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Selection of stable spring wheat (*Triticum aestivum* L.) advanced lines under contrasting environments

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Abstract

Evaluation of varietal candidate lines for their stability and economic value is an important step for their adaptation and commercialization under contrasting environments. Plant breeders generally select breeding materials that show stable performance under contrasting environmental conditions. For this purpose, an experiment was conducted to evaluate the performance of 17 advanced lines along with 3 commercial varieties at 4 different locations for 2 years from 2015-17 in Randomized Complete Block Design with 3 replications. The analysis of variance showed that there was a significant difference (P≤ 0.05) between breeding lines, locations and years. SU-52 and SU-38 were higher grain yielding advanced lines when compared with commercial varieties. SU-168 was the most stable advanced line across all locations and years as per various estimated stability parameters. SU-179 was found specifically adapted to Dera Ghazi Khan location characterized by high temperature and lower rainfall. Biplot analysis was done to select breeding lines with better agronomic and quality traits. The close relationship between the agronomic and quality traits showed that agronomic traits and quality traits were simultaneously present in the newly developed breeding lines. Breeding lines such as SU-18, SU-168, SU-12, SU-6H, PB-11 and SU-134 processed traits related to agronomic value and quality traits.

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Introduction

An increase in the global wheat yield production meeting the demands of populations dependent on wheat as a staple food is the major challenge for international research organizations. The world would require around 840 million tonnes of wheat by 2050 to feed the population increasing at an alarming pace (Sharma *et al.,* 2015). The shortage of wheat grain may destabilize regions that heavily depend on the wheat grain for daily calories, proteins, and micro-elements (Qureeshi *et al.,* 2020). Continues breeding efforts are required to develop high-yielding, better quality, heat and water stress resilience varieties under the current scenario of global climate change (Qureeshi *et al.,* 2020).

The development of high-yield potential cultivars, better adaptable to the targeted environment is one of the prime goals of wheat breeders to meet the goal of self-sufficiency in highly populated regions of the world (Tadesse *et al.,*2019). Climate change is a global phenomenon. An increasing level of greenhouse gases, temperature and irregular rainfall patterns are major indicators of climate change (Noorka and Khaliq 2007; Yue *et al.,* 2019).

Global climate change is posing challenges to the world global production regions such as South Asia including Pakistan, where high temperature, drought, erratic rainfall, hail storms and strong winds causing significant yield reduction and making elite cultivars vulnerable to climatic conditions (Sultana *et al.,* 2009; Tariq *et al.,* 2014). Food insecurity has become a major worldwide concern due to the increasing number of people who remain undernourished amounting to approximately 12% of the total world's population (Noorka and Heslop-Harrison. 2019; Zhou *et al.,* 2019). High demand for wheat grain often causes a shortage in supply and hike in prices even causing instability in the region (Rauf *et al.,* 2015). Wheat production in the south and some parts of central Asia especially are highly prone to global climatic changes where an outbreak of new diseases, high temperature and unavailability of irrigational water can shrink the production of wheat which may affect large masses of population in these areas (Shiferaw *et al.,* 2013; Ali *et al.,* 2017; Kaur *et al.,* 2017). In this regard, breeding and selection are continuously required for targeted environments challenged by global climate changes. Generally, the best performing varieties often differ across a range of environments. The basic cause of the differential performance of genotypes is the wide occurrence of genotype × environment (G × E) interaction (Oladosu *et al.,* 2017). In this scenario, it becomes a challenging task for plant breeders to develop not only high-yielding but also stable varieties. A genotype having higher adaptability and a broad genetic base had higher phenotypic buffering capacity across environments and shows less shift in its performance.

Thus, stability is the sum of variable genetic factors which increase the chances of success of cultivars for large-scale general cultivation (Jeberson *et al.,* 2017; Noorka, 2019). The performance of stable cultivar is more predictable and durable across the years and locations. Based on these grounds, a study was initiated to determine the stability of newly developed wheat advanced lines through various yields and its components at four diverse locations for two years.

Materials and methods

Plant material

An experiment was conducted on 20 wheat (*Triticum aestivum* L.) accessions consisting of 17 advanced lines along with 3 commercial check varieties (FSD-08, Pb-11, and Galaxy-13). These advanced lines were selected through pedigree methods for various traits related to yield. To appraise the stability and adaptability of the yield of wheat genotypes, a comprehensive study was carried out for two years during 2015-2016 and 2016-2017 at four locations in the Punjab province, Pakistan. Two sites i.e., 'Faisalabad' and 'Sargodha' were chosen in the irrigated regions of central Punjab, Pakistan, with high summer temperature and wheat crop may experience, intense climatic conditions during the reproductive phase such as heat stress (Fig. 1A- 1D). Location 'Chakwal' was situated in the arid region of 'Pothohar Plateau' of Punjab. The conditions are

slightly mild in the region but the crop faces water stress during critical reproductive growth stages (Fig. 2). 'Dera Ghazi Khan' is characterized by dry conditions with high heat stress during the reproductive phase (Fig. 1G, 1H).

Growth conditions

Advanced lines were sown in a randomized complete block design (RCBD) with three replications on well-prepared soil at each location. The seeds were sown with an experimental drill. Each advanced line was sown in 6 rows of 5m length, and was 30 cm apart, being plot size of 9m². Sowing was completed from the first week to the middle of November in both years. Cultural practices, fertilizers and irrigations and other crop husbandry practices were applied as per standard production practices applied in the region on the recommendations of the agriculture department for that particular area. Weeds, insects, and diseases were controlled by using standard herbicides and pesticides as required to avoid yield loss.

Data measurements

Grain yield was determined after crop maturity. Manual harvesting was carried out in 9m² (5 m ×1.8m) plots at each location. The plants were cut from the surface and dried to remove any additional moisture. Seeds were threshed from each plot. The detail of traits recorded during the study are given below.

Grain yield per plant: The grains from each ten randomly selected plants in each replication of every genotype were bulked separately. All grains of individually selected plants were threshed manually and weighed by using an electronic balance (Compax-Cx-600). Average grain yield plant⁻¹ was estimated for each genotype in each replication.

Plant height: The plant height of each of ten randomly selected plants was measured from the base of the plant to the tip of the spike excluding awns of mother shoot by using a measuring rod. The average plant height for each genotype was estimated. Peduncle

length of randomly selected plants of each genotype was measured in centimeters by using measuring tape. Peduncle length (cm): Peduncle is a region between the spike base and flag leaf. Peduncle length of randomly selected plants of each genotype was measured in centimeters by using the measuring tape and finally, the average was computed.

Number of tillers per plant: The number of tillers of selected plants of each genotype was counted at maturity in each replication and the average was computed.

Number of tillers per m²: The number of effective tillers of each genotype was counted in an area of 1 m² at the physiological maturity of the crop.

Spike length: Spike length of mother shoot of selected plants was measured in centimeters from base to the tip of spike excluding awns.

Number of spikelets per spike: Spikelets were counted from the mother spike of selected plants and were averaged.

Number of grains per spike: The spike of the mother shoot was threshed manually and a number of grains per spike were counted for each genotype.

Single spike grain mass: The spike of the mother shoot was threshed manually and weighed on electronic balance (Compax-Cx-600).

1000-Grain mass: The grains from each ten randomly selected plants in each replication of every advanced line were bulked separately. 1000 grains were counted randomly and weighed on digital balance (Compax-Cx-600).

Protein contents (%): Grain protein contents were determined using Kernelyzer (OmegAnalyzer, Bruins Instruments, Germany).

Gluten contents (%): The Perten Glutomatic (Huddinge, Sweden) was used to determine the

amount and nature of various flour gluten proteins according to International Method No. 38-12 (AACC, 2000).

Grain hardness: The SKCS apparatus (Single Kernel Characterization System) was used to determine grain hardness according to International Method No. 55-31 (AACC, 2000). SKCS measured kernel/grain hardness index in the form of values ranging from -20 to 120.

Zeleny value: Zeleny sedimentation value of each wheat variety was estimated by using NIR instrument, Inframatic 9100 (Perten Instruments AB, Sweden) following the method as adopted by Hruskova and Famera (2003).

Starch contents (%): The total starch of wheat flour samples were determined according to ACCA method 76-20 (17, 18).

Statistical analyses

The experiment was conducted in a randomized complete block design (RCBD). Traits showing significant G × E were further analyzed for G + GEI to determine stable genotypes. The stable wheat genotypes were identified according to different stability analyses proposed by Eberhart and Russel, (1966), Finlay and Wilkinson (1963), Wricke (1962) and Shukla (1972). Traits showing significant variation were subjected to the biplot analysis. The high-yielding stable genotypes were identified based on KR scores according to Kang (1988). All analyses were carried out by using statistical package R.

Results

Analyses of variance showed significance (P≤ 0.05) of breeding lines, locations and years and all their interactions. The significance of all interactions showed that breeding lines changed their relative ranking across all locations and years.

Table 1. Soil fertility status and texture of four districts of Punjab-Pakistan.

Parameters	Sargodha	Faisalabad	Chakwal	D. G. Khan
Altitude	190	186	523	129
Longitude	72.67	73.08	72.86	70.63
Latitude	32.08	31.42	32.93	30.60
Texture	Silty clay	Silt loam	Sandy loam to loam	Sandy loam
O.M (%)	0.1-1.16	0.35-1.32	0.36-0.61	0.29-0.48
pH	7-10.1	7.8-9.2	7.7-7.8	7.7-9.8
E. C (ds/m)	0.75-9.99	1.36-10.8	0.22-0.38	1.3-2.8
P (ppm)	2.6-25.2	6.2-20.4	5.9-7.1	3.5-6.9
K (ppm)	90-386	130-500	80-180	105-160

O.M = Organic matter; E.C = Electrical conductivity; P = Phosphorus, K = Potassium.

Biplot analysis for yield at various locations

Biplot analysis showed that accession SU-168 and SU-133 were in the middle of the axis and thus were considered stable and independent of environment sensitivity during the year 2015. Genotypes "SU-159" were close to Chakwal location while "SU-134" and SU-12H were adapted to "Sargodha" and "Faisalabad" respectively. SU-179 clustered close to DG khan and thus adapted to DG khan location (Fig. 3A). In 2016, "SU-52', SU-159 and SU-38 were clustered close to "Chakwal" and "Faisalabad" respectively and thus show adaptation to this location. "SU-18" had adaptation to "Sargodha". Accessions such as SU-168, PB-11 and SU-91 and SU-133 and Glaxy-13 clustered

in the middle of the axis and thus were stable genotypes for yield during the year 2016. SU-179 showed adaptation to the arid environment of DG khan for consecutive two years (Fig. 3B).

Estimation of stability of wheat (Triticum aestivum L.) accessions through various stability parameters

The advanced line "SU-52" followed by "SU-38" had the highest yield across all locations (Table 2). Various parameters were used to estimate the stability of accessions under study (Table 2). Wricke (1962) suggested the estimation of ecovalence (Wi²) as a stability parameter and noted that accessions with the lowest Wi² had the highest stability.

Table 2. Estimation of various stability parameters of various breeding lines for yield (g plant^{-1}).

Breeding lines	Averaged Yield (g Plant^{-1})		W_i^2		σ^2_i		s^2d_i		b_i		CV_i		KR	
	2015	2016	2015	2016	2015	2016	2015	2016	2015	2016	2015	2016	2015	2016
SU-91	9.05	5.99	1.27	0.33	0.21	0.06	0.08	0.03	0.63	0.65	10.19	7.96	22.00	21.00
SU-21	11.21	6.96	12.11	1.87	4.22	0.63	1.21	0.14	0.15	0.11	15.10	8.20	21.00	24.00
SU-01	11.15	7.08	6.72	1.73	2.23	0.57	0.93	0.18	0.80	0.35	16.13	9.62	19.00	20.00
SU-12	11.48	7.25	4.90	1.67	1.56	0.55	0.02	0.01	1.97	2.18	22.31	18.70	15.00	16.00
SU-179	10.03	6.53	39.41	10.73	14.34	3.91	4.95	0.90	0.02	-0.97	33.87	24.00	37.00	37.00
SU-6H	11.36	7.48	3.61	1.20	1.08	0.38	0.51	0.17	0.89	1.10	13.95	12.37	15.00	13.00
SU-66	10.41	6.99	7.72	1.86	2.60	0.62	1.10	0.26	1.06	0.83	20.24	13.36	23.00	22.00
SU-38	13.43	8.20	14.71	4.01	5.19	1.42	2.00	0.47	0.62	1.79	17.17	18.60	15.00	14.00
SU-52	13.83	8.52	25.52	7.72	9.19	2.79	2.26	0.43	2.39	3.03	27.83	24.91	19.00	20.00
SU-133	10.40	6.78	2.89	0.76	0.81	0.21	0.41	0.11	1.08	0.99	16.36	11.66	20.00	19.00
SU-159	11.95	7.79	23.92	5.78	8.60	2.08	3.17	0.39	1.58	2.64	28.50	24.21	24.00	21.00
SU-12H	12.51	7.99	20.44	5.18	7.31	1.85	2.74	0.62	1.50	1.84	25.47	20.76	19.00	18.00
SU-134	12.04	7.62	12.43	1.39	4.34	0.45	1.25	0.13	0.14	0.34	14.24	7.70	18.00	13.00
SU-100	10.98	7.12	18.25	4.96	6.50	1.77	2.48	0.67	1.42	0.49	27.55	18.02	27.00	25.00
SU-105	10.46	6.70	12.20	4.79	4.26	1.71	0.63	0.65	-0.25	0.57	11.99	19.17	25.00	29.00
SU-168	9.67	6.47	0.93	0.15	0.09	-0.01	0.11	0.02	1.19	1.11	16.69	11.06	19.00	19.00
Pb-11	9.14	5.92	8.12	2.25	2.75	0.77	1.11	0.26	0.74	0.40	20.50	13.89	28.00	31.00
SU-18	11.52	7.15	1.37	0.41	0.25	0.08	0.15	0.06	0.74	1.08	9.69	10.63	11.00	13.00
FSD-08	12.30	7.66	30.11	6.87	10.89	2.48	4.30	0.77	1.05	-0.13	28.00	17.55	23.00	24.00
Galaxy-13	12.05	7.68	18.64	5.51	6.64	1.97	1.47	0.73	2.29	1.60	28.97	21.30	20.00	21.00

W_i^2 = Wricke's ecovalence (Wricke, 1962); σ^2_i = Shukla's stability variance (Shukla, 1972); b_i = Regression coefficient (Finlay and Wilkinson, 1963); s^2d_i = Variance of deviation from regression (Eberhart and Russel, 1966); CV_i = Coefficient of variance (Francis and Kannenberg 1978); $\theta_{(i)}$ = Peterson's mean variance component (Plaisted and Peterson ,1959); θ_i = Plaisted's GE variance component (Plaisted 1960); KR = Kang scores (Kang, 1988).

According to the estimate of W_i^2, SU-168 had the lowest W_i^2 value and was considered to be the most stable genotype (Table e). Shukla (1972) suggested stability variance (σ^2_i) as a stability parameter. Breeding lines with the lowest value of σ^2_i are considered stable. The genotype SU-168 had the lowest score across both years and was thus considered stable. Regression of slope/Regression coefficient (b_i) is the response of the genotypes to environmental interaction. This famous parameter was proposed by (Finlay and Wilkinson, 1963). The accessions with a value close to unity are considered stable while accessions with a value significantly greater > 1 are sensitive to the environment and maybe adaptable to the high yielding environment while accessions with value <1 are adaptable to low yield environment and show resistance to environmental change. In addition, another parameter i.e., a variance of deviation from regression (s^2d_i) was also considered along with b_i values. Thus, genotypes with b_i value close to unity and s^2d_i value =0 were considered stable.

SU-52 was sensitive and adaptable to a high input environment, while SU-12 had the lowest s^2d_i value but a very high b_i value (Table 2), thus was also considered adaptable to a high yielding environment. SU-168 and SU-113 had a value close to unity and also had lower s^2d_i values, thus considered as stable genotypes through these values. SU-52 was high-yielding but was unstable accession. KR scores were proposed by Kang (1988). According to the scoring, accessions with high yield and lower σ^2_i were used to set scores. Accessions with lower KR scores were considered to be desirable for selections of accessions with yield and stability. SU-18 had the lowest score across both years. Moreover, SU-12 and SU-168 had similar KR scores (Table 2).
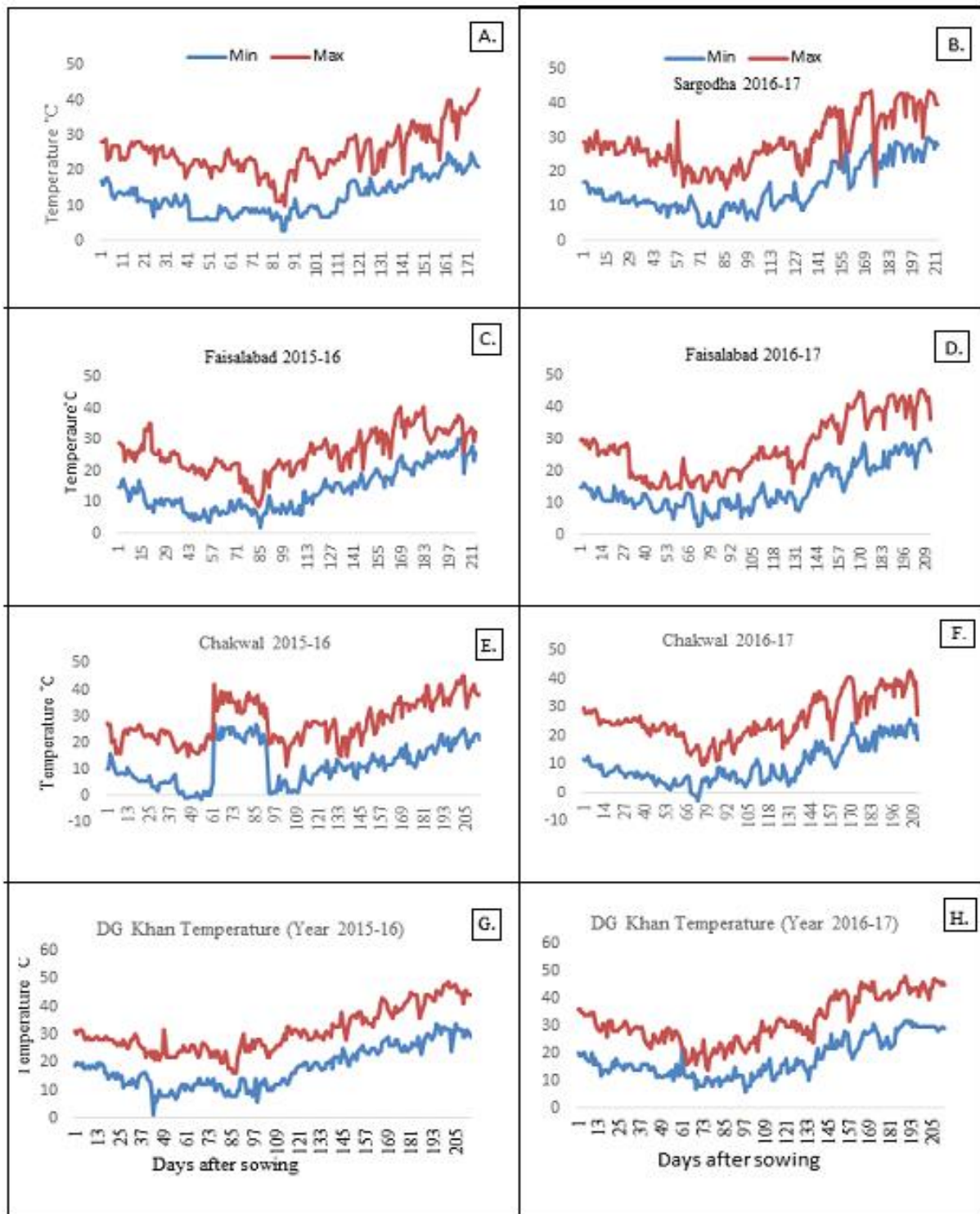
Fig. 1. Mean minimum and maximum temperature during entire growth phase of wheat in 2 years trials conducted at 4 locations of Punjab, Pakistan.

Associations between yield, components and quality traits

Plant height (PH) and number of grain spikes (NGS) clustered together at Sargodha location during 2015-16. The breeding lines SU-168 and SU-18 had the highest NGS. Starch % and 1000-grain mass (1000-GM) clustered with ZelV and PL respectively. SU-133 had higher starch % and ZelV whereas SU-105 showed higher 1000-GM as well as PL. Protein %, grain yield plant^{-1}(GYP), grain hardness (GH), spike length (SL), number of spikelet spike^{-1}(NSS), Gluten % and single spike grain mass (SSGM) clustered

together (Fig 4a). The genotypes SU-100, PB-11 and Galaxy-13 were promising lines for all these traits (Fig 4A) SL, protein%, GYP, PL, SSGM, NGS were clustered together at sargodha location during 2016-17 (Fig 4B). SU-66, SU-12, SU-12H, FSD-08, Galaxy-13 and SU-179 were promising breeding lines for these traits at Sargodha (Fig 4B). Starch%, 1000-GM,

ZelV clustered together at Sargodha location. Breeding line SU-18 had the highest Zeleny value (ZelV). SU-12 and PB-11 had the highest 1000-GM. SU-38 had high starch% while SU-134 had the highest number of spike meter[-1] (NSM) at Sargodha location (Fig 4B). PH, NGS and GH were found to be in the same cluster at Faisalabad location during 2015-16.
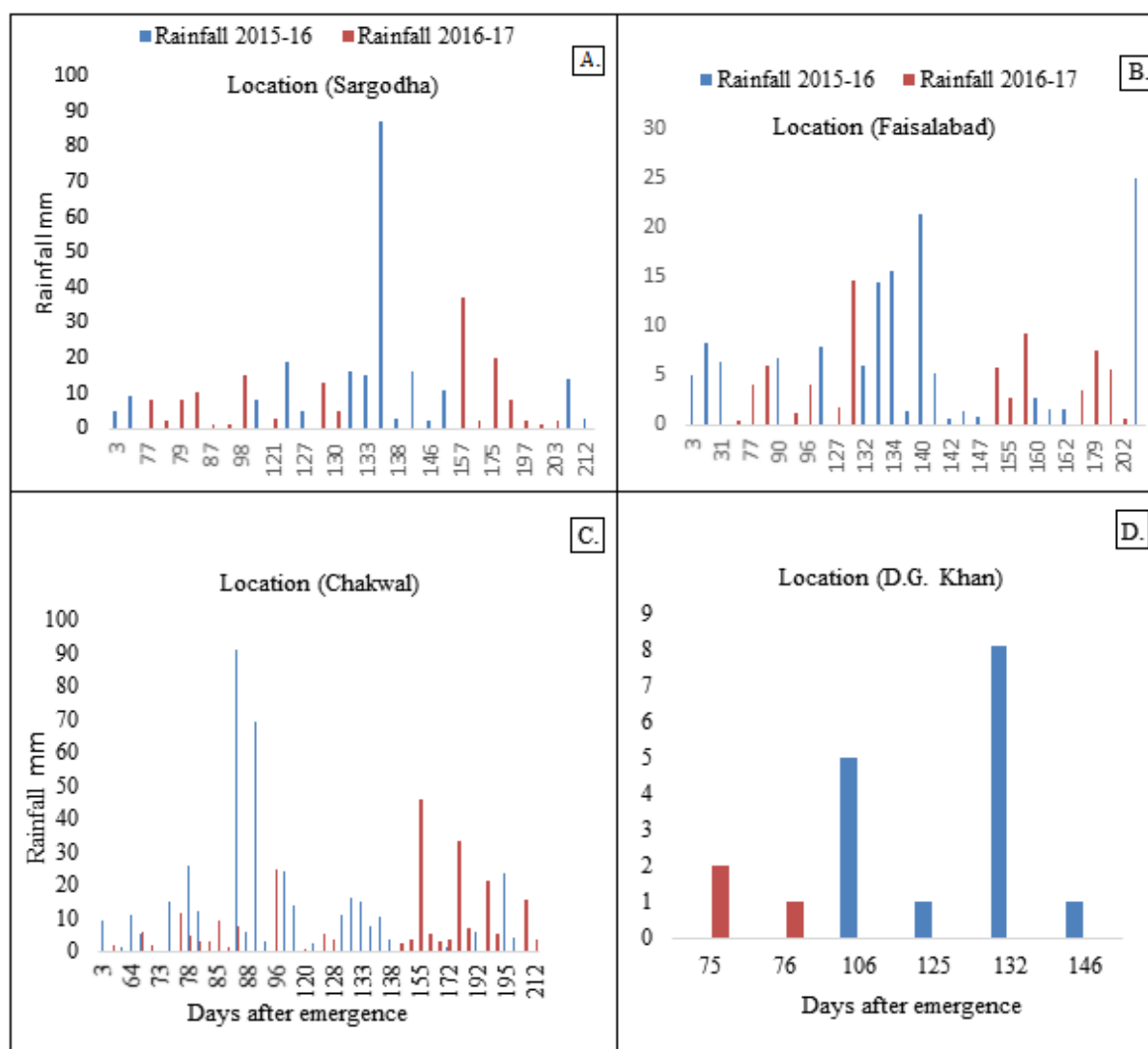
Fig. 2. Rain fall (mm) across 4 locations during years 2015-17.

The genotypes SU-18 and SU-168 showed the best performance for NGS while SU-133 had higher GH (Fig 5A). 1000-GM, ZelV, starch% and PL were closely associated traits at the same location during the first cropping season. SU-105 and SU-134 were best lines for these traits (Fig 5A). GYP, SL, protein% and SSGW also clustered together while SU-21, SU-52, Galaxy-13 and SU-100 were promising lines for all these traits. Moreover, NSS and Gluten% were found

aggregated in the same cluster. SU-179 and FSD-08 showed the best performance for both of these traits (Fig 5A). SU-91 had a higher NSM. SU-38 was the best performing breeding line simultaneously for various traits including gluten%, GYP, SL and NSS at the Faisalabad location during 2015-16 (Fig 5A). Starch%, ZelV, PL, GYP, NSS and protein% were closely related traits at Faisalabad during 2016-17. SU-12 had the highest value for these traits. SL, 1000-

GM and GH clustered together at the Faisalabad location (Fig 5B). SU-21, SU-105 had the highest SL, 1000-GM and GH. NGS, and SSGW were closely spotted together with SU-168 and FSD-08 had the highest value for these traits. SU-38 and SU-159 showed the highest value for NSM (Fig 5B).
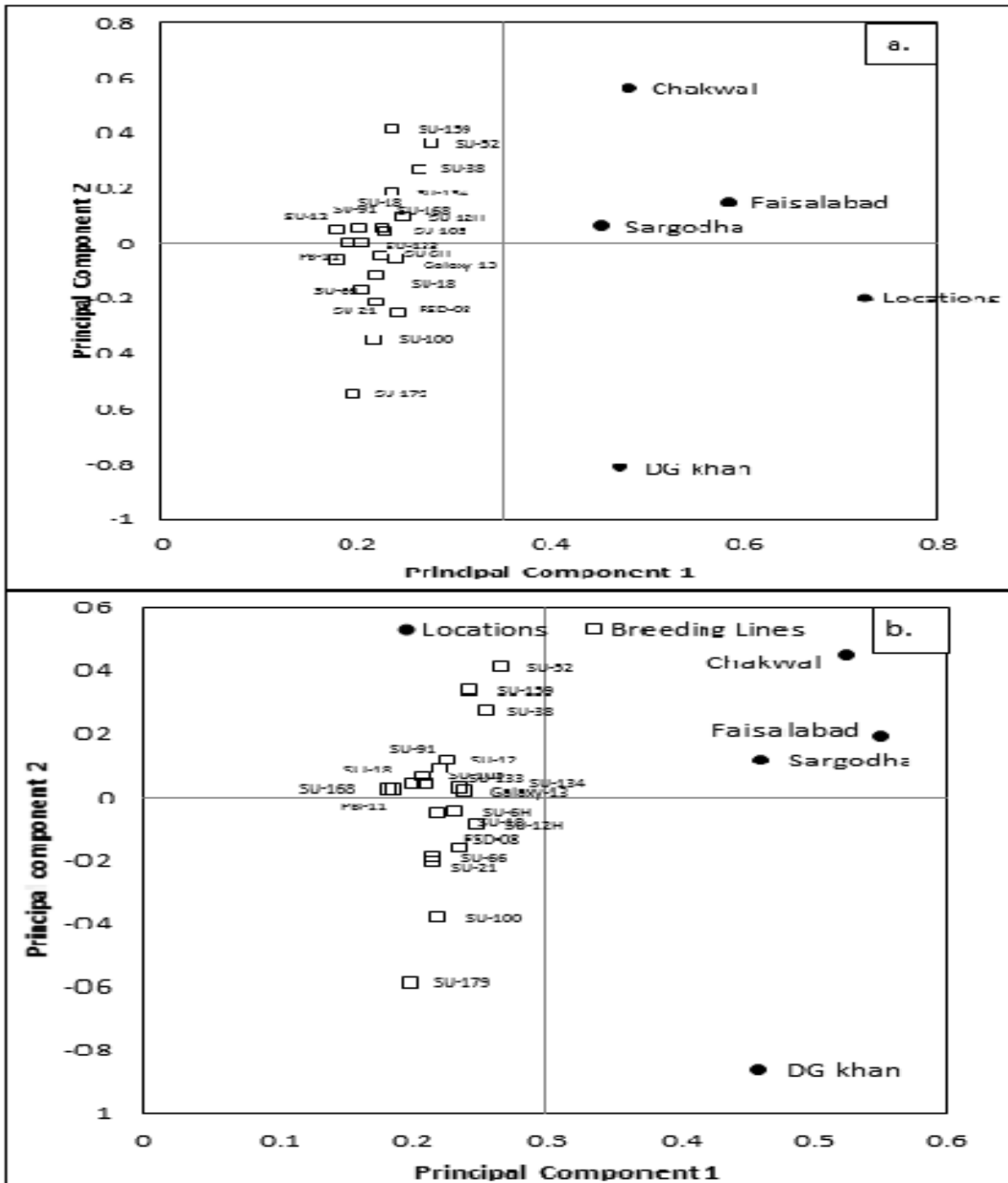

Fig. 3. Genotype + Genotype × Environment interaction of 17 advanced wheat breeding lines (*Triticum aestivum* L.) and 3 commercial varieties for grain yield per plant at various sites of Punjab, Pakistan during a. 2015-16 b. 2016-17.

PH and NGS clustered together at Chakwal location during 2015-16 while SU-179 and SU-21were the best lines for these traits (Fig 6A). SU-91 had higher GH. Starch%, 1000-GM and ZelV also clustered together showing close association among these traits whereas higher values of all these traits were observed in SU-

134 genotype (Fig 6A). FSD-08 had higher NSS as well as gluten%. The traits viz, SL, protein%, GYP and SSGW were also found to be clustered in the same group. SU-12, SU-105, SU-133 and SU-6H were promising lines for all these traits. SU-12 H had higher NSM at Chakwal during 2015-16 Fig 6B). Gluten%, GYP and ZelV clustered together at Chakwal location during 2016-17. SU-105 had the highest ZelV

and gluten%. SU-133 and SU-52 had the highest GYP at Chakwal location (Fig 6B). FSD-08 and SU-21 had the highest Protein% and SL. SU-12H and SU-100 had the highest PL. 1000-GM, SSGW and NGS were located together. Breeding lines SU-134, SU-18 and SU-6H had the highest values for these traits at Chakwal location. SU-91 had the highest NSM at Chakwal (Fig 6B).
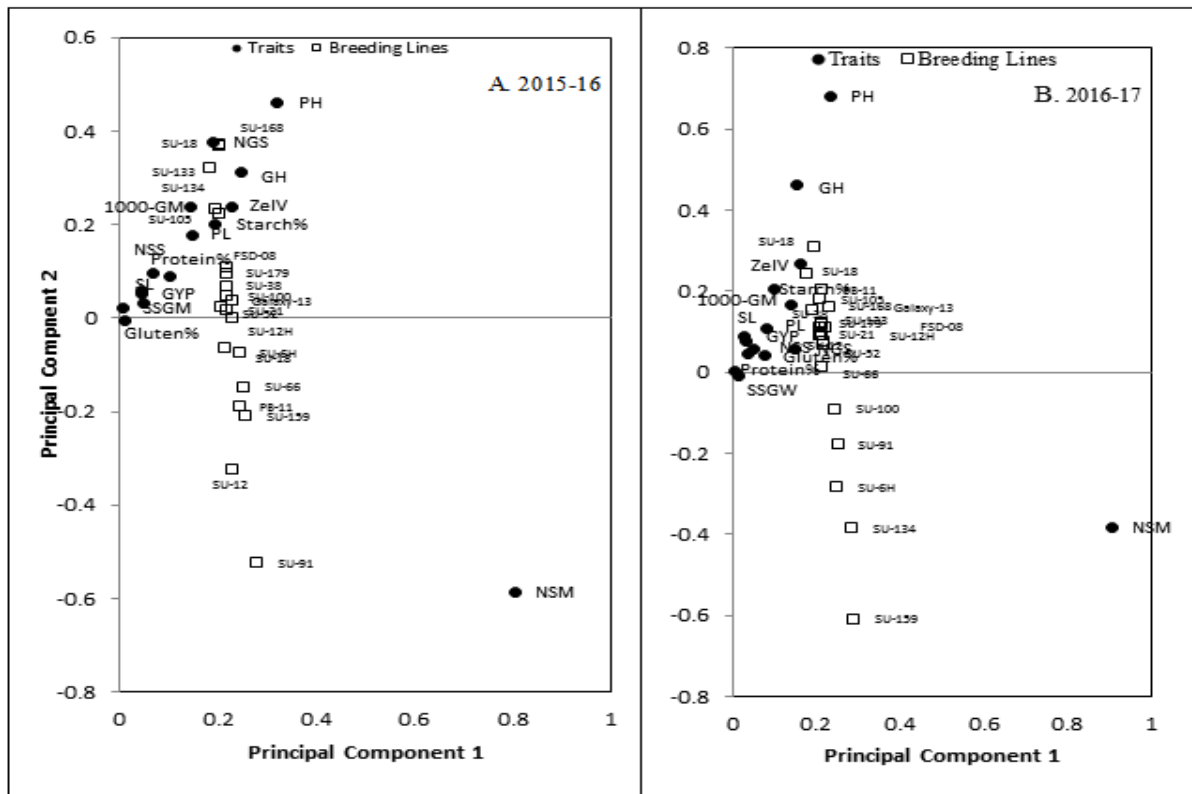
Fig. 4. Biplot analyses of accessions × traits + traits interaction and quality components Sargodha, where plant height (PH), grain yield plant[-1] (GYP), 1000-grain mass (1000-GM,) grain hardness (GH), number of spikelets spike[-1] (NSS), single spike grain mass (SSGM), spike length (SL), number of grain spike[-1](NGS), Peduncle length (PL).

PH, and NGS clustered together at Dera Ghazi Khan location during the first cropping season i.e., 2015-16 (Fig 7A). Breeding lines SU-179 and SU-21 had the highest PH and NGS. Grain hardness (GH) and starch% and 1000-GM (g) and peduncle length (PL) were closely related to each other and breeding lines SU-18 and SU-91 had the highest values for these traits (Fig 7A). SU-134 had the highest 1000-GM, PL, and Zeleny values. Protein% and grain yield plant[-1] (GYP), SSGW were closely related at DG khan site and breeding lines SU-12, SU-133 and SU-105 had the highest values for these traits. NSS and gluten%

clustered together at DG khan. FSD-08 and SU-6H had the highest values for the same traits (Fig 7A). Breeding lines SU-18 and SU-12H had the highest number of spikes meter[-2] (NSM) (Fig 7A).

SL, GH and SSGW clustered together at Dera Ghazi Khan location during the second cropping season (2016-17). The genotype SU-179 had the highest values for all these traits (Fig 7B). 1000 GM, NSS and PL and GYP formed another cluster at the same location. SU-179 also had the highest value for Zeleny sedimentation rate.
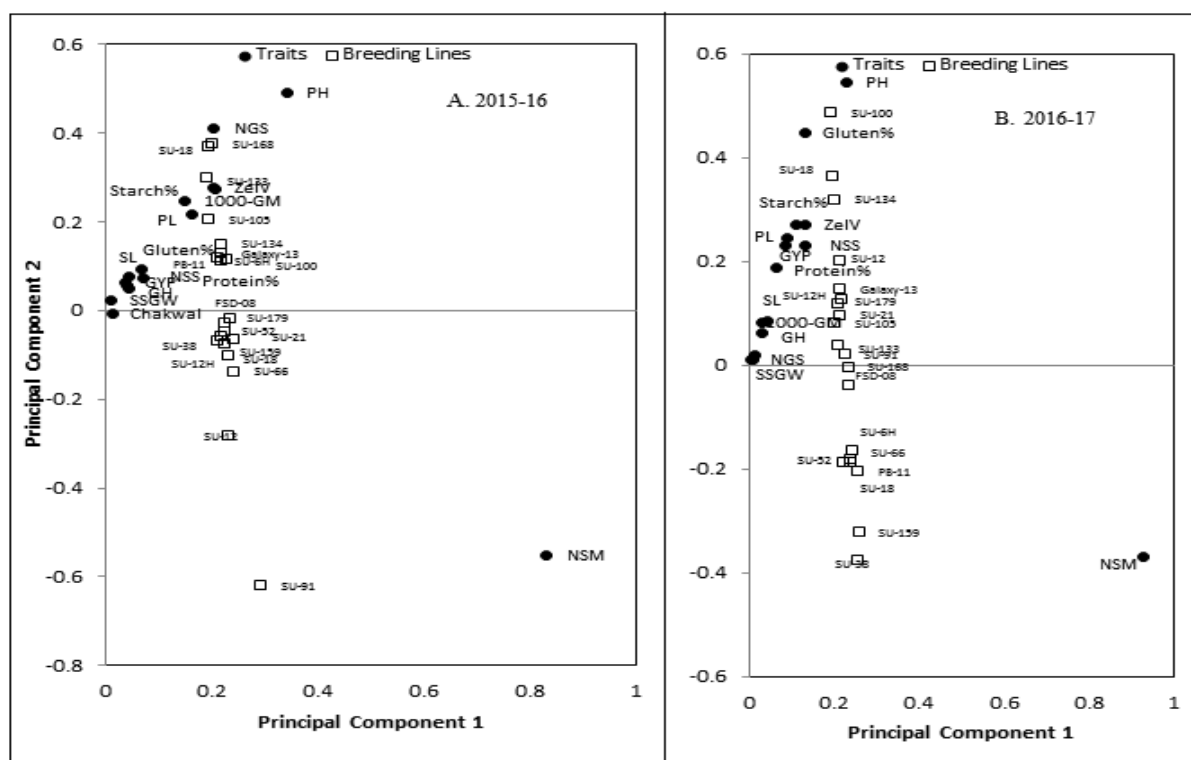
Fig. 5. Biplot analyses of accessions × traits + traits interaction and quality components at Faisalabad, where plant height (PH), grain yield plant^{-1} (GYP), 1000-grain mass (1000-GM,) grain hardness (GH), number of spikelets spike^{-1} (NSS), single spike grain mass (SSGM), spike length (SL), number of grain spike^{-1}(NGS), Peduncle length (PL).

The genotypes SU-134, SU-100 and SU-18 were promising lines for protein%, PH and gluten% respectively (Fig. 7B).

Discussion

The development of breeding lines with high yield, quality and stable performance are an ultimate breeding objective of any crop improvement program. Several parameters were used to estimate the stability of accessions under study (Table 2). According to the estimate of Wi², SU-168 had the lowest Wi² value and was considered to be the most stable genotype.

Similarly, breeding line SU-168 showed the lowest σ²$_i$ and was considered stable (Shukla, 1972). SU-52 was sensitive and adaptable to a high input environment, while SU-12 had the lowest s²d$_i$ value but a very high b$_i$ value, thus was also considered adaptable to a high yielding environment. SU-168 and SU-113 had a value close to unity and also had lower s²d$_i$ values, thus considered as stable accessions. SU-52 was high-yielding but was unstable accession. KR scores were

proposed by SU-18 had the lowest score across both years. Moreover, SU-12 and SU-168 had similar KR scores. The stability of any accession was dictated by many factors such as broad genetic base, resistance to biotic and abiotic stresses (Kendal, 2019; Qureeshi *et al.,* 2020). An accession with stable performance tends to have more predicted yield and may provide yield sustainability over years (Rauf *et al.,* 2015). The prevalence of various yield-limiting factors may also affect the stability of wheat accessions (Rauf *et al.,* 2015). Therefore, unstable accessions may experience more yield losses under climate change (Rauf *et al.,* 2015). Moreover, improvement in stress resistance has also been known to improve the sustainability of yield and quality (Qureeshi *et al.,* 2020). However, stress breeding in wheat may require the utilization of traits that may positively affect the yield to take advantage of both stress and non-stress environment (Rauf *et al.,* 2016). Otherwise, stress breeding based on traits highly adapted to the stress environment may develop cultivars that may be grown only in a stress environment (Rauf *et al.,* 2016).
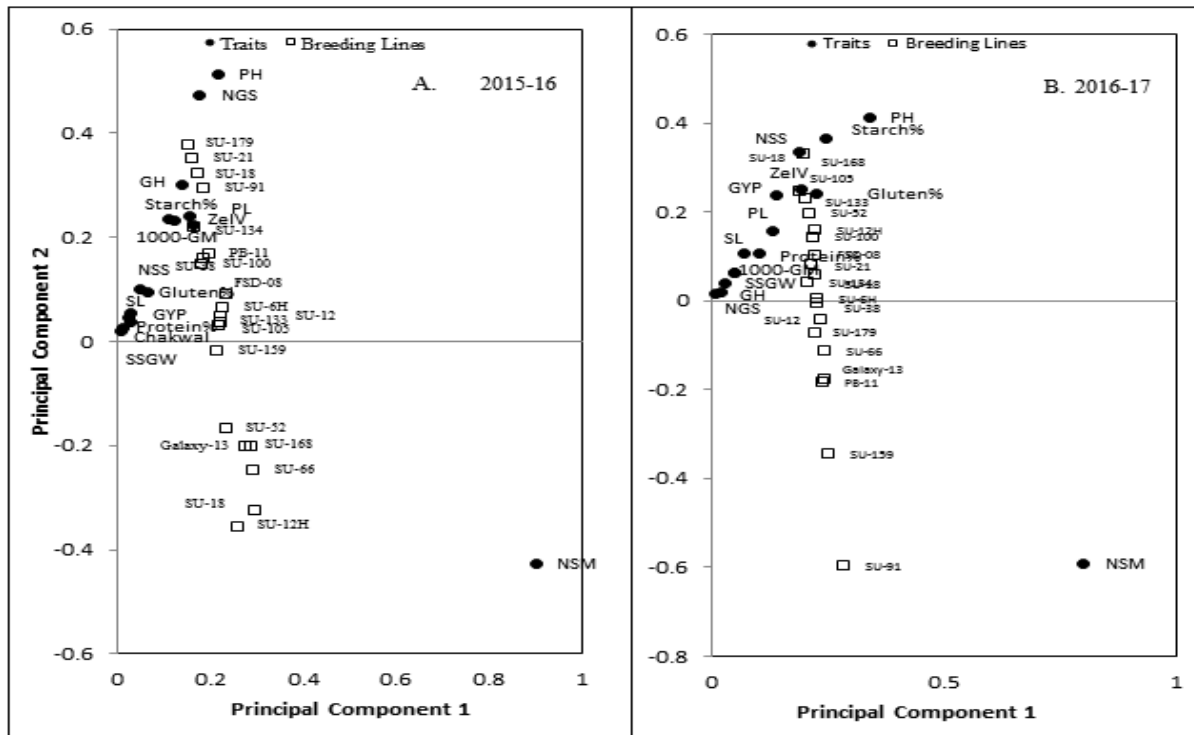
Fig. 6. Biplot analyses of accessions × traits + traits interaction and quality components at Chakwal, where plant height (PH), grain yield plant^{-1} (GYP), 1000-grain mass (1000-GM,) grain hardness (GH), number of spikelet spike^{-1} (NSS), single spike grain mass (SSGM), spike length (SL), number of grain spike^{-1}(NGS), Peduncle length (PL).
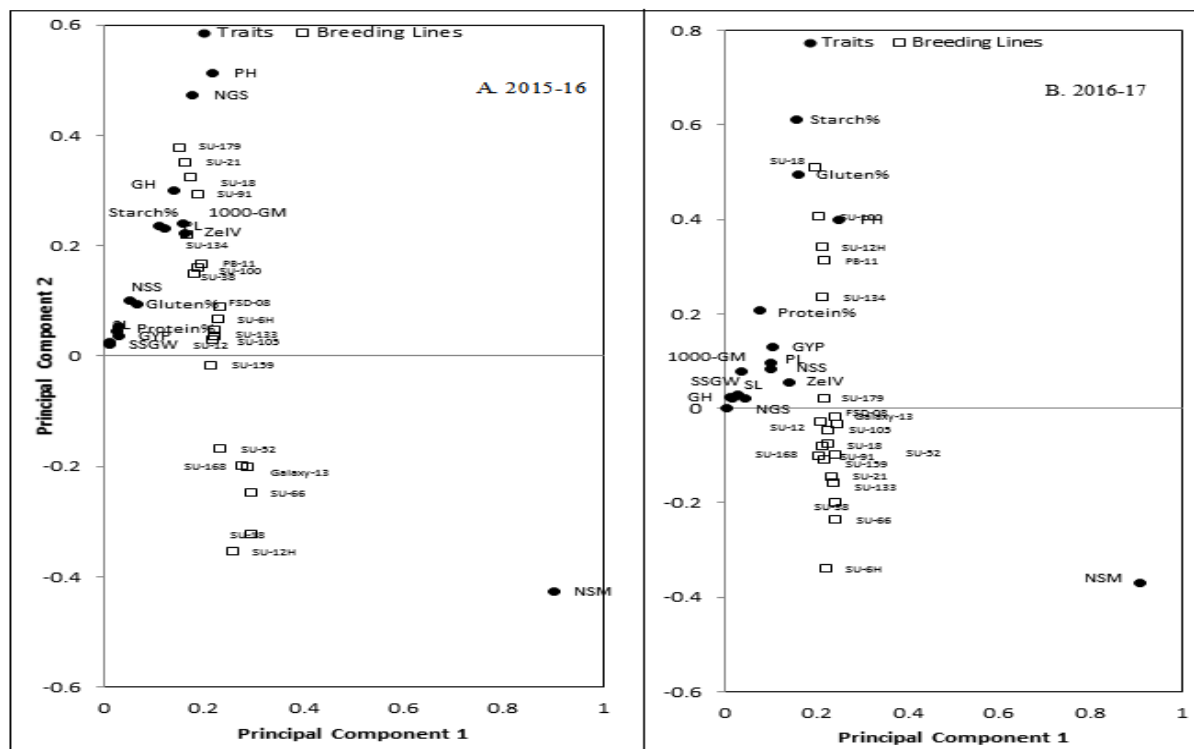

Fig. 7. Biplot analyses of accessions × traits + traits interaction and quality components at DG Khan during 2016-2017, where plant height (PH), grain yield plant^{-1} (GYP), 1000-grain mass (1000-GM,) grain hardness (GH), number of spikelet spike^{-1} (NSS), single spike grain mass (SSGM), spike length (SL), number of grains spike^{-1}(NGS), Peduncle length (PL).

Our study showed that traits related to wheat quality were affected by the environments, provided by variable locations and multiple years, which may have altered associations between yield and quality traits (Kendal, 2019). However, there was some close relationship between the agronomic and quality traits, showing that higher agronomic traits and quality traits were simultaneously present in the newly developed breeding lines. The close - or + relationships between traits may be due to physiological processes such as photosynthates synthesis and mobilization to sink and thus controlled at the functional level, where reaction limits may affect the differential development of traits and were also affected by the environments (Rauf *et al.,* 2015). A genetically significant relationship between traits was explained by linkage or pleiotropic effects, and these relationships were identified in suitable mapping populations (Zhai *et al.,* 2018; Kumar *et al.,* 2019). A positive relationship was observed between the wheat qualities traits i.e., grain protein contents with grain hardness, sedimentation, dough development time and farinograph (Gómez-Becerra *et al.,* 2010). However, a negative relationship was observed between the grain protein contents and agronomic traits such as maturity, grain filling duration and harvest index (Iqbal *et al.,* 2007). Despite negative associations between yield and agronomic traits, genotypes with high grain quality traits, yield and medium maturity were selected from segregating populations (Iqbal *et al.,* 2007).

Breeding lines such as SU-18, SU-168, SU-SU-12, SU-6H, PB-11, SU-134 were promising lines due to their high agronomic value and quality traits.

Conclusion

Accessions such as SU-168 were stable across the environment. Accessions SU-18 had high grain yield plant^{-1} and stable across environments. 6H, SU-12, SU-18, PB-11 and SU-134 had better agronomic and quality traits. Biplot analyses were carried out for simultaneous identification of breeding lines with better agronomic and quality traits. Trait analyses showed that breeding lines having high agronomic

value and better grain quality traits may be present which may be recommended for commercial cultivation under a range of environments.

Data availability statement

The data sets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Conflict of interest

Authors declare no conflict of interest.

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