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Estimating the Inheritance Patterns of Peduncle length and Spike length in Bread Wheat (*Triticum aestivum* L. em Thell.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Estimating the inheritance pattern of peduncle length and spike length in bread wheat is crucial for advancing research in wheat genetics and breeding. To understand this pattern an experiment was conducted using six generations of 4 crosses. This study investigated genetic parameters affecting

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peduncle and spike length in bread wheat across four families (A, B, C and D) using generation mean analysis. For peduncle length, the additive-dominance model was suitable for Family A, indicating significant dominance effects, while higher-order interactions were present in Families B, C, and D with dominance × dominance and additive × additive effects playing major roles. For spike length, digenic interaction models were appropriate for all families, highlighting significant dominance and dominance × dominance effects. Families A, B, and C showed prevalent duplicate epistasis, suggesting potential transgressive segregants. The findings suggest both additive and non-additive gene actions are crucial, indicating early and later generation selection strategies could be effective in improving these traits. Understanding the genetic variability and underlying genetic architecture of these traits can enhance wheat yield and quality, making them ideal targets for breeding programs aimed at improving productivity.

Keywords: Bread wheat; generation mean; inheritance; peduncle length; spike length.

1. INTRODUCTION

Estimating the inheritance pattern of peduncle length and spike length in bread wheat is a crucial area of research that holds significant importance in the field of genetics and wheat breeding. By utilizing inferences from scaling test and generation mean analysis, researchers can delve into the genetic mechanisms underlying these traits and pave the way for targeted breeding strategies to enhance wheat yield and quality. This analysis provides valuable insights into the genetic architecture of various traits, such as yield, quality, and disease resistance, by evaluating the extent of dominance and epistatic gene effects alongside additive gene effects [1,2]. Peduncle length and spike length are key morphological traits in wheat that play a vital role in determining grain yield. Studies have shown that these traits exhibit high heritability, indicating that a substantial proportion of the phenotypic variation observed in these traits is due to genetic factors [3]. High heritability values for peduncle length and spike length suggest that these traits are strongly influenced by the genetic makeup of the wheat plant, making them ideal targets for breeding programs aimed at improving yield potential [4]. The genetic variability observed in peduncle length and spike length underscores the importance of understanding the underlying genetic architecture of these traits [5]. By unraveling the genetic basis of these traits through generation mean analysis, researchers can identify the key genes and alleles responsible for controlling peduncle length and spike length, facilitating targeted breeding efforts to improve these traits in wheat cultivars [6]. Wheat yield is a multifaceted trait influenced by numerous genes, environmental conditions, and developmental stages, making it essential to dissect the genetic components contributing to traits such as peduncle length and spike length to enhance overall productivity [7]. The strong estimates of heritability (>50%) observed for peduncle length and spike length emphasize the genetic control underlying these traits. Understanding the heritability and genetic components influencing these traits is essential for predicting the response to selection and designing effective breeding strategies to enhance wheat productivity [8]. The genetic effects of dwarfing genes on peduncle length underscore the intricate genetic interactions that regulate plant morphology and yield components in wheat, emphasizing the need for detailed genetic analyses to unravel the underlying mechanisms controlling these traits [9]. By dissecting the genetic effects of key genes on peduncle length and spike length, researchers can gain insights into the molecular pathways governing these traits and leverage this knowledge for targeted trait improvement in wheat breeding programs. The research on estimating the inheritance patterns of peduncle length and spike length in bread wheat using scaling test and generation mean analysis is of paramount importance for advancing our understanding of the genetic basis of these traits.

2. MATERIALS AND METHODS

The experimental material include eight wheat genotypes. Information about families evaluated for genetic analysis, is outlined in Table 1. In the rabi season of 2020-21, eight parent lines were chosen based on their morphological traits and subsequently, four crosses were established using these parent lines. All eight parent lines, along with the four hybrid combinations, were evaluated during rabi 2021-22 at the experimental station. Each F_1 hybrid was backcrossed to either of its parent lines to generate BC_1P_1 ($F_1 \times P_1$) and BC_1P_2 ($F_1 \times P_2$)

generations. In rabi 2021-22, F_1 hybrids were once again produced and measures such as covering some F_1 spikes with butter paper bags were implemented to prevent cross-pollination. Selfed seeds of parent lines P_1 and P_1 were also collected for subsequent season assessments. Thus, a total of six generations – P_1, P_2, F_1, BC_1P_1, BC_1P_2 and F_2 were generated for each of the family.

2.1 Experimental Materials and Layout

The experiment encompassed six generations for all four crosses, specifically P_1, P_2, F_1, BC_1P_1, BC_1P_2 and F_2. A compact family block design was employed for planting, with three replications for each generation. The number of rows in a single replication varied, considering the heterozygosity level and the required number of plants for subsequent analysis. Sowing was done on November 12th, 2022, under timely sown conditions, with a row-to-plant spacing of 20 cm × 10 cm. The recommended package of agronomic practices was followed throughout the entire experimental duration.

2.2 Biometrical Analysis

Analysis of variance for the Compact Family Block Design (CFBD) was conducted using the plot means of the studied characters as recommended by Singh and Chaudhary [10]. Then four test of scale effects were applied as proposed by Mather (1949)**.** Generation mean analysis was conducted for each cross using the six-parameter model proposed by Jinks and Jones [11] for each trait of each family. The means of parents (P_1 and P_2), F_1, F_2 and the two backcrosses (BC_1P_1 and BC_1P_2) were calculated for each cross separately. These means from all six generations were utilized to calculate the gene effects for each family individually. The estimates of various model were estimated using the "Joint scaling test" proposed by Cavalli [12], based on means calculated from all available generations. This approach allowed for testing the adequacy of different model, followed by an assessment of the observed generation means against the expected values derived from the estimated genetic parameters of a given model. The parameters were computed using the "weighted least square technique" outlined by Jinks and Jones [11], with weights being the reciprocal of the squared standard error of each mean. The comparison between observed and expected means was achieved by assuming that the sum of squares minimized in the fitting process follows a chi-square distribution with degrees of freedom equal to the difference between the number of available generations means and the number of parameters in the model. The data recorded on all six generations obtained in the present investigation were enough to permit the analysis of the various genetic models. Based on the direction of significant estimates of [h] and [l], the type of epistatic interaction Hayman and Mather, [13] was calculated.

If opposite sign of [h] and [l] : Duplicate epistasis

If same sign of [h] and [l] : Complementary epistasis

Table 1. Description of families utilized for generation mean analysis

S. No.	Crosses				Generations
	Family A	**Family B**	**Family C**	**Family D**	
1	QLD 91	PBW 813	PBW 725	Agra Local	P_1
2	VL 967	HS 490	UP 2572	DBW 222	P2
3	QLD 91 × VL 967	PBW 813 × HS 490	PBW 725 × UP 2572	Agra Local × DBW 222	F1
4	QLD 91 × VL 967	PBW 813 × HS 490	PBW 725 × UP 2572	Agra Local × DBW 222	F2
5	(QLD 91 × VL 967) × QLD 91	(PBW 813 × HS 490) × PBW 813	(PBW 725 × UP 2572) × PBW 725	(Agra Local × DBW 222) × Agra Local	BC1P1
6	(QLD 91 × VL 967) × VL 967	(PBW 813 × HS 490) × HS 490	(PBW 725 × UP 2572) × UP 2572	(Agra Local × DBW 222) × DBW 222	BC1P2

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The data collected for all eleven characteristics of bread wheat were subjected to analysis using the Compact Family Block Design (CFBD). The results of the analysis of variance for peduncle length (cm) and spike length (cm) mean squares for both between-family and within-family were highly significant.

3.2 Peduncle Length

The estimates of the scaling test, along with their corresponding standard errors for peduncle length, are available in Table 2. Scale A was determined to be significantly different from zero in Families B, C and D. Scale B showed significance in Family C whereas Scale C and D exhibited significance in Families B and C. The significance of these scales signifies the presence of non-allelic interactions within Families B, C and D.

Table 3 presented an evaluation of the model's adequacy for peduncle length across all four families. It also exhibited estimates of genetic parameters, with standard errors, tailored to the specific genetic model applicable to each family. Additionally, the table contained the corresponding χ^2 values and specifies the type of epistasis involved in the inheritance of peduncle length.

Non-significant χ^2 value (5.02) in Family A, had reinforced the suitability of the 3-parameter additive-dominance interaction model. In this model significant estimates for the mean [m] (31.02**), dominance [h] effect (5.84**) and additive [d] effect (-1.38**) were found. These results indicated that the dominance [h] effect played a more substantial role in governing the inheritance of the peduncle length. Notably, the additive effect [d] exhibited a significant value in the desired negative direction for the trait.

In Family B, 3, 4, or 5 parameter models were found insufficient, suggesting the presence of higher-order interactions in the inheritance of the trait. Instead the 6-parameter model was deemed to be the most appropriate. Within this model, significant estimates for the mean [m] (39.4**), dominance × dominance [l] effect (13.74**), dominance [h] effect (-11.52**), additive × dominance effect [j] (-9.26**) and additive [d] effect (3.33**) were found. These findings indicated that the dominance × dominance [l] effect and additive × additive [i] effect had a more substantial impact on the inheritance of peduncle length. Family B exhibited a prevalence of duplicate epistasis due to the presence of opposite signs for dominance [h] and dominance × dominance [l] gene effects, suggesting a gene cancellation effect within this specific family. Furthermore, the dominance [h] effect, additive × additive [i] effect and additive × dominance [j] effect displayed significant values in the desired negative direction for peduncle length.

Non-significant χ^2 value (1.95) had confirmed the adequacy of the 4-parameter digenic interaction model in Family C. This model showed significant estimates for the mean [m] (27.88**), dominance [h] effect (10.39**), additive × additive [i] effect (7.58**) and additive [d] effect (-3.49**). These results indicated that the dominance [h] effect exerted a more substantial influence on the inheritance of the peduncle length. Notably, the additive effect [d] exhibited a significant value in the desired negative direction for the trait.

In Family D, non-significant χ^2 value (2.74) had suggested suitability of the 5-parameter digenic interaction model. In this model significant estimates for mean [m] (33.71**), dominance [h] effect (9.77**), additive × dominance effect [j] (-5.3**), additive × additive [i] effect (4.95**), additive [d] effect (3.79**) were observed. These results indicated that the dominance [h] effect had great impact on regulating the inheritance of the peduncle length. Additionally, the additive × dominance [j] effect displayed a significant value in the desired negative direction for the trait. Dominant type of gene action responsible for increasing peduncle length has been also reported by Farooq et al., [14]; Virk and Aulakh, [15].

Table 2. The estimates of scaling test for peduncle length (cm)

	Families			
Scale	**Family A**	**Family B**	**Family C**	**Family D**
A	2.33±1.47	-9.41±1.22**	-3.89±0.66**	-5.21±0.38**
B	-0.89±1.41	-0.15±1.48	-4.84±0.77**	0±0.62
C	1.81±2.06	-5.34±2.42*	-15.19±0.84**	-2.96±4.44
D	0.18±0.87	2.11±0.81**	-3.24±0.44**	1.12±2.2

**Significant at 5% probability level **significant at 1% probability level*

Table 3. Estimates of genetic parameter under the adequate genetic model with respective χ² value and type of epistasis involved for peduncle length (cm)

Families	Model	[m]	[d]	[h]	[i]	[j]	[l]	χ² value	Type of epistasis
A	AD(3PM)	31.02±0.29**	-1.38±0.29**	5.84±0.65**	–	–	–	5.02	–
B	DI(6PM)	39.4±1.72**	3.33±0.54**	-11.52±4.38*	-4.19±1.63	-9.26±1.48**	13.74±3.15**	–	Duplicate
C	DI(4PM)	27.88±0.29**	-3.49±0.17**	10.39±0.44**	7.58±0.36**	–	–	1.95	–
D	DI(5PM)	33.71±0.47**	3.79±0.32**	9.77±0.52**	4.95±0.72**	-5.3±0.71**	–	2.74	–

*AD = Additive-Dominance Model; DI = Digenic Interaction Model; PM = Parameter Model; *significant at 5% probability level;**significant at 1% probability level*

Table 4. The Estimates of Scaling Test for Spike Length (cm)

	Families			
Scale	**Family A**	**Family B**	**Family C**	**Family D**
A	1.41±0.5**	-3.44±0.69**	0.76±0.48	1.93±0.72**
B	2.08±0.41**	-1.64±0.52**	2.68±0.53**	-1.18±0.37**
C	-4.99±0.83**	-5.31±1.33**	-0.89±1.18	0.32±0.69
D	-4.24±0.08**	-0.12±0.59	-2.17±0.56**	-0.22±0.35

**significant at 5% probability level; **significant at 1% probability level*

Table 5. Estimates of Genetic Parameter under the Adequate Genetic Model with Respective χ² Value and Type of Epistasis Involved for Spike Length (cm)

Families	Model	[m]	[d]	[h]	[i]	[j]	[l]	χ² value	Type of epistasis
A	DI(5PM)	2.73±0.18**	0.43±0.07**	21.43±0.66**	8.55±0.15**	–	-12.51±0.84**	–	Duplicate
B	DI(4PM)	12.21±0.29**	0.5±0.18*	-3.27±1.07*	–	–	4.55±0.82**	4.39	Duplicate
C	DI(6PM)	7.58±1.14**	-0.75±0.24*	13.53±2.59**	4.33±1.12*	-1.93±0.67*	-7.79±1.51**	–	Duplicate
D	DI(3PM)	11.69±0.12**	–	1.6±0.25**	–	3.39±0.35**	–	6.7	–

*AD = Additive-Dominance model; DI = Digenic Interaction Model; PM = Parameter Model; *significant at 5% probability level;**significant at 1% probability level*

3.3 Spike Length (cm)

The estimates for the scaling test, along with their corresponding standard errors for spike length are presented in Table 4. Scale A was determined to be significantly different from zero in Families A, B and D. Scale B was revealed to be significant for Families A, B, C and D, while Scale C showed significance for Families A and B and Scale D was significant for Families A and C. The significance of these scales suggested the presence of non-allelic interactions in Families A, B, C and D. Table 5 presented the adequacy of the model for various traits across all four families. It also included estimates of genetic parameters, along with standard errors, within the appropriate genetic model for each specific family. Additionally, the table provided the corresponding χ^2 values and type of epistasis involved in the inheritance of spike length.

Non-significant χ^2 value (0.37) had suggested the adequacy of the 5-parameter digenic interaction model in Family A. In this model significant estimates for the mean [m] (2.73**), dominance [h] effect (21.43**), dominance × dominance [l] effect (-12.51**), additive × additive [i] effect (8.55**) and additive [d] effect (0.43**) were detected. These results indicated that the dominance [h] effect had substantial role in the inheritance of the spike length. Family A exhibited duplicate epistasis due to the presence of opposite signs for dominance [h] and dominance × dominance [l] gene effects, implying gene cancellation effects within this family. Notably, dominance [h] effect, additive [d] effect and additive × additive [i] effect displayed significant values in the positive direction for the trait.

In Family B, non-significant χ^2 value (4.39) had reaffirmed the adequacy of the 4-parameter digenic interaction model. This model, detected significant estimates for the mean [m] (12.21**), dominance × dominance [l] effect (4.55**), dominance [h] effect (-3.27*), additive [d] effect (0.5*) were found. These results suggested that the dominance × dominance [l] effect had a significant impact in controlling the inheritance of spike length. Similar to Family A, Family B exhibited preponderance of duplicate epistasis indicating a gene cancellation effect within this family. Additionally, additive [d] effect and dominance × dominance [l] effect displayed significant values in the desired positive direction for the trait.

In Family C the 3, 4, or 5-parameter models were found inadequate, indicating the presence of higher-order interactions governing the inheritance of this character. For this reason, a 6-parameter model was deemed the most appropriate. In this model, significant estimates were observed for the mean [m] (7.58**), dominance [h] effect (13.53**), dominance × dominance [l] effect (-7.79**), additive × additive [i] effect (4.33*), additive × dominance effect [j] (-1.93*) and additive [d] effect (-0.75*). These results indicated that the dominance [h] effect played a more substantial role in determining the inheritance of the spike length. Family C exhibited a presence of duplicate epistasis suggesting a gene cancellation effect within this family. Notably, dominance [h] effect and additive × additive [i] effect displayed significant values in the desired positive direction for the trait.

Non-significant χ^2 value (6.7) had suggested adequacy of the 3-parameter digenic interaction model in Family D. In this model significant estimates for the mean [m] (11.69**), additive × dominance effect [j] (3.39**) and dominance [h] effect (1.6**) were observed. These results indicated that the additive × dominance [j] effect had a significant control in the inheritance of the spike length. Both dominance [h] effect and additive × dominance [j] effect had significant contribution in desired positive direction for the trait. Dominant type of gene action responsible for increasing Spike length has been also reported by Mahmood and Chowdhry, [16], Nasrullah, [17].

4. CONCLUSION

This study analyzed genetic parameters affecting peduncle and spike length in bread wheat across four families. For peduncle length, the additive-dominance model was suitable for Family A, highlighting a significant dominance effect, while higher-order interactions were evident in Families B, C, and D with notable contributions from dominance × dominance and additive × additive effects. The results suggest both additive and non-additive gene actions are crucial, indicating that early and later generation selection could be effective, and the presence of duplicate epistasis in Family B hints at potential transgressive segregants. For spike length, digenic interaction models were appropriate for all families, with significant roles played by dominance and dominance × dominance effects, particularly in Families A, B, and C, where duplicate epistasis was prevalent. Family D showed significant

additive × dominance interactions. This study confirms the presence of both additive and non-additive gene actions, suggesting that tailored breeding strategies, including selection at both early and later generations, can be effective. The presence of duplicate epistasis in several families indicates potential for obtaining transgressive segregants, which can be exploited for trait improvement. Understanding these genetic interactions provides valuable insights for optimizing wheat breeding programs, ensuring the development of varieties with desirable traits, such as improved peduncle and spike length, ultimately contributing to enhanced yield and quality in bread wheat.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

we declare that NO generative AI technologies such as Large Language Models and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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