

Research Article

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Identifying phosphorus use efficient genotypes by evaluating a chickpea reference set across different phosphorus regimes

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Abstract

Low phosphorus use efficiency (PUE) is one of the abiotic factors that hamper yield and production potential in chickpea (*Cicer arietinum* L.). Higher yield coupled with improved PUE can make this crop more adaptive and competitive to wide cropland area, especially on marginal soils having low-level phosphorus (P). To identify chickpea germplasm lines that assimilate phosphorus more efficiently under P-deficient soils, 288 diverse genotypes of chickpea belonging to reference set were evaluated for yield component traits and PUE under field conditions for two consecutive years at two phosphorus levels (low P – no phosphorus application and high P – phosphorus application at 40 kg/ha). Based on 2-year evaluation of data under high and low P soil conditions, we identified strong correlations for traits like number of primary and secondary branches, number of pods, biological yield and seed yield indicating that these traits can be used as proxy traits for PUE. ICC 6571 was the best performing genotype under low P conditions while ICC 6579 yielded maximum under high P regime. We report 16 genotypes namely ICC 1052, ICC 1083, ICC 1098, ICC 1161, ICC 2072, ICC 4418, ICC 4567, ICC 4991, ICC 5504, ICC 5639, ICC 7413, ICC 8350, ICC 9590, ICC 9702, ICC 11584 and ICC 13357 as phosphorus use efficient genotypes based on their better performance for yield and yield-contributing traits under low P compared to high P conditions. These genotypes can be exploited in future as potential donors for development of phosphorus use efficient chickpea cultivars.

Introduction

Phosphorus (P) is a major macronutrient required for proper plant growth and reproduction. It is entailed in various key physiological and biological processes of the plant such as photosynthesis, energy transfer, nutrients mobilization, carbohydrate transportation including metabolism and also a key component of nucleic acids (Lambers *et al.*, 2015; Meng *et al.*, 2021). Very obvious symptoms like purple-coloured leaves, reduced plant height and reedy stem can be noticed when plants face phosphorus starvation (Zribi *et al.*, 2017). The photosynthetic efficiency of plants is severely affected by phosphorus deficiency (Carstensen *et al.*, 2018; Meng *et al.*, 2021). Reduced number of pods and tillers in legumes and cereals, respectively, has been recorded upon inadequate P supply (Fageria, 2007; Fageria and Santos, 2008). In particular, leguminous crops need more P than other crop species owing to heavy consumption of this macronutrient during nitrogen fixation by legumes (Sprent, 1999; Lyu *et al.*, 2016). However, in almost all crop species, plants use only 10–30% of the applied P (Syers *et al.*, 2008) while rest of P remains in soil creating pool of residual P where it leads to negative environmental impacts (Conijn *et al.*, 2018). Moreover, phosphorus is entering into the list of depleting macronutrients predominantly in acidic and alkaline soils of tropical and sub-tropical regions (Krishnappa *et al.*, 2011). It has been postulated that in coming next 60–130 years, the exploitable P reserves will be completely depleted (Steen, 1998; Liu *et al.*, 2008; Cordell *et al.*, 2009). Additionally, mining of the phosphorus from other possible sources will affect the cost of fertilizer use. Breeding for improved phosphorus use efficiency (PUE) can help to solve both ecological and cost issues (Bovill *et al.*, 2013). PUE can be enhanced by improving phosphorus uptake and utilization efficiency (van de Wiel *et al.*, 2016). P uptake efficiency is more important under low phosphorus environment, whereas P utilization efficiency is more significant under surplus P availability to improve PUE.



Chickpea (*Cicer arietinum* L.) is one of the important legume crops cultivated widely in more than 50 countries. India is the world's leading producer of chickpea contributing about 75% of total global production (Dixit *et al.*, 2019; Gaur *et al.*, 2019). Regardless of having huge potential, chickpea productivity is constrained by various biotic and abiotic stresses along with its poor response to management practices. It is evident that conventional breeding method is not enough to cope up with these problems (Varshney *et al.*, 2010; Garg *et al.*, 2015; Jain *et al.*, 2023). One of the major bottle necks of the chickpea improvement programme is the use of existing variability with limited genetic base. Further, the replacement of landraces and traditional cultivars by genetically uniform high-yielding varieties has led to loss of variability accompanied by more vulnerability to various biotic and abiotic factors (Ficiciyan *et al.*, 2018). Therefore, the genetic potential of chickpea along with stable higher yield with minimal environmental effects needs to be improved that can be achieved by the exploitation of desirable alleles from diverse genotypes as base materials (Sharma and Sharma, 2015). All these factors emphasized the development of stable high-yielding and stress resistance cultivars for which there is a need of conservation and maintenance of different germplasm accessions and further exploit underutilized alleles within wild relatives, landraces and exotic lines. Considering the importance of preservation and utilization of gene pool, a reference set of 300 accessions using allelic diversity data to represent the whole genetic diversity in genus *Cicer* was developed (Upadhyaya *et al.*, 2006; Upadhyaya *et al.*, 2008). This diverse chickpea reference set can be utilized for future chickpea breeding programmes to study and explore underrated or neglected traits like PUE.

At present when P is becoming one of the deficient macronutrients in majority of cultivated land, there is a dire necessity of exploitation of genetic diversity in chickpea with special reference to the PUE that has not been utilized yet. Moreover, use of higher levels of P fertilizers induces Zn deficiency in plants (Srinivasarao *et al.*, 2006) and depletion of exhaustible natural phosphorus deposits (Reijnders, 2014). So, to meet the high demands of exhaustible resources of phosphatic fertilizers, intraspecific genetic variability should be studied and exploited. Therefore, designing crop varieties with high productivity and enhanced PUE may help to make optimum use of P fertilizers without compromising seed yields. This may also help in coping with environmental and hydrological issues arising through heavy fertilizer application (Ahmad *et al.*, 2001). Keeping in view, the present study was attempted to identify the chickpea genotypes with high PUE that further expose new horizons in chickpea breeding programme facing the problem of low phosphorus.

Materials and methods

Plant material

A set of 288 chickpea genotypes from the reference set was evaluated for PUE based on the performance of genotypes for seed yield under low P compared to high P conditions and yield-contributing traits at Punjab Agricultural University (PAU), Ludhiana, India. The chickpea reference set effectively captures a substantial portion of the genetic variation present in the entire chickpea germplasm across the globe. Specifically, it encompasses 78% of the alleles found in the composite collection, indicating that it is a comprehensive representation of genetic diversity. Furthermore, the reference set exhibits variation in seed types,

with *desi*, *kabuli* and pea-shaped accessions among cultivated types, in addition to wild *Cicer* accessions. This diversity is crucial for breeding programmes as it provides a broad genetic base to work with, potentially enhancing resilience, adaptability and overall performance of chickpea varieties.

Evaluation of chickpea reference set

The experiments were conducted for two consecutive years *viz.*, 2018–19 and 2019–20 in alpha-lattice design under two phosphorus regimes (low P – no phosphorus application and high P – phosphorus application at 40 kg/ha). Therefore, four sets of experiments (E) namely, low P 2018–19 (E1), high P 2018–19 (E2), low P 2019–20 (E3) and high P 2019–20 (E4) were set up in two replications. Each genotype was planted in paired rows of 1.5 m length keeping row-to-row and plant-to-plant spacing of 30 cm × 10 cm in Ludhiana. It is positioned at a latitude of 30°54' N, signifying its placement north of the equator, and with a longitude of 75°48' E, the experimental site boasted an altitude of 247 m above sea level.

Agro-morphological traits

Data were meticulously recorded on five random plants for each genotype, encompassing a range of vital traits including plant height (cm), number of primary branches, number of secondary branches, number of pods per plant and seeds per 10 pods (g). The data for all other traits were recorded on per plot basis including days to germination, days to flower initiation, days to 50% flowering, days to maturity, as well as crucial photosynthetic parameters such as chlorophyll content at the pre-flowering stage. The chlorophyll content was measured using SPAD Chlorophyll Meter Readings (SCMR) obtained from a SPAD-502 meter (Minolta Konica Co. Ltd., Japan). Additionally, other important traits contributing to yield were documented on per plant basis as an average including biological yield per plant (g), seed yield per plant (g) and harvest index (%). Harvest index (%) was calculated as: economic yield/biological yield × 100; where economic yield corresponds to total grain yield per plant (g); and biological yield is the total dry weight per plant (g).

Soil analysis and phosphorus use efficiency

The soil texture in the experimental site was loamy sand as the content of sand, silt and clay in the experimental field was 78.8, 7.9 and 13.2%. On soil test basis, the average pH of the experimental site was 7.8 and EC was 0.11 dS/m. Organic carbon, available nitrogen (N), phosphorous (P) and potassium (K) were 0.26%, 128 kg/ha, 9.85 kg/ha and 152 kg/ha, respectively. The available Zn, Fe and Cu were 0.82, 5.32 and 24 ppm, respectively. PUE was estimated using equation adopted from Moll *et al.* (1982): seed yield (kg/ha)/P_{Soil} + P_{Applied}; where P_{Soil} corresponds to natural P content of soil (kg/ha) and P_{Applied} is P dose allocated through fertilizer (kg/ha).

Statistical analyses

The data were subjected to analysis of variance (ANOVA) using proc GLM procedure of SAS software (SAS 2013). Correlation among various traits was estimated using R software (R Core Team, 2020). Phenotypic and genotypic correlation coefficients

Table 1. Pooled analysis of variance for low P and high P regimes (2018–19 and 2019–20)

SV	DF	Traits													
		GERMI	FI	F50	SCMR	NPB	NSB	DTM	PH	NOP	SP10P	SW100	BY	SY	HI
Mean sum of squares under low P regime															
G	287	0.51*	82.08*	128.57*	87.31*	0.24*	19.60*	76.71*	281.10*	213.96*	13.37*	136.15*	112.98*	14.51*	32.11*
Rep	1	0.17	88.88*	119.48*	6.91	0.03	59.89*	0.50	151.38*	12958.48*	8.37*	9.89	321.35*	18.00*	3.62
Block (Rep)	30	0.29	11.89	4.72	207.27*	0.12	3.73	4.08	9.44	13.64*	2.49	1.46	15.72	1.39	12.75
Year	1	4.5*	249.39*	89.44*	0.27	133.10*	81.65*	2194.53*	90.90*	4275.20*	48.27*	73.83*	2501.20*	453.38*	34.66
G × year	287	0.41*	7.36*	13.55*	4.42	0.28*	4.28	12.44*	25.67*	143.15*	4.64*	2.53*	113.43*	8.63*	25.73*
Mean sum of squares under high P regime															
G	287	0.67*	190.43*	184.13*	113.88*	0.15*	18.57*	25.49*	332.60*	362.21*	12.01*	139.82*	82.53*	9.91*	15.70*
Rep	1	52.95*	5.98	140.98*	0.004	1.16*	510.28*	1.32	362.47*	9860.99*	11.68	6.32	2761.94*	507.87*	63.89*
Block (Rep)	30	0.45	7.57	12.88	111.04	0.11	28.50*	6.27*	16.32	137.91*	2.45	3.73	29.04	3.29	6.56
Year	1	10.31*	221.38*	82.88*	0.53	39.87*	30.21*	9.93*	3.31	1011.52*	1.25	170.33*	32505.60*	1640.02*	2742.07*
G × year	287	0.40*	8.03*	17.35*	4.73	0.14*	4.26	156.79*	28.94*	11.15	4.02*	3.46*	56.75*	6.93*	14.98*

SV, source of variation; DF, degrees of freedom; GERMI, days to germination; F50, days to flower initiation; SCMR, chlorophyll content; NPB, number of primary branches; NSB, number of secondary branches; DTM, days to maturity; PH, plant height (cm); NOP, number of pods per plant; SP10P, seeds per 10 pods; SW100, 100-seed weight (g); BY, biological yield (g); SY, seed yield per plant (g); HI, harvest index (%); G, genotype; Rep, replication. *Significant at $P=0.05$.

were estimated using the standard procedure suggested by Miller *et al.* (1958) and Kashiani and Saleh (2010).

Results

Phenotypic variation under different phosphorus (P) regimes

The ANOVA results revealed significant variability among the genotypes for all the investigated traits under both phosphorus regimes for two cropping seasons during 2018–19 and 2019–20 except chlorophyll content in individual environments (Table 1; online Supplementary Tables S1 and S2).

Days to germination in all four environments ranged from 7 to 10 days with a mean of 8.06 in E1, 8.65 in E2, 8.18 in E3 and 8.46 in E4. Days to flower initiation was observed to be increased under high P conditions in both years, mirroring the trend observed for days to 50% flowering (Table 2). The mean values for number of primary branches were 2.26 in E1, 2.07 in E2, 1.58 in E3 and 1.70 in E4. Similarly, for number of secondary branches, observed mean values were 13.54 (E1), 16.39 (E2), 14.07 (E3) and 16.06 (E4) (Table 2) revealing positive impact of high P on the trait.

The days to maturity showed a decline under high P conditions, while plant height was observed to be more under high P than low P regime. The number of pods per plants showed positive effect of high P in both the years of experiment, although seeds per 10 pods decreased (Table 2). The 100-seed weight also followed a similar (decreasing) trend under high P conditions. Biological yield reduced in the first year but increased in the second year under high P. Mean seed yield per plant demonstrated a positive effect of high P; 13.52 g (E1), 14.01 g (E2), 14.77 g (E3) and 16.40 g (E4). The positive effect of high P on harvest index was observed only during the first year with a mean of 33.11, 36.38, 33.45 and 33.29 in E1, E2, E3 and E4, respectively.

The mean values and range for morphological data have been given in Table 2.

Better performing genotypes under different phosphorus conditions

The genotype ICC 5639 was found with highest mean increase (44.65%) in seed yield during the cropping seasons 2018–19 and 2019–20 under low P conditions in comparison to high P conditions followed by genotypes namely, ICC 7413, ICC 11584, ICC 13357, ICC 9590, ICC 2072, ICC 4418, ICC 4567, ICC 9702, ICC 5504, ICC 1161, ICC 1098, ICC 1052, ICC 1083, ICC 4991 (Fig. 1(a)). These results indicated that these genotypes were more efficient for P-use efficiency for seed yield. In addition, PUE under low P conditions was compared with PUE at high P conditions through scatter diagram to determine the efficiency of genotypes. This classified the reference set into four classes *viz.*, non-efficient non-responder, efficient non-responder, non-efficient responder and efficient responder (Fig. 1(b)). Under low P conditions, above average genotypes were considered as efficient. Overall, efficient genotypes have higher utilization of absorbed P over non-efficient genotypes.

The genotypes ICC 4567, IG 10419, ICC 13187, ICC 1923, IG 6343, ICC 8350, ICC 5504, ICC 13357, ICC 3410, ICC 1715, ICC 7668, ICC 15762, ICC 8151, ICC 15888 and ICC 8200 recorded remarkably higher number of pods per plant under low P conditions as compared to high P conditions during both the cropping seasons 2018–19 and 2019–20 (Fig. 2(a)).

Likewise, the genotypes having variation for seeds per 10 pods, biological yield and harvest index with highest per cent increase under low phosphorus conditions than high phosphorus conditions have been depicted in Fig. 2(b)–2(d), respectively. The

Table 2. Mean and range of various traits across different environments

Traits	Low P 2018–19 (E1)		High P 2018–19 (E2)		Low P 2019–20 (E3)		High P 2019–20 (E4)	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Germination	8.06	7.00–10.00	8.65	7.00–10.00	8.18	7.00–10.00	8.46	7.00–10.00
Days to flower initiation	96.03	80.00–115.00	97.61	78.00–120.00	95.10	77.00–115.00	96.73	83.00–121.00
Days to 50% flowering	106.11	87.00–124.00	107.58	87.00–127.00	105.55	91.00–121.00	108.11	93.00–128.00
Chlorophyll content (SPAD)	52.74	36.54–64.77	52.72	31.95–64.99	52.71	37.41–65.27	52.77	35.14–67.10
Number of primary branches	2.26	1.16–3.45	2.07	1.43–3.20	1.58	0.91–2.66	1.70	0.91–2.70
Number of secondary branches	13.54	9.18–24.81	16.39	8.66–23.95	14.07	6.42–28.54	16.06	7.91–26.55
Days to maturity	156.69	150.00–169.00	155.53	146.00–165.00	159.45	151.00–175.00	154.79	149.00–166.00
Plant height (cm)	49.91	29.21–77.57	50.14	28.56–85.27	49.35	23.72–82.15	50.03	30.67–90.67
Number of pods per plant	49.81	29.59–80.78	50.35	29.48–87.30	45.96	25.12–76.36	52.23	28.65–91.77
Seeds per 10 pods	12.70	9.28–20.72	12.57	9.35–21.12	13.11	9.46–21.22	12.64	8.97–19.65
100-seed weight (g)	17.81	8.87–39.64	17.76	8.57–38.27	17.30	9.53–46.41	16.99	8.43–38.17
Biological yield (g)	41.46	25.44–82.71	38.74	29.53–68.22	44.41	30.79–80.64	49.36	37.38–86.52
Seed yield per plant (g)	13.52	9.69–24.58	14.01	11.05–26.55	14.77	9.51–22.19	16.40	11.46–24.55
Harvest index (%)	33.11	17.66–45.61	36.38	25.22–43.69	33.45	20.01–45.66	33.29	23.69–41.19

genotype ICC 13357 performed better for seed yield and yield-contributing traits like number of pods per plant and harvest index under low P conditions (Figs 1(a), 2(a), 2(d)). Similarly, the genotype ICC 11584 performed better under low P conditions for seed yield and harvest index (Figs 1(a) and 2(d)). Some other genotypes showed remarkably higher values for the yield-contributing traits *viz.*, number of pods per plant, seeds per 10

pods, biological yield and harvest index under low P conditions. The genotypes ICC 4567 and ICC 5504 performed better under low P for the seed yield and yield-contributing traits namely number of pods and biological yield (Figs 1(a), 2(a), 2(c)). Genotype ICC 16654 also showed promise for seeds per 10 pods and biological yield (Fig. 2(b) and 2(c)). The genotypes ICC 1161 and ICC 4991 performed better under low P regime as compared to

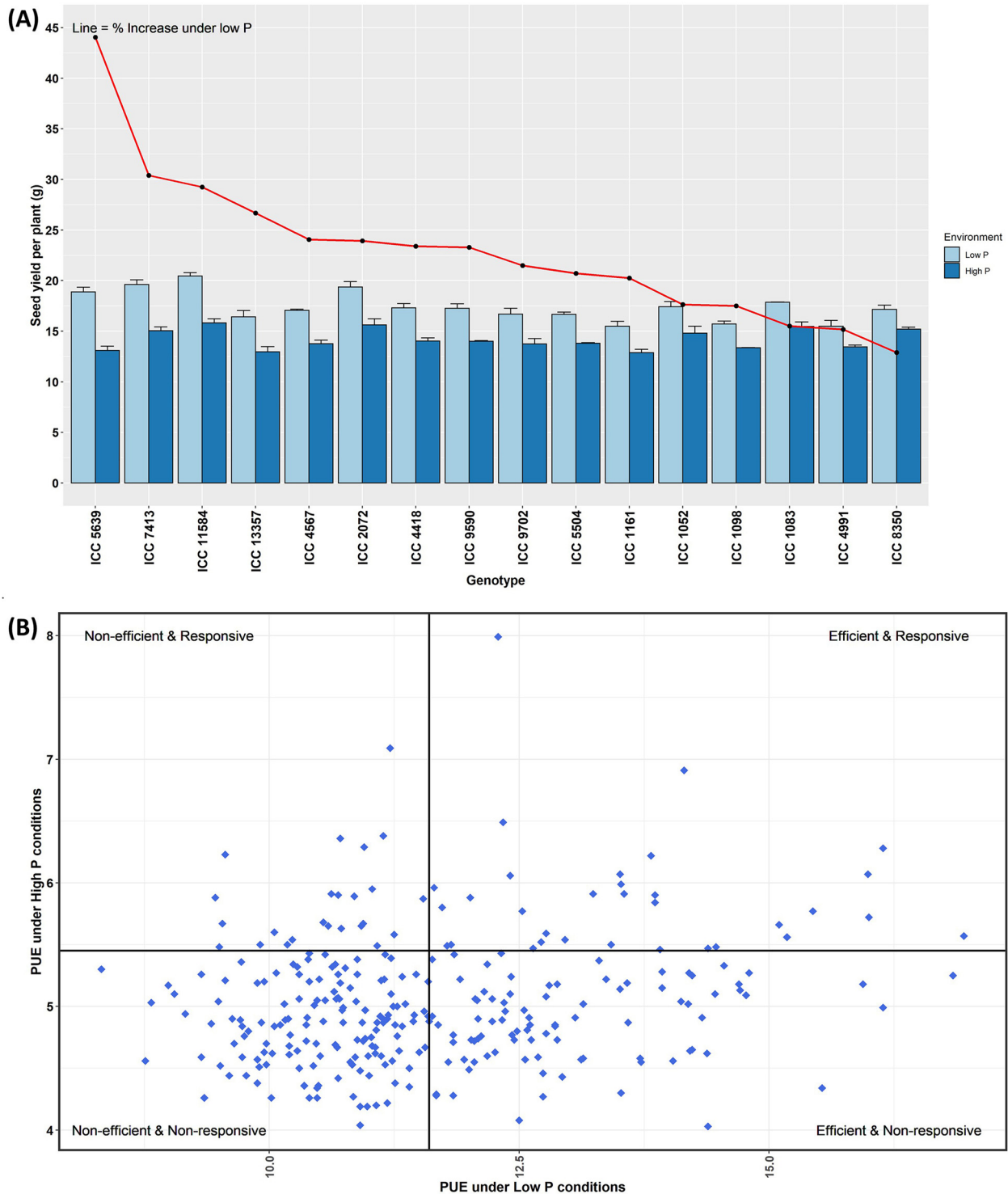


Figure 1. (a) Promising genotypes for seed yield per plant under low P conditions in comparison to high P conditions. (b) Scatter plot representing relationship between genotypes performance for PUE under two phosphorus regimes.

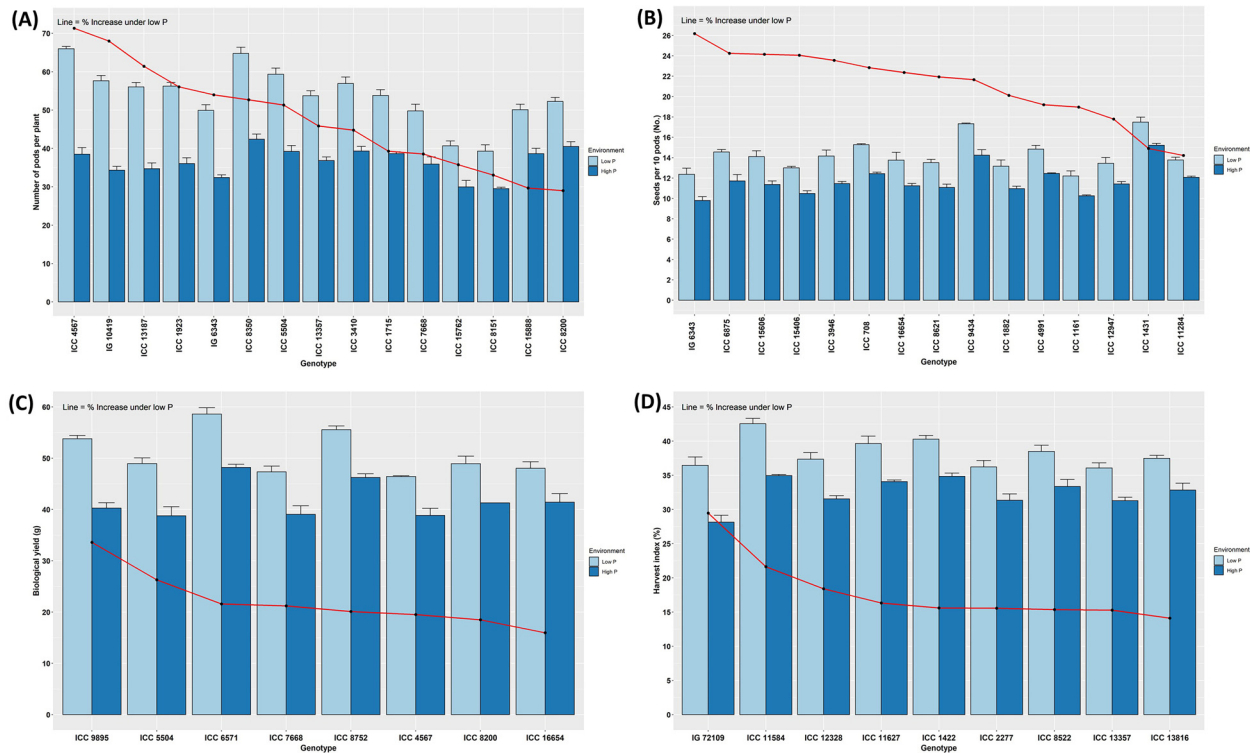


Figure 2. Variation for (a) number of pods per plant, (b) seeds per ten pods, (c) biological yield, (d) harvest index, in chickpea reference set under low P conditions in comparison to high P conditions.

high P conditions for seed yield and seeds per 10 pods (Figs 1(a) and 2(b)). The observations for number of pods per plant and biological yield were higher for the genotypes ICC 7668 and ICC 8200 under low P conditions as compared to high P regime (Fig. 2(a) and 2(c)).

Overall, 15 *desi* chickpea genotypes ICC 1052, ICC 1083, ICC 1098, ICC 1161, ICC 2072, ICC 4418, ICC 4567, ICC 4991, ICC 5504, ICC 5639, ICC 7413, ICC 8350, ICC 9590, ICC 9702, ICC 11584 and one *kabuli* chickpea genotype ICC 13357 were considered as promising for PUE with respect to higher yield and yield-attributing traits (Table 3). Thus, the outcomes of the present investigation are encouraging for low input chickpea breeding. Under high P regime the genotypes ICC 6579, ICC 6263, IG 10500, ICC 5337, ICC 16487, ICC 13124, ICC 16374, ICC 15610, ICC 13863 and ICC 1915 were found promising for yielding ability. These genotypes can thus be considered as good sources for breeding for high phosphorus conditions to improve productivity. Moreover, the genotype ICC 15610 was in the top ten entries in term of yield under both high and low P regimes, thus exhibiting stable PUE across the P regimes as well as cropping seasons.

Correlation studies

Correlation analysis revealed significant and positive correlations between seed yield and biological yield, number of pods, harvest index, number of primary branches with Pearson coefficient values (r) of 0.74 and 0.82; 0.66 and 0.55; 0.47 and 0.32; 0.23 and 0.16 under low and high P conditions, respectively (Fig. 3(a) and 3(b)). Phenotypic and genotypic correlation coefficient among the traits under low and high phosphorus regimes during both the years of experiment is presented in online

Supplementary Tables S3–S6. These results revealed that under both phosphorus regimes, selection for harvest index, biological yield, seeds per 10 pods and number of pods per plant will help in improving seed yield of chickpea. Under low P regimes (online Supplementary Tables S3 and S4), significant positive correlations of biological yield with seeds per 10 pods, number of pods per plant and number of primary branches; seeds per 10 pods with number of pods per plant and days to maturity and significant negative correlation with 100-seed weight were observed. Positive correlations were observed for the trait number of secondary branches with plant height, number of primary branches with number of pods per plant, days to 50% flowering with days to maturity and days to flower initiation.

Under high phosphorus regimes (online Supplementary Tables S5 and S6) during both the seasons 2018–19 and 2019–20, biological yield was found to be significantly and negatively correlated with harvest index whereas positively correlated with 100-seed weight, plant height and number of secondary branches. For the trait 100-seed weight, negative correlations with seeds per 10 pods and number of pods per plant and positive correlation with plant height and chlorophyll content were observed. The trait seeds per 10 pods were found to be negatively correlated with plant height and chlorophyll content. Number of pods per plant had significant negative correlations with days to flower initiation and days to 50% flowering and significant positive correlation with number of secondary branches. Chlorophyll content was found to be positively correlated with days to maturity. The trait days to flower initiation was found to be positively correlated with days to 50% flowering but it was negatively correlated with number of secondary branches (online Supplementary Tables S5 and S6).

Table 3. Promising genotypes based on seed yield and yield contributing under low P in comparison to high P conditions

Genotypes	Seed yield (g)		Harvest index (%)		Biological yield (g)		Seeds per 10 pods		Number of pods	
	Low P	High P	Low P	High P	Low P	High P	Low P	High P	Low P	High P
ICC 1052	17.41	14.80	38.14	35.62	45.92	41.63	15.55	16.04	38.87	45.44
ICC 1083	17.87	15.47	40.30	38.84	44.53	39.44	11.82	11.17	59.14	56.07
ICC 1098	15.71	13.37	34.62	34.34	45.64	39.09	16.04	14.98	53.16	47.43
ICC 1161	15.49	12.88	37.37	36.50	41.71	35.94	12.20	10.26	50.38	40.06
ICC 2072	19.37	15.63	39.61	34.05	48.99	45.93	16.19	15.69	61.54	56.66
ICC 4418	17.30	14.02	38.97	35.21	44.12	40.02	13.28	10.68	56.94	48.45
ICC 4567	17.06	13.75	37.09	35.48	46.42	38.84	17.48	18.04	65.98	38.51
ICC 4991	15.48	13.44	36.99	35.06	41.93	38.45	14.84	12.45	53.25	45.69
ICC 5504	16.66	13.80	34.38	35.62	48.95	38.76	14.20	12.17	59.34	39.22
ICC 5639	18.87	13.10	40.09	32.76	47.47	41.51	13.77	13.25	52.12	47.46
ICC 7413	19.61	15.04	34.09	32.84	58.10	46.52	12.85	11.31	59.15	63.57
ICC 8350	17.16	15.20	31.08	29.02	55.29	52.83	10.82	11.92	64.78	42.42
ICC 9590	17.26	14.00	38.52	34.84	44.96	40.21	10.93	12.67	48.82	72.06
ICC 9702	16.68	13.73	37.75	34.42	43.57	39.88	12.09	10.90	48.21	46.79
ICC 11584	20.46	15.83	42.53	34.97	47.96	45.31	14.78	12.28	56.18	59.20
ICC 13357	16.43	12.97	36.07	31.29	45.71	41.46	11.75	10.34	53.74	36.85

Discussion

Chickpea stands as a vital legume crop globally, contributing significantly to food security and agricultural sustainability. Harnessing genetic diversity and employing modern molecular tools can facilitate the development of chickpea varieties with enhanced PUE, ensuring sustainable crop productivity in phosphorus limited environments. Henceforth, understanding the mechanisms underlying phosphorus acquisition, uptake and utilization in chickpea plants is fundamental to address this issue.

ANOVA indicated presence of significant variability among the genotypes in all the four experimental environments for all the traits except chlorophyll content. This significant variance implies the scope for selection and utilization of the diversity within the reference set for chickpea improvement programmes. The results concur with the various studies on core and mini core subsets of ICRISAT germplasm collection and other collections that reported significant variability for various traits such as days to 50% flowering, days to maturity, plant height, number of primary and secondary branches, 100-seed weight, number of pods per plant, seed yield per plant (Upadhyaya and Ortiz, 2001; Upadhyaya *et al.*, 2001; Gowda *et al.*, 2011; Chrigui *et al.*, 2021; Eker *et al.*, 2022) and seeds per 10 pods (Upadhyaya *et al.*, 2002). In disparity to present results, Chaturvedi *et al.* (2009) reported non-significant results for plant height and seeds per pod in chickpea germplasm collection. This difference and extent of variability can be ascribed to various causes including magnitude of the environmental impact on the expression of traits.

In the present study, different genotypes from the reference set were recognized as P-efficient genotypes under low P regimes. Similarly, Pang *et al.* (2018) studied P-use efficiency in a set of 100 genotypes taken from the reference set and reported the genotype ICC 8350 to be more efficient for P use, which supported the results of present study as the same genotype also revealed higher

values for the traits namely number of pods per plant and seed yield. Similarly, the genotype ICC 2277 that showed higher harvest index (Fig. 2(d)) was also reported as phosphorus-efficient by Pang *et al.* (2018). In another study, Keneni *et al.* (2015) identified the genotype ICC 4918 as P-efficient which had higher seeds per 10 pods in the current study. In the present investigation, on overall mean basis, seed yield per plant was observed to be increased with P application revealing the positive effect of high P on the trait. These results are in tune with the earlier report by Madzivhandila *et al.* (2012) where grain yield was reported to be increased with P fertilizer application but only on summer sowing in chickpea cultivars. But on the contrary, Wen *et al.* (2008) reported no response of the chickpea varieties to P fertilization with negligible increase in grain yield with P fertilizer. These findings can be attributed to the fact that most of the current cultivars have been bred for yield only, without any emphasis on nutrient use efficiency. Thus, the present study has facilitated the identification of potential germplasm lines that perform better under low phosphorus conditions. The improvement of PUE of chickpea can be achieved by using the P-use efficient genotypes identified in the present study as potential donors. Additionally, genotypes ICC 6579, ICC 6263, IG 10500, ICC 5337, ICC 16487, ICC 13124, ICC 16374, ICC 15610, ICC 13863 and ICC 1915 were identified as best performing under high P conditions, facilitating breeding for high input chickpea cultivation.

Yield is a complex character which is jointly determined by a number of yield-attributing traits. So, efficiency of selection for higher yield can be improved with the knowledge of the association between yield and yield-contributing traits. The estimated correlations generally vary with the set of genotypes under study. In the current study, seed yield per plant showed significant and positive association with harvest index under all the four

environments. Earlier studies also suggest significant correlation between harvest index and seed yield (Sharma *et al.*, 1989; Gumber *et al.*, 2000; Vaghela *et al.*, 2009; Chopdar *et al.*, 2017). Positive correlation of seed yield per plant with biological yield

in low and high P regimes was also found effective in crop improvement programme (Thakur and Sirohi, 2009; Vaghela *et al.*, 2009; Ali *et al.*, 2011; Chopdar *et al.*, 2017; Hagos *et al.*, 2018). Under high P conditions major traits *viz.*, seed yield per

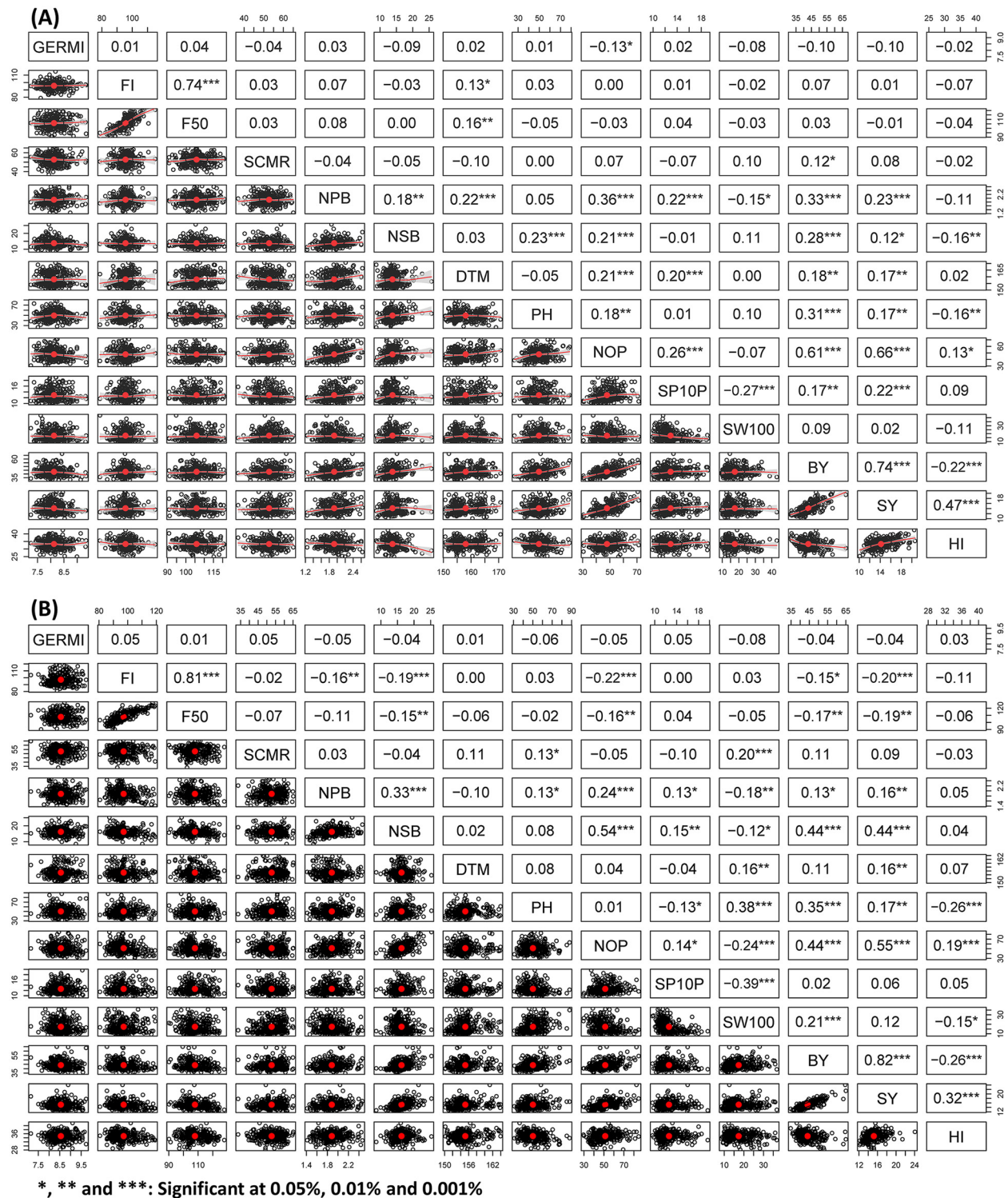


Figure 3. Correlation chart among estimated traits under (a) low P, and (b) high P conditions.

plant and harvest index were found to be positively correlated with number of pods per plant and seeds per 10 pods suggesting that selection for these yield-contributing traits will help to enhance chickpea productivity (Bahl and Jain, 1977; Sharma *et al.*, 1989; Upadhyaya *et al.*, 2001; Malik *et al.*, 2010; Salgotra, 2016; Hagos *et al.*, 2018). Prior studies were conducted with a restricted range of genotypes, contrasting with current research utilizing the chickpea reference set, which encompasses 288 of the most genetically diverse accessions worldwide. This set represents approximately 78% of the alleles present in the broader composite collection, thereby offering a comprehensive representation of genetic diversity, aiming to identify genotypes and key component traits crucial for breeding P-efficient cultivars in the present investigations.

Consequently, it can be concluded that the traits such as number of primary branches, number of pods per plant, seeds per 10 pods, biological yield and harvest index can serve as valuable criteria in a selection programme aimed at enhancing yield under different P regimes. Selecting traits that positively and significantly contribute to yield will ultimately result in increased yields. Therefore, these traits can be used as indirect selection indices for seed yield. The significant correlations identified in the present study will undoubtedly facilitate future achievements in breeding phosphorus use efficient chickpea varieties.

Conclusion

Genetic improvement in PUE of chickpea is most efficient and fundamental approach for sustainable crop growth and yield, particularly under low phosphorus soils. Nonetheless, genetic upgradation of chickpea PUE is determined by the nature as well as extent of genetic variability present in the gene pool. The present study was executed with the aim to identify P-efficient genotypes in a reference set of 288 genotypes under different phosphorus regimes. Sufficient variation was observed for all the traits under study in the current reference set under both the P regimes. The *desi* chickpea genotypes ICC 1052, ICC 1083, ICC 1098, ICC 1161, ICC 2072, ICC 4418, ICC 4567, ICC 4991, ICC 5504, ICC 5639, ICC 7413, ICC 8350, ICC 9590, ICC 9702, ICC 11584 and *kabuli* chickpea genotype ICC 13357 proved to be the most efficient in terms of yield and yield-attributing traits under low P conditions for two consecutive years of experiments. Moreover, understanding the correlation between traits linked to PUE is crucial for improving chickpea cultivation in low phosphorus environments. Promising accessions identified within reference set will serve as valuable genetic resources for chickpea breeding programme. Genotypes exhibiting high PUE discovered in this research will be utilized as parental lines in breeding crosses to develop new chickpea varieties suitable for low input conditions, while the best genotypes under high P conditions will be prioritized for breeding cultivars in high input cropping systems.

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Data availability. All relevant data that support this study are present within the manuscript and supplementary files.

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