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Research Article

Genetic architecture of F_2 and identified transgressive segregants for yield and its component traits in bread wheat (*Triticum aestivum* L.)

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Abstract

Two crosses of bread wheat viz., K 1006 x LOK 1 and PBW 343 x HUW 234 were investigated to explore the useful variability parameters, correlation along with inheritance study (skewness and kurtosis) in the segregating F_2 and F_3 population for yield and its component traits respectively. Narrow difference between phenotype and genotype coefficient of variation showed less influence of environment on expression of traits under investigation. High heritability coupled with high genetic advance as per cent of mean (GAM) were registered in F_2 segregants of both crosses for majority of the characters. Among identified transgressive segregants it was higher for most of the traits like Grain filling duration (GFD), Spike length (SPL), Awn length (AL), Peduncle length (PL), Plant height (PLH), No. of spikelet's per spike (SLPS), Net effective tiller (NET), and Area under SPAD decline curve (AUSDC) in F_3 generation depicting the predominance of additive gene action, followed by selection along with progeny testing that can be utilized for improving of these traits. Significance of mean sum of square for traits under study among identified transgressive segregants indicated the presence of adequate amount of genetic variability among the plants. Grain yield plant⁻¹ showed significant and positive correlation with NET, SPL, PLH, SLPS, GPS in F_2 segregants of both the crosses revealed that selection for these traits leads to increase in overall productivity of the crop. Inheritance study revealed that traits with a negatively skewed Platykurtic distribution (1000 grain weight, AL, NET, PLH, PL, DM, GFD and AUSDC) were governed by many genes exhibiting dominant and dominant based duplicate epistasis in F_2 population. Similarly, positively skewed Platykurtic distribution for traits like GYPP, GPS, SLPS, SPL, NET, DF in F_2 population suggested the presence of large number of genes showing dominant and dominant based complementary epistasis. Hence, intense selection is required for rapid genetic gain. Inheritance studies are more powerful than first and second-degree statistics which disclosed interaction genetic effects.

Keywords: Wheat, Skewness, Kurtosis, Transgressive Segregants, Variation, Correlation.

INTRODUCTION

Wheat (*Triticum spp.*) is recognized as a key staple food crop, in many regions of the world, both in terms of the area under cultivation and as a reliable supply of food (Barman *et al.*, 2020). It is a crucial cereal crop for people all over the world, holding a dominant position in Indian agriculture, which makes up 33% of the nation's

overall output of food grains and occupies 28% of the cereal region (Mohammadi-joo *et al.*, 2015). In India it is grown in an area of 30.47 mha with the production of 106.84 mt of wheat grain with productivity of 35.07 quintal per hectare (Department of Agriculture, Cooperation and Farmers Welfare, 2023). Three different species

namely bread wheat, *T. durum* and *T. dicoccum* can be grown in India due to the country's unique environmental circumstances and dietary preferences. 95 % of the overall output of these comes from bread wheat, while four percent comes from durum wheat and almost one percent from dicoccum (Kumar *et al.*, 2014). Besides having satisfactory crop yield and good nutritional profile, wheat grains also contains, iron, minerals and vitamins. However, still there is need to improve the crop yield as well as other desirable traits of wheat because of huge demand of rapidly growing population.

The ultimate goal of every plant breeding effort is to create cultivars with great potential and consistent output in a variety of situations. In plant breeding programme, improvement in a crop usually involves exploitation of genetic variability for yield related traits. Genetic improvement through conventional breeding approaches like hybridization, selection depends mainly on presence of enormous genetic variability. The genetic variability in a population can be categorized into heritable and non-heritable variation using genetic parameters such as variance, genotypic coefficient of variation (GCV), heritability and genetic advance (GA), which serve as a basis for selecting certain outstanding genotypes from existing genotypes (Tsegaye *et al.*, 2012). Heritability along with genetic advance is helpful in anticipating the gain under selection (Johnson *et al.*, 1955). Crop improvement for grain yield can be attained through identification of transgressive segregants based on parent and progeny performance in F_2 and F_3 segregating population and fixing desirable character combination. Further, awareness of the relationship between yield and its component characters is of immense value to the breeder, as it forms the basis for selection. Correlation is helpful in determining the component characters that are positively and negatively influencing the complex yield trait. Skewness and kurtosis were formulated as per Snedecor and Cochran (1994) to interpret the nature of distribution of F_2 population for growth and yield related traits. Skewness helps us to know about the gene action for a particular trait while Kurtosis will occur if either a few genes are controlling the phenotypic distribution or there are inequalities in the additive genetic effects at different loci. Keeping above scenario in mind, present investigation has been made to assess the genetic architecture of F_2 generation and identified transgressive segregants for productivity *per se* traits in order to select outstanding genotypes from existing population.

MATERIALS AND METHODS

The investigation was carried out in the *rabi* season of 2018-19 and 2019-20 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India. The experimental material consisted of F_2 population of two wheat crosses *viz.*, K 1006 x LOK 1 and PBW 343 x HUW 234. In *rabi*, 2018-19, F_2 population of both crosses along with parents were sown in un-replicated plots.

The recommended package of practices was followed during crop growth period to raise a good crop. Data were collected on 100 randomly selected individual plants in cross K 1006 x LOK 1 and 105 plants in PBW 343 x HUW 234 cross and 10 plants in each parent for 13 quantitative traits *viz.*, Days to 50% flowering (DF), Days to maturity (DM), Grain filling duration (GFD), Net effective tiller (NET), Area under SPAD decline curve (AUSDC), Spike length (SPL), Awn length (AL), Peduncle length (PL), Plant height (PLH), No. of spikelet's per spike (SLPS), No. of grains per spike (GPS), 1000 grain weight (TW), Grain yield per plant (GYPP). Nineteen transgressive segregants were identified based on yield (Nine in K 1006 x LOK 1 and ten in PBW 343 x HUW 234). In *rabi* 2019-20, identified transgressive segregants along with parents were grown in RCBD (Randomized complete block design) with three replications. Data were collected on ten randomly selected plants from each F_3 families of transgressive segregants and parents in each replication. The F_2 population was grown in 20 rows of 2m length and parents in 4 rows of 2m length. The parents, F_2 and F_3 population of identified segregants were sown in line spaced 22.5 cm apart with plant-to-plant distance of 10 cm.

Descriptive statistics such as mean, range and genetic parameters PCV, GCV, heritability and genetic advance (Robinson, 1949) were estimated using MS Excel program. The mean data of identified segregants were subjected to analysis of variance to test the level of significance among the segregants for different characters by using Windostat version 9.3. Correlation analyses were also preformed to get a clearer understanding of how different characters are associated with grain yields. Skewness and kurtosis were formulated as per Snedecor and Cochran (1994) to interpret the nature of distribution of F_2 population for growth and yield related traits. The mean values of quantitative traits of above cross were used to formulate the coefficients of skewness and kurtosis using 'SPSS' software program.

RESULTS AND DISCUSSION

In general, a wide range of variation was observed for productive *per se* traits which indicated existence of variability among the plants. The maximum range in F_2 population was estimated for AUSDC followed by PLH and GPS while it was maximum for AUSDC followed by PLH (cross 1) and GPS (cross 2) among the identified transgressive segregants respectively (Table 3,4). These findings were reported by Alam *et al.* (2013). The highest mean was observed for AUSDC followed by DM in F_2 population (Table 3) and among identified transgressive segregants in both the crosses (Table 1, 2). Analysis of variance among identified transgressive segregants indicated highly significant differences for all the traits in both the crosses in F_3 generation, revealed the presence of adequate genetic variation and substantiates the worthiness of experimental material used in present investigation (Table 5,6).

Table 1. Mean performance of identified transgressive segregants in F₃ generation of cross K 1006 × LOK 1

Segregants*	DF	DM	GFD	NET	SPL	AUSDC	AL	PL	PLH	SLPS	GPS	TW	GYPP
L2	79	114	34.67	10.89	9.83	436.66	6.35	12.61	87.60	22.11	67.89	43.67	27.12
L6	72.67	118.67	46.00	12.44	8.89	459.66	4.13	15.83	88.68	20.89	63.22	36.50	26.45
L25	80.33	111.67	31.33	10.33	12.57	376.33	5.33	13.53	100.05	27.56	78.67	38.83	27.79
L36	79.00	113.00	34.00	10.22	10.21	414.22	6.55	16.19	78.42	23.89	71.67	37.17	28.16
L59	79.67	109.33	29.67	12.11	10.77	409.06	5.34	12.87	91.24	23.56	70.89	39.33	27.92
L88	79.67	120.00	40.33	10.22	12.15	477.89	4.51	12.56	86.84	24.56	75.78	40.42	31.07
L89	80.33	116.67	36.33	10.78	10.89	491.68	5.42	17.83	92.58	24.11	71.54	39.81	25.98
L91	73.33	117.00	43.67	12.45	8.73	459.96	6.14	15.72	92.58	24.11	71.54	39.81	25.98
L96	73.33	110.33	37.00	10.45	9.86	398.67	5.64	15.72	82.17	19.00	61.32	40.44	29.87
Mean	77.52	114.52	37.0	11.09	10.43	436.01	5.49	14.76	89.01	23.39	70.41	39.46	27.89
Parents mean K 1006	83	116.3	33.3	10.7	10.16	415.1	4.15	15.85	87.51	24.07	72.6	35.19	26.50
Parents mean LOK 1	78.4	115.4	37	9.8	8.73	412.15	7.25	16.1	75.17	18.88	57.5	36.04	20.31
C.V.	2.29	1.97	7.86	9.04	7.00	2.19	8.38	8.19	5.21	7.06	7.40	3.41	6.07
F ratio	10.52	8.31	10.52	2.74	9.73	49.68	9.16	7.46	5.67	6.73	3.39	7.09	2.86
S.E.	1.03	1.30	1.68	0.58	0.42	5.53	0.27	0.69	2.68	0.95	3.01	0.78	0.98
C.D.5%	3.08	3.91	5.03	1.74	1.26	16.57	0.79	2.09	8.03	2.86	9.02	2.33	2.93
C.D.1%	4.25	5.39	6.94	2.39	1.74	22.83	1.09	2.88	11.06	3.94	12.43	3.21	4.04

*L2, L6, L25, L36, L59, L88, L91, L96 = Identified segregants plant number

Table 2. Mean performance of identified Transgressive Segregants in F₃ generation of cross PBW 343 × HUW 234

Segregants*	DF	DM	GFD	NET	SPL	AUSDC	AL	PL	PLH	SLPS	GPS	TW	GYPP
K3	77.00	119.67	42.67	10.89	10.08	389.05	5.30	14.84	97.58	21.78	68.45	39.82	27.76
K5	86.33	116.67	30.33	13.77	9.03	431.39	4.23	15.68	97.60	21.12	63.46	31.99	26.82
K9	85.00	122.00	37.00	10.78	10.57	421.28	4.96	17.18	103.55	22.38	67.71	40.61	27.67
K28	79.00	115.67	36.67	12.55	9.53	349.91	5.52	20.58	98.25	20.44	62.11	39.40	27.67
K30	93.67	120.33	26.67	13.34	10.77	393.78	6.96	17.00	101.01	24.71	75.71	36.89	32.62
K40	80.67	117.00	36.33	14.22	8.11	498.72	5.45	10.89	101.38	15.60	49.60	43.93	29.86
K52	81.67	118.00	36.33	11.11	9.74	408.83	5.78	15.37	102.41	24.79	74.12	39.22	28.01
K60	84.67	118.00	33.33	10.00	10.30	476.18	4.97	16.22	102.75	24.00	75.33	40.66	28.47
K68	79.67	116.33	36.67	10.77	8.33	445.89	7.73	11.89	84.15	22.06	67.06	39.69	28.62
K100	76.67	113.33	36.67	15.55	9.22	425.87	6.01	19.06	88.74	16.66	50.11	40.12	28.11
Mean	82.43	117.70	35.27	12.29	9.57	424.09	5.69	15.87	97.74	21.36	65.37	39.23	28.56
Parents mean PBW 343	88.4	118.7	30.3	10.7	10.34	414.7	4.81	11.09	91.41	23.91	72.1	35.75	27.00
Parents mean HUW 234	81.9	115.5	33.6	10.5	9.57	417.1	4.75	14.83	90.57	20.81	62.8	30.42	20.06
C.V.	2.22	1.94	8.27	10.31	7.16	2.48	8.53	8.96	4.61	8.08	9.51	4.33	6.17
F ratio	23.73	3.59	6.58	6.41	5.19	50.17	13.19	12.76	6.09	9.84	6.87	9.85	2.58
S.E.	1.06	1.32	1.68	0.73	0.39	6.08	0.28	0.82	2.59	0.99	3.59	0.98	1.02
C.D.5%	3.14	3.92	5.00	2.18	1.18	18.07	0.83	2.44	7.72	2.96	10.66	2.92	3.02
C.D.1%	4.31	5.37	6.86	2.98	1.61	24.76	1.14	3.34	10.58	4.05	14.61	3.99	4.14

*K3, K5, K9, K28, K30, K40, K52, K60, K68, K100 = Identified segregants plant number

DF, Days to 50% flowering; DM, Days to maturity; GFD, Grain filling duration; NET, Net effective tiller; SPL, Spike length; AUSDC, Area under SPAD decline curve; AL, Awn length; PL, Peduncle length; PLH, Plant height; SLPS, No. of spikelet's per spike; GPS, No. of grains per spike; TW, 1000 grain weight; GYPP, Grain yield per plant.

Table 3. Variability parameters of 13 characters in F₂ population of Cross 1 (K 1006 × LOK 1) and Cross 2 (PBW 343 × HUW 234)

Trait*	Range		Mean		PCV (%)		GCV (%)		h ² (broad sense)		GA as % of mean	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
DF	70-88	75-96	79.95	85.69	4.83	7.01	4.51	6.73	87.20	92.11	8.68	13.31
DM	106-121	109-125	114.53	118.34	3.40	2.69	3.20	2.52	88.82	87.36	6.22	4.85
GFD	23-48	17-45	34.58	32.64	15.65	20.30	14.86	19.72	90.12	94.37	29.05	39.47
NET	2-14	4-16	8.58	8.11	26.30	33.19	20.18	25.73	58.88	60.10	31.91	41.10
SPL	4.4-12.3	4.4-13	8.74	9.09	15.24	14.94	13.70	13.27	80.77	78.85	25.37	24.27
AUSDC	370.5-506	301-534.5	5.44	5.67	7.16	12.29	6.75	10.14	88.95	68.08	13.12	17.24
AL	1.8-8.8	2.2-9.8	429.65	418.83	20.63	24.40	14.18	22.48	47.24	84.89	20.08	42.67
PL	8.8-22.5	4.1-27.6	14.92	14.02	19.95	29.36	18.01	23.44	81.53	63.75	33.51	38.56
PLH	46.2-101	67.4-113	80.66	90.83	9.97	10.92	7.90	10.30	62.84	89.05	12.90	19.03
SLPS	11-27	14-28	18.90	20.59	21.25	17.65	19.39	16.58	83.27	88.25	36.45	32.10
GPS	35-78	42-86	57.07	62.27	20.74	18.09	19.16	17.39	85.37	92.36	36.47	34.43
TW	24.7-50.1	29.8-56.86	38.62	38.60	12.87	13.63	10.79	12.26	70.32	80.93	18.64	18.42
GYPP	4.45-30.81	6.72-35.49	18.59	18.89	31.17	31.01	23.67	17.59	57.69	32.16	37.04	20.54

Table 4. Variability parameters for 13 traits in identified transgressive Segregants of Cross 1 (K 1006 × LOK 1) and Cross 2 (PBW 343 × HUW 234) in F₃ generation

Trait*	Range		Grand mean		PCV (%)		GCV (%)		h ² (broad sense)		GA as % of mean	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
DF	72.67-80.33	76.66-93.66	82.43	82.43	4.69	6.51	4.09	6.11	76	88.30	7.36	11.84
DM	109.33-120	113.33-122	117.70	117.70	3.66	2.65	3.08	1.80	70.90	46.30	5.34	2.53
GFD	29.67-46	26.66-42.66	35.27	35.27	16.06	13.99	14.00	11.28	76	65	25.16	18.74
NET	10.22-12.45	10-15.55	12.29	12.29	11.36	17.26	6.88	13.85	36.70	64.30	8.59	22.87
SPL	8.73-12.57	8.1-10.76	9.57	9.57	13.85	11.09	11.94	8.47	74.40	58.30	21.23	13.24
AUSDC	376.33-491.68	349.90-498.72	424.09	424.09	9.11	10.36	8.85	10.06	94.20	94.20	17.68	20.11
AL	4.13-6.55	4.22-7.73	5.69	5.69	16.17	19.19	13.83	17.19	73.10	80.30	24.36	31.74
PL	12.56-17.83	10.89-20.57	15.87	15.87	14.54	19.88	12.02	17.74	68.30	79.70	20.46	32.62
PLH	78.42-100.05	84.14-103.54	97.74	97.74	8.34	7.57	6.51	6.00	60.90	62.90	10.46	9.81
SLPS	19-27.56	15.60-24.79	21.35	21.35	12.04	16.05	9.75	13.86	65.60	74.70	20.86	24.66
GPS	61.32-78.67	49.60-75.71	65.37	65.37	9.92	16.35	6.61	13.30	44.40	66.20	9.076	22.29
TW	36.50-43.67	31.99-43.93	39.23	39.23	5.95	8.61	4.87	7.44	67	74.70	8.21	13.24
GYPP	25.98-31.07	26.81-35.62	28.56	28.56	7.72	7.62	4.78	4.47	38.30	34.50	6.09	5.41

*DF, Days to 50% flowering; DM, Days to maturity; GFD, Grain filling duration; NET, Net effective tiller; SPL, Spike length; AL, Awn length; AUSDC, Area under SPAD decline curve; PL, Peduncle length; PLH, Plant height; SLPS, No. of spikelet's per spike; GPS, No. of grains per spike; TW, 1000 grain weight; GYPP, Grain yield per plant.

F₂ segregant population of cross K 1006 x LOK 1 showed highest PCV and their corresponding GCV for grain yield per plant followed by net effective tiller while in cross PBW 343 x HUW 234 segregants it was highest for net effective tiller, peduncle length and awn length respectively (Table 3). These findings were in accordance with the Kumar *et al.* (2017), Arya *et al.* (2017) and Ahamad *et al.* (2022). Similarly, moderate value of PCV and their corresponding GCV was estimated for PL, GFD, SPL and TW in segregant population of cross 1 while in cross 2 segregants it was proclaimed moderate for GPS, SLPS, SPL, TW, AUSDC and PLH. The findings were in conformity with the findings of Mecha *et al.* (2017). Among identified transgressive segregants of both the crosses no character reveals high PCV and their corresponding GCV while moderate value of PCV and GCV was observed for AL, GFD and PL in cross 1. Traits viz., SLPS, NET along with AUSDC, GPS (in cross 2) had moderate GCV and PCV. Lowest value of PCV and GCV was observed for DF followed by TW and GYPP in F₃ generation (Table 4). These findings were in broad conformity with the findings of Safi *et al.* (2017). In the present study, PCV values were higher than GCV for all studied traits in F₂ and F₃ which could be due to genotype environment interaction to some extent indicating environmental factors affecting the expression of these characters and effective selection would be applicable for these traits in succeeding generation. These results were similar to the findings of Gaur (2019) and Adhiena *et al.* (2016).

In F₂ population of the cross 1, high heritability coupled with high genetic advance as per cent of mean (GAM) was observed for GFD, SPL, PL, SLPS and GPS, whereas in

another population generated from cross 2, it was revealed for most of the characters viz., GFD, NET, SPL, AL, PL, SLPS and GPS (Table 3). These results are similar to the findings of Naik *et al.* (2015), Bhardwaj *et al.* (2018) and Wolde *et al.* (2016). GYPP revealed moderate heritability along with high genetic advance in both F₂ population. Desheva and Cholakov (2014) reported the same findings. Among the identified transgressive segregants from both cross in F₃ generation, high heritability coupled with high GAM were observed for GFD, SPL, AL, PL, SLPS and PLH in cross 1, whereas in cross 2 it was conveyed for NET, AUSDC, AL, PL, SLPS and GPS (Table 4). GYPP reported moderate heritability along with low genetic advance among the transgressive segregants of both crosses. Ali *et al.* (2008) and Dutamo *et al.* (2015) reported results were in agreement with present finding. This property revealed presence of additive component of genetic variation which responds to selection in early generation. Therefore, it might be possible to select outstanding and high yielding genotypes by practicing selection for these characters.

Among the F₂ population of cross 1, grain yield plant⁻¹ exhibited highly significant positive correlation with NET (0.652), SPL (0.553), SLPS (0.568), GPS (0.558) and PLH (0.372), while in F₂ population of cross 2, GYPP found highly significant and positively associated with NET (0.754), GPS (0.298), SPL (0.259) and SLPS (0.266) (Fig.1). These findings were in accordance with the results remarked by Ali *et al.* (2008); Singh *et al.* (2017); Ojha *et al.* (2018) and Mecha *et al.* (2017). Genetic correlation among morphological traits allows breeder for indirect selection of those traits which are significantly correlated with grain yield plant⁻¹.

Table 5. Analysis of variance for 13 quantitative traits in identified Transgressive Segregants in F₃ generation of cross K 1006 × LOK 1

Source of variation	Df	MEAN SUM OF SQUARES												
		DF	DM	GFD	NET	SPL	AUSDC	AL	PL	PLH	SLPS	GPS	TW	GYPP
Replication	2	7.26	3.81	4.33	0.02	0.08	193.37	0.02	0.16	13.11	0.85	1.99	1.13	0.18
Treatment	8	33.43**	42.43**	89**	2.76*	5.19**	4553.65**	1.94**	10.90**	122.16**	18.35**	92.17*	12.88**	8.19*
Error	16	3.16	5.11	8.46	1.01	0.53	91.66	0.21	1.46	21.53	2.73	27.15	1.81	2.86

Table 6. Analysis of variance for 13 quantitative traits in identified Transgressive Segregants in F₃ generation of PBW 343 × HUW 234

Source of variation	Df	MEAN SUM OF SQUARES												
		DF	DM	GFD	NET	SPL	AUSDC	AL	PL	PLH	SLPS	GPS	TW	GYPP
Replication	2	0.13	2.10	1.43	2.70	0.54	5.01	0.11	6.55	59.0	9.66	36.36	6.98	2.12
Treatment	9	79.63**	18.70*	55.98**	10.31**	2.44**	5568.07**	3.11**	25.80**	123.54**	29.27**	265.51**	28.43**	7.99*
Error	18	3.36	5.21	8.50	1.60	0.47	110.98	0.24	2.02	20.26	2.98	38.65	2.89	3.10

**significant at p<0.01, *significant at p<0.05

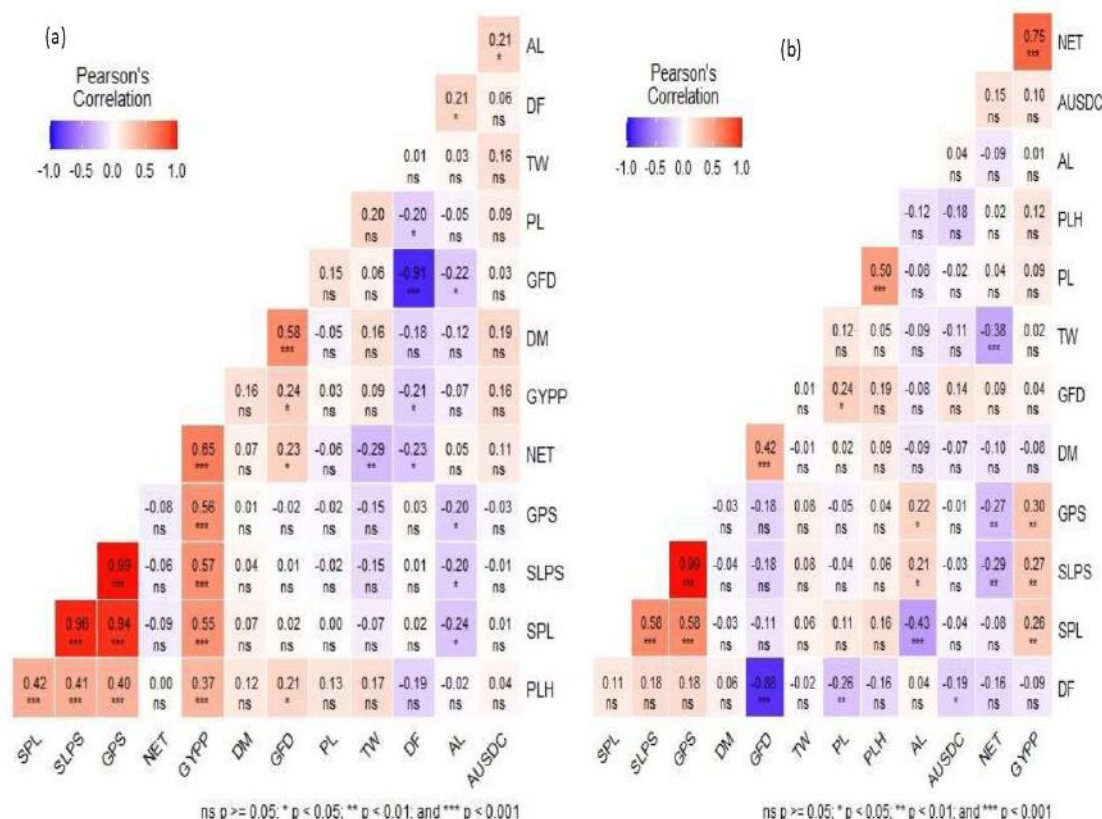
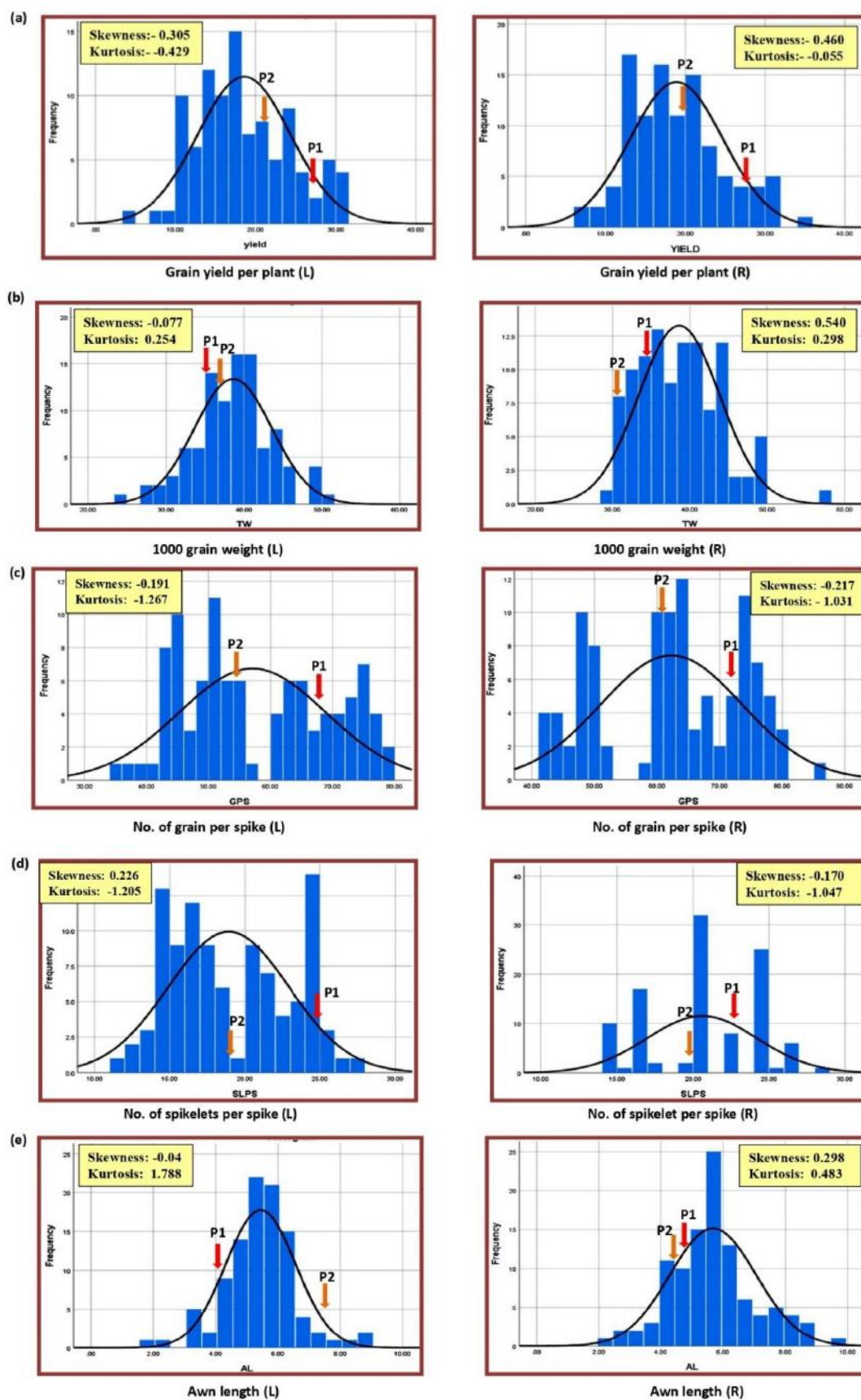


Fig. 1. Correlation matrix plot among traits under investigation in F₂ Population of K 1006 × LOK 1 cross (a) and PBW 343 × HUW 234 cross (b)

The investigation on distribution properties such as coefficients of skewness and kurtosis, furnished the nature of gene action and number of genes controlling the traits respectively. They are more powerful than first and second-degree statistics which disclosed interaction genetic effects. Traits viz., TW, AL, NET, PLH, PL, DM, GFD and AUSDC in F₂ population of cross first and GPS, SLPS, SPL, PLH, DF, DM, GFD traits for cross second showed negatively skewed Platykurtic distribution suggested that these traits were controlled by a number of genes and the majority of them exhibiting dominant and dominant based duplicate epistasis. Hence, mild selection is predicted to result in a rapid genetic gain for these traits. Positively skewed platykurtic distribution was showed by traits like GYPP, GPS, SLPS, SPL, NET, DF in F₂ population of cross 1 while in cross 2 the traits GYPP, TW, AL, NET, PL and AUSDC showed similar trend, suggesting that these traits were governed by a large number of genes and the most of them with dominant and dominant based complementary epistasis. This trend indicated that intense selection is required for rapid genetic gain (Fig. 2). Similar results were reported by Kumar *et al.* (2020) and Pooni *et al.* (1977). The present investigation revealed that characters like GFD, SPL,

PL, SLPS, GPS in F₂ population of cross 1 while in cross 2 GFD, NET, SPL, AL, PL, SLPS, GPS were governed by large no. of genes (Platykurtic distribution) along with involvement of both additive and non-additive gene action with more influence of additive gene action in SPL, GPS (positively skewed nature) in cross 1 and AL, PL, NET in cross 2 respectively. On other hand, remaining traits were under the influence of non-additive gene action (negatively skewed nature) in both the crosses for which selection is not beneficial in early generation. These results are in accordance with the findings of Menon *et al.* (2016) and Harshiya and Jagadeesh, (2014). The present study confirms the usefulness of genetic variability in a population which serve as a basis for selecting outstanding genotypes from existing population. Importance of early generation selection *i.e.*, identification and study of transgressive segregants may have a greater influence on the breeding programme of wheat with respect to yield and its component characters. Traits showing additive gene action respond to selection in early generation as compared to traits under the control of non-additive gene action. Study of inheritance revealed the interaction genetic effects and based on that selection intensity can be formulated to acquired rapid genetic gain.



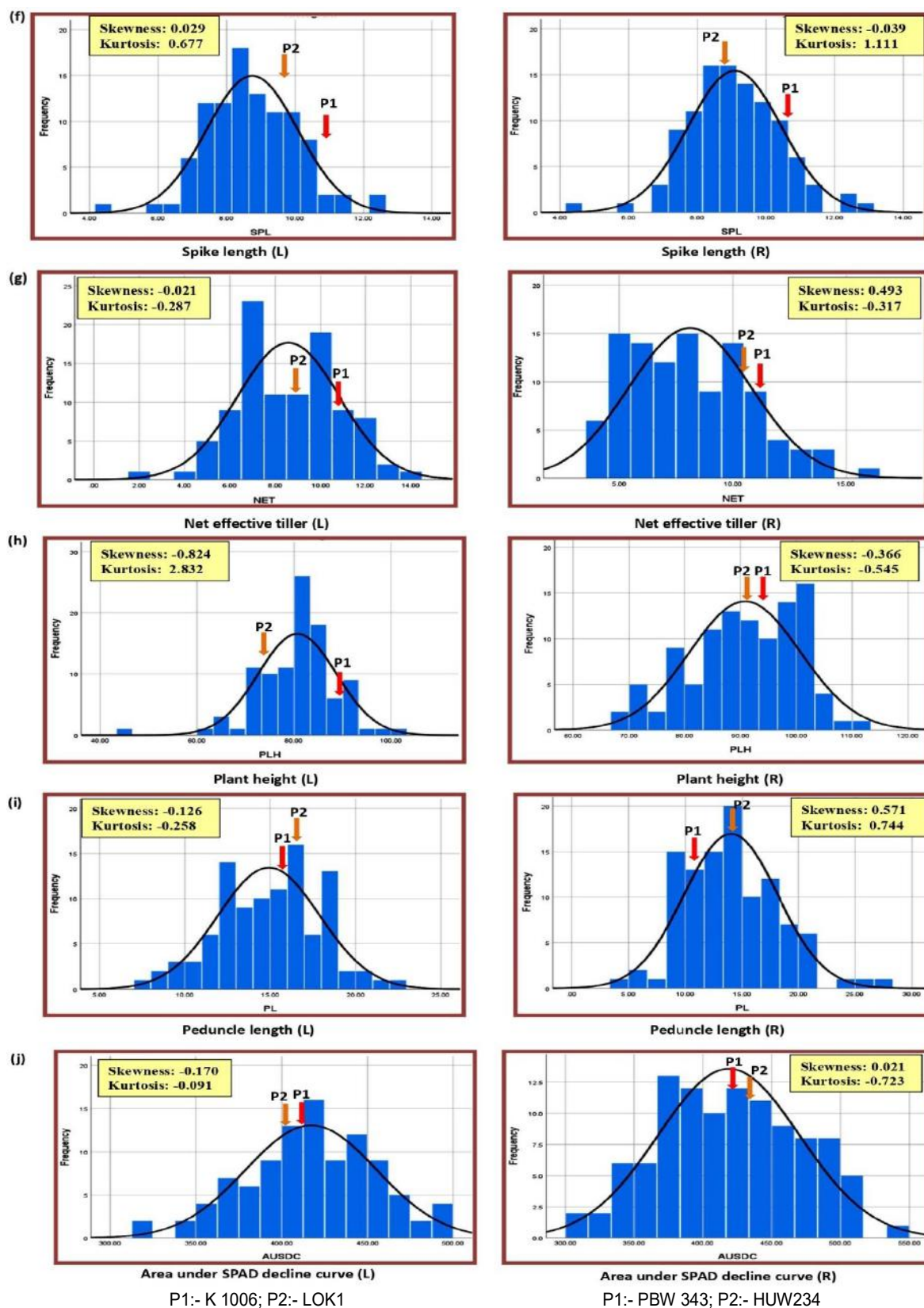


Fig. 2 Frequency distribution patterns of different traits (a to j) in the F_2 generation of K 1006 x LOK 1 (Left) and PBW 343 x HUW 234 (Right)

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