

Correlation and genetic component studies for peduncle length affecting grain yield in wheat



Muhammad Umer Farooq¹, Asim Ali Cheema², Iqra Ishaq³, Jianqing Zhu^{1,*}

¹Crop Genetics and Breeding, Sichuan Agricultural University, Chengdu, China

²Department of Renewable Resources, University of Alberta, Canada

³Department of Plant Breeding and Genetics, University of Agriculture, Pakistan

ARTICLE INFO

Article history:

Received 3 May 2018

Received in revised form

11 August 2018

Accepted 14 August 2018

Keywords:

Gene action

Line × tester analysis

Peduncle length

Metric yield traits

Correlations

ABSTRACT

The main emphasis of wheat breeders is to strive for genetically more stable, high yielding varieties than the pre-released ones to sustain the yield. Yield improvement efforts should be made while considering all contributing factors that can improve it. The role of peduncle length influencing yield and other supporting features are barely taken into consideration, and still not fully elucidated. Understanding and utilization of plant natural response will help to develop genetically and morphologically more adaptable genotypes for ever-increasing feed demand. The present research was conducted to assess the nature of gene action controlling inheritance of these traits coupled with manipulating role for yield traits. In this regard, 27 F₁ hybrids were developed by crossing 9 female and 3 male parents using Line × Tester (L×T) mating design and evaluated for yield and its related traits. The analysis of variance for combining ability pointed out the presence of broad genetic variation in material with highly heritable nature. Correlation studies portrayed strong phenotypic and genotypic association between peduncle length, plant height, flag leaf area, spike length and grain weight/plant. Strong association of peduncle length with other yield contributing traits may be utilized as an indirect selection criterion for yield improvement. Hence, short stature and high yielding varieties can be developed by controlling the favourable genes for peduncle length. All yield related traits except peduncle length, spike length, and flag leaf area were controlled by dominant genes. Selection in the later generations for peduncle length may indirectly improve yield.

© 2018 The Authors. Published by IASE. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

Wheat is major cereal crop in the world. Wheat characteristic properties i.e. broad genetic base, good storage qualities and high nutritive value, make it 3rd important staple food after rice and maize (Nazeer et al., 2013). Wheat also provides cheap source of energy, a useful source of minerals, calories, fibres, proteins and vitamins (Hammad et al., 2013). It accounts for 9.6% of value added in agriculture and 1.9% of GDP of Pakistan (MOFA, 2017). The total wheat production in Pakistan declined due to drought, flooding and rapid population growth (Chandio et al., 2016). Production of wheat for growing population in changing conditions has some associated problems, which can

be compensated through the modification of genome by breeding. Successful breeding program depends on the selection of desirable parents, and their progenies in pedigree breeding. Better selection of parents provides genetic diversity and their combining ability effects aids in achieving targets, which were also assessed by Kempthorne (1957) (Basbag et al., 2007; Rashid et al., 2007; Jain and Sastry, 2012). Performances do not obligatorily predict the ability of parents to be best or poor combiner. To overcome this arduousness, it is essential to amass knowledge about gene actions.

It is valuable to predict the selection response in the prospering generations. Additive gene actions and complementary epistatic gene interactions are fixable while non-additively controlled type of gene actions are not reliably fixable (Xiang and Li, 2001; Iqbal et al., 2007). Heritability drives information about genetic variability (additive and non-additive); that can be determined by the type of gene action (Hasnain et al., 2006; Chowdhary et al., 2007). Understanding genetic mechanism underlying

* Corresponding Author.

Email Address: zhujianqing1963@163.com (J. Zhu)

<https://doi.org/10.21833/ijaas.2018.10.010>

2313-626X/© 2018 The Authors. Published by IASE.

This is an open access article under the CC BY-NC-ND license

(<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

genetic control of traits will be helpful in breeding of favourable traits. Heritability assessment along with the determination of genetic advance make genetic amendment more authentic (Verma et al., 2007; Mangi et al., 2007).

Researchers determined genetic mechanism for different traits, (Chowdhry et al., 2005) pointing towards dominant type of gene action for inheritance of peduncle length (Malik et al., 2005; Sial, 2007) and significant effects of specific combining ability (Kempthorne, 1957) for grain weight/spike. It was observed that grain yield/plant and 1000-kernel weight had significant SCA effects (Hassan et al., 2007). Correlation studies (Desheva and Kyosev, 2017) suggested that spike length, 1000-kernel weight, grain weight/spike and grains per spike showed valuable contribution in grain yield, while, grain yield also affected by plants/m² and spikes/m² significantly (Asrar et al., 2016). The role of peduncle length in yield improvement is not fully understood. However, nature of genes influencing inheritance of these traits provides better image. Coupled with other divergent analyses, the correlation between peduncle length and cognate yield traits will provide better understanding about the inheritance as well as influence of peduncle length on yield contributing traits.

In view of above literature, this study was conducted to assess wheat lines/varieties and their hybrids regarding combining ability, the nature and magnitude of gene action, heritability and genetic gain in a line × tester fashion and further correlations were calculated for yield and its cognate traits in *Triticum aestivum L.*

2. Materials and methods

2.1. Experimental conditions

Present investigation was accomplished at the research area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad with coordinates (31.4310° N, 73.0695° E) during 2013-15 cropping season. The Parentage utilized in experiment were crossed in 9×3 line × tester fashion according to Kempthorne (1957) during 2013-14 and sown subsequent year in three blocks to observe the genetic variation. Parents and hybrids randomized separately in the same block to reduce the experimental error and make it statistically more acceptable

2.2. Selection of parents

2.2.1. Choice of testers

Testers were selected from CIMMYT segregating material ESWYT (Elite Spring Wheat Yield Trial), not related by pedigree to the lines, represented broad genetic base, with commercial adaptation and with

waxiness on stem which was later observed in F₁ viz; E-108, E-113 and E-114.

2.2.2. Choice of lines

Six widely divergent advanced inbred lines and three approved varieties i.e. 9730, 9731, 9733, 9859, 9860, 9861, AARI-11, AAS-11 and PB-11 (Table 1) were selected to be crossed with the testers.

2.3. Agronomic practices and data collection

The experiment was conducted under normal conditions from sowing till maturity for agronomic demands of crop (irrigation, fertilization and weeding etc.). Hand emasculation followed by cross pollination was practiced, while seeds were collected at maturity. The 27 F₁ crossed seeds as well as their parental seed were planted in triplicate replications under randomized complete block design (RCBD) during 4th week of November 2014. Plant × plant distance of 15cm and row × row distance of 30cm were maintained. Two seeds were sown in each hole followed by thinning to maintain one plant/hole after emergence. At maturity, ten competitive guarded plants were tagged before heading stage of plants. Data was collected for seven metric traits except area of flag leaf (which was measured before on-set of maturity, when leaves were green and rigid in the morning hours) i.e. peduncle length (cm) was taken from first node of mother tiller to the base of the spike with measuring scale. Plant height (cm) was taken using meter rod from ground level to spike tip of mother shoot excluding awns at maturity. Length of main spike (cm) was measured from the rachis base to the spike tip (excluding the awns). Main spikes used to measure spike length were utilised for measuring grains/spike, grain weight/spike (Sayre et al., 1997). Finally, average grain yield was computed by weighing total produced grains of ten plants of each genotype using an electronic balance (G and G T-500 version). Area of flag leaf (cm²) was computed as (Muller, 1991) i.e.

$$\text{Flag leaf area} = \text{flag leaf width} \times \text{flag leaf length} \times 0.74 \quad (1)$$

Ratios of general combining ability (GCA) and specific combining ability (Kempthorne, 1957) variance were used to determine the relative influence of both types of gene action i.e. additive versus nonadditive (Verma and Srivastava, 2004). Additive and dominance genetic variances were calculated by taking inbreeding coefficient (F) as one, because both lines and testers were inbred (Fellahi et al., 2013). All type of variances (Genotypic, phenotypic, environmental) were computed through the formula given by Uguru (2005). Heritability estimates were taken from these computed variances (Burton and Devane, 1953), which were categorized as low (0-29%), moderate (30-59%) and highly heritable (60% or above). Expected genetic advance with one selection cycle

and 10 % selection intensity was calculated by formula of Panse (1954) i.e.:

$$GA = K \times \sqrt{\sigma^2_p} \times h^2 \tag{2}$$

Table 1: Parentage

Material (Lines and Testers)	9730, 9731, 9733	9859, 9860	9861	AARI-2011	PB-2011	AAS-2011	E-108	E-113	E-114
Parentage	Inq-91/BWON84 (1998-99)	Pasban-90/30 th SAWSN ₉₀ (1998-99)	WLRG1 (1993-94) /5039	SH-88/90A-204//MH-97	Amsel/Attila// Inq-91/Pe wS	PRL/Pastor/ /2236	MX111-12 /M34ESWYT /208	MX111-12 /M34ESWYT /228	MX111-12 /M34ESWYT/4

2.4. Statistical analysis

The experiment was replicated thrice in field conditions. Analysis of variance was used to analyse recorded data (Steel and Torrie, 1981). Data was then subjected to least significant difference (LSD) test to separate and compare the means. Line × tester method as per Kempthorne (1957) was used to determine combining ability effects. T-test applied to check significance at probability $p \leq 0.05$ and 0.01 (1 and 2-tail) for combining ability and correlations respectively. All statistical analyses were performed using the Microsoft Excel 2007 and GenStat statistical package 10th edition while phenotypic (r_P) and genotypic (r_G) correlations were built under statistical software R version 3.1.2. (CoreTeam, 2014).

3. Results and discussion

3.1. Estimation of mean square values

The analysis of variance depicted that treatments were significant for all parameters under study while non-significant differences can be observed between replications. Sufficient genetic variability observed among lines, testers as well as in hybrids to assess combining ability effects. All treatments showed significant variation except for area of flag leaf (Table 2). Parents (testers) depicted differences that were non-significant for three parameters viz; area of flag leaf, grains per ear and per spike grain weight whereas significant for grain yield/plant. Length of peduncle and spike showed highly significant differences. Parents vs crosses (interaction) exhibited significant differences for grain weight per ear whereas all the other traits were non-significant in them. Highly significant differences for plant height, grains/spike and grain yield/ plant were observed in interaction (line × tester).

3.2. Study of mean values among parents

Genetic variations and mean performances can be exploited for genotypic evaluation of parents and hybrids. The Mean value were 32.7 cm, 94.09 cm, 12.5 cm, 22.8 cm², 59.09, 2.83 g, and 16.9 g for length of peduncle, height of plant, length of spike, area of flag leaf, grains/spike, weight of grains/spike and per plant grain yield respectively. Moreover, overall mean differences between parents and their hybrids revealed that testers were 3.44 cm and 1 cm short in height and peduncle length respectively than parent lines, with advantage of 60.8 grains/spike suggesting for development of short stature genotypes avoiding lodging problems. The differences between overall mean values suggested lines to be best for spike length (13 cm), flag leaf area (25.24 cm²) while for per plant yield hybrids performed best over parents with advantage of 1.4 g grain weight. Parents including their hybrids compared at $LSD_{0.05}$ for traits.

Table 2: Mean squares from ANOVA for some metric traits in wheat derived from line × tester analysis

Source of variation	d.f	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYP ⁻¹
Replications	2	16.666*	0.690 ^{NS}	0.183 ^{NS}	76.401*	6.745 ^{NS}	0.106 ^{NS}	1.263 ^{NS}
Treatments	38	20.035**	61.296**	2.343**	30.610*	57.484**	0.196**	35.576**
Parents	11	45.807**	80.931**	4.063**	52.454**	64.532**	0.202**	44.115**
Parents vs crosses	1	0.042 ^{NS}	24.514 ^{NS}	0.180 ^{NS}	3.914 ^{NS}	55.607 ^{NS}	0.398*	36.339 ^{NS}
Crosses	26	9.900**	54.403**	1.699**	22.395 ^{NS}	54.575**	0.185**	31.933**
Lines	8	19.007**	76.067**	3.168**	29.711 ^{NS}	40.166 ^{NS}	0.278**	20.009 ^{NS}
Testers	2	29.246**	135.573**	3.849**	38.259 ^{NS}	27.852 ^{NS}	0.093 ^{NS}	42.098*
Lines x Testers	16	2.929 ^{NS}	33.425**	0.696*	16.754 ^{NS}	65.120**	0.150*	36.625**
Error	76	4.664	10.267	0.374	19.117	23.217	0.08	11.338

**=P≤0.01, *=P≤0.05, NS=Non-significant

Average mean values of lines for aforementioned metric traits were 9.078 cm, 14.889 cm, 4.077 cm, 12.94 cm², 14.533 grains, 0.72 g and 10.456 g respectively, revealing significant differences among all nine lines (Fig. 1). Among parent’s minimum mean value for peduncle length (27.72 cm) was observed in AARI-11 while for spike length (14.33 cm) and flag leaf area (32.34 cm²) line 9731 exhibited least mean value. To prepare photosynthetic assimilates, role of flag leaf area is of immense importance in a plant. Line 9859 was best for grains/ spike (63.80) and grain yield/ plant (23.9 g). Line 9733 was prominent for kernel weight (3.34 g). The differences between extreme values among testers were 11.3 cm, 0.56 cm, 2.12 cm², 6.46 grains, 0.71 g and 10.989 g for mentioned metric traits respectively. Among testers, E-113 was superior for PL (24.73cm) and SL (12.28cm), E-108 was superior

for FLA (20.68 cm²) while E-114 performed best for yield related traits like grains/spike (63.6), Kernel weight/spike (3.06) and per plant grain yield (23.4 g). AARI-11× E-114 among hybrids was superior for yield related traits. Unlike parents, average hybrids mean was more for almost all the traits. Crosses 9730 × E-108 and 9860 × E-114 observed to have highest mean value for per plant kernel yield and grain weight per spike respectively, while mean value of spike length and flag leaf was more for 9859 × E-113 and 9731 × E-108 respectively (Fig. 2). Although mean performances could be used to exploit variability, but it’s not satisfactory to rely on just mean values for complex genetic mechanisms of inheritance in nature. These abilities are estimated in terms of GCA and SCA effects among hybrid and parents.

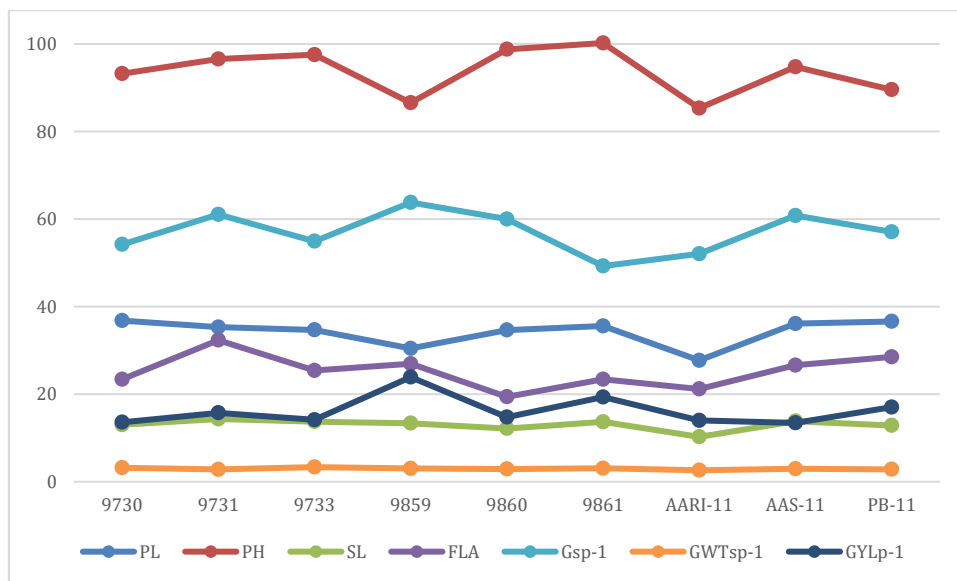


Fig. 1: Mean performance for twelve parents (Nine lines and three testers)

3.3. Estimation of GCA and SCA effects

L × T design employed as-a rapid measure of screening of genetic stocks based on GCA/SCA effects, rather than their variances. Dominance gene action was found in all parameters (Javaid et al., 2001; Hassan et al., 2007; Kashif and Khan, 2008; Nazeer et al., 2013) revealed by ratio of GCA/SCA variances except peduncle length, spike length and flag leaf area for that additive components were greater.

The significance for GCA and SCA effects were estimated by comparing with t-tabulated 1- tail values to get more stable and reliable results. The estimates of GCA for peduncle length ranged from -3.31 to 2.10 (Table 3). The line 9861 was a potential parent for all the studied characters except for flag leaf area. Most of the parental material revealed significant combining ability for traits. Among parents, E-113 and E-114 proved to be best male parents for yield improvement traits while E-108 was good combiner for peduncle length, plant height and flag leaf area. Among lines 9733 and PB-11

shared significant homology for per plant yield, flag leaf and spike length while differed for plant height and peduncle length respectively. Tiwari et al. (2011) described that in cross combinations, where one parent has good GCA, could be best utilized to develop pure lines having high yield due to predominance of additive gene action, even though their cross combinations depicted non-significant SCA effects.

As described by Singh et al. (2005) the better performance of a specific cross combination may be achieved by combining dominant alleles from good combiners and recessive alleles from poor combiners. Verma and Srivastava (2004) pointed out that effects of SCA were positively associated with hybrids where one parent is common as a good general combiner.

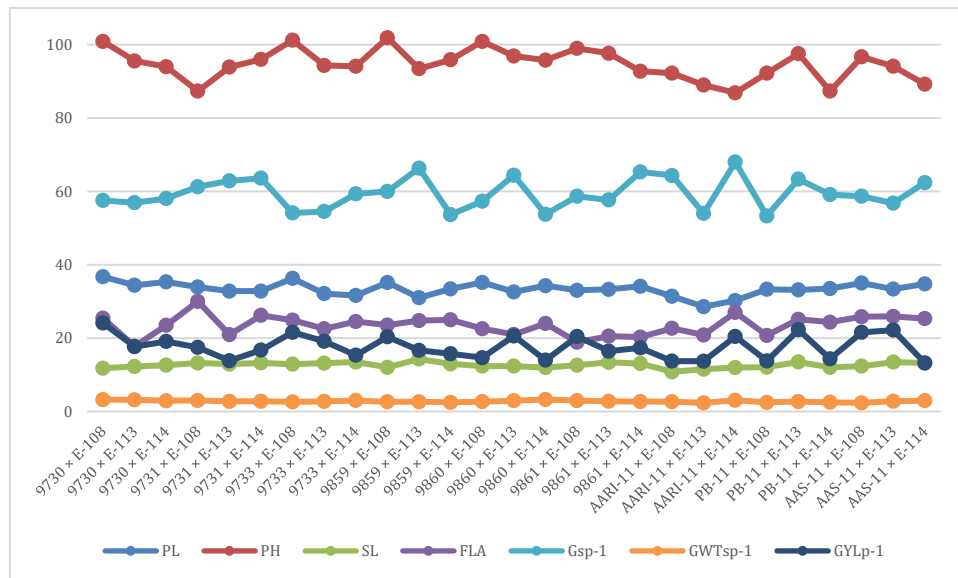


Fig. 2: Mean performance for twenty-seven cross combinations

Yet SCA effects do not subsidise noticeably in self-pollinated crops improvement, except in situations where exploitation of heterosis is practicable, Potent homozygous lines could be selected in transgressive segregants, which could be possible only by selecting finest hybrids (Fellahi et al., 2013). Among hybrids AARI-11 × E-114, PB-11×E113, AAS-11×E-114, 9859×E-108, 9733×E-108, 9731×E-113, 9731×E-108 and 9730×E-108 revealed positive highly significant SCA effects in respect of per plant grain yield and other traits under study. Concomitant significance of combining ability effects due to line × tester for peduncle length, spike length, height of plant, flag leaf area and grains related traits selected for present study suggested 9730×E-108 as supreme specific combiner for all metric traits except spike length (Table 4).

3.4. Proportional contribution of lines and testers

The corresponding proportion of lines, testers as well as their interactions for seven indicated characters are mentioned in Fig. 3. The proportional contribution of maternal and paternal influence was significant in interaction (line × tester) for parameters like flag leaf area (46.038%), grains/spike (73.429%), grain weight/spike (49.935%) and yield/plant (70.579%). Lines played a positive influential role towards spike length

(57.36%), plant height (43.02%) and peduncle length (59.07 %), Which indicate that maternal effect was predominant for these parameters (Rashid et al., 2007). Paternal influence was non-significant for almost all the characters. The results depicted that lines and hybrids contribute more towards genetic variation in the expression of the mentioned characters which was in paradox with (Fellahi et al., 2013).

3.5. Genetic components and degree of dominance

We found additive nature for inheritance pattern of peduncle length, spike length and flag leaf area. GCA variance was lower than SCA variance for all yield traits except for peduncle length, spike length and flag leaf area indicating additive genetic effect in action for the latter traits, favoured by additive and dominance genetic variances than followed by ratio of GCA/SCA variance which was smaller than unity except for length of spike and peduncle and flag leaf area (Table 5). Importance of non-additive gene action for height of plant and grain yield was also suggested by Premlatha et al. (2011). Gnanasekaran et al. (2006) found gene action that was non-additive for weight of grain/spike and height of plant, while additive gene action was observed by Sharma (2006).

Table 3: General combining ability effects for some metric traits in wheat

Lines	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYLp ⁻¹
9730	2.102 ^{NS}	2.119**	-0.433 ^{NS}	-1.263 ^{NS}	-1.949 ^{NS}	0.324 ^{NS}	2.636*
9731	-0.209 ^{NS}	-2.288 ^{NS}	0.467*	2.234**	3.117**	0.071**	-1.634 ^{NS}
9733	-0.050 ^{NS}	1.860**	0.530*	0.498**	-3.460 ^{NS}	0.000 ^{NS}	1.044**
9859	-0.194 ^{NS}	2.379*	0.445*	0.942**	0.540**	-0.194 ^{NS}	-0.061 ^{NS}
9860	0.639**	3.156 ^{NS}	-0.418 ^{NS}	-0.980 ^{NS}	-0.961 ^{NS}	0.180**	-1.227 ^{NS}
9861	0.095**	1.786**	0.371**	-3.582 ^{NS}	1.095**	0.026**	0.433**
AARI-11	-3.313 ^{NS}	-5.325 ^{NS}	-1.214 ^{NS}	0.023**	2.651**	-0.096 ^{NS}	-1.693 ^{NS}
AAS-11	-0.068 ^{NS}	-2.325 ^{NS}	-0.114 ^{NS}	-0.083 ^{NS}	-0.860 ^{NS}	-0.225 ^{NS}	-0.841 ^{NS}
PB-11	0.998**	-1.362 ^{NS}	0.364**	2.211**	-0.171 ^{NS}	-0.087 ^{NS}	1.344**
E-108	1.061**	2.230*	-0.412 ^{NS}	0.350**	-1.098 ^{NS}	-0.046 ^{NS}	-1.402 ^{NS}
E-113	-1.019 ^{NS}	0.021**	0.330**	-1.326 ^{NS}	0.191**	-0.020 ^{NS}	0.409**
E-114	-0.042 ^{NS}	-2.251 ^{NS}	0.081**	0.976 ^{NS}	0.906**	0.066**	0.993**
S.E for lines	0.72	1.068	0.204	1.457	1.606	0.094	1.122
S.E for testers	0.416	0.617	0.118	0.841	0.927	0.054	0.648

*, **= significance at the 0.05 and 0.01 levels of probability, respectively (1-tailed)

Table 4: Specific combining ability effects for crosses in wheat

Hybrids	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYLp ⁻¹
9730 × E-108	0.187**	1.844**	-0.026 ^{NS}	2.839**	1.120**	0.171**	2.829**
9730 × E-113	-0.066 ^{NS}	-1.280 ^{NS}	-0.301 ^{NS}	-3.125 ^{NS}	-0.769 ^{NS}	0.091**	-3.031 ^{NS}
9730 × E-114	-0.121 ^{NS}	-0.564 ^{NS}	0.326**	0.286 ^{NS}	-0.351 ^{NS}	-0.262 ^{NS}	0.202**
9731 × E-108	-0.313 ^{NS}	-7.305 ^{NS}	0.508**	3.940**	-0.213 ^{NS}	0.211**	0.478**
9731 × E-113	0.645**	1.461**	-0.545 ^{NS}	-3.447 ^{NS}	0.097**	-0.089 ^{NS}	-2.594 ^{NS}
9731 × E-114	-0.332 ^{NS}	5.844 ^{NS}	0.037**	-0.493 ^{NS}	0.116**	-0.122 ^{NS}	2.117**
9733 × E-108	1.872**	2.436**	0.112**	0.567**	-0.769 ^{NS}	-0.118 ^{NS}	1.922**
9733 × E-113	-0.192 ^{NS}	-2.243 ^{NS}	-0.330 ^{NS}	-0.132 ^{NS}	-1.658 ^{NS}	-0.024 ^{NS}	0.039**
9733 × E-114	-1.680 ^{NS}	-0.193 ^{NS}	0.219**	-0.435 ^{NS}	2.427**	0.142**	-1.961 ^{NS}
9859 × E-108	0.905**	2.584**	-0.637 ^{NS}	-1.235 ^{NS}	1.098**	0.088**	1.779**
9859 × E-113	-1.170 ^{NS}	-3.650 ^{NS}	0.855 ^{NS}	1.670**	6.142 ^{NS}	0.082**	-1.334 ^{NS}
9859 × E-114	0.265**	1.066**	-0.218 ^{NS}	-0.436 ^{NS}	-7.240 ^{NS}	-0.171 ^{NS}	-0.445 ^{NS}
9860 × E-108	0.083**	0.807**	0.537**	-0.308 ^{NS}	-0.071 ^{NS}	-0.232 ^{NS}	-2.752 ^{NS}
9860 × E-113	-0.403 ^{NS}	-0.984 ^{NS}	-0.205 ^{NS}	-0.191 ^{NS}	5.710 ^{NS}	-0.004 ^{NS}	3.776*
9860 × E-114	0.320**	0.177**	-0.333 ^{NS}	0.499**	-5.639 ^{NS}	0.236**	-1.024 ^{NS}
9861 × E-108	-1.506 ^{NS}	0.288**	-0.007 ^{NS}	-1.360 ^{NS}	-0.791 ^{NS}	0.202**	1.378**
9861 × E-113	0.830**	1.165**	0.040**	1.942**	-3.080 ^{NS}	-0.024 ^{NS}	-2.039 ^{NS}
9861 × E-114	0.676**	-1.453 ^{NS}	-0.033 ^{NS}	-0.582 ^{NS}	3.871**	-0.178 ^{NS}	0.661**
AARI-11 × E-108	0.268**	0.621**	-0.211 ^{NS}	-1.201 ^{NS}	3.320**	0.011**	-3.219 ^{NS}
AARI-11 × E-113	-0.474 ^{NS}	-0.391 ^{NS}	-0.253 ^{NS}	-1.332 ^{NS}	-8.303 ^{NS}	-0.315 ^{NS}	-2.668 ^{NS}
AARI-11 × E-114	0.205**	-0.230 ^{NS}	0.463**	2.533**	4.983*	0.305*	5.887 ^{NS}
PB-11 × E-108	-1.076 ^{NS}	-2.379 ^{NS}	-0.044 ^{NS}	-3.027 ^{NS}	-4.169 ^{NS}	-0.034 ^{NS}	-4.015 ^{NS}
PB-11 × E-113	0.849**	5.165 ^{NS}	0.636*	3.061**	4.542*	0.160**	5.057 ^{NS}
PB-11 × E-114	0.228**	-2.786 ^{NS}	-0.592 ^{NS}	-0.034 ^{NS}	-0.373 ^{NS}	-0.126 ^{NS}	-1.043 ^{NS}
AAS-11 × E-108	-0.421 ^{NS}	1.103**	-0.233 ^{NS}	-0.215 ^{NS}	0.476**	-0.298 ^{NS}	1.600**
AAS-11 × E-113	-0.018 ^{NS}	0.757**	0.103**	1.554**	-2.680 ^{NS}	0.122**	2.795**
AAS-11 × E-114	0.439**	-1.860 ^{NS}	0.130**	-1.340 ^{NS}	2.205**	0.176**	-4.394 ^{NS}
S.E for crosses	1.247	1.850	0.353	2.524	2.782	0.163	1.944

*, **= significance at the 0.05 and 0.01 levels of probability, respectively (1-tailed)

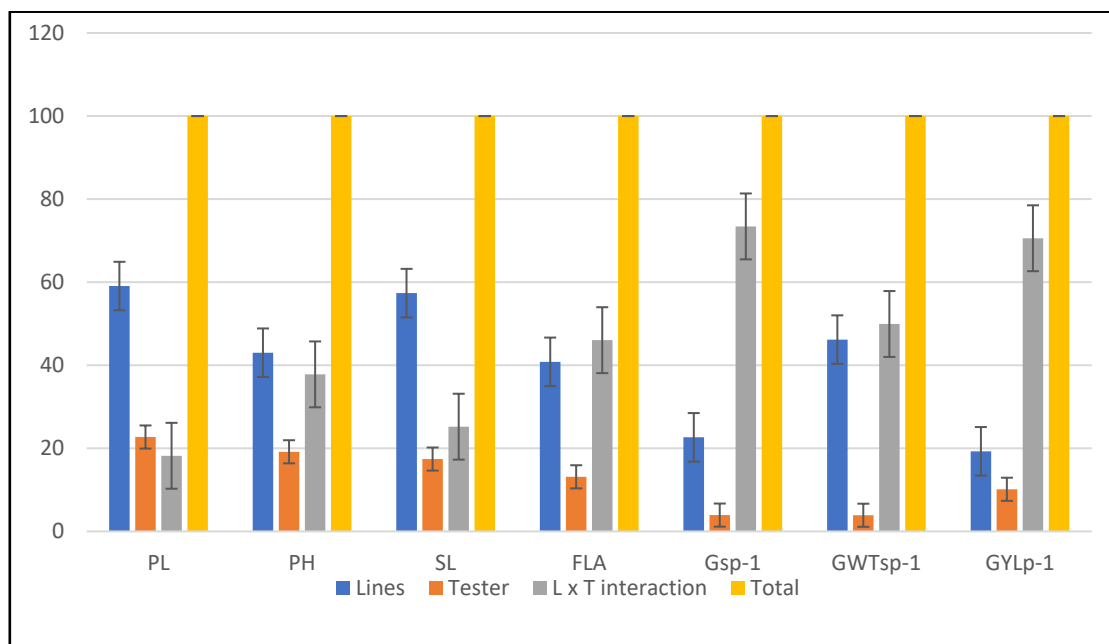


Fig. 3: Proportional contribution of lines, testers and their interaction towards total genetic variation

Predominance of SCA variance over GCA one was also investigated for barley (Verma et al., 2007), while Borghi and Perenzin (1994) discovered additive effects for yield traits. Degree of dominance relative to the pre-existing allele(s) strongly influences evolutionary impact, because both lines and testers were inbred. Differences in results found may be due to variability of breeding material or genotype × environment interaction. The inheritance pattern of peduncle length, spike length and flag leaf area depicted complete additive nature. But, all other yield traits revealed complete dominance (Table 5) (Fellahi et al., 2013). The additive effects revealed that selection of superior genotypes for peduncle length, spike length and Flag leaf area should be delayed to later generations, where improvement in characters can be made by recombinants selection in the segregating populations.

3.6. Heritability, genetic advance, and correlations

Magnitude of heritability and genetic advance favoured process of selection. It was found that genotypic variances were more than corresponding environmental variances, showing strong estimates of heritability (>50%) for spike, peduncle length and plant height (Table 6) (Hussain et al., 2017). Low heritability was perceived for flag leaf area (16.6%) while yield related traits were moderately heritable like grains spike⁻¹ (32.9%), grains weight/ spike (32.5%) and grain yield plant⁻¹(41.6%) (Fellahi et al., 2013) escorted by genetic advance, which ranged from 0.1 g (grain weight per spike) to 3.42 grains/spike (Yadav et al., 2011). Flag leaf area and traits related to yield observed to be moderately heritable.

Table 5: Genetic components

Genetic Variation	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYLp ⁻¹
Variance of GCA	1.63	3.45	0.25	2.23	1.96	0.02	1.36
Variance of SCA	-0.58	7.72	0.11	-0.79	13.97	0.03	8.43
Additive genetic variance	3.25	6.90	0.50	4.46	3.92	0.02	2.72
Dominance genetic variance	-0.58	7.72	0.11	-0.79	13.97	0.03	8.43
Variance ratio of GCA to SCA	-2.81	0.45	2.35	-2.83	0.14	0.50	0.16
degree of dominance	-0.42	1.06	0.46	-0.42	1.89	1.19	1.76

Table 6: Heritability, genetic variation and genetic advance

	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYLp ⁻¹
Ve	4.70	10.3	0.40	19.10	23.20	0.10	11.30
Vg	5.12	17.00	0.66	3.83	11.42	0.04	8.08
Vp	9.79	27.27	1.03	22.95	34.64	0.12	19.42
H ₂ (h.s)	0.52	0.62	0.64	0.17	0.33	0.33	0.42
GA	2.88	5.73	1.14	1.41	3.42	0.20	3.23

Most of the traits studied exposed significant positive association at phenotypic and genotypic levels (2-tailed). The association revealed the importance and contribution of peduncle length towards yield traits, how it affects stature and grains morphology of plants affecting yield is very limited. The assessments of correlation clearly manifested that association of peduncle length with plant height ($r_p= 0.63$; $r_G=0.49$), length of spike ($r_p= 0.31$; $r_G=0.29$), flag leaf area ($r_p= 0.30$; $r_G=0.34$) and grain weight/spike ($r_p=0.28$; $r_G=0.61$) is highly positive and significant at both phenotypic and genotypic levels (Table 7) while for grains per spike negative and strong relationship was observed at genotypic

level ($r_G= -0.485$). Grains/spike and per plant yield at both levels were independent to peduncle length. Peduncle length ameliorates all the related parameters primarily plant height, spike length and flag leaf area which ultimately influence yield. Although it has no direct association with yield/plant, it may be utilized as an indirect selection criterion for yield improvement. Flag leaf area showed strong and positive correlation with length of peduncle, spike length and grains weight/spike at both levels which is in contradiction with (Hussain et al., 2017). Genotypic and phenotypic correlations of grain yield and grain weight/spike were significant.

Table 7: Genotypic and phenotypic correlations

	PL	PH	SL	FLA	Gsp ⁻¹	GWTsp ⁻¹	GYLp ⁻¹
PL	1**	0.49513**	0.28959**	0.33505**	-0.485**	0.61377**	0.1639ns
PH	0.63132**	1**	0.15741ns	-0.3589**	-0.2766**	0.19041*	0.41348**
SL	0.31135**	0.23495*	1**	0.71929**	0.06542ns	0.25585**	0.04778ns
FLA	0.30271**	-0.0345ns	0.36925**	1**	0.06998ns	0.40336**	0.0369ns
Gsp ⁻¹	0.07581ns	-0.0694ns	0.20299*	0.17223ns	1**	0.01303ns	0.17952ns
GWTsp ⁻¹	0.2809**	0.17739ns	0.15864ns	0.03921ns	-0.0050ns	1**	0.38778**
GYLp ⁻¹	0.21253*	0.26832**	0.15603ns	0.21599*	0.22199*	-0.02579ns	1**

*, **= Correlation is significant at the 0.05 and 0.01 level of probability, respectively (2-tailed)

A common pattern was observed between association studies for flag leaf area, length of spike, plant height and peduncle length. Very strong association exist between flag leaf area influencing length of peduncle which will ultimately affects

length of spike and resulting phenotype of plant. Hence, short stature and high yielding varieties can be developed by controlling the favourable genes for peduncle length. Additionally, this study indicated involvement of gene action particularly additive in

present scenario for inheritance of flag leaf area, spike length especially peduncle length with highly heritable features.

4. Conclusion

The major emphasis of the present work was to access the role of peduncle length in the manipulation of important yield traits and to understand the nature of genes controlling inheritance of major traits. Dominant type of gene action condition yield traits with moderate heritability. The lines and the interaction (lines × testers) contributed more for expression of different traits. Line 9861 was supreme general combiner for all traits under study except flag leaf area. Testers E-113 and E-114 were good general combiners for spike length, grains/spike, grain weight/spike and grain yield per plant while lines 9860,9861 and PB-11 along with E-108 were good general combiners for peduncle length. Cross combination 9730×E-108 proved to be best specific combiner for all traits except for length of spike. Among hybrids AARI-11×E-114, PB-11×E-113 and AAS-11×E-113 exhibited significant potential to be best hybrids. Additive genetic effect prevailed for peduncle length, spike length and flag leaf area, concomitant significance for high heritability in peduncle length, plant height and length of spike was also observed. Further association studies between the characters strengthen the results, indicating that peduncle length has significant and strong influence on morphology and inheritance of major yield contributing traits. Although it has no direct association with yield/plant, it may be utilized as an indirect selection criterion for yield improvement. Hence, late generation selection could be fruitful for traits like peduncle length, spike length and flag leaf area for full exploitation of genetic potential.

Acknowledgment

The author's thanks, to Dr. Muhammad Akbar (Senior research officer at Wheat research institute) AARI, Faisalabad, Pakistan for fruitful discussion and guidance.

References

- Asrar M, Usama K, Abdul R, Ghazanfar H, and Zulqarnain H (2016). Heritability of yield and yield components in hexaploid wheat. *Academia Journal of Agricultural Research*, 4(5): 277-280.
- Basbag S, Ekinci R, and Gencer O (2007). Combining ability and heterosis for earliness characters in line× tester population of *Gossypium hirsutum* L. *Hereditas*, 144(5): 185-190.
- Borghi B and Perenzin M (1994). Diallel analysis to predict heterosis and combining ability for grain yield, yield components and bread-making quality in bread wheat (*T. aestivum*). *Theoretical and Applied Genetics*, 89(7-8): 975-981.
- Burton GW and Devane EH (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. *Agronomy Journal*, 45(10): 478-481.
- Chandio AA, Jiang Y, Joyo MA, and Rehman A (2016). Impact of area under cultivation, water availability, credit disbursement, and fertilizer off-take on wheat production in Pakistan. *Journal of Applied Environmental and Biological Sciences*, 6(10): 10-18.
- Chowdhary MA, Sajad M, and Ashraf MI (2007). Analysis on combining ability of metric traits in bread wheat, *triticum aestivum*. *Journal of Agricultural Research*, 45(1): 11-17.
- Chowdhry MA, Saeed MS, Khaliq I, and Ahsan M (2005). Combining ability analysis for some polygenic traits in a 5×5 diallel cross of bread wheat (*Triticum aestivum* L.). *Asian Journal of Plant Sciences*, 4(4): 405-408.
- CoreTeam R (2014). R: A Language and Environment for Statistical Computing. The R Foundation for Statistical Computing, Vienna, Austria.
- Desheva G and Kyosev B (2017). Study of genetic parameters and association between characters in einkorn genotypes. *Trakia Journal of Sciences*, 15(2): 141-148.
- Fellahi ZEA, Hannachi A, Bouzerzour H, and Boutekrabi A (2013). Line× tester mating design analysis for grain yield and yield related traits in bread wheat (*Triticum aestivum* L.). *International Journal of Agronomy*, 2013: Article ID 201851, 9 pages. <https://doi.org/10.1155/2013/201851>
- Gnanasekaran M, Vivekanandan P, and Muthuramu S (2006). Combining ability and heterosis for yield and grain quality in two line rice (*Oryza sativa* L.) hybrids. *Indian Journal of Human Genetics*, 66(1): 6-9.
- Hammad G, Kashif M, Munawar M, Ijaz U, Muzaffar M, Raza MM, and Abdullah M (2013). Genetic analysis of quantitative yield related traits in spring wheat (*Triticum aestivum* L.). *American-Eurasian Journal of Agricultural and Environmental Sciences*, 13(9): 1239-1245.
- Hasnain Z, Abbas G, Saeed A, Shakeel A, Muhammad A, and Rahim MA (2006). Combining ability for plant height and yield related traits in wheat (*Triticum aestivum* L.). *Journal of Agricultural Research*, 44(3): 167-173.
- Hassan, G., Mohammad, F., Afridi, S. S., and Khalil, I. H. (2007). Combining ability in the F₁ generations of diallel cross for yield and yield components in wheat. *Sarhad Journal of Agriculture*, 23(4): 937-942.
- Hussain I, F Mohammad, T Iqbal, GHassan S K, F Anwar F N, S Gao N A, and Nauman M (2017). Comparative analysis of some production traits in F_{5,9} recombinant inbred lines (RILs) of bread wheat. *American-Eurasian Journal of Agricultural and Environmental Sciences*, 17(2): 148-154.
- Iqbal M, Navabi A, Salmon DF, Yang RC, Murdoch BM, Moore SS, and Spaner D (2007). Genetic analysis of flowering and maturity time in high latitude spring wheat. *Euphytica*, 154(1-2): 207-218.
- Jain SK and Sastry EVD (2012). Heterosis and combining ability for grain yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *Journal of Agriculture and Allied Science*, 1(1): 17-22.
- Javaid A, Masood S, and Minhas NM (2001). Analysis of combining ability in wheat (*Triticum aestivum* L.) using F₂ generation. *Pakistan Journal of Biological Sciences*, 4(11): 1303-1305.
- Kashif M and Khan AS (2008). Combining ability studies for some yield contributing traits of bread wheat under normal and late sowing conditions. *Pakistan Journal of Agricultural Sciences*, 45(1): 45-49.
- Kempthorne O (1957). An introduction to genetic statistics. John Wiley and Sons, Inc., New York, USA.
- Malik MFA, Awan SI, and Ali S (2005). Genetic behavior and analysis of quantitative traits in five wheat genotypes. *Journal of Agriculture and Social Sciences*, 1(4): 313-315.

- Mangi SA, Sial MA, Ansari BA, and Arain MA (2007). Study of genetic parameters in segregating populations of spring wheat. *Pakistan Journal of Botany*, 39(7): 2407-2413.
- MOFA (2017). Economic wing. Ministry of Food and Agriculture Islamabad, Pakistan.
- Muller J (1991). Determining leaf surface area by means of linear measurements in wheat and triticale (brief report). *Archiv Fuchtforsch*, 21(2): 121-123.
- Nazeer W, Hussain T, Khan MA, Naeem M, Amjad MW, and Hussain K (2013). Mechanism of inheritance for quantitative traits in interspecific crosses of *Triticum aestivum* L. *World Applied Sciences Journal*, 22(10): 1440-1448.
- Panse VG (1954). *Statistical methods for agricultural workers*. Indian Council of Agricultural Research, New Delhi, India.
- Premlatha M, Kalamani A, and Nirmalakumari A (2011). Heterosis and combining ability for grain yield and quality in maize (*Zea mays* L.). *Advances in Environmental Biology*, 5(6): 1264-1267.
- Rashid M, Cheema AA, and Ashraf M (2007). Line x tester analysis in basmati rice. *Pakistan Journal of Botany*, 39(6): 2035-2042.
- Sayre KD, Rajaram S, and Fischer RA (1997). Yield potential progress in short bread wheats in northwest Mexico. *Crop Science*, 37(1): 36-42.
- Sharma RK (2006). Studies on gene action and combining ability for yield and its component traits in rice (*Oryza sativa* L.). *The Indian Journal of Genetics and Plant Breeding*, 66(3): 227-228.
- Sial MA (2007). Genetic heritability for grain yield and its related characters in spring wheat (*Triticum aestivum* L.). *Pakistan Journal of Botany*, 39(5): 1503-1509.
- Singh NB, Singh YP, and Singh VPN (2005). Variation in physiological traits in promising wheat varieties under late sown condition. *Indian Journal of Plant Physiology*, 10(2): 171-175.
- Steel RGD and Torrie JH (1981). *Principles and procedures of statistics: A biometrical approach*. 2nd Edition McGraw-Hill, London, UK.
- Tiwari DK, Pandey P, Giri SP, and Dwivedi JL (2011). Prediction of gene action, heterosis and combining ability to identify superior rice hybrids. *International Journal of Botany*, 7(2): 126-144.
- Uguru MI (2005). *Crop genetics and breeding (Revised)*. Epharata Press, Nsukka, Enugu State, Nigeria.
- Verma AK, Vishwakarma SR, and Singh PK (2007). Line x Tester analysis in barley (*Hordeum vulgare* L.) across environments. *Barley Genetics Newsletter*, 37: 29-33.
- Verma OP and Srivastava HK (2004). Genetic component and combining ability analyses in relation to heterosis for yield and associated traits using three diverse rice-growing ecosystems. *Field Crops Research*, 88(2-3): 91-102.
- Xiang B and Li B (2001). A new mixed analytical method for genetic analysis of diallel data. *Canadian journal of forest Research*, 31(12): 2252-2259.
- Yadav AK, Maan RK, Kumar S, and Kumar P (2011). Research note variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding*, 2(3): 405-408.