Research Article

Phenotypic Diversity in Yield Determining Traits of Pea (*Pisum sativum* L.) Genotypes under the growing Conditions of Dera Ismail Khan, Khyber Pakhtunkhwa, Pakistan

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Abstract | Field experiments were conducted to assess the phenotypic diversity in diverse pea genotypes for yield determining traits under the growing condition of D. I. Khan, KPK. Experiment was laid out in Randomized Complete Block Design (RCBD) replicated thrice during two normal growing seasons (2013-14 and 2014-15). At physiological maturity, data were collected for yield contributory traits. In Season 1, the genotype Minarellet proved to be early maturing by taking lesser number of days to flower initiation (55.48 days) followed by Rando and Coronado. Statistically maximum variability was shown by Climax and Green feast for plant height (81.33 and 80.77 cm), number of pods plant^{-1} (18.64 and 17.77), weight of pods plant^{-1} (51.74 and 50.89 g), pod length (11.09 and 11.31 cm), pod width (2.51 and 2.31 cm), number of grains pod^{-1} (8.02 and 7.64), and pod yield (5.61 and 5.50 t ha^{-1}), respectively. Almost similar results were obtained in S_2. Results concluded that the best yielding capability of genotypes Climax and Green feast were mainly because of high pod yield. Results also indicated a huge variation in different varietal performance in climatic conditions of D. I. Khan which could be utilized in pea breeding programs.

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Introduction

Yield is the inter-play of genetics, growing environment, and their interactions (Quarrie *et al.*, 2006). Indigenous varieties show high degree of genetic and phenotypic diversity. Plant biologists are faced with the challenge of how to effectively breed for high yielding and resistant genotypes. Assessing the phenotypic diversity among genotypes for yield-related traits may become effective tool for developing better yielding varieties for specific and/or multi-environments (Casadebaig *et al.*, 2016). Vegetables are an economical wellspring of protein for both humans consuming fewer calories. Assessing the phenotypic diversity among genotypes for yield-related traits may become effective tool for developing better yielding varieties for specific and/or multi-environments (Santalla *et al*., 2001; Ali *et al*., 2007; Jatoi *et al*., 2011). Pea (*Pisum sativum* L.) is one of the world's most developed vegetable crops. It is one of the major agricultural produces and is a significant segment, alongside different vegetables and oats, of the eating routine of early human advancements in the Middle East and the Mediterranean Basin. Wild pea relatives include the species *P. fulvum* and *P. sativum* subsp. elatius. Developed peas for the most part have a place with *P. sativum* subsp. sativum. *P. sativum* subsp. abyssinicum is a less often developed pea, limited to Yemen and Ethiopia (Duc *et al*., 2015).

Field pea (*Pisum sativum* L.) is among the top ranked legume crops that is consumed by humans to meet their dietary needs all over the world. It is a rich source of protein (21-25 %), carbohydrates, vitamin A and C, calcium, phosphorous, amino acids, lysine and tryptophan (Bhat *et al*., 2013). In Pakistan, total production of pea is about 149 thousand tonnes from an area of 23.6 thousand hectares (FAOSTAT, 2016). Pod yield of pea highly depends on climatic conditions of the cultivated area and genotypic variability of variety grown for better adoptability and high yield (Khichi *et al*., 2017). Existence of genotypic differences among grain legumes is an indication for improvement through conventional selection procedures (Coulibaly *et al*., 2002). Seboka and Fikresilassie (2013) conducted experiments on sixteen field pea genotypes and reported that seed yield had positive and significant correlation with grain filling periods, plant height, number of seeds pod^{-1}, seed plant^{-1} and pod length. Kosev (2015) highlighted the cumulative effect of yield contributing traits and indicated that number of grains plant^{-1}, pod length and grain weight had the highest effect on seed yield.

Actual yield as characterized is the immensity of seed collected than the immensity of seed planted. Especially in large seeded vegetables in low yielding situations, yield in essence is certifiably not an ideal estimation of financial efficiency. Two cultivars of peas with a similar yield potential (6735 kg/ha) yet extraordinary seed sizes, were compared that showed differences in yield due to varietals differences. Actual yield is a greater amount of productivity than the basic estimation of grain yield at crop since it signifies seed cost. Yield potential is the genetically decided capacity of a harvest to produce ideal yield in a given agro-climatic environmental condition. Yield potential is believed to be in part verbalized by seed evaluation, and various investigations have attempted to comprehend the correlation between seed size and yield in pea. All these actual and potential yield differences were due to genotypic variability and different agro-climatic conditions (Biger, 2009; Gusmao *et al*., 2012).

Agricultural research in developing countries is mainly focused to assess various cultivars for their suitability to be grown in suitable growing conditions for guaranteeing best yield potential of that crop within available resources. Explicit zones need specific variety that could better grow under the prevailing conditions of the area. Little consideration has been given to varietals improvement of peas outside the temperate region of developed countries. Hence, keeping in view the importance of pea crop for ensuring food security with recommendation of specific variety for a specific area, present investigations were carried out to evaluate pea varieties for yield and its contributory traits under the agro-climatic conditions of Dera Ismail Khan (D. I. Khan), Khyber Pakhtunkhwa, Pakistan during two normal growing seasons.

Materials and Methods

Field experiments were conducted to assess the phenotypic diversity in diverse pea genotypes for yield determining traits under the tropical environment of D. I. Khan, Khyber Pakhtunkhwa, Pakistan (latitude 32^0 4' N, longitude 71^0 2', altitude of 173m) during two growing seasons (2013-14 and 2014-15). To reduce chance of error, experiments in both seasons were planted in Randomized Complete Block Design (RCBD) with three replications. Plant material included ten genotypes (Indeterminate) that are designated as Climax (Cli), Coronado (Cor), Dasan (Das), Faisalabad (Fsd), Green feast (Gre), Meteor (Met), Minarellet (Min), PS-40 (P4), Rando (Ran), and Shareen (Sha) genotypes.

Soil was sampled before starting the experiment, for various physico-chemical properties according to standard procedures (Table 1). Organic matter was determined by dicrome oxidation method Walkley and Black (1943). EC and soil pH were measured in a 1/5 soil/water extract. Soil Nitrogen was measured by method given by Hesse (1971). The available P was measured with the method given Olsen *et al*. (1954). K was determined by the procedure given Junsomboon and Jakmunee (2011). All plant production and protection measures were adopted accordingly. Both experiments were planted at 26th September and seeds were planted at ridges, where R×R and P×P distance was maintained 100 cm and 30 cm, respectively. These ten genotypes were commonly grown in Pakistan. The objective of determining phenotypic diversity was to evaluate most suitable genotype specially for this climatic condition. The source seed was NARC and Ayub Agriculture Research Institute, Faisalabad. Data regarding climate was collected from meteorological station located nearby the experimental site (Table 2). The plants were harvested at last week of February on both years. At physiological maturity, five plants from each treatment were selected and data were recorded on days to flowering (D_F), plant height (PL_H, cm), number of pods plant^{-1} (P_N), weight of pods plant^{-1} (P_{WT}, g), pod length (P_L, cm), pod width (P_W, cm), number of grains pod^{-1}(G_N), and pod yield (P_Y, t ha^{-1}). Collected data were subjected to analysis of variance technique as outlined by Steel *et al*. (1997). Least Significance Difference (LSD) at 5% probability was used to assess the extent of variability among pea genotypes. All statistical analyses were performed in IBM SPSS, version 22 (IBM corp., NY, USA).

Table 1: *Physical and chemical properties of the experiment soil.*

Property	Unit	2013-14	2014-15
N	(mg kg^{-1})	12.98	13.03
P	(mg kg^{-1})	0.52	0.71
K	(mg kg^{-1})	327.87	332.13
Organic matter	%	0.60	0.71
pH	-	8.20	8.10
EC	dS m^{-1}	4.38	4.47
Sand	%	14.89	14.70
Silt	%	75.10	74.50
Clay	%	10.00	10.80
Textural class	-	Silt loam	Silt loam

Results and Discussion

Days to flowering

Pea genotypes presented significant ($P<0.05$) differences for days to flowering (D_F) in both the growing seasons (2013-14 and 2014-15) (Figure 1). It ranged from 55.48 to 78.77 in 2013-14 and from 54.84 to 75.13 in 2014-15. Genotype Min and Ran took minimum days to flowering (55.48, 56.55 respectively) whereas Das took maximum days to flowering (78.77) in 2013-14. Almost similar results were recorded in 2014-15, however, genotype M*et al*so took maximum (75.13) days to flowering (Table 1). Finding enclosed that all the other genotypes intermediary responded to flowering during both the seasons. Previously conducted studies had also drawn similar conclusion of differential response of varieties to flower initiation (Khokhar *et al*., 1988).

Table 2: *Mean agro-meteorological data recorded during two growing seasons.*

Growing Season	Temperature (^{0}C)		Relative humidity (%)		Pan evaporation (mm day^{-1})	Total rainfall (mm)
	Max	Min	08:00 hrs	14:00 hrs		
2013-14	24.5	10.0	79.5	45.5	2.1	100.5
2014-15	24.3	9.7	82.0	51.2	2.4	160.3

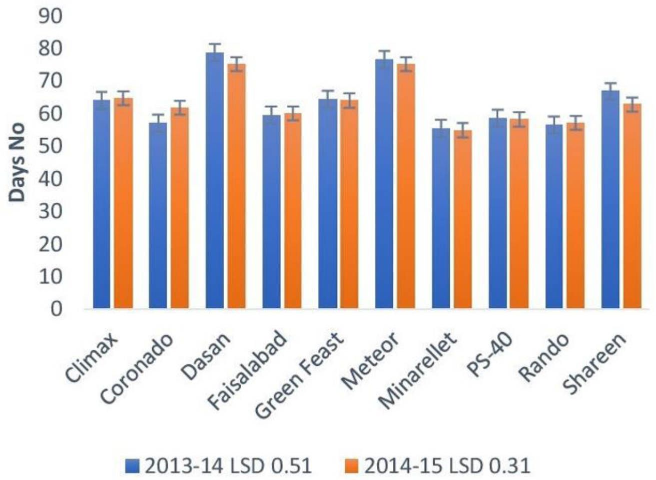

Figure 1: *Days to flowering of ten genotypes in two growing seasons.*

Plant height (cm)

Effects of genotype were highly significant ($P<0.05$) on plant height (PL_H) in both the growing seasons (*i.e.* 2013-14 and 2014-15) (Figure 2). PL_H ranged from 48.02 to 81.33 in 2013-14 and 48.01 to 83.61 cm in 2014-15. Maximum PL_H was recorded in Cli (81.33, 83.61 cm) and Gre (79.89, 79.63 cm) in both the seasons (*i.e.* 2013-14 and 2014-15), respectively. Both genotypes were statistically alike and differed considerably from the rest of genotypes. Genotype Cor attained lowest PL_H (48.02, 48.01 cm) in 2013-14 and 2014-15, respectively. However, it was interesting to note that this genotype was followed by statistically similar values recorded in genotypes Min (49.35, 55.44 cm), P4 (50.78, 54.79 cm), and Ran (53.23, 52.71 cm) in 2013-14 and 2014-15, respectively. These results clearly indicated the existence of genotypic variability among the genotypes (Ali *et al*., 2007; Khan *et al*., 2013; Umar *et al*., 2014).

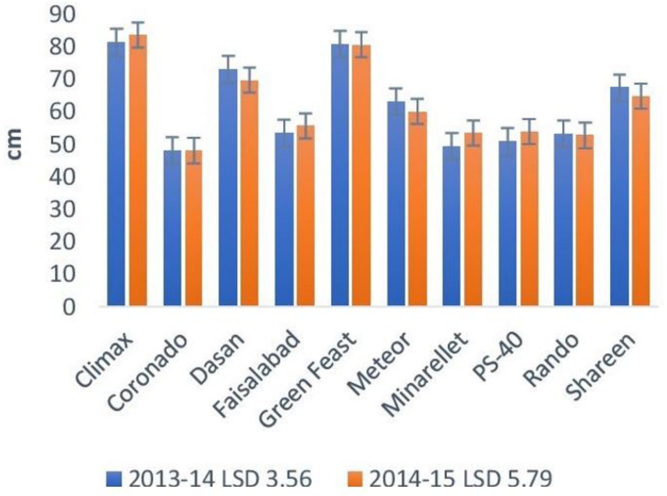

Figure 2: *Plant height (cm) of ten genotypes in two growing seasons.*

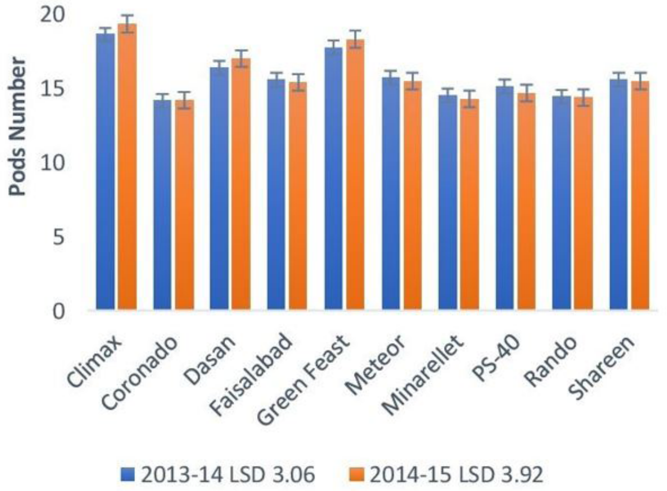

Figure 3: *Number of pods plant^{-1} of ten genotypes in two growing seasons.*

Number of pods plant^{-1}

Significant (P<0.05) genotypic variability was found to be present for pods plant^{-1} (P_N) among the different pea genotypes in both the growing seasons (*i.e.* 2013-14 and 2014-15) (Figure 3). In 2013-14, genotype Cli produced maximum P_N (18.64) with a very low or no differences of varieties Gre, Das, Sha, Met, and Fsd due to statistical similar ranks. Lowest P_N (15.01) were registered in genotype Ran succeeded by Min (15.10) and all these two genotypes were statistically identical to each other. In 2014-15, as expected, the genotype Cli produced maximum P_N (19.34), while genotype Ran produced the lowest P_N (13.39). The rest of genotypes indicated similar trends as in 2013-14. The presence of significant genetic variation in pod formation has been reported by Ashraf *et al.* (2011), and Kosev *et al.* (2013).

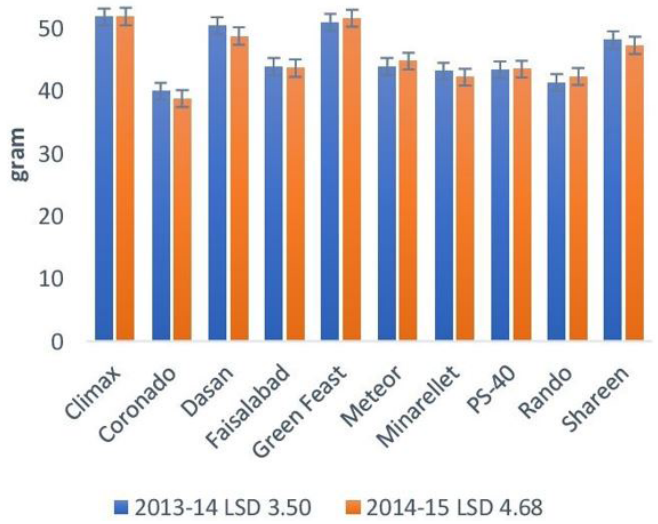

Figure 4: *Weight of pods plant^{-1} of ten genotypes in two growing seasons.*

Pods plant^{-1}weight (g)

Fresh pods plant^{-1} weight (P_{WT}) differed significantly (P<0.05) among the pea genotypes in both the growing seasons (*i.e.* 2013-14 and 2014-15) (Figure 4). In 2013-14, the genotype Cli exhibited maximum P_{WT} (51.83 g) followed by Gre, Das, and Sha with non-significant P_{WT} (51.08, 49.98, 47.14 g, respectively). Minimum P_{WT} was recorded in genotype Cor (40.05 g) which was followed by statistically at par P_{WT} (41.99, 42.19, 42.85, 42.98 and 44.65 g) in PS-40, Ran, Min, Fsd and Met, respectively. Results from the second season (*i.e.* 2014-15) revealed almost similar results for genotype Cli with maximum P_{WT} (51.90 g). However, it was followed by statistically non-significant P_{WT} in the rest of genotypes except for Fsd and Cor with minimum P_{WT} (41.65 and 39.76 g, respectively). The variation in P_{WT} may be attributed to the inherent capability of some genotypes particularly Cli to produce high number of pods as these traits have close inter-relationship that affect crop yield considerably. Such relationships are discussed in detail in later section. Findings are inter-linked to previously deduced results of Tan *et al.* (2012) and Khan *et al.* (2013).

Pod length (cm)

Different pea genotypes designated significant (P<0.05) differences in pod length (P_L) in both growing seasons (*i.e.* 2013-14 and 2014-15) (Figure 5). In 2013-14, maximum P_L (11.09 cm) was presented in genotype Cli, however, it was statistically not different to the rest of the genotypes except Min and Cor with minimum P_L (8.23 and 9.17 cm, respectively). Almost similar results were obtained in the second growing season (2014-15), where Cli exhibiting maximum (11.01 cm) pod length. Present findings are in accordance with the findings of Ghafoor *et al*. (2005) and Khan *et al*. (2013). Both these studies depicted that considerable genetic variation were found to be present in pod length of different pea cultivars.

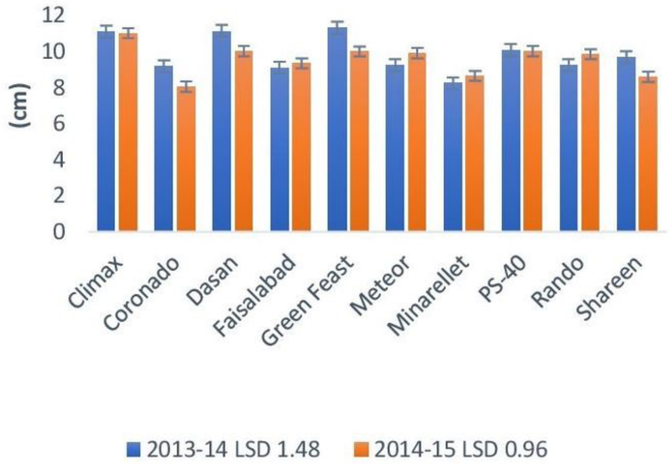

Figure 5: *Pod length (cm) of ten genotypes in two growing seasons.*

Pod width (cm)

Findings showed huge (P<0.05) contrasts in the pea cultivars for pod width (*P*w) in both the growing seasons (2013-14 and 2014-15) (Figure 6). In 2013-14, greatest pod width (2.51 cm) was recorded from Cli pursued by Gre with 2.31 cm for said trait and the two genotypes were measurably indistinguishable however differed really from every single other cultivar. Measurably comparative outcomes for *Pw* (cm) were significantly different in genotypes Ran, Sha, Cor, Min, Met, and Fsd with *Pw* 2.21, 1.65, 1.51, 1.61, 1.54, and 1.81 cm, respectively. The narrowest *Pw* (1.49 cm) was found in genotype Das pursued by P4 with 1.76 cm *Pw* and the two genotypes were identical to one another. Results relating to second growing season (2014-15) uncovered most extreme *Pw* (2.67 cm) in genotype. Cli showed measurably similar *Pw* (2.89 cm) to Gre which differed significantly from every single other genotype. It was trailed by measurably comparative *Pw* recorded in Sha (2.12 cm), Ran (1.79 cm), and Fsd (1.99 cm). Smallest *Pw* (1.71 cm) was found in Das that was factually indistinguishable to PS-40, Cor, Met, Min, and Fsd with 1.69, 1.70, 1.69, 1.69 and 1.91 cm *Pw*, respectively. These outcomes demonstrated that various genotypes indicated heterogeneous differences in *Pw* being most astonishing in Cli and Gre, while the least in Das. Past researchers like Khan *et al*. (2013) and Umar *et al*. (2014) likewise announced dissimilarity in *Pw* in various genotypes of *Pisum sativum*.

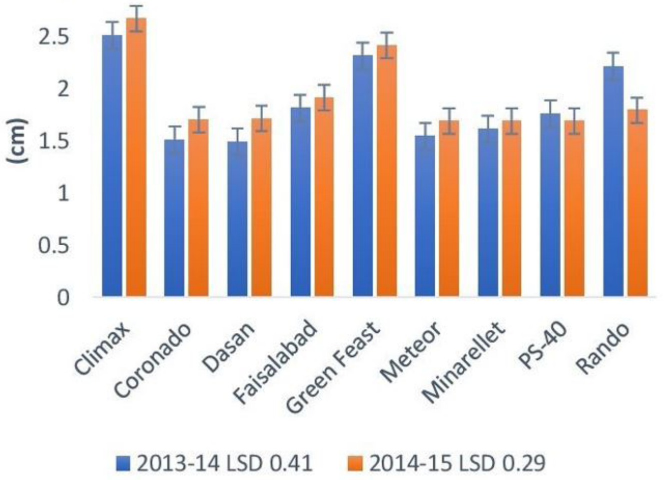

Figure 6: *Pod width (cm) of ten genotypes in two growing seasons.*

Grains pod^{-1}

Critical contrasts were recorded among the distinctive pea genotypes in regards to G_N in both the growing seasons (2013-14 and 2014-15) (Figure 7). In 2013-14, maximum G_N (8.02) were recorded in genotype Cli all around intently pursued by Gre, Das, Sha, Ran, and Met with 7.64, 7.12, 6.93, 6.65 and 6.92 G_N, respectively. In any case, all these six genotypes did not vary altogether from one another. Statistically alike results were reported for genotypes P4 and Fsd, both delivering 6.33 and 6.51 G_N respectively. The least G_N (5.19) were recorded in Cor that varied essentially from every single other cultivar aside from Min producing 5.72 G_N. In the second growing season (2014-15), the fundamentally maximum G_N (7.36) was recorded in Cli, statistically similar pursued by Gre, PS-40, and Das creating 7.07, 6.81, and 6.69 G_N, respectively. The genotype Cor recorded least GN (5.56), trailed by factually non-huge qualities in genotypes for example Ran, Min, Fsd, Sha, and Met with 6.04, 5.87, 5.93, 6.01 and 6.03 G_N, respectively. These results demonstrated that G_N differed significantly among the pea genotypes. Pea cultivar Cli, Gre and Das produced the highest G_N as contrasted with different genotypes, while the most minimal G_N were recorded in Cor during both the growing seasons (2013-14 and 2014-15), demonstrating differential grain production capability of pea genotypes. Previously researchers Bozoglu *et al*. (2007), Muhammad *et al*. (2009), and Khan *et al*. (2013) furthermore found different G_N in various genotypes of *Pisum sa-*

tivum which indicates presence of genetic fluctuation for this attribute in pea germplasm.

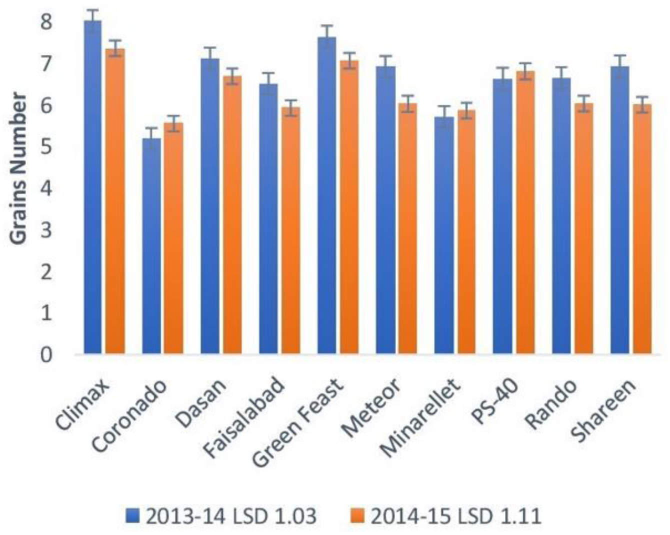

Figure 7: *Number of grains pod^{-1} of ten genotypes in two growing seasons.*

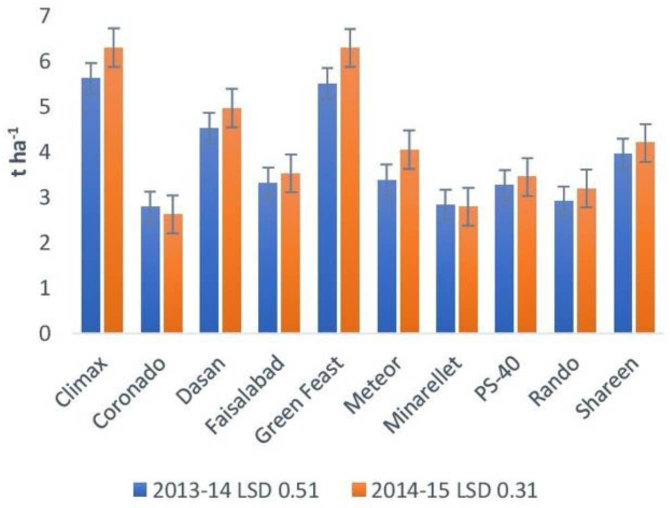

Figure 8: *Pods yield t ha^{-1} of ten genotypes in two growing seasons.*

Pod yield (t ha^{-1})

Exceptionally remarkable variation in P_Y was recorded among various pea genotypes in both the growing seasons (2013-14 and 2014-15) (Figure 8). In 2013-14, the most elevated P_Y (5.61 t ha^{-1}) was recorded in genotype Cli which was in all respects intently prevailing by Gre (5.50 t ha^{-1}) and the two genotypes fundamentally contrasted from the remainder of genotypes. These were trailed by Das (4.52 t ha^{-1}), Sha (3.95 t ha^{-1}), and Met (3.38 t ha^{-1}). Genotype Met with 3.38 t ha^{-1} P_Y in turn was factually much the same as Fsd, PS-40, and Ran producing P_Y of 3.31, 3.26, and 2.90 t ha^{-1}, separately. Cor created the least PY (2.78 t ha^{-1}) which was measurably at standard with genotypes Min, Ran, and PS-40. In S_2, practically comparable outcomes were gotten. The genotype Cli created essentially greatest P_Y (6.29 t ha^{-1}) which showed up measurably at standard with Gre (6.28 t ha^{-1}), in any case, both these genotypes were fluctuated fundamentally from the remainder of genotypes.

It was trailed by genotypes Das, Sha and Met with P_Y of 4.96, 4.19, and 4.04 t ha^{-1}, respectively, however, the last two genotypes were non-significant to each other. Factually comparable outcomes were likewise seen in Fsd and P4 with P_Y 3.52 and 3.44 t ha^{-1}, individually. Be that as it may, genotype S-40 was likewise factually like Ran (3.19 t ha^{-1}). The genotype Cor and Min exhibited the most reduced P_Y (2.62 and 2.79 t ha^{-1}, separately) and varied from the remainder of genotypes. These outcomes uncovered impressive contrasts among pea genotypes for P_Y. Comparable outcomes were cited by Arshad *et al.* (2011) and Khan *et al.* (2015), who additionally discovered Cli as stature pea yield genotype among the various studied genotypes. These outcomes are fairy supported by Jilani (2008), Muhammad *et al.* (2009) and Khan *et al.* (2013) who enlisted huge contrasts in pod yields of pea germplasm.

Conclusions and Recommendations

This study concluded that there exists significant phenotypic diversity among the pea genotypes for plant growth, yield, and yield contributing traits under the growing conditions of D.I. Khan, Khyber Pakhtunkhwa, Pakistan. Findings revealed that genotype Cli very closely followed by Gre were promising varieties among tested genotypes in enhancing the yield of peas substantially.

Novelty Statement

There exists significant phenotypic diversity among the pea genotypes for plant growth, yield, and yield contributing traits under the growing conditions of D. I. Khan, Khyber Pakhtunkhwa, Pakistan.

Author's Contribution

Tehseen Ali Jilani: Conducted the research.
Muhammad Saleem Jilani, Hasnain Saleem and Javeria Sherani: Reviewed the manuscript.
Kashif Waseem: Helped in preperation of graphs.
Muhammad Sohail Khan: Wrote and reviewed the manuscript.
Abdul Manan: Approved the final draft.

Rashid Jawad: Helped during research and method.
Sami Ullah: Helped in interpretation of results.

Conflict of interest

The authors have declared no conflict of interest.

References

Achakzai, A.K.K. and M.I. Bangulzai. 2006. Effect of various levels of nitrogen fertilizer on the yield and yield attributes of pea (*Pisum sativum* L.) cultivars. Pak. J. Bot., 38 (2): 331-340.

Achakzai, A.B.K. 2012. Effect of various levels of nitrogen fertilizer on some vegetative growth attributes of pea (*Pisum sativum* L.) cultivars. Pak. J. Bot., 44(2): 655-659.

Ali, Z., A.S. Qureshi, W. Ali, H. Gulzar, M. Nisar and A. Ghafoor. 2007. Evaluation of genetic diversity present in pea (*Pisum sativum* L.) germplasm based on morphological traits, resistance to powdery mildew and molecular characteristics. Pak. J. Bot., 39: 2739-2747.

Arshad, M., S.A. Hussain, S.A.N. Ali, N. Muhammad and Ziaullah. 1998. Screening of pea (*Pisum sativum* L.) cultivars in Kohat valley. Sarhad J. Agric., 14(6): 559-562.

Ashraf, M.I., M.A. Pervez, M. Amjad, R. Ahmad and M. Ayub. 2011. Qualitative and quantitative response of Pea (*Pisum sativum* L.) cultivars to judicious applications of irrigation with phosphorus and potassium. Pak. J. Life Soc. Sci., 9(2): 159-164.

Bhat, T.A, M. Gupta, M.A. Ganai, R.A. Ahanger and H.A. Bhat. 2013. Yield, soil health and nutrient utilization of field pea (*Pisum sativum* L.) as affected by phosphorus and biofertilizers under subtropical conditions of Jammu. Int. J. Modern Plant Anim. Sci., 1(1): 1-8.

Biger, B.T. 2009. The effect of seed size on yield and yield components of chickpea and lentil. Afr. J. Biotechnol., 8(8): 1482–1487.

Bozoglu, H., E. Peksen, A. Peksen and A. Gulumser. 2007. Determination of the yield performance and harvesting periods of fifteen Pea (*Pisum sativum* L.) cultivars sown in autumn and spring. Pak. J. Bot., 39(6): 2017-2025.

Casadebaig, P., E. Mestries and P. Debaeke. 2016. A model-based approach to assist variety evaluation in sunflower crop. Eu. J. Agron., 81: 92-105. https://doi.org/10.1016/j.eja.2016.09.001

Coulibaly, S., R.S. Pasquet, R. Papa and P. Gepts. 2002. AFLP analysis of the phonetic organization and genetic diversity of *Vigna unguiculata* L. Walp. reveals extensive gene flow between wild and domesticated types. Theor. Appl. Gen., 104: 358-366. https://doi.org/10.1007/s001220100740

Duc, G., H. Agrama, S.Y. Bao, J. Berger, V. Bourion and A.M. De Ron. 2015. Breeding annual grain legumes for sustainable agriculture: new methods to approach complex traits and target new cultivar ideotypes. CRC. Crit. Rev. Plant Sci,. 34: 381–411. https://doi.org/10.1080/07352689.2014.898469

FAOSTAT (FAO Statistics Division). 2016. http://faostat.fao.org.

Ghafoor, A., Z. Ahmad and R. Anwar. 2005. Genetic diversity in *Pisum sativum* and strategy for indigenous biodiversity conservation. Pak. J. Bot., 37(1): 71-77.

Gusmao, M.K.H., M. Siddique, K. Flower, H. Nesbitt and E.J. Veneklaas. 2012. Water deficit during the reproductive period of grass pea (*Lathyrus sativus* L.) reduced grain yield but maintained seed size. J. Agron. Crop Sci., 6(198): 430–441. https://doi.org/10.1111/j.1439-037X.2012.00513.x

Hesse, P.R. 1971. A textbook of soil chemical analysis (No. 631.41 H4).

Jatoi, S.A., A. Javaid, M. Iqbal, O.U. Sayal, M.S. Masood and S.U. Siddiqui. 2011. Genetic diversity in radish germplasm for morphological traits and seed storage protein. Pak. J. Bot., 43: 2507-212.

Jilani, T.A. 2008. Performance of different pea (*Pisum sativum* L.) cultivars for seed production under the agro-climatic conditions of Dera Ismail Khan. M.Sc. thesis (unpublished). Deptt. of Hort., Gomal Uni., D. I. Khan.

Junsomboon, J. and J. Jakmunee. 2011. Determination of potassium, sodium, and total alkalies in Portland cement, fly ash, admixtures, and water of concrete by a simple flow injection flame photometric system. J. Autom. Meth. Manage. Chem., 1:1–9. https://doi.org/10.1155/2011/742656

Khan, A., I.A. Khan and K. Habib. 2015. Response of pea varieties to insect pests in Peshawar. J. Ent. Zool., 3(3): 403-407.

Khan, T.N., A. Ramzan, G. Jilani and T. Mehmood. 2013. Morphological performance of peas (*Pisum sativum*) genotypes under rainfed conditions of Potowar region. J. Agric. Res., 51(1): 51-60.

Khichi, P., R. Pant and S. Upadhayay. 2017. Performance of garden pea varieties for their growth and yield characteristics in Vidharbha region of Maharashtra, India. J. Appl. Nat. Sci., 9(4): 2300-2304. https://doi.org/10.31018/jans.v9i4.1527

Khokhar, K.M., M.A. Khan, S.I. Hussain, T. Mahmood and H. Rehman. 1988. Comparative evaluation of some foreign and local pea cultivars. Pak. J. Agric. Res., 9(4):1-3.

Kosev, V., I. Pachev and A. Mikic. 2013. Assessing the breeding value of nine spring field pea (*Pisum sativum* L.) cultivars. Plant Breed. Seed Sci., 68: 55-64. https://doi.org/10.2478/v10129-011-0080-4

Kosev, V. 2015. Model of high-productive varieties in forage pea. J. Central Eu. Agric., 16(2): 172-180.

Muhammad, S., S. Bacha, M. Arshad, R. Din and A. Ghafoor. 2009. Genetic diversity for determining yield potential and selection criteria in *Pisum sativum* L., genetic resources. Pak. J. Bot., 41(6): 2987-2993.

Olsen, S.R., F.S. Watanabe., H.R. Cosper., W.E. Larson and L. B. Nelson. 1954. Residual phosphorus availability in long-time rotations on calcareous soils. Soil Sci., 78(2):141-152. https://doi.org/10.1097/00010694-195408000-00008

Peksen, E., A. Peksen, H. Bozoglu and A. Gulumser. 2004. Comparison of fresh pod yield and pod related characteristics in pea (*Pisum sativum* L.) cultivars sown in autumn and spring under Samsun ecological conditions. Turkish J. Agric., 28: 363-370.

Quarrie, S., Q.S. Pekic, Radosevic, R. Rancic, D. Kaminska, A. Barnes, J.D. Leverington, M. Ceoloni and C. Dodig. 2006. Dissecting a wheat QTL for yield present in a range of environments: from the QTL to candidate genes. J. Exp. Bot., 57(11): 2627-37. https://doi.org/10.1093/jxb/erl026

Santalla, M., J.M. Amurrio and A.M.D. Ron. 2001. Food and feed potential breeding of green dry and vegetable pea germplasm. Canadian J. Plant Sci., 81:601-610. https://doi.org/10.4141/P00-114

Seboka, H. and M. Fikresilassie. 2013. Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. Academic J., 55: 78-87. https://doi.org/10.5897/IJGMB2013.0080

Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and Procedures of Statistics. A Biometric Approach. 3rd ed. McGraw Hill Book Co., Inc, Singapore. 172-177.

Tan, M., A. Koc and Z.D. Gul. 2012. Morphological characteristics and seed yield of east Anatolian local forage pea (*Pisum sativum* L.) ecotypes. Turkish J. Field Crops, 17(1): 24-30.

Umar, H.M.I., S. Rehman, M. Bilal, S.A.H. Naqvi, S.A. Manzoor, A. Ghafoor, M. Khalid, M.T. Iqbal, A. Qayyum, F. Ahmad and M.A. Irshad. 2014. Evaluation of genetic diversity in pea (*Pisum sativum* L.) based on morpho-agronomic characteristics for yield and yield associated traits. J. Biol. Environ. Sci., 4(5): 321-328.

Walkley, A. and I.A. Black. 1934. An examination of the Degtjareff method for determining soil organic matter, and a proposed modification of the chromic acid titration method. Soil Sci., 37(1): 29-38. https://doi.org/10.1097/00010694-193401000-00003