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Gene action for yield and yield contributing traits in Wheat (*Triticum aestivum* L.)

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Abstract

In a comprehensive study conducted at Lovely Professional University, Punjab, India, thirteen diverse traits in wheat (*Triticum aestivum* L.) were investigated using the Line × Tester mating approach, analyzing 27 F₁ hybrids derived from crossing 9 lines and 3 testers. The main goal was to understand the gene action governing agronomic and yield-contributing characteristics. The findings showed that all thirteen traits exhibited non-additive gene action, indicating the significant influence of complex gene interactions on their expression in hybrids. Moreover, the predictability ratios for all traits were below 1, providing further evidence of non-additive gene action and highlighting the limitations of relying solely on parental information to predict trait outcomes accurately. The study highlights the importance of considering gene interactions in wheat breeding programs, offering insights to enhance crop productivity and quality in sustainable agriculture. Moreover, the results advocate the strategic development of hybrids, leveraging non-additive genetic effects, to improve agricultural practices and food security through more effective and targeted wheat breeding efforts.

Keywords: Line × tester, gene action, non-additive, predictability ratio

1. Introduction

Wheat (*Triticum aestivum* L.) is an essential annual grass, self-pollinated, belonging to the Gramineae family and *Triticum* genus, originating from the "Fertile Crescent" region (Wang *et al.*, 2021; Peng *et al.*, 2011) [1, 13]. Globally, it holds the top position among cereals in terms of cultivated area and ranks second in production, earning the titles "king of cereals" or "golden grain" (Mohan *et al.*, 2006) [11]. FAO estimates the projected global wheat production for 2021-22 to reach approximately 775.4 million metric tons, with India contributing around 103.9 million metric tons (Santhosini A *et al.*, 2023) [16]. Wheat cultivation traces back to the Neolithic era in the Nile valley around 5000 B.C., and it later spread to regions like the Indus and Euphrates valleys, China, and England, expanding from domestication sites in the Mediterranean. Throughout history, wheat played a pivotal role in the development of West Asian and European civilizations, serving as the primary staple for bread production in Europe and the Middle East since the advent of agriculture (Reddy *et al.*, 2023) [15]. *Triticum aestivum* is an allopolyploid with a complex genome, having a ploidy level of 2n=6x=42. Bread wheat accounts for approximately 95% of total wheat production, while durum wheat contributes around 4%, and *T. dicoccum* wheat makes up the remaining 1% (Grewal *et al.*, 2015) [7]. Wheat grains contain vital components such as starch (60-68%), protein (6-21%), fat (1.5-2%), lipids (1.8%), reducing sugar (2%), cellulose (2.0-2.5%), minerals (1.8%), and vitamins. It serves as a valuable source of minerals and vitamins, including calcium, nicotinic acid, thiamine, iron, and riboflavin (Gill *et al.*, 1991; Nelson *et al.*, 1995; Acevedo *et al.*, 2002) [6, 12, 1].

In the agricultural year 2021-2022, India achieved a wheat production of 106.41 million tonnes from a cultivated area of 31.76 million hectares (MoA, DA & FW, 2021-2022) [4]. Among Indian states, Uttar Pradesh led with the highest cultivation area of 9.35 million hectares and a production of 32.08 million metric tons. Punjab, on the other hand, boasted the highest productivity, producing 18.20 million metric tons from a cultivated area of 3.5 million hectares, with a productivity rate of 5190 kilograms per hectare. Additionally, significant wheat-growing states included Haryana, Madhya Pradesh, and Rajasthan.

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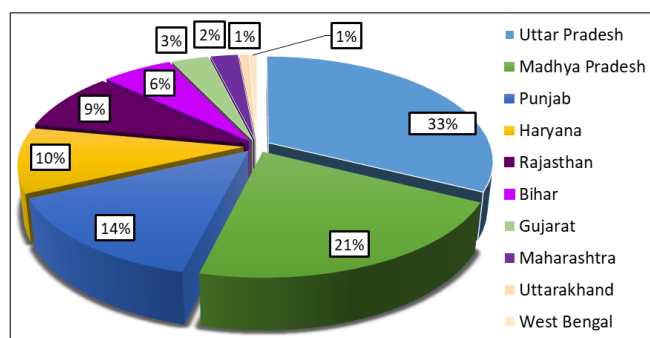


Fig 1: Wheat production in India in thousand tonnes (2021-2022)

In recent times, the production and productivity of wheat have faced a decline, necessitating extensive research to enhance its yield potential through genetic improvement. Enhancing the genetic potential of wheat presents a significant challenge due to the complex nature of grain yield, which is governed by the intricate interactions of multiple genes. In order to tackle this challenge, the research employed a line \times tester design based on the methodology proposed by Kempthorne O' (1957) [8], which bears similarities to the North Carolina Design-II introduced by Comstock and Robinson (1948, 1952). This design allowed for the examination of gene action for thirteen traits. The evaluation of gene action involved analyzing various components of genetic variances and effects. The variance of general combining ability (*gca*) mainly represents additive genetic variance, potentially including additive \times additive epistasis. In contrast, the variance of specific combining ability (*sca*) primarily reflects non-additive genetic variance, encompassing additive \times dominant and dominant \times dominant epistasis if present. Since wheat is a self-pollinated crop, its ability to benefit from hybrid vigor depends on the type of gene action and the level of heterosis observed in different combinations. By carefully analyzing gene interactions, researchers can work towards increasing wheat productivity and meeting the demands of a growing population.

2. Materials and Methods

The experiment aimed to study the gene action of 27 F_1 hybrids produced by crossing 9 lines (used as female parent) and 3 testers (used as male parent) in a line \times tester mating design during the *Rabi* season 2021-2022 and 2022-2023 (evaluation) at Lovely Professional University, Jalandhar, Punjab using a Randomized Block Design (RBD) with three replications. The hand emasculatation method followed by brushing method of pollination was adopted for crossing. The plot size and spacing followed during the experiment was double rows of 2.5 m length and 0.5 \times 22.5 cm intra and inter-row spacing. The thirteen traits recorded were days to 50% flowering (DFL), days to maturity (DM), plant height (PH), number of productive tillers plant⁻¹ (PT), length of main spike (SL), flag leaf area (FLA), peduncle length (PL), number of spikelets main spike⁻¹ (NS), number of grains main spike⁻¹ (NG), test weight (TW), biological yield plant⁻¹ (BY), grain yield plant⁻¹ (GY) and harvest index (HI). List of parental genotypes and crosses obtained are listed below in Table no. 1 and Table no. 2.

Table 1: List of parental genotypes

Sl. No	List of Genotypes used
Female Parent/Lines	
1	10 th HYPT 427
2	10 th HYPT 428
3	10 th HYPT 435
4	10 th HYPT 437
5	10 th HYPT 439
6	10 th HYPT 440
7	10 th HYPT 441
8	10 th HYPT 444
9	10 th HYPT 450
Male Parent/Tester	
1	Unnat PBW 550
2	WH 711
3	WH 1105
Standard Check	
1	DBW 187
2	HD 3086

Table 2: List of crosses made

Sl.no	Crosses obtained	Sl.no	Crosses obtained
1.	Unnat PBW 550 \times 10 th HYPT 427	2.	WH 1105 \times 10 th HYPT 439
3.	WH 711 \times 10 th HYPT 427	4.	Unnat PBW 550 \times 10 th HYPT 440
5.	WH 1105 \times 10 th HYPT 427	6.	WH 711 \times 10 th HYPT 440
7.	Unnat PBW 550 \times 10 th HYPT 428	8.	WH 1105 \times 10 th HYPT 440
9.	WH 711 \times 10 th HYPT 428	10.	Unnat PBW 550 \times 10 th HYPT 441
11.	WH 1105 \times 10 th HYPT 428	12.	WH 711 \times 10 th HYPT 441
13.	Unnat PBW 550 \times 10 th HYPT 435	14.	WH 1105 \times 10 th HYPT 441
15.	WH 711 \times 10 th HYPT 435	16.	Unnat PBW 550 \times 10 th HYPT 444
17.	WH 1105 \times 10 th HYPT 435	18.	WH 711 \times 10 th HYPT 444
19.	Unnat PBW 550 \times 10 th HYPT 437	20.	WH 1105 \times 10 th HYPT 444
21.	WH 711 \times 10 th HYPT 437	22.	Unnat PBW 550 \times 10 th HYPT 450
23.	WH 1105 \times 10 th HYPT 437	24.	WH 711 \times 10 th HYPT 450
25.	Unnat PBW 550 \times 10 th HYPT 439	26.	WH 1105 \times 10 th HYPT 450
27.	WH 711 \times 10 th HYPT 439	28.	

Table 3: Nature of gene action involved in inheritance of thirteen characters

Sl. No	Variance components	DFL	DM	PH	PT	SL	FLA
1	$\sigma^2 l$	1.55	1.49	8.95	0.90	0.30	0.44
2	$\sigma^2 t$	0.25	0.23	0.50	0.06	0.04	0.02
3	$\sigma^2 lt$	9.25**	9.07**	12.90**	2.13**	0.82**	1.07**
4	$\sigma^2 gca$	0.57	0.54	2.62	0.27	0.10	0.13
5	$\sigma^2 sca$	9.25	9.07	12.90	2.13	0.82	1.07
6	Average degree of dominance	2.85	2.9	1.57	1.99	2.02	2.03
7	Predicatability ratio	0.06	0.06	0.17	0.12	0.11	0.11

*, ** Significant at 5% and 1% against error, respectively

The estimation of genetic variance contributed by lines ($\sigma^2 l$) and testers ($\sigma^2 t$)

Table 3: (Contd...) Nature of gene action involved in inheritance of thirteen characters

Sl. No	Variance components	PL	NS	NG	TW	BY	GY	HI
1	$\sigma^2 l$	1.35	0.87	21.98	0.58	15.44	6.41	1.7
2	$\sigma^2 t$	2.23	0.08	1.57	0.06	1.83	0.15	-0.02
3	$\sigma^2 lt$	7.16**	2.38**	44.13**	1.13*	42.17**	11.87**	1.20**
4	$\sigma^2 gca$	2.01	0.28	6.67	0.19	5.23	1.72	0.41
5	$\sigma^2 sca$	7.16	2.38	44.13	1.13	42.17	11.87	1.20
6	Average degree of dominance	1.33	2.06	1.82	1.72	2.01	1.86	1.21
7	Predicatability ratio	0.22	0.11	0.14	0.15	0.12	0.13	0.26

*, ** Significant at 5% and 1% against error, respectively

The estimation of genetic variance contributed by lines ($\sigma^2 l$) and testers ($\sigma^2 t$)

3. Results and Discussion

The study's findings showed that the interaction between lines and testers (line \times tester) significantly affected all thirteen traits, highlighting the importance of gene interactions in shaping trait expression in hybrid offspring. Non-additive gene action was identified as the primary mode of inheritance for these traits, with specific combining ability (*sca*) having a more substantial impact on trait expression than general combining ability (*gca*). This suggests that the dominance effects and epistatic interactions between different gene combinations play a more substantial role in shaping these traits than the additive effects of individual genes. Additionally, the predictability ratio being less than unity value *i.e.*, 1 emphasized the significance of non-additive gene action. This finding indicates that the genetic expression of the traits in the hybrid offspring cannot be entirely predicted based solely on parental information, underscoring the complexity and importance of considering gene interactions in the breeding process. This highlights the need for incorporating heterosis breeding strategies to capitalize on the inherent non-additive genetic effects and develop wheat varieties with desirable traits.

To harness the advantages of non-additive gene action, the strategic development of hybrids for commercial use becomes essential. By selectively choosing parent lines with desirable non-additive genetic effects, breeders can create high-yielding wheat varieties with early maturity, increased productive tillers, higher spikelets, and more grains per plant. These insights provided by the study offer significant potential for enhancing wheat productivity and quality, contributing to global food security and sustainable agriculture. The understanding of gene action and heterosis can guide breeders in making informed decisions and selecting superior parent lines to achieve improved wheat varieties for the ever-growing demands of a growing population. Similar results are in conformity with several workers Singh *et al.*, (2012)^[18], Singh *et al.*, (2013)^[17] Khan *et al.*, (2016)^[9], Tabassum *et al.*, (2017)^[20] and Maida *et al.*, (2017)^[10].

4. Conclusion

The investigation into gene action in wheat traits has highlighted the substantial influence of gene interactions and non-additive genetic effects on the expression of these traits in hybrid offspring. The prevalence of specific combining ability (*sca*) over general combining ability (*gca*) suggests that the interactions between parental genes have a more pronounced impact on trait outcomes compared to the individual contributions of parental genes. The predictability ratio being below unity underscores the complexity of gene interactions and highlights the limitations of solely relying on parental information to predict trait expressions accurately. These findings emphasize the importance of incorporating heterosis breeding strategies to harness the inherent non-additive genetic effects and develop high-yielding wheat varieties with desirable agronomic characteristics. By understanding the complexities of gene action and considering heterosis in selecting parent lines, breeders can develop improved wheat varieties that contribute to global food security. The findings from this study have important implications for wheat breeding programs focused on improving crop productivity and tackling the issues arising from decreasing wheat production.

5. Conflict of Interests

The authors have stated that they have no conflicts of interest.

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