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Research Article

Assessment of Morpho-Physiological, Yield and Yield Attributing Traits Related to Post Anthesis Drought in Wheat Genotypes Under Rainfed Condition in Rampur, Chitwan

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Abstract

A set of twenty wheat (*Triticum aestivum* L.) genotypes was evaluated to assess morpho-physiological, yield and yield attributing traits related to post-anthesis drought in wheat genotypes under rainfed condition in a Randomized completely block design with three replications at research farm of Faculty of Agriculture, Rampur, Chitwan, during winter season of 2016/2017. The result revealed highly significant genotypic effects for number of tillers per m^2 area, plant height, spike length, number of grains per spike, weight of grains per spike, 1000 kernels weight, days to booting, days to heading, days to anthesis, days to flag leaf senescence, days to maturity, SPAD meter reading, peduncle length, grain filling duration and reproductive growth period. Significant genotypic effects were found for grain yield, biological yield and harvest index and an array of variation was found among the genotypes for each trait. But non-significant genotypic effect was found for canopy temperature depression. WK2373 gave highest grain yield kg/ha (3035 kg/ha) and biomass yield kg/ha (8080 kg/ha).

This study presented WK2373, WK2379, WK2380, WK2386, WK2388, WK2383, WK 2378 and WK1481 the best genotypes governing different valuable traits. These potential genotypes for valuable traits found in different clusters. Crossing genotypes belonging to different clusters could maximize the opportunities for transgressive segregation as there is a higher probability that unrelated genotypes would contribute unique desirable alleles at different loci. Therefore, this study can help breeders to increase genetic diversity by selecting materials of divergent parentage for crosses, thereby reducing vulnerability to diseases and climate changes.

Keywords: Traits; post anthesis; drought; rainfed; wheat genotypes

Introduction

Wheat (*Triticum aestivum* L.), one of the largest cereal crops of the world. Wheat contributes 17% of the total cultivated land in the world. It contributes 35% of the world's diet than any others crop as a staple food (Bajracharya, 1995).

In Nepal, it contributes third after rice and maize. In winter it is major cereal crops grown. More than 80% of wheat is grown in rice-wheat cropping pattern. It occupies 20.4 % of total cereal area and contributes 18.8% of the total cereal production in the country. Wheat production and productivity in Nepal is 2005665 mt and 2.85 t/ha respectively (MoALD, 2019/2020). Wheat grows well in temperature 15-18°C during grain filling period. Due to heavy uses of chemical in food production, large amount of fossil fuel uses in factory results in emission of greenhouse gases which has effect in increase in temperature and have changed the precipitation pattern resulting the incidence of drought and flood globally (Wassmann, 2008). This result is shifting of cropping pattern. Food production and its productivity have decreased annually.

The drought problem in Nepal is increasing in crop growing season resulting to failure of crop. Within average of 0.006°C/year, a rise in temperature from 1975 to 2006 by 1.8°C has been recorded in the country (Regmi, 2007). Climate change has several effects like landslides, drought, serve floods, in agricultural crop production in Nepal. Now a day's world is facing a serious and most important problem i.e., scarcity of food grains. Production of wheat is dependent upon many factors like biotic and abiotic. At present farmer are growing improved varieties of wheat mostly under irrigated conditions but much area in hill and terai are grown under rainfed conditions of Nepal.

Demand for wheat in the developing world is projected to increase by 60% by 2050 (Rosegrant and Agcaoili, 2010). At the same time, climate change induced temperature increases are estimated to reduce wheat production in the developing countries by 20-30 % (Rosegrant and Agcaoili, 2010). Wheat production will suffer the effects of stagnating or decreasing on farm productivity, reduced irrigation water, declining soil productivity, threats of emerging diseases and insect pest. In the absence of unprecended, coordinated measures to raise wheat productivity, consumers will pay more than twice today's prices for their staple food by 2050 (Rosegrant and Agcaoili, 2010).

With the increase in global warming erratic rain fall is seen more than 65% of the rain fall occur in rainy season. Rest of the period has less rainfall occurs in other season but in winter it is more drought. To cope this problem research should focus to increase the better adaptive varieties in these environments so we can increase the productivity of wheat. The identification of strategies to increase plant productivity under unfavorable environmental conditions is a big challenge for plant physiologists, biochemists, plant breeder and geneticians. As water scarcity poses a major threat to food production, especially in the developing countries, 'more crops per drop' is needed.

The present scenario of the grain scarcity, increasing trend of population growth and increasing climate change is forcing to intensify the grain production. This intensification can only be reached by the search of the cultivars those can be grown in non-conventional areas by the improvement in them, the ability to withstand the abiotic production hazards. Drought, being the major abiotic production hazard in our country and probably in the world, the study is outmost necessary.

World food production is limited primarily by environmental stresses. It is very difficult to find 'stress free' areas where crops may approach their potential yield. Abiotic environmental factors are considered to be the main source of yield reductions (Boyer, 1982). Drought is one of the most common environmental stresses that affects growth and development of plants through alterations in metabolism and gene expression. It is a permanent constraint to agricultural production in many developing countries. In Nepal, more than 80 % wheat area is under rice-wheat cropping system. Due to cultivation of long duration rice varieties, wheat sowing is delayed after rice harvesting. Late sown wheat is always exposed to high temperature stress and drought during flowering and grain filling stages, which force crop to precocious ripening and decrease grain yield (Giri, 1998). It is proven that wheat growing after second week of November decline grain yield @ 40 kg/day/ha in Nepal (Hobbs *et al.,* 1996). Abiotic stresses are the primary source of yield losses. It is estimated that only 10% of the world's arable area is not subjected to the abiotic stress. Drought is the main abiotic factor as it affects 26% of the arable area (Singh, 2005).

Improvement of productivity of wheat cultivars under drought conditions is one of the important breeding objectives in wheat. Mechanism of drought tolerance are drought escape, dehydration avoidance and dehydration tolerance. Hence, study of varietal response on drought condition is much needed for understanding and improvement of varieties on this stress. Hence, keeping this thing in consideration, this study was conducted to assess morpho-physiological, yield and yield attributing traits related to post-anthesis drought in wheat genotypes under rainfed conditions.

Materials and Methods

Site Description

The field experiment was conducted at the research farm of Agriculture and Forestry University, Faculty of Agriculture, Rampur, Chitwan, Nepal from October 2016 to June 2017.The location of the research site was 27°64"-N latitude and 84°34"-E longitude and at an altitude of 228 meters above the sea level.

Plant Material

The plant material for the research study was taken from the Agriculture Botany Division NARC, Khumaltar, Nepal. Twenty wheat genotypes were tested in this research.

Experimental Layout

The experiment was carried out using rainfed condition in randomized completely block design with three replications. All genotypes were randomized. The plot size was 1.5 m x 1.0 m.

Land Preparation, Sowing and Inter Cultural Operations

After final land preparation, the seeds were sown giving 25 cm row to row spacing. The chemical fertilizers were applied at the rate of 100:60:40 N-P-K/ha respectively. Manure was applied at the rate of five ton/ha. All manure, P, K and half dose of N was applied at the time of final land preparation. The remaining half dose of N was applied at the time of booting stage. Two hoeing were done 30 and 60 days after sowing.

Data to be Taken

Data of the morpho-physiological traits, yield and yield attributing traits were recorded. They were number of tillers per m^2 area (NT), plant height (PH), spike length (SL), number of grains per spike (NGS), weight of grains per spike (WGPS), grain yield (GY), 1000 kernels weight (TKW), biomass yield (BY), harvest index (HI), days to booting (DB) , days to heading (DH), days to anthesis (DA), days to flag leaf senescence (DFLS), days to maturity (DM), SPAD meter reading, canopy temperature depression (CTD), peduncle length (PL), grain filling duration (GFD) and reproductive growth period (RGP).

Ten randomly selected plants per genotype per replication was used for each trait except - days to booting, days to heading, days to anthesis, days to flag leaf senescence, grain filling duration, reproductive growth period, 1000 kernels weight, canopy temperature depression, number of tillers per m^2 and days to maturity.

Harvesting and Threshing

Each plot was harvested separately, threshed, well dried and stored properly.

Statistical Analysis

Statistical analysis was carried out with the help of MS – Excel 2013. Analysis of Variance and comparison of means was done by GenStat software packages. Cluster analysis and principal component analysis was done with the help of Minitab.

Results and Discussions

Mean values of morpho-physiological, yield and yield attributing traits of 20 wheat genotypes is presented in Table 1. An LSD test at 5% level of significance was performed among genotypes to evaluate the performance of number of tillers per m^2 area, plant height, spike length, number of grains per spike, weight of grains per spike, grain yield, 1000 kernels weight, biomass yield, harvest index, days to booting , days to heading, days to anthesis, days to flag leaf senescence, days to maturity, SPAD meter reading, canopy temperature depression, peduncle length, grain filling duration and reproductive growth period. Non-significant result was found for canopy temperature depression. Likewise, significant result was found for harvest index, grain yield and biomass yield. Except these traits, highly significant results were found for all traits among tested genotypes that indicated the presence of genotypic differences suggesting the importance of their genetic value in order to identify the best genetic makeup for a particular condition (Table 1).

A. Yield and Yield Attributing Traits

1. Grain yield (GY), Biomass yield (BY) and harvest index (HI)

A significant variation was found for grain yield among the genotypes (Table 1). The mean grain yield was found 2204 kg/ha and varied from 3035 kg/ha (WK 2373) to 1307 kg/ha (WK 2382) (Table 1). ANOVA showed significant genotypic differences among genotypes indicating substantial variation existed for grain yield. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5% level of significance, genotypes were categorized in four groups. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 2373 was found superior to and WK 2382 was found inferior to check. Rest all genotypes were found similar to check.

Highly significant positive correlation of grain yield was observed with BY (r=0.81) and HI (r=0.5). Similarly, significant positive correlation was observed with TKW (r=0.27), WGPS (r=0.31), GFD (r=0.27) and RGP (r=0.31) (Table 2). This suggests that with increase in the value of these traits increases grain yield significantly. This finding was found similar to the previous findings obtained by Ojha, 2010; Ojha, 2011; Ojha, 2012; Sharma, 1992; Sharma, 1993; Sharma, 1994; Neupane, 2009; Al-Otayk, 2010, who found that grain yield was positively correlated with biomass yield and harvest index. Likewise, significant negative correlation of grain yield was found with DB (r= -32), DH (r= -26), DA (r=-27) and PH (r= -28) (Table 2). This suggests that with increase in the value of these traits decreases grain yield. It means DB, DH, DA and PH cannot be increased only by increasing grain yield. This finding supported to the previous findings obtained by Ojha and Ojha, 2012, who found that grain yield and these traits were negatively correlated. This suggests that higher grain yield can be obtained by growing early booting, heading and flowering genotypes.

Similarly, a significant variation was found for biomass yield among the genotypes (Table 1). The mean biomass yield was found 6450 kg/ha and varied from 8080 kg/ha (WK 2373) to 3340 kg/ha (WK 2382) (Table 1). ANOVA showed significant genotypic differences among genotypes indicating an array of variation existed for biomass yield. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5% level of significance, genotypes were categorized in four groups. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 2373 was found superior to and WK 2382 was found inferior to check. Rest all genotypes were found similar to check.

Highly significant positive correlation of biomass yield was observed with GY (r = 0.81), GFD (r = 0.34), TKW (r = 0.42) and RGP (r = 0.39). Similarly, significant positive correlation was observed with WGPS (r = 0.29) and NT (r = 0.27) (Table 2). This suggests that with increase in the value of these traits increases biomass yield significantly. This finding did agree with the previous findings obtained by Ojha, 2010; Ojha 2011; Ojha 2012; Sharma, 1993; Neupane, 2009; Al-Otayk, 2010, who found that biomass yield and these traits were positively correlated. Likewise, highly significant negative correlation of biomass yield was found with DB (r = - 42), DH (r = - 38) and DA (r = - 41) (Table 2). This means with increase in the value of these traits decreases biomass yield. This suggests that higher biomass yield can be obtained by growing early booting, heading and flowering genotypes. This finding supported to the previous findings obtained by Ojha and Ojha, 2012 who found that biomass yield and these traits were negatively correlated.

Likewise, a significant variation was found for harvest index among the genotypes (Table 1). The mean harvest index was found 0.34 and varied from 0.4 (WK 2379) to 0.27 (WK 2369) (Table 1). ANOVA showed significant genotypic differences among genotypes indicating variability existed for harvest index. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5 % level of significance, genotypes were categorized in six groups. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 2379 was found superior to check and none genotypes were found either similar to or inferior to check.

Highly significant positive correlation of harvest index was observed with GY (r=0.50) (Table 2). This suggests that with increase in the value of grain yield increases harvest index significantly. This finding did not differ from the previous findings who found that harvest index and grain yield was positively correlated (Ojha, 2010; Ojha, 2011; Ojha, 2012; Sharma, 1992; Sharma, 1993; Sharma, 1994; Neupane, 2009; Al-Otayk, 2010). Likewise, highly significant negative correlation of harvest index was found with PH (r= - 46) and PL (r= - 36) (Table 2). This suggests that with increase in the value of these traits decreases harvest index. It means by growing dwarf cultivars, harvest index can be increased because of distribution of photosynthetates in the storage organs.

2. Number of grains/spike (NGS), number of tillers/m^2(NT), 1000 kernels weight (TKW)and weight of grains/spike (WGPS)

A highly significant variation was found for number of grains/spike, number of tillers/m^2, 1000 kernels weight and weight of grains/spike among the genotypes (Table 1). The mean Number of grains/spike, number of tillers/m^2, 1000 kernels weight and weight of grains/spike were found 40, 243, 37 g and 1.51 g respectively. number of grains/spike ranged from 54 (WK 2380) to 31 (WK 2369, WK 2363), Number of tillers/m^2 ranged from 303 (WK 2374) to 200 (WK 1481) and 1000 kernels weight ranged from 45.2 g (WK 2386) to 23.4 g (WK 2382). Weight of grains/spike ranged from 2.26 g (WK 2380) to 0.85 g (WK 2382) (Table 1).

ANOVA showed highly significant genotypic variation among genotypes indicating substantial variability existed for these traits. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5 % level of significance, genotypes were categorized in seven groups for numbers of grains/spike. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. No genotypes were found superior to check, and WK 2363, WK 2369 and WK 2385 were found inferior to check. Rest all genotypes were found similar to check. Similarly, genotypes were categorized in seven groups for number of tillers/m^2. WK 2374 and WK 2378 were found superior to check but none genotypes were found inferior. Likewise, genotypes were categorized in nine groups for 1000 kernels weight. WK 2382 was found inferior to check and except WK 2356, WK 2378 and WK 2408, rest all genotypes were found superior to check. Similarly, genotypes were grouped in five groups for weight of grains/spike. None genotypes were found superior and similar to check but WK 2408 and WK 2382 were found inferior to check.

Highly significant positive correlation of numbers of grains/spike were observed with WGPS (r = 0.81) GFD (r=0.36) and RGP (0.36) (Table 2). This suggests that with increase in the value of these traits increases numbers of grains/spike significantly. It means longer GFD and RGP help in increasing NGS and finally results in better WGPS production. Similarly, significant positive correlation of number of tillers/m^2 was observed with BY (r = 0.27) and negative correlation was observed with number of grains/spike and 1000 kernels weight (Table 2). Likewise, highly significant positive correlation of 1000 kernels weight were observed with WGPS (r = 0.38), GY(r = 0.27), BY(r = 0.42), GFD (r = 0.37) and RGP (r = 0.38) indicating improving such characters ultimately improves the value of 1000 kernels weight (Table 2). Highly significant negative correlation of 1000 kernels weight was found with DB (r= - 67), DH (r = - 64), DA (r = - 59), DFLS (r = - 48) and DM (r = - 55) (Table 2). Likewise, negative correlation was observed with number of grains/spike. This suggest that by growing early booting, heading, flowering, flag leaf senescencing and maturing genotypes higher 1000 kernels weight can be achieved. Those genotypes which flower and mature lately and because of lower GFD, TKW is to be found decreased.

Highly significant positive correlation of weight of grains/spike were observed with NGS (r = 0.81), TKW (r = 0.38), GFD (r = 0.44) and RGP (r = 0.48) (Table 2). This suggests that with increase in the value of these traits increases weight of grains/spike significantly. Similarly, significant positive correlation of weight of grains/spike was observed with BY (r=0.29) and GY (r = 0.31). It indicates that higher weight of grains/spike gives higher BY and GY. Highly significant negative correlation was found with DB (r = -0.41), DH (r = -0.34) and DA (r= -0.43). This suggest that by growing early booting, heading and flowering genotypes weight of grains/spike can be maximized. This finding was found in favour of the previous findings who found that numbers of grains/spike was positively correlated with grain filling duration and grain yield (Ojha, 2012; Baral, 2011; Thapa *et al.*, 2009; Rosyara, 2005; Pirayvatlou, 2001) and with WGPS (Pant, 2011; Baral, 2011). This suggest that by growing genotypes having longer grain filling duration higher numbers of grains/spike can be achieved that ultimately helps in increasing grain yield. Likewise, this finding supported to the previous findings obtained by Ojha, 2011; Ojha and Ojha, 2012; Pant, 2011, who found that 1000 kernels weight was negatively correlated with DH, DA, DFLS and DM. This finding did not support to the previous findings obtained by Ojha, 2011who found that TKW and NGS was positively correlated. Similarly, this finding was found similar to the previous findings who found that number of tillers/m^2 and BY was positively correlated (Ojha, 2010; Ojha 2012; Sharma, 1993; Neupane, 2009; Thapa *et al.*, 2009), and with TWK and NGS negatively correlated (Ojha, 2012). But this finding differed from the previous findings who found that NT and TKW (Sharma, 1993; Thapa *et al.*, 2009) and NT and NGS (Pant, 2011) were positively correlated.

B. Morpho-physiological traits

1. Spike length (SL), peduncle length (PL) and plant height (PH)

A highly significant variation was found for spike length, peduncle length and plant height among the genotypes (Table 1). The mean spike length, peduncle length and plant height were found 9.6 cm, 38.8 cm and 86.9 cm respectively and varied from 12.7 cm (WK 2382) to 8 cm (WK 2363), 52.5 cm (WK 2378) to 29.9 cm (30 ESWYT 104) and 112 cm (WK 1481) to 68.5 cm (WK 2379) respectively (Table 1).

ANOVA showed highly significant genotypic differences among genotypes indicating an array of variation existed for spike length, peduncle length and plant height. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5 % level of significance, genotypes were categorized in eight, ten and seven groups for spike length, peduncle length and plant height respectively. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 2374, WK 2378 and WK 2373 were found superior to and WK 2363 and WK 2356 were found inferior to check for spike length. Rest all genotypes were found similar to check for spike length. Similarly, except WK 2386, WK 2380, WK 2408 and WK 2374, all WK lines were found superior to check for peduncle length. All ESWYT lines and WK 2386, WK 2380, WK 2408 and WK 2374 were found similar to check for peduncle length. Likewise, WK 1481, WK 2378, WK 2369, WK 2388, WK 2356, WK 2382 and WK 2383 were found superior to check and WK 2379 was found inferior to check for plant height. Rest all genotypes were found similar to check for this trait.

Highly significant positive correlation of spike length was observed with DB (r=0.34), DH (r = 0.38), DA (r = 0.34), DFLS (r = 0.48), DM (r = 0.41) and SPAD (r = 0.34) (Table 2). This suggests that with increase in the value of these traits increases spike length significantly. Likewise, significant negative correlation of spike length was found with BY (r= - 27) (Table 2). This suggests that with lowering the value of BY increases spike length and it can help in increasing sink capacity of the plant by increasing NGS. Highly significant positive correlation of PH was observed with PL (r = 0.55). Significant positive correlation was found with spike length (r = 0.27). This suggests that with increase in the value of these traits increases plant height significantly. This finding was found in favour of the previous findings where plant height was positively associated with peduncle length and spike length (Khadka, 2007; Baral, 2011). Likewise, significant negative correlation of plant height was found with GY (r = - 28) and highly significant negative correlation was observed with HI (r = -0.46) (Table 2). This suggests that growing dwarf cultivars harvest index and grain yield can be maximized. Because if the height of the plant is lowered, the assimilates can be accumulated to the sink. Similarly, highly significant positive correlation of peduncle length was observed with GFD (r = 0.38) and PH (r = 0.55) but highly significant negative correlation was found with DA (r = -0.38), DH(r = -0.38), DB (r = -0.34), HI (r = -0.36), and DM (r = -0.33) (Table 2). This suggests that with increasing the value of GFD and PH increases PL. And, with decreasing the value of DA, DH, DM, DB and HI increases PL This finding supported to the previous findings obtained by Khadka, 2007, who found that peduncle length was negatively correlated with DB, DH and DM.

2. SPAD and canopy temperature depression (CTD)

A highly significant variation was found for SPAD among the genotypes (Table 1). The mean SPAD was found 34.1 and varied from 39.1 (30 ESWYT 123) to 26 (WK 2363). But a non-significant variation was found for CTD. The mean CTD was found 5.08 ^{O}C and varied from 5.89 ^{O}C (WK 2374 to 3.84 ^{O}C (WK 1481) (Table 1).

ANOVA showed highly significant genotypic differences among genotypes indicating substantial variability existed for SPAD. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5 % level of significance, genotypes were categorized in six groups for SPAD. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. 30 ESWYT 123 and WK 2380 were found superior to check for SPAD. Rest all genotypes were found similar to check for this trait.

Highly significant positive correlation of SPAD was observed with DB (r = 0.42), DH (r = 0.51), DA (r = 0.40), DFLS (r = 0.63), DM (r = 0.58) and SL (r = 0.34). Similarly, positive correlation of SPAD with NGS, GY, HI and GFD were observed (Table 2). This suggests that with increase in the value of these traits increases SPAD value significantly. It means photosynthesis rate is increased and ultimately helps in higher grain production. Chlorophyll depression during GFD is harmful for production. If chlorophyll depression occurs during this period, plant breeders have to think alternative ways to compensate yield by other biological processes (Reynolds et al 1994, Reynolds et al 1998). This finding did not differ from the previous findings who found that SPAD reading with GY, GFD, DA, DH, DM and DFLS were positively correlated (Rosyara *et al.*, 2006; Khadka, 2007; Baral, 2011; Pant, 2011; Ojha and Ojha, 2012).

3. Grain filling duration (GFD) and reproductive growth period (RGP)

A highly significant variation was found for GFD and RGP among the genotypes (Table 1). The mean GFD and RGP were found 28 and 32 days respectively. The GFD and RGP ranged from 33 days (WK 1481, WK 2380) to 23 days (WK 2382) and 37 days (WK 2380) to 25 days (WK 2382) respectively) (Table 1).

ANOVA showed highly significant genotypic differences among genotypes indicating substantial variation existed for GFD and RGP. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds. On the basis of LSD test at 5 % level of significance, genotypes were categorized in five and six groups for GFD and RGP respectively. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 1481, WK 2380, WK 2383, WK 2388 and WK 1204 were found superior to check for GFD. Rest all genotypes were found similar to check for this trait. Similarly, WK 2380, WK 1481 and WK 2383 were found superior to check for RGP and WK 2382 was found inferior to check for this trait.

Highly significant positive correlation of GFD was observed with RGP (r = 0.87), WGPS (r = 0.44), TKW (r = 0.37), NGS (r = 0.36), BY (r = 0.34) and PL (r = 0.38). Similarly, significant positive correlation was observed with GY (r=0.27) (Table 2). This suggests that with increase in GFD the value of these traits increases significantly. This finding was found in agreement with the previous findings that GFD was positively correlated with GY, RGP, NGS, TKW, BY (Sharma, 1992; Sharma, 1994; Adhikari, 2007; Ojha, 2009; Ojha, 2012; Neupane, 2009; Baral, 2011). On the other hand, highly significant negative correlation of GFD was found with DB (r= - 43), DH (r= - 42) and DA (r= - 60) (Table 2). This suggests that by growing early booting, heading and flowering genotypes higher GFD can be achieved. This finding was found in favour of the previous findings who found that GFD was negatively correlated with DB, DH and DA (Ojha, 2011; Ojha, 2012; Neupane, 2009; Baral, 2011).

Likewise, highly significant positive correlation of RGP was observed with GFD (r = 0.87), WGPS (r = 0.48), TKW (r = 0.38), NGS (r = 0.36) and BY (r = 0.39). Similarly, significant positive correlation was observed with GY (r = 0.31) and PL (r = 0.26) (Table 2). This suggests that with increase in RGP the value of these traits increases significantly. This finding supported to the previous findings obtained by Sharma, 1992; Sharma, 1994; Adhikari, 2007; Ojha, 2009; Ojha, 2012; Neupane, 2009; Baral, 2011, who found that RGP was positively correlated with GFD, TKW and GY. On the other hand, highly significant negative correlation of RGP was found with DB (r= - 52), DH (r= - 50) and DA (r= - 71) (Table 2). This suggests that by growing early booting, heading and flowering genotypes higher RGP can be achieved. This finding was found similar to the previous findings who found that RGP with DA and DH were negatively correlated (Sharma, 1992; Sharma, 1994; Adhikari, 2007).

4. Days to booting (DB), days to heading (DH), days to anthesis (DA), days to flag leaf senescence (DFLS) and days to maturity (DM)

A highly significant variation was found for DB, DH, DA, DFLS and DM among the genotypes (Table 1). The mean days to DB, DH, DA, DFLS and DM were found 77, 83, 89, 117 and 121 days respectively. The mean days to DB, DH, DA, DFLS and DM varied from 101 days (WK 2382) to 66 days (WK 2379), 106 days (WK 2382) to 72 days (WK 2379), 110 days (WK 2382) to 83 days (WK 2363, WK 2379), 132 days (WK 2382) to 108 days (WK 2379) and 135 days (WK 2382) to 113 days (WK 2379) respectively) (Table 1).

ANOVA showed highly significant genotypic differences among genotypes indicating substantial variation existed for all these traits. This result indicates that variations among genotypes might partially reflect their different genetic backgrounds for these traits. On the basis of LSD test at 5 % level of significance, genotypes were categorized in seven, nine, five, six and seven groups for DB, DH, DA, DFLS and DM respectively. Genotypes falling under each respective group indicate no genotypic variation among genotypes of each respective group. WK 2382 was found superior to check indicating a late genotype for all these traits. WK 2379 was found earliest genotype for all these traits except DA. WK 2379, WK 2388 and WK 2363 were found similar for DB, DH and DM. WK 2388, WK 2379, WK 2363, WK 2383, WK 1481 and WK 2380 were found inferior to check for DA and earlier flowering genotypes. WK 2382 and WK 2374 were found similar for days to maturity and later maturing genotypes. WK 2379, WK 2363, WK 2388, WK 2383 and WK 1481 were found inferior to check for DM and earlier maturing genotypes.

Highly significant positive correlation of DB was observed with DH (r = 0.97), DA (r = 0.93), DM (r = 0.91), DFLS (r = 0.85), SPAD (r = 0.47) and SL (r =0.34) (Table 2). This suggests that with increase in DB the value of these traits increases significantly. This finding was found similar to the previous findings who found that DB was positively correlated with DH, DA and DM (Ojha, 2012; Pokharel, 2011; Pant, 2011). On the other hand, highly significant negative correlation of DB was found with TKW (r = - 67), RGP (r = - 52), GFD (r = -0.43), BY (r = -0.42), WGPS (r = -0.41) and PL (r = - 34). And, significant negative correlation of DB was found with GY (r = -0.32) (Table 2) indicating early booting genotypes have higher GFD and RGP. Such genotypes can give higher yield because of longer grain filling duration. This suggests that by growing late booting genotypes decreases the value of these traits. This finding did not differ from the previous findings obtained by Pant, 2011, who found that DB was negatively correlated with GY and TKW.

Similarly, highly significant positive correlation of DH was observed with DB (r = 0.97), DA (r = 0.94), DM (r = 0.93), DFLS (r = 0.87), SPAD (r = 0.51) and SL (r = 0.38) (Table 2). This suggests that with increase in DH the value of these traits increases significantly. It indicates that late heading genotypes mature lately. This finding was found in favour of the previous findings that DH was positively correlated with DA and DM (Khadka, 2007; Pokharel, 2011; Baral, 2011; Ojha and Ojha, 2012; Ojha, 2012; Ojha, 2011). On the other hand, highly significant negative correlation of DH was found with TKW (r = - 64), RGP (r = - 50), GFD (r = -0.42), BY (r = -0.38), WGPS (r = -0.34) and PL (r = - 38). And, significant negative correlation of DH was found with GY (r= -0.26) (Table 2). This suggests that by growing late heading genotypes decreases the value of these traits. And it indicates that yield can be maximized by growing early heading genotypes. This finding was found similar to the previous findings that DH was negatively correlated with GY and TKW (Adhikari, 2007; Ojha, 2011; Pant, 2011).

Likewise, highly significant positive correlation of DA was observed with DB (r = 0.93), DH (r = 0.94), DM (r = 0.88), DFLS (r = 0.83), SPAD (r = 0.63) and SL (r =0.48) (Table 2). This suggests that with increase in DA the value of these traits increases significantly. It means those genotypes which flower earlier mature earlier and vice versa. This finding supported to the previous findings that DA and DM was positively correlated (Khadka, 2007; Pokharel 2011; Baral, 2011; Ojha and Ojha, 2012; Ojha, 2012; Ojha, 2011). On the other hand, highly significant negative correlation of DA was found with TKW (r = - 59), RGP (r= - 71), GFD (r = -0.60), BY (r = -0.41), WGPS (r = -0.43) and PL (r = - 38). And, significant negative correlation of DA was found with GY (r = -0.27) (Table 2) indicating by growing late flowering genotypes decreases the value of these traits. It suggests that by growing early flowering genotypes, RGP and GFD can be increased and better yield can be obtained. This finding was found similar to the previous findings that DA was negatively correlated with TKW and GY (Adhikari, 2007; Ojha, 2011; Ojha, 2012; Pant, 2011; Pokharel, 2011; Sharma, 1992; Sharma, 1994).

Similarly, highly significant positive correlation of DFLS was observed with DB (r = 0.85), DA (r = 0.83), DM (r = 0.94), DH (r = 0.87), SPAD (r = 0.58) and SL (r =0.41) (Table 2). This suggests that lengthening DFLS value helps in increasing the value of these traits significantly. On the other hand, highly significant negative correlation of DFLS was found with TKW (r = - 48). And, significant negative correlation of DFLS was found with BY (r = -0.27) and RGP (r = -0.27) (Table 2). Likewise, highly significant positive correlation of DM was observed with DB (r = 0.91), DA (r = 0.88), DH (r = 0.93), DFLS (r = 0.94), SPAD (r = 0.58) and SL (r = 0.41) (Table 2). This suggests that late maturing genotypes have larger value of these traits. On the other hand, highly significant negative correlation of DM was found with TKW (r = - 55), and PL (r = - 34). And, significant negative correlation of DM was found with BY (r = -0.29) and RGP (r = -0.28) (Table 2). This suggests that by growing late maturing genotypes decreases the value of these traits. This finding supported to the previous findings that DM was positively correlated with DA and DH, and negatively correlated with TKW (Khadka, 2007; Ojha, 2011, Ojha, 2012; Pant, 2011; Pokhrel, 2011; Baral, 2011).

Table 1: Mean, SEM, F-Test, LSD 0.05 and CV % of 19 characters of 20 wheat genotypes grown at Rampur, Chitwan, Nepal in 2016/2017.

S.N.	**Genotypes**	**BY (Kg/ha)**	**GY (Kg/ha)**	**HI**	**NGS**	**NT**	**TKW (g)**	**WGPS (g)**	**DB**	**DH**	**DA**	**DFLS**	**DM**	**RGP**	**PL (cm)**	**PH (cm)**	**SPAD**	**GFD**	**CTD (ºC)**	**SL (cm)**
1	30 ESWYT 104	6770	2457	0.36	45	263	37.8	1.71	78	86	92	117	121	29	30.1	85.7	34.1	25	5.27	9.9
2	30 ESWYT 123	6715	2535	0.38	36	279	34.7	1.33	82	88	92	119	123	31	29.9	86	39.1	27	5.36	8.3
3	30 ESWYT 144	6343	2385	0.38	39	225	34.9	1.21	75	81	87	116	121	34	36.1	75.1	31	29	5.12	9.1
4	Gautam (check)	6343	2073	0.33	44	232	28.6	1.7	79	87	92	117	121	30	33.2	80.2	32.2	25	4.87	9.6
5	WK 1204	7210	2557	0.36	43	245	38.1	1.66	75	83	88	118	122	33	39.2	75.9	35.5	30	4.54	9
6	WK 1481	6328	2018	0.32	47	200	43.7	2.17	73	80	84	117	120	36	48.7	112.2	34.6	33	3.84	9.9
7	WK 2356	6980	2330	0.33	46	231	34.1	1.62	82	86	92	119	124	32	38.4	95.2	35.6	27	5.27	7.3
8	WK 2363	6600	1978	0.31	31	237	40.5	1.38	68	73	83	109	113	31	43.3	79.1	26	26	4.99	8
9	WK 2369	5830	1532	0.27	31	248	37.1	1.26	81	87	91	119	121	30	40.8	102	35.7	28	4.98	11.3
10	WK 2373	8080	3035	0.38	38	284	40.8	1.41	73	81	89	118	122	33	41.7	79.9	32.1	29	5.24	10.1
11	WK 2374	6837	2198	0.32	37	303	37.7	1.41	84	88	93	120	125	32	31.2	83.8	36.6	27	5.89	9.1
12	WK 2378	7513	2507	0.32	49	299	32.6	1.6	80	85	90	118	121	31	52.5	103	35	28	5.69	9.8
13	WK 2379	5737	2290	0.4	44	201	37.9	1.61	66	72	83	108	113	30	38.1	68.5	27.4	25	4.87	8.5
14	WK 2380	6507	2310	0.35	54	208	39.3	2.26	73	81	85	118	121	37	34.8	80.7	38.9	33	4.96	10.4
15	WK 2382	3340	1307	0.39	37	231	23.4	0.85	101	106	110	132	135	25	36.8	94.1	38.1	23	5.12	12.7
16	WK 2383	6435	2070	0.32	42	207	40.8	1.61	71	77	84	115	119	35	47.6	93.5	33.3	31	5.16	11.4
17	WK 2385	6298	2022	0.32	30	233	40.7	1.2	78	84	91	118	122	31	38.1	80.4	34.8	27	5.17	9.6
18	WK 2386	6427	2382	0.37	40	239	45.2	1.71	74	82	90	118	121	32	36	84.2	38	29	5.28	10.1
19	WK 2388	7038	2112	0.3	35	244	40.1	1.35	68	75	82	113	116	34	46.7	98.3	29.7	31	4.78	9.5
20	WK 2408	5672	2015	0.35	33	257	31.1	1.13	81	88	91	117	124	33	32.8	81	34.6	25	5.16	9
	Mean	6450	2204	0.34	40	243	37	1.51	77	83	89	117	121	32	38.8	86.9	34.1	28	5.08	9.6
	SEM	599	266	0.02	3.97	19	1.6	0.19	0.83	0.9	1.3	1.33	0.87	1.26	1.23	2.2	2.27	1.5	0.44	0.49
	F--Test	*	*	*	**	**	**	**	**	**	**	**	**	**	**	**	**	**	ns	**
	LSD $_{0.05}$	1714	762	0.06	11	55	4.7	0.56	2	3	4	4	3	4	3.5	6.4	6.5	4	1.27	1.4
	CV %	15	16	11	16	13.6	7.7	20	2	2	2.4	2	2	7	5.5	4.5	11.5	9.6	15	8.8

* and ** indicate significant and highly significant at 0.05 and 0.01 level of significance. BY = biomass yield kg/ha, GY = grain yield kg/ha, NGS = number of grains/spike, HI = harvest index, NT = number of tillers/m^2, TKW = 1000 kernels weight, WGPS = weight grains/spike, GFD = grain filling duration, RGP = reproductive growth period, CTD = canopy temperature depression, PL = peduncle length, PH = plant height, SL = spike length, DB = days to booting, DH = days to heading, DA = days to anthesis, DFLS = days to flag leaf senescence, DM = days to maturity and SPAD = chlorophyll reading.

Table 2: Correlations coefficient matrix among 19 characters of 20 wheat genotypes grown at Rampur, Chitwan, Nepal in 2016/2017.

	SL	**NGS**	**TKW**	**WGPS**	**GY**	**BY**	**HI**	**NT**	**GFD**	**DB**	**DH**	**DA**	**DFLS**	**DM**	**SPAD**	**CTD**	**PH**	**PL**	**RGP**
SL	1	0.188	-0.141	0.091	-0.23	-0.27	0.015	0.031	0.094	0.34	0.377	0.336	0.484	0.408	0.341	-0.052	0.266	0.167	-0.073
NGS		1	-0.03	0.806	0.234	0.114	0.244	-0.057	0.36	-0.134	-0.097	-0.184	0.025	-0.008	0.206	0.013	0.063	0.112	0.355
TKW			1	0.376	0.269	0.415	-0.185	-0.178	0.365	-0.672	-0.643	-0.591	-0.478	-0.548	-0.195	-0.045	0.007	0.23	0.376
WGPS				1	0.31	0.288	0.094	-0.153	0.436	-0.413	-0.339	-0.425	-0.221	-0.248	0.117	-0.128	0.083	0.129	0.483
GY					1	0.809	0.501	0.165	0.271	-0.322	-0.263	-0.267	-0.141	-0.152	0.197	0.151	-0.283	-0.058	0.309
BY						1	-0.085	0.265	0.341	-0.418	-0.375	-0.409	-0.268	-0.293	0.083	0.14	-0.053	0.153	0.386
HI							1	-0.114	-0.059	0.098	0.131	0.187	0.19	0.211	0.219	0.092	-0.459	-0.36	-0.063
NT								1	-0.053	0.23	0.211	0.149	0.148	0.175	0.14	0.165	0.068	-0.075	-0.041
GFD									1	-0.432	-0.416	-0.595	-0.036	-0.215	0.192	-0.005	0.184	0.375	0.869
DB										1	0.967	0.926	0.847	0.908	0.465	0.169	0.239	-0.336	-0.515
DH											1	0.938	0.873	0.933	0.513	0.116	0.2	-0.382	-0.503
DA												1	0.825	0.876	0.395	0.173	0.09	-0.381	-0.709
DFLS													1	0.938	0.626	0.212	0.241	-0.21	-0.27
DM														1	0.582	0.151	0.164	-0.338	-0.282
SPAD															1	0.151	0.179	-0.244	0.066
CTD																1	-0.168	-0.194	-0.125
PH																	1	0.549	0.061
PL																		1	0.264
RGP																			1

Where, BY = biomass yield kg/ha, GY = grain yield kg/ha, NGS = number of grains/spike, HI = harvest index, NT = number of tillers/m^2, TKW = 1000 kernels weight, WGPS = weight grains/spike, GFD = grain filling duration, RGP = reproductive growth period, CTD = canopy temperature depression, PL = peduncle length, PH = plant height, SL = spike length, DB = days to booting, DH = days to heading, DA = days to anthesis, DFLS = days to flag leaf senescence, DM = days to maturity and SPAD = chlorophyll reading.

C. Multivariate Analysis

This technique is helpful to describe phenotypic variation among the genotypes. Cluster analysis and principal component analysis (PCA) were used in this study. Twenty wheat genotypes were used for this study and are presented in the following Fig. 1 and Fig. 2.

1. Cluster analysis

In this technique genotypes were splitted into various groups on the basis of their performances which are displayed in a dendogram. The dendogram for wheat based on the morpho-physiological and yield and yield attributing traits of 20 different genotypes was constructed and presented in Figure 1. Based on the similarity percentage and related characters five clusters were constructed.

In cluster 1, thirteen genotypes are grouped, which represent 65 % of the total genotypes. It has been observed that high value of traits like thousand seeds weight, number of grains/spike, weight of grains/spike, reproductive growth period, grain filling duration are associated with the genotypes found in this cluster.

In cluster 2, two genotypes are grouped, which represent 10 % of the total genotypes. It has been observed that high value of trait like peduncle length is associated with the genotypes found in this cluster.

In cluster 3, three genotypes are grouped, which represent 15 % of the total genotypes. It has been observed that high value of trait like harvest index and low value of traits like plant height, days to booting, days to heading and days to maturity are associated with the genotypes found in this cluster.

Likewise, in cluster 4, one genotype is grouped, which represents 5 % of the total genotypes. It has been observed that high value of traits like biomass yield and grain yield are associated with the genotype found in this cluster.

Similarly, in cluster 5, one genotype is grouped, which represents 5 % of the total genotypes. It has been observed that high value of traits like spike length, days to booting, days to heading, days to anthesis, days to flag leaf senescence and days to maturity are associated with the genotype found in this cluster.

Clustering these genotypes can be useful in identify accessions with similar traits, which can be useful in breeding programs. It is important that genotypes belonged to respective cluster could be used in crop improvement program for respective character. Crossing genotypes belonging to different clusters could maximize the opportunities for transgressive segregation as there is a higher probability that unrelated genotypes would contribute unique desirable alleles at different loci (Beer *et al.*, 1993).

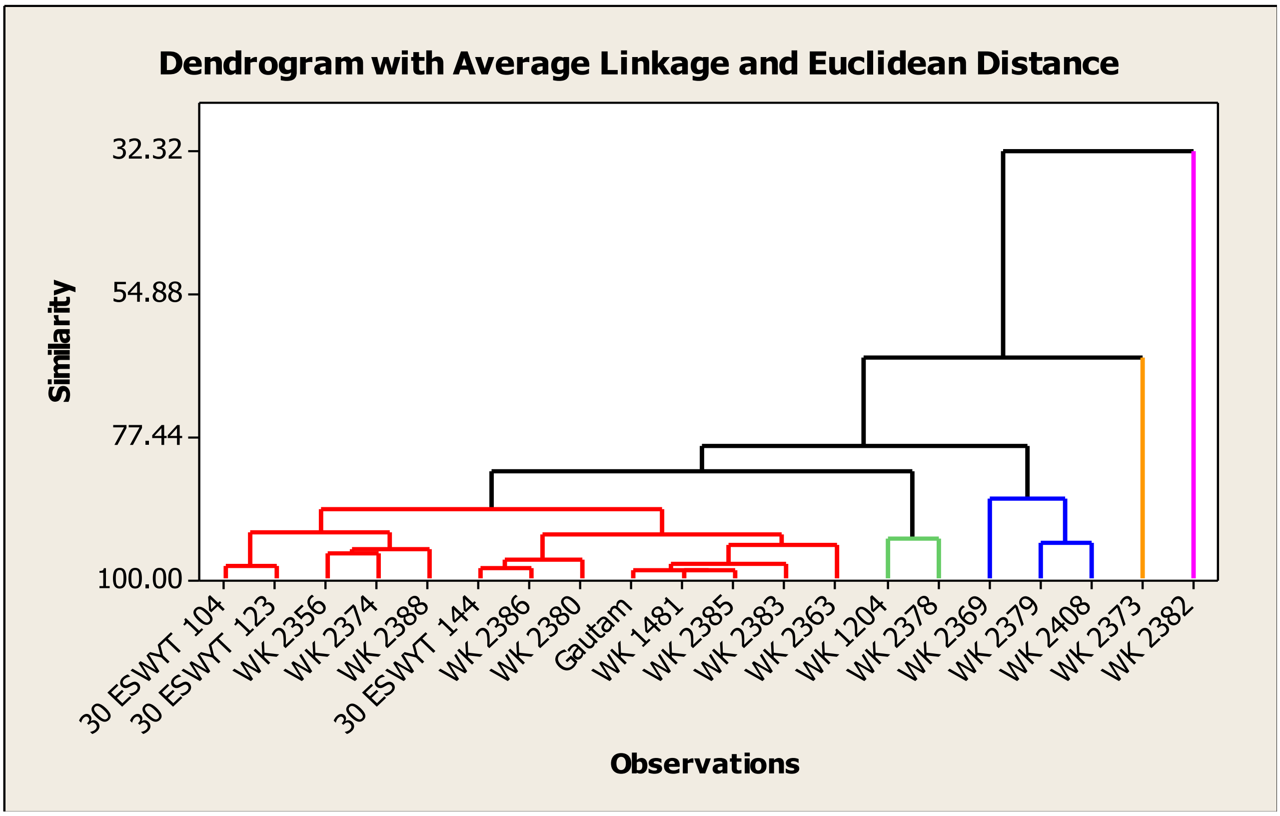

Fig. 1: UPGMA (unweighted pair group method arithmetic average) clustering of 20 wheat genotypes grown at Rampur, Chitwan, Nepal in 2016/2017.

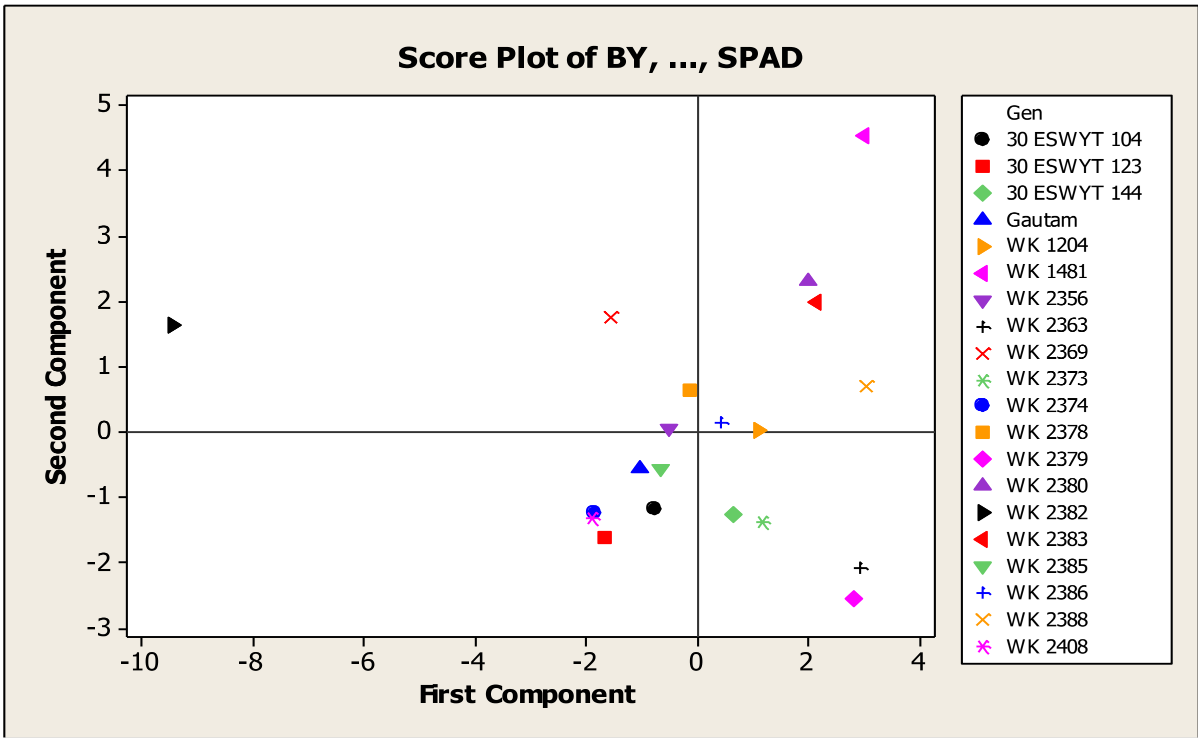

Fig. 2: Principal component analysis of first two components of 20 wheat genotypes grown at Rampur, Chitwan, Nepal in 2016/2017.

Table 3: The Eigen analysis of the correlation matrix of 20 wheat genotypes grown at Rampur, Chitwan, Nepal in 2016/2017.

Variable	PC1	PC2	PC3	PC4	PC5
Eigenvalue	7.916	3.098	2.560	1.961	0.977
Proportion	0.417	0.163	0.135	0.103	0.051
Cumulative	0.417	0.580	0.714	0.818	0.869
Eigen vector					
BY	0.234	-0.113	0.333	-0.300	-0.087
GY	0.170	-0.221	0.449	-0.006	-0.072
HI	-0.080	-0.219	0.198	0.480	0.019
NGS	0.087	0.208	0.343	0.310	-0.528
NT	-0.102	-0.224	0.286	-0.483	-0.063
SL	-0.155	0.332	-0.085	0.015	0.163
TKW	0.272	0.071	0.056	-0.089	0.428
WGPS	0.213	0.239	0.262	0.228	-0.209
GFD	0.226	0.346	0.182	-0.045	0.276
CTD	-0.133	-0.281	0.223	-0.300	-0.008
DB	-0.344	0.072	0.072	-0.050	-0.061
DH	-0.343	0.087	0.102	-0.002	-0.021
DA	-0.349	0.010	0.051	0.019	-0.049
DFLS	-0.308	0.205	0.172	-0.012	0.095
DM	-0.317	0.127	0.184	0.021	0.107
RGP	0.259	0.193	0.188	0.012	0.295
PL	0.150	0.278	-0.166	-0.280	-0.344
PH	-0.035	0.431	-0.038	-0.340	-0.256
SPAD	-0.189	0.233	0.376	0.002	0.276

2. Principal Component Analysis (PCA)

The PCA in general confirmed the groupings obtained through cluster analysis. Results of PCA are given in Table 3 and Figure 2 Variation among 20 wheat genotypes was studied by PCA. The first five principal components with ≥ 1 eigen value accounted for 86.9 % of the total variance. The contribution by the first two principal components is

58%. Individually, PC 1, PC 2, PC 3, PC 4 and PC 5 contributed 41.7, 16.3, 13.5, 10.3 and 5.1 % of total variation respectively. The traits, which contributed more positively to PC 1 are BY, TKW, WGPS, GFD and RGP. This reveals that population with high PC 1 values have higher biomass yield, thousand grains weight, weight of grains/spike, grain filling duration and reproductive growth period. The traits, which contributed more negatively to PC 1 are days to booting, days to heading, days to anthesis, days to flag leaf senescence and days to maturity. This reveals that population with negative PC 1 values have lower values of the respective traits. The traits, which contributed more positively to PC 2 are PH, NGS, SL, WGPS, GFD and DFLS. This reveals that population with high PC 2 values have higher numbers of grains/spike, spike length, weight of grains/spike, grain filling duration, days to flag leaf senescence and higher plant height. The traits, which contributed more negatively to PC 2 are CTD, NT, GY and HI. This reveals that population with negative PC 2 values have lower values of the respective traits.

The traits, which contributed more positively to PC 3 are GY, BY, NGS and NT. This reveals that population with high PC 3 values have higher grain yield, biomass yield, number of tillers/m^2 and numbers of grains/spike. The traits, which contributed more positively to PC 4 are HI, NGS and WGPS. The traits, which contributed more positively to PC 5 are TKW and GFD. Categorizing wheat genotypes into morphological similar and presumably genetically similar groups in this study might be useful for selecting parents for crossing. The PCA also supported the findings from cluster analysis. This study can help breeders to increase genetic diversity by selecting materials of divergent parentage for crosses, thereby reducing vulnerability to diseases and climate changes.

Conclusions

Recent trends of a decline in the yield of wheat of the world have raised serious concerns about the food security. The effect of future climate change on crop production adds to the complex problem.

In Nepal, more than 80 % wheat area is under rice-wheat cropping system. Due to cultivation of long duration rice varieties, wheat sowing is delayed after rice harvesting. Late sown wheat is always exposed to high temperature stress and drought during flowering and grain filling stages, which force crop to precocious ripening and decrease grain yield. Abiotic stresses are the primary source of yield losses. It is estimated that only 10% of the world’s arable area is not subjected to the abiotic stress. Drought is the main abiotic factor as it affects 26% of the arable area. The research of the study suggests that suitable replacements of Gautam and WK 1204, which are the popular cultivars in farmers’ field, are available. Considering, yield and yield attributing traits like biomass and grain yield, harvest index, number of grains/spike and weight of grains/spike, 1000 kernels weight, and number of tillers/m^2; WK 2373, WK 2379, WK 2380, WK 2386 and WK 2374 genotypes bear potential for replacing Gautam and WK 1204 respectively. Reproductive growth period and grain filling duration are the main traits at the time of sink development and assimilates accumulation. WK 2380, WK 1481, WK 2383 and WK 2388 bear potential for replacing Gautam and WK 1204. With regards to maturity traits like days to booting, heading, flowering and maturity; earlier genotypes like WK 2379, WK 2388, WK 2363 and WK 2383 can replace Gautam and WK 1204. Genetic diversity among genotypes represents scope for either improving or replacing Gautam and WK 1204 varieties for these traits through selective breeding.

The potential genotypes for valuable traits found in different clusters. Crossing genotypes belonging to different clusters could maximize the opportunities for transgressive segregation as there is a higher probability that unrelated genotypes would contribute unique desirable alleles at different loci. Therefore, this study can help breeders to increase genetic diversity by selecting materials of divergent parentage for crosses, thereby reducing vulnerability to diseases and climate changes.

Authors’ Contribution

Both authors contributed equally at every stages of research work and manuscript preparation of this publication.

Conflict of Interest

The authors declare that there are no conflicts of interest with this research.

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