



Research Article

Evaluation of Elite Spring Wheat (*Triticum aestivum* L.) Genotypes for Yield and Yield Attributing Traits under Irrigated Condition

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Abstract

Thirty International Maize and Wheat Improvement Centre (CIMMYT) elite lines and Nepalese commercial wheat varieties were grown at Agriculture and Forestry University, Chitwan in Alpha-lattice design to identify high yielding genotypes, yield attributing parameters and correlations between them. Observations were taken for different morpho-physiological and yield attributing traits i.e., days to booting, heading, anthesis, maturity, flag leaf senescence, flag leaf duration, grain filling duration, plant height, spike length, number of grains per spike, thousand kernel weight, hectoliter weight, grain yield and biomass yield. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation among genotypes for each character. The mean grain yield was 2148 kg/ha and it ranged from 1000 to 3425 kg/ha. BLOUK#1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/MUNAL #1 (35th ESWYT138) was the highest grain yielding genotype among all followed by CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE#1/5/CHIBIA//PRLII/CM65531/3/KAUZ/BAV92 (ESWYT 141), Gautam, Vijay and CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER (ESWYT129). Grain yield had significant strong positive correlation with grain filling duration (0.685**), plant height (0.606**), thousand kernel weight (0.675**), biomass yield (0.892**) and hectoliter weight (0.586**). Four clusters were formed by cluster analysis and genotypes were grouped in a particular cluster on the basis of similarity of morpho-physiological traits. So, these genotypes may be exploited for their direct release or as parents in hybridization programmes to develop high yielding wheat varieties.

Keywords: Wheat; *Triticum aestivum* L.; CIMMYT Elite lines; yield; correlation

Introduction

Wheat (*Triticum aestivum* L.) is considered as one of the major cereal crops which belongs to the grass family (Class *Liliopsida*, Family Poaceae and Tribe Triticeae) (Shewry, 2009). It produces large edible grains which acts as a source of about one half of human food and a major portion of nutrient requirement. Wheat also known as king of cereals is a direct source of food for human beings. It is the most important cereal crop of the world providing staple food for around 35% of the world population and about 36% of the world's production is in Asia (FAOSTAT, 2014).

The primary objective of the spring bread wheat improvement program at International Maize and Wheat Improvement Centre (CIMMYT) is to develop wheat germplasm that is widely adapted, higher yielding, high

quality, disease resistant, and stress tolerant. International distribution and testing of CIMMYT-derived advanced wheat breeding lines across diverse environments worldwide with a focus on CIMMYT has characterized the world's diverse wheat production zones into several mega-environments, and its wheat improvement priorities are targeted accordingly (Rajaram *et al.*, 1995; Braun *et al.*, 2010). The importance of international wheat improvement efforts for fulfilling wheat global demands by developing improved varieties was underlined by Dr. Norman E. Borlaug in the early 1960s (Borlaug, 1968). Historically, CIMMYT's bread wheat breeding program has produced outstanding genotypes with significantly increased grain yield potential (Rajaram, 2005). 'Kalyansona' and 'Sonalika' are considered wheat mega-varieties of the "Green Revolution" era (Rajaram *et al.*, 1995). Although

numerous CIMMYT-derived varieties have subsequently been released and grown, hallmark post-green revolution mega-varieties developed from 'Veery', 'Kauz', and Attila crosses were widely grown in many developing countries under different names. Previous studies have documented the wide adaptation of outstanding bread wheat genotypes developed at CIMMYT (Trethowan *et al.*, 2001; Singh, *et al.*, 2007). In addition, outstanding CIMMYT-derived bread wheat lines have been widely used in crossing programs across the developing world (Braun *et al.*, 1996) and have greatly enriched the genetic diversity of wheat cultivars in many countries (Smale *et al.*, 2002).

The CIMMYT-derived high yielding wheat varieties have also exhibited resistance or tolerance to serious biotic and abiotic stresses. For example, targeted breeding for the rust resistance have achieved success in incorporating high levels of disease resistance into CIMMYT-derived high yielding wheat genotypes (Van Ginkel and Rajaram, 1993). Use of synthetic hexaploids derived from crosses between tetraploid durum wheat (*Triticum turgidum* L.) and diploid *Aegilops tauschii* Coss. in the 1990s resulted in several outstanding wheat lines that combine high yield with disease resistance (Villareal *et al.*, 1994) and tolerance to abiotic stresses (Trethowan *et al.*, 2001). The world food demand is increasing continuously, thus it is now a compulsion to develop wheat varieties having higher yield potential, higher tolerance to warmer temperatures, and have improved water use efficiency and drought tolerance. Wheat yield stagnation has been reported in the past decade from South Asia (Mehlka *et al.*, 2000) and Europe (Petersen *et al.*, 2010). Each year since 1981, CIMMYT's spring bread wheat breeding program has been distributing the Elite Spring Wheat Yield Trial (ESWYT), which includes new elite lines targeted for irrigated environments worldwide.

Adoption of improved varieties has potential to increase the production and productivity of wheat by at least two folds. Therefore, there is need to analyze and evaluate the advance lines developed by National Agriculture Research System, CIMMYT with wider genetic base to develop cultivars suitable for our environments. Hence, this study was conducted with the objective to study genotypic performance of wheat lines developed by Nepal Agriculture Research Council and CIMMYT on phenological, agromorphological, grain yield and its components and others traits and to study relationship among various yield attributing traits and economic yield.

Methodology

The experiment was conducted at the research farm of Agriculture and Forestry University, Rampur, Chitwan, Nepal, from November 2015 to June 2016. The research site was located at 27.64768°N latitude and 84.34750°E

longitude and at an altitude of 171 meters above sea level. The site contained sandy loam soil with acidic reaction. Thirty bread wheat genotypes were used as plant material in this study (Table 1). They were obtained from the Agriculture Botany Division, Nepal Agriculture Research Council, Khumaltar, Nepal which included 23 elite lines selected from 35th Elite Spring Wheat Yield Trial (ESWYT), 5 biofortified harvest plus lines from 5th Harvest Plus Yield Trial (HPYT) developed from CIMMYT, Mexico, and 2 Nepalese commercial cultivars, namely Vijay and Gautam. The experiment was conducted in Alpha-lattice design with thirty wheat genotypes as treatments with three replications. Each replication consisted of 5 blocks and six plots were formed in each block. Each plot was 2 m in length and 2 m in width. Each plot consisted of 8 rows with a spacing of 25 cm between rows and continuous sowing was done in each row. The planting was done in 4th December 2015. The chemical fertilizers were applied at the rate of 120:60:60 kg NPK per hectare. First irrigation was done at the crown root initiation (CRI) stage (Zadoks' growth stage Z1.3, Z2.1) second at the time of booting stage (Zadoks' growth stage) and third at grain filling stage.

Observations were recorded for days to booting, days to heading, days to anthesis, days to maturity, days to flag leaf senescence, flag leaf duration, grain filling duration, plant height, spike length, grains per spike, thousand kernel weight, biomass yield, grain yield and hectoliter weight. Data entry and processing was carried out using Microsoft Office Excel 2007. Analysis of variance, mean comparison between genotypes based on LSD by using R Studio software package. Pearson's correlation analysis was performed using SPSS v.16.

Results and Discussions

Days to Booting, Heading and Anthesis

Analysis of variance showed that there was highly significant difference between the wheat genotypes for booting, heading and anthesis days (Table 2). The mean number of booting days for thirty wheat genotypes was 75 days (Table 4). BAJ #1 booted earliest in 70 days followed by NELOKI/3/IWA 8600211//2*PBW343*2/KUKUNA (72 days), KACHU#1 (72 days) and Vijay (73 days) while KACHU #1 took longest days to boot i.e. 80 days. Majority of the genotypes (70%) booted in the range of 73 to 77 days.

Similarly, the mean number of days to heading was 81 days (Table 2). BAJ#1 headed earliest in 75 days followed by Vijay (77 days) and NELOKI/3/IWA 8600211//2*PBW343*2/KUKUNA (78 days) while CHIBIA/PRLII/CM65531/3/FISCAL/4/DANPHE#1/5/C HIBIA/PRLII/CM65531/3/SKAUZ/BAV92 (ESWYT 141) and KACHU#1 (HPYT 403) took maximum number of days for heading i.e. 85 days. About 70% of the genotypes headed in the range of 78 to 80 days.

Table 1: List of wheat genotypes grown for the field experiment, 2015/2016

Trt.	Genotypes	Cross/Pedigree
1	Vijay	Vijay
2	Gautam	Gautam
3	ESWYT 104	MISR 1
4	ESWYT 105	MUNAL #1
5	ESWYT 106	BECARD #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ
6	ESWYT 109	KACHU//KIRITATI/2*TRCH
7	ESWYT 110	KACHU/CHONTE
8	ESWYT 111	KIRITATI//HUW234+LR34/PRINIA/3/BAJ #1
9	ESWYT 112	MUTUS//ND643/2*WBLL1
10	ESWYT 114	ND643/2*WBLL1//KACHU
11	ESWYT 115	SUP152/QUAIU #2
12	ESWYT 118	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92/6/ND643/2*WBLL1
13	ESWYT 119	BAJ #1/KISKADEE #1
14	ESWYT 120	CHEWINK #1/MUTUS
15	ESWYT 121	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/2*MUNAL
16	ESWYT 123	QUAIU #1/2*SUP152
17	ESWYT 129	CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER
18	ESWYT 138	BLOUK #1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/MUNAL #1
19	ESWYT 139	BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47/4/ND643/2*WBLL1/5/ BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47
20	ESWYT 140	QUAIU #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW/ /KAUZ/6/BECARD
21	ESWYT 141	CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE #1/5/CHIBIA/ /PRLII/CM65531/3/KAUZ/BAV92
22	ESWYT 143	KACHU*2/CHONTE
23	ESWYT 145	ND643/2*WBLL1//2*KACHU
24	ESWYT 147	FRANCOLIN #1*2//ND643/2*WBLL1
25	ESWYT 148	BECARD//KIRITATI/2*TRCH/3/BECARD
26	HPYT 402	BAJ #1
27	HPYT 403	KACHU #1
28	HPYT 414	FRANCOLIN #1/7/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)/ /PGO/4/HUITES/5/T.SPELTA PI348599/6/REH/ HARE//2*BCN/3/CROC_1/ AE.SQUARROSA (213)//PGO/4/HUITES
29	HPYT 420	NELOKI/3/IWA 8600211//2*PBW343*2/KUKUNA
30	HPYT 438	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/ PASTOR/3/T.DICOCCON PI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/ MILAN//PI 610750

For days to anthesis, the mean value was 84 days (Table 2). The early anthesis occurred in genotype BAJ#1 (HPYT 402) in 78 days while the genotype KACHU#1 (HPYT 403) was late at anthesis with 88 days.

Flag Leaf Senescence and Duration

There was highly significant variation among genotypes for flag leaf senescence and flag leaf duration as analyzed from Analysis of Variance (Table 2). The mean number of days for flag leaf senescence was 107 days and flag leaf duration was 36 days (Table 2). ND643/2*WBLL1//KACHU, MISHR1 and BAJ#1(HPYT 402) were the earliest genotypes to have their flag leaf senescence in 103 days and

Gautam was late to have its flag leaf senescence with 113 days followed by KACHU/CHONTE and TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCON PI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/MILAN//PI 610750 (HPYT 438) (111 days). Flag leaf duration was minimum for ND643/2*WBLL1//KACHU i.e. 29 days. Similarly, flag leaf duration was maximum for Gautam i.e. 43 days followed by KACHU*2/CHONTE (42 days) and BLOUK#1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/MUNAL #1 (40 days).

Table 2: Mean values of Days to booting (DB), Days to heading (DH), Days to anthesis (DA), Days to Flag leaf senescence (FLS), Flag leaf duration (FLD), Days to maturity (DM) and Grain filling duration (GFD) of thirty wheat genotypes under study

Genotypes	DB	DH	DA	FLS	FLD	DM	GFD
Vijay	73.00	77.33	80.33	106.00	35.00	114.33	34.00
Gautam	77.00	81.66	84.00	113.00	43.33	121.66	37.66
ESWYT 104	72.00	78.66	81.66	103.00	34.33	112.66	31.00
ESWYT 105	79.00	84.33	88.00	108.33	34.33	114.00	26.00
ESWYT 106	78.00	84.00	87.00	108.33	36.00	115.66	28.66
ESWYT 109	77.00	81.66	84.00	107.33	36.33	116.66	32.66
ESWYT 110	78.33	82.66	86.33	111.33	39.66	118.00	31.66
ESWYT 111	73.33	81.00	84.33	105.00	34.66	114.33	30.00
ESWYT 112	75.33	81.66	84.66	108.33	38.33	114.33	29.66
ESWYT 114	73.66	80.66	83.66	103.00	29.66	113.66	30.00
ESWYT 115	73.33	78.33	82.66	106.00	34.00	113.33	30.66
ESWYT 118	76.33	82.00	85.33	105.00	35.33	114.00	28.66
ESWYT 119	74.33	80.33	83.00	108.33	37.33	116.00	33.00
ESWYT 120	75.33	80.33	83.00	108.66	35.00	116.33	33.33
ESWYT 121	75.00	81.00	84.33	104.33	32.00	113.33	29.00
ESWYT 123	75.66	81.00	83.66	107.33	33.66	115.33	31.66
ESWYT 129	75.00	80.33	83.33	106.33	37.00	113.33	30.00
ESWYT 138	73.33	78.33	82.33	108.00	40.00	115.33	35.33
ESWYT 139	75.66	81.00	83.33	108.00	40.00	115.66	32.33
ESWYT 140	75.00	80.66	84.66	105.33	32.66	115.66	31.00
ESWYT 141	79.00	85.00	87.66	107.66	38.66	114.66	31.66
ESWYT 143	78.00	84.33	87.66	110.66	42.33	117.33	29.66
ESWYT 145	77.00	84.00	87.00	108.66	35.66	117.66	30.66
ESWYT 147	77.00	82.00	85.00	106.00	33.33	113.33	28.33
ESWYT 148	74.33	80.00	84.00	106.00	35.00	114.33	30.33
HPYT 402	70.00	75.66	78.66	103.66	33.33	113.33	34.66
HPYT 403	80.00	85.33	88.33	108.66	39.00	117.00	28.66
HPYT 414	75.33	81.66	84.66	105.33	36.66	112.33	27.66
HPYT 420	72.33	78.00	82.33	108.00	38.33	114.33	34.00
HPYT 438	78.00	83.00	86.33	111.00	38.00	117.66	31.33
Grand mean	75.52	81.2	84.37	107.22	36.3	115.18	31.11
F-Statistic	11.63**	13.82**	16.48**	11.00**	3.86**	3.67**	4.46**
CV%	1.54	1.33	1.14	1.17	7.44	1.56	6.57
LSD _{0.05}	1.91	1.78	1.58	2.07	4.44	2.96	3.36

*: significant in 5% level, **: significant in 1% level

Days to Maturity and Grain Filling Duration

For days to maturity and grain filling duration, highly significant difference was observed among the genotypes (Table 2). The average number of days to maturity was 115 days (Table 2). FRANCOLIN #1/7/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)/ PGO/4/HUITES/5/T.SPELTA PI348599/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)/PGO/4/HUITES (HPYT 414) and MISHRI

(ESWYT 104) were early maturing genotypes in 112 days and Gautam was the late maturing with 121 days. The mean value for grain filling duration was 31 days. Gautam had longest grain filling duration of 37 days followed by BLOUK

#1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBL L1/5/MUNAL#1 (ESWYT 138) (35 days) and Baj#1(HPYT 402) (34 days) and Munal#1(ESWYT 105) had the shortest i.e. 26 days.

Plant Height

The average plant height was 86 cm (Table 3). Analysis of variance showed highly significant variation among genotypes for plant height. Plant height was in the range of 73 to 98 cm. Gautam (98 cm) was the tallest among thirty genotypes followed by Vijay (96 cm) and TRAP#1/BOW/3/VEE/PJN/2*TUI/4/BAV92/RAYON/5/

KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCON PI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/MILAN//PI 610750 (HPYT 438) (92 cm) while Kachu#1(HPYT 403) (73 cm) had the least plant height. Twenty three genotypes had plant height in the range of 80 to 90 cm, five genotypes had above 90 cm and two genotypes had below 80 cm.

Table 3: Mean values of Plant height (PH), Spike length (SL), Grain per Spike (Gps), Thousand kernel weight (TKW), Grain yield (GY), Biological Yield (BY) and Hectolitre weight (Kg/hl) of thirty wheat genotypes under study

Genotypes	PH	SL	Gps	TKW	GY	BY	Kg/hL
Vijay	96.00	9.43	40.66	43.60	2960.00	8623.00	80.00
Gautam	98.00	12.40	49.00	45.75	3015.00	8383.00	80.70
ESWYT 104	83.00	9.06	41.00	38.50	2117.00	6083.00	74.50
ESWYT 105	80.16	9.00	49.00	27.05	2103.00	6937.00	74.33
ESWYT 106	89.00	11.10	48.33	27.54	1707.00	5417.00	72.50
ESWYT 109	84.96	8.80	41.33	41.17	2510.00	6583.00	78.00
ESWYT 110	84.36	9.66	45.66	33.26	1963.33	6583.00	73.66
ESWYT 111	85.60	8.96	41.00	30.41	1640.00	5333.00	74.16
ESWYT 112	86.86	10.06	47.66	25.64	1483.33	4500.00	71.00
ESWYT 114	82.06	9.90	51.33	39.29	1636.66	4917.00	71.16
ESWYT 115	90.33	10.10	45.00	40.29	2056.66	5667.00	74.66
ESWYT 118	87.63	9.90	41.33	32.26	1000.00	4000.00	75.16
ESWYT 119	89.06	10.03	40.66	42.85	2640.00	7433.00	75.33
ESWYT 120	89.83	9.33	43.66	36.07	2206.66	6750.00	76.50
ESWYT 121	84.50	9.03	33.66	36.53	2076.66	4433.00	70.50
ESWYT 123	89.66	9.83	47.33	37.19	2390.00	6750.00	77.16
ESWYT 129	86.93	10.36	38.33	42.41	2823.33	5517.00	71.66
ESWYT 138	89.10	9.80	48.33	42.95	3425.00	8453.33	79.33
ESWYT 139	79.10	8.06	48.66	38.91	2000.00	6200.00	74.33
ESWYT 140	82.16	9.20	41.66	30.42	1186.66	4250.00	73.50
ESWYT 141	89.13	9.93	37.33	43.86	3160.00	8286.66	73.33
ESWYT 143	83.63	9.66	46.66	32.01	2126.66	5633.33	74.66
ESWYT 145	86.90	10.30	45.33	38.70	2273.33	6750.00	78.50
ESWYT 147	81.16	9.93	35.33	30.82	1670.00	4423.33	70.83
ESWYT 148	86.76	10.30	52.66	42.75	1920.00	6000.00	73.66
HPYT 402	90.53	9.73	41.00	37.43	2455.00	6968.33	76.00
HPYT 403	73.13	10.33	45.33	35.47	1186.66	4433.33	73.66
HPYT 414	80.43	9.10	45.33	40.88	1446.66	4600.00	73.66
HPYT 420	84.66	11.40	51.66	39.70	2650.00	7310.00	77.50
HPYT 438	91.70	10.40	48.33	41.05	2603.33	7020.00	77.66
Grand mean	86.21	9.83	44.42	37.16	2147.72	6141.27	74.92
F-Statistic	3.58**	5.99**	5.29**	10.63**	10.41**	6.69**	2.36**
CV%	5.34	6.03	8.19	7.9	15.17	14.78	4.12
LSD _{0.05}	7.57	0.97	5.98	4.82	535.74	1492.48	5.07

*: significant in 5% level, **: significant in 1% level

Spike Length

Analysis of variance revealed highly significant difference among genotypes for spike length (Table 3). The average spike length was 9.8 cm (Table 3). It varied from 8.1 cm to 12.4 cm with the maximum spike length observed on Gautam and minimum on BAJ #1/KISKADEE #1 (ESWYT 139). Twenty two genotypes had spike length between 8 to 10 cm and eight genotypes had above 10 cm.

Number of Grains per Spike

There was highly significant variation among genotypes for number of grains per spike (Table 3). The average number of grains per spike was 44 (Table 3). BECARD//KIRITATI/2*TRCH/3/BECARD (ESWYT 148) had the maximum number of grains per spike i.e. 52 followed by NELOKI/3/IWA 8600211//2*PBW343*2/KUKUNA (HPYT 420) (51), ND643/2*WBL1//KACHU (ESWYT 114) (51) and Munal#1 (ESWYT 105) (49). SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/2*MUNAL (ESWYT 121) had the minimum number of grains per spike i.e. 33. Majority of the genotypes (23) had between 40 to 50, three genotypes had above 50 and four genotypes had below 40 grains per spike.

Thousand Kernel Weight

Analysis of variance showed highly significant variation among genotypes for thousand kernel weight (Table 3). The mean thousand-kernel weight for genotypes was 37.2 gm within the range of 25.6 to 45.8 gm (Table 3). Among the genotypes, Gautam (45.8 gm) had highest thousand kernel weight followed by CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE#1/5/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92 (ESWYT 141) (43.9 gm) and Vijay (43.6 gm) while (ESWYT 112) (25.6 gm) and Munal#1(ESWYT 105) (27.1 gm) had the least.

Grain Yield

There was highly significant difference among the genotypes for grain yield (Table 3). The average grain yield was 2147.72 kg/ha (Table 3). The grain yield varied from 1000 kg/ha to 3425 kg/ha. The highest grain yield was recorded for BLOUK #1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBL1/5/MUNAL#1 (3425 kg/ha), followed by CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPH#1/5/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92 (3160 kg/ha), Gautam (3015 kg/ha), Vijay (2960 kg/ha) and CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER (2823 kg/ha). The lowest grain yield was recorded for SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92/6/ND643/2*WBL1,

Kachu#1 and QUAIU #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/6/BECARD.

Biomass Yield

The mean biomass yield was 6141.27 kg/ha (Table 3). Analysis of Variance showed highly significant variation among genotypes for biomass yield (Appendix 4). It varied from 4000 to 8623 kg/ha. Vijay had the highest biomass yield followed by ESWYT 138 (8453 kg/ha), Gautam (8383 kg/ha) and CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE #1/5/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92 (8286 kg/ha). ESWYT 118 had the lowest biomass yield. Majority of the genotypes (65%) had biomass yield between 5000 to 7000 kg/ha.

Hectoliter Weight

There was highly significant variation among genotypes for hectoliter weight (Table 3). The mean value of hectoliter weight was 74.92 kg/hL (Table 3). The genotype with highest hectoliter weight was Gautam i.e. 80.66 kg/hL followed by Vijay (80 kg/hL) and ESWYT 138 (79.33 kg/hL) and the genotypes with lowest test weight were ESWYT 121 and ESWYT 147 i.e. 70.50 kg/hL.

Correlation Analysis

Pearson's correlation analysis showed significant correlations among the variables studied (Table 4). Days to heading showed significant positive correlation with days to maturity (0.40*) but negatively correlated with grain filling duration (-0.53**). Days to maturity was positively correlated with flag leaf duration (0.64**) and hectoliter weight (0.52**) at high level of significance and positively correlated with grain filling duration (0.46*), spike length (0.43*) and biomass yield (0.38*). Flag leaf duration was positively correlated with grain yield (0.35) and hectoliter weight (0.363*). Grain filling duration had highly significant positive correlation with plant height (0.63**), thousand kernel weight (0.60**), grain yield (0.69**), biomass yield (0.73**) and hectoliter weight (0.71**). Plant height was positively correlated with spike length (0.45*), thousand kernel weight (0.40*), grain yield (0.61**), biomass yield (0.61**) and hectoliter weight (0.56**). Spike length and number of grains per spike were positively correlated (0.33). Thousand kernel weight showed highly significant positive correlation with grain yield (0.68**), biomass yield (0.59**) and hectoliter weight (0.497**). There was highly significant positive correlation of grain yield with biomass yield (0.89**) and hectoliter weight (0.59**). Biomass yield and hectoliter weight were positively correlated (0.75**).

Table 4: Pearson's correlation coefficient among different traits of thirty wheat genotypes under study

	DH	DM	FLD	GFD	PH	SL	NGPS	TKW	GY	BY	Kg/hL
DH	1	.403*	.304	-.531**	-.361	.073	.055	-.355	-.285	-.233	-.256
DM		1	.638**	.458*	.280	.426*	.313	.138	.239	.378*	.519**
FLD			1	.367*	.129	.340	.288	.202	.353	.387*	.363*
GFD				1	.632**	.308	.117	.604**	.685**	.730**	.714**
PH					1	.448*	-.010	.404*	.606**	.608**	.564**
SL						1	.333	.207	.242	.228	.242
NGPS							1	.013	-.024	.181	.266
TKW								1	.675**	.586**	.497**
GY									1	.892**	.586**
BY										1	.747**
Kg/hL											1

Values are significantly different at 5% level of significance (*) and highly significantly different at 1% level of significance (**). DH= Days to heading, DM= Days to maturity, FLD= Flag leaf duration, GFD= Grain filling duration, PH= Plant height, SL= Spike length, NGPS= Grains per spike, TKW= Thousand kernel weight, GY= Grain yield, BY= Biomass yield, Kg/hL= Hectoliter weight

Production of wheat yield fluctuates widely as a result of its interaction with environment because grain yield is a complicated quantitative parameter and is the product of several contributing factors affecting grain yield directly or indirectly. Wheat production can be increased through development of productive varieties which better adapt to various agro-climatic conditions and also resist all types of stresses. Selection for grain yield improvement can only be effective if sufficient genetic variability is present in the breeding material (Ali *et al.*, 2008). Genotypic and phenotypic correlations are important breeding parameters used for determining the degree of association of various yield contributing parameters with grain yield (Ali *et al.*, 2008). Many earlier researchers studied phenotypic correlations of various grain yield components with wheat grain yield for its genotypic improvement (Shahid *et al.*, 2002; Aycicek and Yildirim, 2006).

Grain yield of wheat is a complex trait and is affected by various components like; number of tillers/m², number of grains per spike, 1000 grain weight, and plant height and spike length. There were significant differences among the genotypes for all the traits studied which are in agreement with Sharma (1994); Kamat (1996); Ginkel *et al.*, (1998); Dwivedi *et al.*, (2002); Sinha *et al.*, (2006); Kamboj (2007) and Baloch, *et al.*, (2013) who reported high variability for different traits in wheat. Thus, it is implied that there was reasonably sufficient variability in the research material, which provides ample scope for selecting superior and desired genotypes by the plant breeder for further improvement.

Successful breeding of high yielding varieties depends on the yield contributing morphological traits and choosing small number of important traits having positive correlation. There were significant positive correlations among different variables and yield components. These results are in agreement with Akram *et al.*, (2008) who reported positive correlation between grain yield and 1000-grain weight, while Kashif and Khaliq (2004) also found that yield components like tillers per plant had significantly contributed towards grain yield development. They also noted that number of heads per m², grains/spike and 1000 grain weight were main contributors to grain yield in wheat. It was also reported that the grain yield per plant showed significantly positive association with productive tillers per plant, plant height, 1000-grain weight and spike length at both genotypic and phenotypic levels (Aycicek and Yildirim, 2006). The present study suggests that high yielding varieties of wheat may be selected by the indirect selection through grain filling duration, plant height, thousand kernel weight, biological weight and the hectoliter weight.

The correlation results were also in agreement with (Ojha, 2012) who reported a significant positive correlation between grain yield and thousand seeds weight, number of grains per spike, flag leaf duration, grain filling duration and plant height. Similar findings were reported by Thapa *et al.* (2009) also.

Based on the study, ESWYT 141 (CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE#1/5/C HIBIA//PRLII/CM65531/3/SKAUZ/BAV92), ESWYT 138 (BLOUK

#1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/MUNAL #1), Vijay and Gautam were the most important genotypes for showing excellent performance among the studied lines on grain yield and its attributes. Grain yield had strong and positive correlation with its attributing traits. Thousand kernel weight, grain filling duration, plant height and hectoliter weight were the key contributors to grain yield suggesting that more emphasis on these components is needed for increasing grain yield in wheat. So, these genotypes may be exploited for their direct release or as parents in hybridization programmes to develop high yielding wheat varieties.

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