

Multi-Locations Evaluation of Garden Pea Genotypes for Pod Characters and Yield

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Abstract

Pea genotypes developed by national breeding program exhibit wide geographical adaptation. To identify the best high yielding and wide adaptive genotypes, fourteen garden pea genotypes (13 improved and commercial) were studied for their phenotypic traits at two locations (Horticulture Research Station, Dailekh and Agriculture Research Station, Dhankuta) during 2018–2019. Field experiments were conducted at randomized complete block design with three replications in both locations. Combined analysis over the locations revealed that genotypes had highly significant ($p \leq 0.01$) effect on pod length, pod diameter, seed number/pod, pod weight and fresh pod yield. HRSDGP-11-18-1 produced the highest (12.5 t/ha) fresh pod yield, followed by HRSDGP-11-18-11 (12.3 t/ha) and the lowest (8.2 t/ha) fresh yield was recorded in HRSDGP-11-18-9. HRSDGP-11-18-1 and HRSDGP-11-18-11 had 25.0 and 23.0% higher yield advantage over Sikkim Local variety, respectively. Pod length, pod diameter and seed number/plot were significantly ($p \leq 0.01$), and positively correlated with fresh pod yield, and selection of these traits aid for the improvement of yield in garden pea genotypes. HRSDGP-11-18-1 and HRSDGP-11-18-11 were found superior at both locations and can be recommended to evaluate them at on-farm condition for further verification.

Keywords : Combined analysis, fresh pod yield, on-farm, phenotypic traits, pod characters

Introduction:

Pea (*Pisum sativum* L.) is one of the oldest important domesticated vegetable legumes in the world. Globally, it ranks fourth among the pulses and is grown in many countries. Regarding its production, China is the top producer of green peas with 11.2 million tons, followed by India (5.7 million tons) and USA (0.31 million tons) (FAOSTAT, 2021). In Nepal, it is also an important vegetable legume where fresh immature seeds are used as green vegetables. It is grown in winter in terai, autumn in mid hills and summer in high hills. It is one of the cheap source of protein having essential amino acids (23–25%) which have high nutritional values for poor people (Nawab et al., 2008). Being a legume crop, it also plays an important role in soil fertility management.

In Nepal, it is cultivated in 8,072 ha land with total production 73,936 t and average productivity of 9.2 t/

ha (MoALD, 2021). But in Karnali Province, it is cultivated in 518.0 ha land with production 4,425.0 t and productivity of 8.5 t/ha, and the productivity is lower than the national average. The productivity of green peas in Nepal is lower than India (10.12 t/ha) (FAOSTAT, 2021). In Koshi Province, the area of pea cultivated is 1,376 ha with total production of 10,580 t and productivity of 7.7 t/ha (MoALD, 2021). Lack of high yielding pea varieties is one of the serious factors for low green pea productivity in Nepal (Luitel et al., 2021). Three varieties of pea namely; 'Sarlahi Arkel', 'New Line' and 'Sikkime' are released (<https://sqcc.gov.np>) so far and limited varietal diversity in pea is also compelled to farmers for growing old pea varieties. As compared to major cereals and other vegetable crops, improved pea varieties available for farmers are very limited. But the farmers are cultivated pea crop as a source of income generation at hill and mountain regions.

Several studies have been done for the evaluation of horticultural traits in garden pea genotypes in different countries (Poudel et al., 2017; Kumar et al., 2018; Ofga, 2019; Luitel et al., 2023). But the genotypic performance across the locations has not been conducted so far. HRS, Dailekh and ARS, Dhankuta represent the mid-hill regions of Nepal where peas are predominantly grown. The high yielding genotypes are required for sustained production in these regions and therefore, advanced pea genotypes are needed to test in particular domain of the country. Crop yield is a complex trait and is associated with some yield contributing characters. The knowledge of association of characters is important for developing the breeding program. Correlation studies also provide the information about relationship between any two traits (Ofga, 2019). Therefore, the present study was conducted to assess the horticultural traits of pea genotypes at diverse environments, to examine the association among the phenotypic traits and to select high yielding genotypes for commercial cultivation particularly at mid-hills condition.

Materials and Methods:

Study site and climate

This study was conducted at two locations i.e. Horticulture Research Station (HRS), Dailekh (28°50' 49.8" N longitude and 81° 43' 19.4" E latitude, 1,255 meters above sea level) and Agriculture Research Station (ARS), Pakhribas, Dhankuta (27.046033 °N and longitude 87.292939° E, 1,730 m asl) during Oct. 2018 – Mar. 2019. At Dailekh, the annual rainfall amount ranges between 140 and 160 mm and the distribution is high around June-July (HRS, 2019). The maximum and minimum temperature, relative humidity and total rainfall distribution during pea trials at both locations is presented in Table 1. Minimum temperature at Dailekh ranges from 6.3 to 13.5°C and the maximum temperature ranges from 9.2 to 27.6°C. Dhankuta is a relatively warmer region than Dailekh, but similar rainfall pattern was observed at both experimental sites (Table 1). The soil texture at HRS, Dailekh was loamy type with pH ranges from 5.5 to 6.0. At ARS, Pakhribas, the trial was established at 1,700 m asl and it receives the average

annual rainfall of 1,600 mm. Minimum temperatures ranges from 2.0 to 9.0°C and maximum temperature ranges from 15.7 to 23.5°C. The soil texture at Dhankuta consisted of 56.61% sand, 27.62% silt and 15.77% clay and is categorized as loamy to sandy loam type (Khadka et al., 2019).

Plant materials and cultivation

Seeds of 13 improved pea genotypes (HRSDGP-11-18-1, HRSDGP-11-18-2, HRSDGP-11-18-3, HRSDGP-11-18-4, HRSDGP-11-18-5, HRSDGP-11-18-6, HRSDGP-11-18-7, HRSDGP-11-18-8, HRSDGP-11-18-9, HRSDGP-11-18-10, HRSDGP-11-18-11, HRSDGP-11-18-11, HRSDGP-11-18-12, HRSDGP-11-18-13) and one commercial variety, Sikkim Local from HRS, Dailekh were used for the experiments at both research stations. These genotypes were indeterminate types and selected from Preliminary Yield Trial (PYT) of pea at HRS, Dailekh. Field was prepared by tilted at both locations, then pulverized and leveled. Two seeds were manually placed in each hill, and the plants were thinned when they emerged to maintain plant population. Seeds were sown on October, 2018 at both stations and inter- and intra-row spacing was maintained at 75 cm and 10 cm, respectively. Experiments were laid out in randomized complete block design (RCBD) with three replications, and total 24 plants were maintained at each plot with the plot size of 6 m² (3 m × 2 m). A total of 15 t/ha of farmyard manure (FYM) and 30:40:40 kg/ha of NP₂O₅K₂O fertilizer were applied. The sources of nutrients to be supplied were fertilizers: urea (46% N), di-ammonium phosphate (46% P₂O₅, 18% N) and muriate of potash (60% K₂O). Before planting at land preparation, the full amount of nitrogen, phosphorus and potassium were applied. During the crop growing season, crop management

Table 1 : Weather data of HRS, Dailekh and ARS, Dhankuta during the garden pea experiments, 2018/2019

Months	HRS, Dailekh				ARS, Dhankuta			
	Av. Temp. (°C)		RH (%)	Total rainfall (mm)	Av. Temp. (°C)		RH (%)	Total rainfall (mm)
	Max.	Min.			Max.	Min.		
Oct.	27.6	13.5	78.9	0.0	23.5	9.0	74.5	1.0
Nov.	23.8	10.4	81.7	0.08	19.4	6.8	66.1	0.0
Dec.	19.7	6.9	72.5	0.0	16.5	2.0	64.5	1.0
Jan.	9.2	6.3	74.3	1.3	15.7	2.4	55.4	1.0
Feb.	9.3	7.5	76.6	7.2	16.4	3.0	68.9	7.0
Mar.	9.7	7.5	71.1	1.5	19.9	3.5	66.4	2.0

RH = Relative humidity. Source: Department of Hydrology and Meteorology, Surkhet, Karnali and Koshi Province, 2018/2019

techniques including weeding, staking, and watering were performed as recommended by Chalise and Pun (2015).

Data collection and statistical analysis

Observations including days to 50% flowering (DTF), pod length (cm) and diameter (mm), seed number/pod, pod weight (kg/plot) and fresh pod yield (t/ha) were measured at two rows (3 m²). DTF was recorded when 50% of the plant at each plot produced flower. The average length (cm) and diameter (mm) of pod was measured on randomly selected 10 pods at commercial maturity stage using scale and Vernier caliper (150 mm, Model: DC-515), respectively. The number of seeds were counted on 10 pods of each five plant at commercial maturity stage and averaged. Fresh pod weight (kg) was measured at each two rows and cumulative weight was accounted to calculate it and then, fresh pod yield (t/ha) was determined.

Data were summarized using Microsoft Excel (version

16.0, Microsoft, Redmond, WA, USA) and analyzed using GenStat Release 10.3 DE Software (VSN International Ltd., UK). Phenotypic correlation coefficients were analyzed using SPSS (SPSS Inc., Chicago, Ill., USA).

Results and Discussion:

DTF and pod length

Genotypes, locations and genotypes, and their interaction effect on DTF was non-significant ($p \geq 0.05$) (Table 2). However, highly significant ($p \leq 0.01$) differences in pod length was observed among the genotypes. The combined mean over the locations revealed that the highest pod length (9.3 cm) was measured in HRSDGP-11-18-8 and the lowest (7.2 cm) was measured in HRSDGP-11-18-6. Pod length is a genetic trait and earlier researchers (Lakic et al., 2017; Luitel et al., 2021; 2023) have reported the significant ($p \geq 0.05$) differences for pod length in pea genotypes. Locations had significant ($p \leq 0.05$) effect on pod length, but the interaction effect between genotypes and locations was non-significant ($p \geq 0.05$) (Table 2).

Table 2 : DTF and pod length of garden pea genotypes evaluated at HRS, Dailekh and ARS, Pakhribas, 2018/19

Genotypes	DTF		Mean	Pod length (cm)		Mean
	HRS, Dailekh	ARS, Pakhribas		HRS, Dailekh	ARS, Pakhribas	
HRSDGP-11-18-1	64.0	66.0	65.0	7.4	7.6	7.5
HRSDGP-11-18-2	64.0	67.0	65.0	7.6	7.3	7.4
HRSDGP-11-18-3	68.0	67.0	68.0	7.4	7.3	7.4
HRSDGP-11-18-4	69.0	68.0	68.0	7.5	7.2	7.4
HRSDGP-11-18-5	64.0	67.0	65.0	7.4	7.5	7.5
HRSDGP-11-18-6	68.0	66.0	67.0	7.1	7.4	7.2
HRSDGP-11-18-7	74.0	66.0	70.0	8.9	8.3	8.6
HRSDGP-11-18-8	55.0	68.0	61.0	9.3	9.3	9.3
HRSDGP-11-18-9	64.0	68.0	66.0	8.6	8.3	8.5
HRSDGP-11-18-10	65.0	67.0	66.0	7.3	7.4	7.4
HRSDGP-11-18-11	63.0	68.0	66.0	8.2	8.1	8.1
HRSDGP-11-18-12	68.0	68.0	68.0	8.3	8.2	8.2
HRSDGP-11-18-13	69.0	66.0	68.0	8.5	8.1	8.3
Sikkim Local (Check)	70.0	68.0	69.0	8.3	8.2	8.2
Mean	66.0	67.14	66.57	7.99	7.87	7.93
Genotypes (G)			NS			**
Locations (L)			NS			*
G × L			NS			NS
LSD						
Genotypes (G)			7.35			0.33
Locations (L)			2.78			0.12
G × L			10.40			0.47
CV (%)			9.5			3.7

NS, *, and **; non-significant or significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

Pod diameter and number of seed/pod

Genotypes showed highly significant ($p \leq 0.01$) effect on pod diameter and number of seed /pod (Table 3). The highest (12.4 mm) pod diameter was measured in HRSDGP-11-18-8, followed by HRSDGP-11-18-9 (12.0 mm) and the lowest (9.7 mm) diameter was measured in HRSDGP-11-10. Likewise, maximum (7.0) number of seed/pod was counted in HRSDGP-11-18-11 and the lowest (5.0) number was counted in HRSDGP-11-18-8, HRSDGP-11-18-9, HRSDGP-11-18-12 and Sikkim Local. Genotypes and locations interaction in number of seed/pod was significant ($p \leq 0.05$) (Table 3). The significant ($p \leq 0.05$) variation in pod diameter and number of seed/pod in pea cultivars have reported in previous studies (Khichi et al., 2017; Poudel et al., 2017; Luitel et al., 2023).

Pod weight and fresh pod yield

Pod weight/plot and fresh pod yield were highly significantly ($p \leq 0.01$) influenced by the genotypes (Table 4). The highest pod weight (3.8 kg/plot) was recorded in HRSDGP-11-18-1, followed by HRSDGP-11-18-2 (3.6 kg/plot) and the lowest (2.4 kg/plot) pod weight was recorded in HRSDGP-11-18-12. Similarly, the highest (12.5 t/ha) pod yield was recorded in HRSDGP-11-18-1, followed by HRSDGP-11-18-11 (12.3 t/ha) and HRSDGP-11-18-2 (12.1 t/ha) and the lowest (8.2 t/ha) was measured in HRSDGP-11-18-9. Significant ($p \leq 0.05$) differences in fresh pod yield in pea genotypes have reported by many researchers (Khichi et al., 2017; Din et al., 2019; Luitel et al., 2023). Poudel et al. (2017) have reported the highest fresh pod yield (18.14 t/ha) in DGP-09, but this study found the highest fresh pod yield (12.5

Table 3 : Pod diameter and number of seed/pod of garden pea genotypes evaluated at HRS, Dailekh and ARS, Pakhribas, 2018/19

Genotypes	Pod diameter (mm)		Mean	Seed/pod (no.)		Mean
	HRS, Dailekh	ARS, Pakhribas		HRS, Dailekh	ARS, Pakhribas	
HRSDGP-11-18-1	12.4	10.4	11.4	6.0	6.0	6.0
HRSDGP-11-18-2	12.4	11.2	11.8	6.0	6.0	6.0
HRSDGP-11-18-3	12.7	11.0	11.9	6.0	5.0	6.0
HRSDGP-11-18-4	11.9	11.1	11.5	6.0	5.0	6.0
HRSDGP-11-18-5	10.8	10.8	10.8	6.0	5.0	6.0
HRSDGP-11-18-6	11.2	10.3	10.7	6.0	6.0	6.0
HRSDGP-11-18-7	12.1	11.6	11.8	7.0	5.0	6.0
HRSDGP-11-18-8	12.5	12.3	12.4	5.0	5.0	5.0
HRSDGP-11-18-9	13.9	10.2	12.0	5.0	5.0	5.0
HRSDGP-11-18-10	10.8	8.7	9.7	6.0	5.0	6.0
HRSDGP-11-18-11	12.4	10.0	11.2	7.0	6.0	7.0
HRSDGP-11-18-12	12.7	10.3	11.5	5.0	4.0	5.0
HRSDGP-11-18-13	13.0	8.9	10.9	7.0	5.0	6.0
Sikkim Local (Check)	14.3	9.0	11.6	5.0	5.0	5.0
Mean	12.37	10.41	11.39	5.9	5.2	5.8
Genotypes (G)			**			**
Locations (L)			**			**
G × L			**			*
LSD						
Genotypes (G)			0.71			0.52
Locations (L)			0.26			0.19
G × L			1.01			0.73
CV (%)			5.4			8.3

*, and **, significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

t/ha) in HRSDGP-11-18-1. This might be due to genetic-make up the cultivars. Besides, the growth habit of the cultivar also differs the yield potential. Shinde (2000) has reported the genetic variability for phenotypic traits in 73 pea genotypes. The locations effect on fresh pod yield was significant ($p \leq 0.05$), but the effect of genotypes and locations on pod yield was highly significant ($p \leq 0.01$) (Table 4). The locations effect on fresh pod yield might be due to the variation in agro-climatic and soil edaphic factors. The fresh yield was relatively higher at Dailekh than Dhankuta and this might be due to frost and powdery mildew disease problems (data not shown). But the variation in fresh pod yield was not statistically different. Yield is a complex trait determined by the interaction of many heritable characters with soil, climate and agronomic conditions (Makasheva, 1983). Proper vegetative growth requires to achieve the highest yield (Muehlbauer and McPhee, 1997). In the present study, genotypes HRSDGP-11-18-1 and HRSDGP-11-18-11 had good pod characters and more number of seed/pod that resulted in higher fresh yields compared to commercial variety Sikkim Local. Though some genotypes had good pod characters and more seed number/pod, they resulted low yield which might be due to the agro-climatic condition. The genotypes performed differently at different locations. Khichi et al. (2017) have reported the similar results in the study of pea genotypes.

Phenotypic correlation

The phenotypic correlation coefficients of studied traits in pea genotypes are presented in Table 5. DTF was significantly ($p \leq 0.01$) and positively correlated with pod length ($r = 0.42$) but it showed significant ($p \leq 0.01$) and negative correlation with pod weight/plot ($r = -0.65$). Pod length had significantly ($p \leq 0.01$) and negative correlated with pod diameter ($r = -0.62$), but it showed significant ($p \leq 0.01$) positive association with number of seed/pod ($r = 0.41$), pod weight ($r = 0.51$) and fresh yield ($r = 0.54$). Luitel et al. (2021) have also reported the significant ($p \leq 0.05$) positive association of pod length with fresh pod yield in garden pea genotypes. The positive correlation between pod length and pod weight has also mentioned in a study by Kumawat et al. (2018). The significant and positive association between pod length and number of seed/pod has reported in pea (Kaur et al., 2023). Pod diameter was positively and significantly ($p \leq 0.05$) correlated with pod weight/plot ($r = 0.52$) and fresh pod yield ($r = 0.61$). Similarly, seed number/pod showed the significant ($p \leq 0.01$) positive correlation with pod weight ($r = 0.72$) and fresh yield ($r = 0.66$). This result agrees with the findings of Pandey et al. (2017) who reported significant ($p \leq 0.05$) and positive correlation between seed number/pod and fresh pod yield. The highly significant ($p \leq 0.01$) positive correlation ($r = 0.61$) was observed between pod weight/plot and fresh yield (Table 5).

Table 4 : Pod wt. and fresh pod yield (t/ha) of garden pea genotypes evaluated at HRS, Dailekh and ARS, Pakhribas, 2018/19

Genotypes	Pod wt./plot (kg)		Mean	Fresh pod yield (t/ha)		Mean
	HRS, Dailekh	ARS, Pakhribas		HRS, Dailekh	ARS, Pakhribas	
HRSDGP-11-18-1	3.6	3.9	3.8	11.9	13.0	12.5
HRSDGP-11-18-2	3.9	3.3	3.6	13.1	11.1	12.1
HRSDGP-11-18-3	3.0	3.2	3.1	10.0	10.5	10.3
HRSDGP-11-18-4	2.6	2.9	2.8	8.7	9.7	9.2
HRSDGP-11-18-5	2.7	4.3	3.5	9.1	14.3	11.7
HRSDGP-11-18-6	3.1	3.6	3.4	10.4	12.0	11.2
HRSDGP-11-18-7	3.2	2.8	3.0	10.7	9.3	9.9
HRSDGP-11-18-8	2.7	2.9	2.8	8.9	9.8	9.4
HRSDGP-11-18-9	2.9	2.1	2.5	9.5	6.8	8.2
HRSDGP-11-18-10	3.9	2.5	3.2	12.9	8.3	10.6
HRSDGP-11-18-11	3.9	2.7	3.3	13.4	11.2	12.3
HRSDGP-11-18-12	2.8	1.9	2.4	9.3	7.9	8.6
HRSDGP-11-18-13	4.5	2.0	3.3	15.2	6.7	10.9
Sikkim Local (Check)	3.3	2.7	3.0	10.3	9.7	10.0
Mean	3.29	3.25	3.27	10.95	10.02	10.80
Genotypes (G)			**			**
Locations (L)			**			*
G × L			**			**
LSD						
Genotypes (G)			0.86			1.41
Locations (L)			0.46			0.91
G × L			1.73			2.40
CV (%)			22.1			19.3

NS, *, and **, non-significant or significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

Table 5 : Phenotypic correlation coefficients of measured traits in garden pea genotypes at HRS, Dailekh and ARS, Pakhribas, 2018/19

Traits	DTF	PL	PD	SN	PWT	FPY
DTF	1.0	0.42**	0.19	0.10	-0.65**	-0.12
PL		1.0	-0.62**	0.41**	0.51**	0.54**
PD			1.0	0.27*	0.52**	0.61**
SN				1.0	0.72**	0.66**
PWT					1.0	0.61**
FPY						1.0

*, ** significant at $p \leq 0.05$ and $p \leq 0.01$, respectively. DTF; Days to 50% flowering (days), PL; Pod length (cm), PD; Pod dia. (mm), SN; Seed number/pod, PWT; Pod weight/plot (kg), and FPY; Fresh pod yield (t/ha).

Conclusion:

We evaluated the phenotypic traits of 14 garden pea genotypes (13 improved genotypes and commercial) at HRS, Dailekh and ARS, Dhankuta. Except DTF, genotypes and locations influenced significantly ($p \leq 0.05$) in all the studied traits. From the combined analysis, average fresh pod yield showed higher in HRSDGP-11-18-1 (12.5 t/ha), followed by HRSDGP-11-18-11 (12.3 t/ha) and HRSDGP-11-18-2 (12.1 t/ha) than commercial variety, Sikkim Local (10.0 t/ha). Pod length, pod diameter, seed number/pod and pod weight had significantly ($p \leq 0.01$) and positively correlated with fresh pod yield and hence, selection of these traits infers the improvement of yield through simple selection. From this study, HRSDGP-11-18-1 and HRSDGP-11-18-11 are identified as high yielding genotypes at both locations and can be recommended to grow at similar agro-climatic regions of the country. Furthermore, these genotypes should be up-scaled further at on-farm for commercial production.

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Declaration of conflict of interest and ethical approval:

BP Luitel involved in designing the experiments, analyzing the data and writing the manuscript. KP Poudel and BB Bhandari conducted the experiments at ARS, Pakhribas and HRS, Dailekh, respectively. The authors declare no conflict of interest for the publication of this article.

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