out throughout the experiment, random selection of ten plants from each replication were done and tagged. Data were recorded for traits such as plant height (cm), spike length (cm), peduncle length (cm), number of tillers, stem diameter (mm), number of nodes per stem, height of basal node (cm), basal internodes distance (cm), number of grains/spike, 1000-kernel weight (g) and grain yield/plant (g) with respect to growth stages especially critical stages for lodging (heading, anthesis and maturity). The averages of individual plant were analyzed using ANOVA (Steel *et al.* 1997). The generation mean analysis given by Mather and Jinks (1982) was followed to study the gene action for each trait.

Results and Discussion

ANOVA revealed significant differences for all factors such as genotypes, treatments and their interaction and also revealed significant statistical differences under both nitrogen level for all the parameters expect number of nodes per stem (Tables 1 and 2). Morphological traits that correlate with lodging can be used as a selection parameter that gives an indirect estimation to assess the lodging resistance (Berry *et al.* 2003). The traits under study were significantly affected by the double nitrogen (240 kg/ha) levels (lodging field condition), these results were in accordance with many researchers lines as increase in nitrogen rate increased tillering, plant height, length of basal internodes and decreased the stem diameter and first node length which ultimately increase the chances of crop lodging (Pinthus 1974, Wei *et al.* 2008).

The additive-dominance model of generation mean analysis was followed for analyzing the differences between generations and all tests shown significance at 5% level of confidence. The both wheat crosses were evaluated under normal (N) and lodging (L) field conditions. The results obtained by generation mean analysis are presented in Tables 3 and 4. Under both environments, different model parameters were operated for different traits.

Under normal condition, in cross-I the additive (md) gene action was observed for plant height, spike length, peduncle length, stem diameter, while height of basal node and basal internodes distance exhibited additive × additive and additive × dominance gene actions, respectively. Number of tillers/plant, number of grain/spike, 1000-kernel weight and grain yield/plant showed presence of duplicate type of epistasis. In lodging condition traits of cross-I such as stem diameter, height of basal nodes and basal internodes distance showed additive gene

Table 1. Mean squares values for traits under different nitrogen levels for Cross-I (Aas-2011 × Chenab-2000).

SOV	Df	PH	SL	PL	SD	HBN	BID	NTP	NGS	TKW	GYP
Replication (R)	1	0.224	0.00046	0.0396	0.0028	0.0004	0.001760	0.006	0.2262	0.215	0.095
Treatment (T)	1	449.8**	9.20**	0.09*	9.27**	9.35**	12.76*	19.24**	3.58*	524.44**	694.34**
Error (R×T)	1	0.052	0.00005	0.0518	0.00735	0.00027	0.00202	0.0009	2.4257	0.006	0.152
Genotype	5	51.94**	1.53**	18.38**	0.17**	1.59**	1.06**	4.07**	10.59*	4.56**	3.80**
G×T	5	7.83**	5.99**	10.31**	0.23**	0.34**	0.08**	1.42**	3.07*	6.80**	1.48*
Error R×G×N	10	0.465	0.00750	0.4922	0.00419	0.00250	0.00404	0.0073	1.9630	0.377	0.344

*p < 0.05, **p < 0.01.

PH (Plant height, cm), SL (Spike length, cm), PL (Peduncle length, cm), SD (Stem diameter, mm), HBN (Height of basal node, cm), BID (Basal intermodal distance, cm), NT (Number of tillers per plant), NGS (Number of grain per spike), TKW (1000-kernel weight, g) and GYP (Grain yield per plant, g).

Table 2. Mean squares values for traits under different nitrogen levels for Cross-II (Saher-2006 × Bhakkar-2001).

SOV	Df	PH	SL	PL	SD	HBN	BID	NTP	NGS	TKW	GYP
Replication (R)	1	0.205	0.0016	0.115	0.144	0.008	0.004	0.0004	0.476	0.003	0.457
Treatment (T)	1	857.05**	0.582**	0.052*	1.480**	0.710*	14.648**	5.811*	2.801*	344.2**	554.7**
Error (R×T)	1	0.144	0.001	0.173	0.00082	0.0015	0.00041	0.0035	0.260	0.008	0.175
Genotype	5	88.71**	4.58**	5.15**	1.80**	1.06**	0.45**	0.88932*	2.47571*	7.068**	15.919**
G×T	5	14.61**	0.20**	3.29**	0.14**	0.18**	0.38**	3.81864 *	3.10730 *	5.047**	3.316**
Error R×G×N	10	0.189	0.016	0.246	0.060	0.007	0.0016	0.002	0.290	0.233	0.070

* = p < 0.05, ** = p < 0.01.

PH (Plant height, cm), SL (Spike length, cm), PL (Peduncle length, cm), SD (Stem diameter, mm), HBN (Height of basal node, cm), BID (Basal intermodal distance, cm), NT (Number of tillers per plant), NGS (Number of grain per spike), TKW (1000-kernel weight, g) and GYP (Grain yield per plant, g).

Table 3. Estimates of the best fit model for generation means parameters (± standard error) by weighted least squares analysis Cross-I (Aas-2011 × Chenab-2000) under normal (N) and lodging (L) conditions in the field.

Traits	Cross-I	Genetic effects						$\chi2$ (df)
	Treatment	m ± SE	[d] ± SE	[h] ± SE	[i] ± SE	[j] ± SE	[l] ± SE	
Plant height	N	103.4± 0.34	1.91± 0.36	-	-	-	-	4.51(3)
	L	118.9±0.3	3.75±0.26	-	4.26±0.6	-	-	2.85(3)
Spike length	N	14.78 ±0.12	0.34± 0.15	-	-	-	-	1.35(2)
	L	13.71±0.09	1.98±0.18	-	3.29±0.93	-	-	2.89(4)
Peduncle length	N	36.5 ±0.15	7.9± 0.15	-	-	-	-	3.23(4)
	L	49.49±0.13	5.53±0.91	-	41.23± 0.47	-	-	5.62(4)
Stem diameter	N	16.06 ±0.045	5.02 ± 0.08	-	-	-	-	6.52(4)
	L	16.05±0.02	3.46± 0.41	-	-	-	-	4.52(4)
Height of basal node	N	4.77 ± 0.05	0.92±0.06	-	0.26± 0.09	-	-	5.87(3)
	L	6.22± 0.05	0.29± 0.06	-	-	-	-	4.27(4)
Basal internodal distance	N	8.64±0.04	0.36±0.11	-	-	1.647±0.324	-	7.09(4)
	L	9.97± 0.06	0.42± 0.08	-	-	-	-	3.16(4)
No. of tillers/ plant	N	11.3±0.16	1.08±0.18	-	1.24±0.25	5.270± 0.775	-	2.58(2)
	L	13.1±1.14	2.02±1.19	6.19±2.52	3.02±1.13	3.62±0.50	3.07± 1.48	0.027(1)
No. of grain/ spike	N	48.03 ±0.2	3.08± 0.44	4.56±0.911	-	10.11 ± 1.829	5.9±2.11	6.01(3)
	L	31.06±0.12	4.8± 0.21	3.58±0.15	-	9.44±1.876	-	6.23(4)
Thousand kernel weight	N	38.83±0.13	9.21± 0.24	6.64±2.14	9.56±0.45	6.57±0.347	-	6.21(4)
	L	31.1±0.55	3.57±0.21	3.31±0.76	5.99±0.6	-	-	2.52(2)
Grain yield/plant	N	37.7±0.14	0.49±0.22	2.57±2.12	4.53±2.3	3.651±0.332	-	5.44(4)
	L	26.7±0.08	0.74±0.15	3.1±1.5	3.8±0.65	-	-	4.89(4)

Table 4. Estimates of the best fit model for generation means parameters (± standard error) by weighted least squares analysis Cross-II (Saher2006 × Bhakkar-2001) under normal (N) and lodging (L) conditions in the field.

Traits	Cross-II	Genetic Effects						χ2 (df)
	Treatment	m ± SE	[d] ± SE	[h] ± SE	[i] ± SE	[j] ± SE	[l] ± SE	
Plant height	N	1.226 ± 0.041	0.166 ± 0.064	-	-	-	-	4.996 (4)
	L	4.52 ± 0.039	1.43 ± 0.060	-	-	-	-	5.249 (4)
Spike length	N	16.93 ± 0.120	0.751 ± 0.189	-	-	-	-	4.932 (4)
	L	46.53 ± 0.118	19.82 ± 0.185	-	-	-	-	5.042 (4)
Peduncle length	N	8.88 ± 0.0647	4.469 ± 0.106	-	-	-	-	5.63 (4)
	L	8.36 ± 0.115	4.000 ± 0.07	0.479±0.216	-	-	-	5.28 (3)
Stem diameter	N	62.52 ± 0.158	124.3 ± 0.219	-	-	-	-	6.42 (4)
	L	249.81 ± 0.109	205.43 ± 0.22	-	-	-	-	3.55 (4)
Height of basal node	N	199.73 ± 0.174	5.852 ± 0.273	-	-	-	-	5.592 (4)
	L	228.60 ± 0.89	5.91± 0.28	212.56±0.18	212.5 ± 0.96	-	-	3.82 (2)
Basal internodal distance	N	302.4 ± 0.144	103.6 ± 0.232	-	-	-	-	5.392 (4)
	L	285.15 ± 0.133	237.6 ± 0.208	-	-	-	-	5.375 (4)
Number of tillers/plant	N	24.14 ± 0.122	3.19 ± 0.192	-	4.35 ± 1.9	3.26 ± 0.36	-	4.369 (4)
	L	18.1 ± 0.129	1.307 ± 0.201	-	4.87 ± 0.8	3.98 ± 0.14	-	5.326 (4)
Number of grain/spike	N	11.84 ± 0.058	4.63 ± 0.090	3.76 ± 1.435	-	5.46 ± 0.95	-	5.782 (4)
	L	9.45 ± 0.059	2.85 ± 0.091	2.16 ± 0.981	-	3.16 ± 1.16	-	4.5872(4)
Thousand kernel weight	N	12.51 ± 0.068	2.23 ± 0.1162	3.77 ± 0.776	3.45 ± 1.16	4.654 ± 1.23	-	5.782 (4)
	L	10.42 ± 0.076	0.555 ± 0.124	1.098 ± 1.34	-	1.243 ± 1.07	-	5.234 (4)
Grain yield/plant	N	3.71 ± 0.467	1.92 ± 0.137	4.46 ± 0.628	3.16 ± 0.501	3.854 ± 0.56	-	3.5452 (2)
	L	12.52 ± 0.105	0.33 ± 0.163	2.763 ± 0.487	1.564 ± 1.245	2.01 ± 1.98	-	5.6214 (4)

action, whereas additive × additive gene action was observed for plant height, spike length and peduncle length. Double epistasis exhibited by grain yield/plant, 1000-kernel weight, number of grain/spike and number of tillers/plant (Table 3).

Similarly, the cross-II showed additive nature of gene action for plant height, spike length, peduncle length, stem diameter and basal internodes distance under both lodging and no lodging condition except height of basal node that showed additive in normal condition while epistasis effects in lodging condition. Double epistasis effects persisted under both conditions with different magnitude for number of tillers per plant, number of grains per spike, 1000-kernel weight and grain yield per plant (Table 4).

These aforementioned results indicated that gene actions (additive, dominance and epistastic effects) operated differently for traits under studay and showed the different levels of significane but magnitude changed with each cross. Stem morpohological traits like basal internodal distance was under epistatic interaction (Zuber *et al.* 1999, Berry *et al*. 2000). Pinthus (1974), Islam *et al.* (2007) reported that plant height and stem morphological traits were closely related to lodging resistance and by increasing the stem diameter the lodging resistance can be improved in crops (Kong *et al.* 2013, Peng *et al.* 2014). Herein, plant height, stem diameter, and average stem wall thickness were controlled by additive gene effects. Dominance × dominance interaction effect was the most active component on non-allelic effects and observed significant for most of the traits (basal inter-nodal distance, number of tillers per plant, number of grains per spike, 1000-kernel weight and grain yield per plant). Magnitude of dominance × dominance gene action exerted greater influnced than additive × dominance gene action upon most of the traits in both crosses under both field conditions. These collaborated with the findings of Misra *et al.* (1994), Sarker *et al.* (2007).

From the present study it may be concluded that the traits exhibited additive gene action would be more responsive as compared to the dominance and other non-allelic genetic effects. Increasing nitrogen fertilizer increases the risk of lodging significantly. Selection in early segregating generations restrict the expression and would not be effective for the flexible components of variation. The present findings are considered valuable for enhancing lodging resistance of wheat and improving grain yield and quality.

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