



Leveraging genetic variability for MGIDI based identification of chickpea (*Cicer arietinum*) landraces with improved phosphorus use efficiency

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ABSTRACT

Known for its high nutritional content, chickpea (*Cicer arietinum* L.) is grown around the world, but its productivity is constrained by numerous biotic and abiotic factors including low phosphorus (P) stress. As it is grown majorly in marginal lands, the availability of P to the crop is greatly reduced. To overcome the problem, phosphorus use efficiency (PUE) of the chickpea needs to be improved. The first step to any breeding programme is to understand the phenotypic variability and adaptive responses of the plants under stress conditions and to employ the effective approaches to identify the superior genotypes with desirable traits. The present study was carried out during 2024–25 at ICAR-Indian Agricultural Research Institute, New Delhi, and utilized a hydroponic system to analyze the root traits under contrasting P conditions in chickpea. The experiment was laid out in a completely randomized design (CRD) with 5 replications of each genotype. The majority of root associated traits in genotypes tolerant to low P exhibited marked increase in growth and development under low P conditions. The PUE index was used to categorize the genotypes, identifying IG5860, ILC0 (Moldova), and ILC1906 as efficient, and ILC0 (CR), ILC12022, and ILC595 were classified as inefficient. The MGIDI served as a powerful, easy-to-use, and adaptable tool for conducting multitrait analysis on complex multivariate data and MGIDI analysis revealed IG5876, ILC0 (Moldova) and ILC1906 as the best genotypes under low P conditions and ILC0 (Russia), IG5848, and ILC0 (Moldova) under adequate P conditions. These contrasting genotypes represent promising candidates for subsequent field evaluation and, upon confirmation under field conditions, for incorporation into breeding and mapping programme.

Keywords: Chickpea, Landraces, MGIDI, Phosphorus use efficiency, PUE index

Chickpea (*Cicer arietinum* L.), a premier pulse crop that thrives on residual soil moisture, is a rich source of dietary proteins, vitamins, fiber, and minerals. As the crop is predominantly grown in marginal regions, it faces various kinds of biotic and abiotic stresses including low phosphorus (P) stress, which hinder the crop from reaching its yield potential (Thakro *et al.* 2023). P, being the second most crucial macronutrient, is a major component of nucleic acids, membrane proteins, and lipids (Lambers *et al.* 2022). Extreme pH limits P availability by forming complexes with iron and aluminium under acidic soils and with calcium under alkaline soils. In arid and semi-arid regions, water stress shrinks pores and hinders P diffusion and mass flow (Sharma *et al.* 2021). Large amounts of P fertilizers are used to mitigate P deficiency and their production relies on rock phosphate mined in a few global locations (McDowell *et al.* 2024). However, plants absorb only 10–25% of

applied P, leaving most unutilized (Rajamanickam *et al.* 2024). Breeding P use efficient cultivars that can better utilize available P is the best alternative (Wen *et al.* 2023). P use efficiency (PUE) refers to the ability of the plants to absorb, translocate and utilize P from the soil or applied fertilizers for growth and development. Therefore, PUE has two major components, P uptake efficiency (PU_pE) and P utilization efficiency (PU_tE). PU_pE describes how effectively roots can extract P from the soil, whereas PU_tE determines internal transport or redistribution, usually assessed by the extent of P absorbed per unit biomass (Kumar *et al.* 2024). This study screened twenty landraces to assess phenotypic variability in 12 root-related traits and one shoot-related trait associated with PUE in order to understand the behavioural growth patterns. To identify the best and most efficient genotypes across multiple traits, we employed the multi-trait genotype ideotype distance index (MGIDI), a novel selection method that requires no weighting coefficients and avoids multicollinearity, thereby providing a distinct and straightforward selection criterion (Olivoto *et al.* 2022).

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MATERIALS AND METHODS

Experimental materials and environmental setup: The present study was carried out during 2024–25 at ICAR-Indian Agricultural Research Institute, New Delhi. Twenty chickpea landraces were selected for the study to assess various PUE associated traits (Supplementary Table 1). The research was undertaken in hydroponics system in two different setups. In one setup adequate P (1000 μM) was provided and in the other low P (10 μM) was provided. We chose a hydroponic system to overcome the difficulty of analysing root characteristics in soil at the seedling stage and to benefit from precise control of nutrient supply and assessment of uptake efficiency. Furthermore, the controlled environment eliminates the confounding soil factors, enabling an unambiguous focus on P availability and plant responses. The entire experimental setup was established in a regulated environmental facility at ICAR-Indian Agricultural Research Institute, New Delhi. The growth parameters maintained over the study period include a 12 h photoperiod, 85% relative humidity, and daytime and nighttime temperatures of 25°C and 16°C, respectively. After 3 min of thorough cleaning with 0.1% (w/v) HgCl_2 , the seeds were washed with double distilled water. Sterilized seeds are wrapped in germination paper to facilitate germination. Seven-day old seedlings of consistent size were transplanted into 15 L capacity nutrient solution trays, which were provided with aeration from an aquarium pump. The nutrient solution contained $\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$ (4 mM), KNO_3 (6 mM), $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ (4 mM), $\text{NH}_4\text{H}_2\text{PO}_4$ (1 mM), H_3BO_3 (0.01 mM), $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ (0.002 mM), $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ (0.0003 mM), $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ (0.0002 mM), $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$ (0.00008 mM), $\text{Co}(\text{NO}_3)_2 \cdot 6\text{H}_2\text{O}$ (0.025 mM), NaOH (0.16 mM), Fe-EDTA (0.1 mM). Plants were spaced 5 cm $\times$ 5 cm apart in 2-inch plastic sheets. The pH of the solution is maintained at 6.5 and monitored regularly. Solution was changed for every 48 h and data was collected at day 35.

Trait measurements: The primary root length (PRL) (cm) was measured manually, while the detailed root system architecture namely, total root length (TRL) (cm), total root volume (TRV) (cm^3), average root diameter (AVD) (mm), and total surface area (TSA) (cm^2) was analysed using WinRHIZO Pro 2016a software after scanning with an Epson V700 Pro. The plant samples underwent oven drying for 72 hours at a temperature of 62°C to determine the root dry weight (RDW) (g/plant), shoot dry weight (SDW) (g/plant), and total dry weight (TDW) (g/plant) along with the root mass ratio (RMR).

Quantification of tissue P status: The P content analysis was performed by digesting the 0.3 g of the ground plant material in a 9:4 HNO_3 : HClO_4 solution which is then diluted to 50 ml with double distilled water and filtered through Whatman No.1 filter paper. From this a 5 ml of the sample was mixed with bartons reagent (containing 100 g ammonium metavanadate, 500 g ammonium molybdate and 500 g potassium dihydrogen phosphate) and measured spectrophotometrically at 420 nm. The P concentration (PCON) was calculated in mg/g, which was then used

along with root and shoot dry weights to determine total P uptake (TPU), P uptake efficiency (PUpE) and P utilization efficiency (PUtE) under contrasting P treatments with the help of following formulas (Rajamanickam *et al.* 2024).

$$\text{TPU (mg/plant)} = \text{PCON} \times (\text{RDW} + \text{SDW})$$

$$\text{PUpE (mg/g root dry weight)} = \text{TPU} / \text{RDW}$$

$$\text{PUtE (\%)} = [(\text{RDW} + \text{SDW}) / \text{PCON}] \times 100$$

Variability analysis: The experiment was set up in a hydroponic system using two factors (genotypes and P levels) in a completely randomized design (CRD) with 5 replications of each genotype. Using the R stats package version 4.4.3 in R- studio version 4.4.3, two-way analysis of variance (ANOVA) was calculated. Descriptive statistics and variability analysis were determined using variability package version 0.1.0 in R-Studio version 4.4.3.

Classification of genotypes based on PUE index: The studied genotypes were classified into three most efficient, three most inefficient and the remaining as moderate performers based on a PUE index computed using the following formula. The three genotypes that scored the highest and three genotypes that scored the lowest in the PUE index were considered the most efficient and the most inefficient genotypes, respectively.

$$\begin{aligned} \text{PUE Index} = & \frac{(\text{PRL})_{\text{LP}} \times (\text{PRL})_{\text{AP}}}{(\overline{\text{PRL}})_{\text{AP}}^2} + \frac{(\text{TRL})_{\text{LP}} \times (\text{TRL})_{\text{AP}}}{(\overline{\text{TRL}})_{\text{AP}}^2} + \\ & \frac{(\text{TSA})_{\text{LP}} \times (\text{TSA})_{\text{AP}}}{(\overline{\text{TSA}})_{\text{AP}}^2} + \frac{(\text{RVL})_{\text{LP}} \times (\text{RVL})_{\text{AP}}}{(\overline{\text{RVL}})_{\text{AP}}^2} + \frac{(\text{AVD})_{\text{LP}} \times (\text{AVD})_{\text{AP}}}{(\overline{\text{AVD}})_{\text{AP}}^2} + \\ & \frac{(\text{RDW})_{\text{LP}} \times (\text{RDW})_{\text{AP}}}{(\overline{\text{RDW}})_{\text{AP}}^2} + \frac{(\text{SDW})_{\text{LP}} \times (\text{SDW})_{\text{AP}}}{(\overline{\text{SDW}})_{\text{AP}}^2} + \frac{(\text{TDW})_{\text{LP}} \times (\text{TDW})_{\text{AP}}}{(\overline{\text{TDW}})_{\text{AP}}^2} + \\ & \frac{(\text{RMR})_{\text{LP}} \times \text{RMR}_{\text{AP}}}{(\overline{\text{RMR}})_{\text{AP}}^2} + \frac{(\text{PCON})_{\text{LP}} \times (\text{PCON})_{\text{AP}}}{(\overline{\text{PCON}})_{\text{AP}}^2} + \frac{(\text{TPU})_{\text{LP}} \times (\text{TPU})_{\text{AP}}}{(\overline{\text{TPU}})_{\text{AP}}^2} + \\ & \frac{(\text{PUpE})_{\text{LP}} \times (\text{PUpE})_{\text{AP}}}{(\overline{\text{PUpE}})_{\text{AP}}^2} + \frac{(\text{PUtE})_{\text{LP}} \times (\text{PUtE})_{\text{AP}}}{(\overline{\text{PUtE}})_{\text{AP}}^2} \end{aligned}$$

The description of the PUE index is as follows. For example, in the above formula $(\text{PRL})_{\text{LP}}$ refers to the trait value of a particular genotype in low P condition, $(\text{PRL})_{\text{AP}}$ refers to the trait value of the same genotype in adequate P condition and $(\overline{\text{PRL}})_{\text{AP}}^2$ refers to the mean value of all the genotypes of a given trait under adequate P condition. Summation of all the traits results in a cumulative stress tolerance index called as PUE index.

MGIDI based selection of genotypes: The calculation of MGIDI involves a systematic four-step process as described by Olivoto and Nardino (2021), i) Rescaling the trait measurements to ensure they fall within a standardized 0-100 range; ii) Performing factor analysis to assess the correlation matrix and reduce dimensional complexity; iii) Conceptualizing an ideotype by defining target values for each desired trait; iv) Finally computing the MGIDI index as a deviation of each genotype from this constructed ideotype.

$$\text{MGIDI}_p = \sqrt{\sum_{j=1}^z (Y_{pj} - Y_j)^2}$$

where MGIDI_p is the multitrait genotype ideotype distance

index for the p^{th} genotype; Y_{pj} is the score of the p^{th} genotype in the j^{th} factor ($p=1, 2, \dots, u$; $j = 1, 2, \dots, z$), being u and z the number of genotypes and factors, respectively; and Y_j is the j^{th} score of the ideotype.

The contribution of the MGIDI index for the p^{th} genotype attributed by the j^{th} factor (ω_{pj}) is utilized to highlight the strengths and weaknesses of genotypes. Its computation is given by the formula:

$$\omega_{pj} = \frac{\sqrt{D_{pj}^2}}{\sum_{j=1}^z \sqrt{D_{pj}^2}}$$

where, D_{pj} is the distance between the p^{th} genotype and ideotype for the j^{th} factor.

The predicted genetic gain, expressed as SG (%), was estimated for each trait by applying a selection intensity of $\alpha\%$, and computed as follows:

$$SG(\%) = \frac{(\bar{X}_s - \bar{X}_0) \times h^2}{\bar{X}_0} \times 100$$

Where, $\bar{X}_s$, Mean of the selected genotypes; $\bar{X}_0$, Mean of the original population and h^2 , Heritability.

The statistical analysis of MGIDI was computed using MGIDI function in metan package version 1.18.0 in R-Studio version 4.4.3.

RESULTS AND DISCUSSIONS

ANOVA, descriptive statistics, genetic parameters:

The results of the ANOVA have been presented in Supplementary Table 2. The maximum, minimum and mean values of all the investigated traits are represented in the Table 1 along with the results of genetic variability parameters and percentage change in mean of all the traits. A higher genotypic coefficient of variation and phenotypic coefficient of variation was observed for the investigated traits across the varying P levels demonstrating the presence of significant variability among the chickpea landraces included in the study. The observed higher heritability of the traits demonstrates a solid genetic stability across the evaluated genotypes. Our experimental results corroborate previous research findings in green gram (Reddy *et al.* 2020). The investigated traits exhibited the varied growth pattern under low P and adequate P conditions. Under low P conditions, traits PRL, TSA, TRL, AVD, RDW, TDW, RVL, RMR, and PUE exhibited enhanced growth, whereas SDW, PCON, TPU, and PUE declined. Enhanced growth in root associated traits under low P has also been documented in wheat (Soumya *et al.* 2021), and soybean (Krishnapriya and Pandey 2016). An increased RMR under low P conditions is due to the higher stimulation of the root growth, which occurs at the expense of shoot growth. Similar findings were also reported in chickpea (Pang *et al.* 2022), and rice (Sandhu *et al.* 2016).

Classification of genotypes based on PUE index: To classify the studied genotypes, we developed a PUE index that integrates all trait values into a robust framework for efficient, moderate or inefficient categorization. Three genotypes IG5860, ILC0 (Moldova), and ILC1906 had the highest PUE indices (43.5621, 31.9092, and 29.7408,

Table 1 Estimates of ranges and means, genotypic and phenotypic coefficient of variation, heritability (broad sense), percent change in mean response to low P condition of all the traits

Trait	Maximum			Minimum			Mean		Genotypic coefficient of variation		Phenotypic coefficient of variation		Heritability (Broad sense)		Percent change in mean
	LP	AP	LP	LP	AP	LP	LP	AP	LP	AP	LP	AP	LP	AP	
PRL	67	71.2	20.5	16.5	37.5325	24.8752	38.185	31.8229	30.7213	38.6991	0.6556	0.6762	0.6556	0.6762	1.7385
TRL	1724.85	1576.45	145.65	111.14	639.7995	68.8405	714.634	71.6647	72.1979	75.027	0.9092	0.9124	0.9092	0.9124	11.6966
TSA	332.2	270.89	31.4	23.01	117.3175	68.0934	136.0595	68.5688	71.6279	70.5573	0.9037	0.9444	0.9037	0.9444	15.9755
AVD	0.72	0.7	0.43	0.42	0.5875	5.8171	0.5955	11.4182	9.4993	13.1846	0.375	0.75	0.375	0.75	1.3617
RVL	5.59	3.71	0.42	0.38	1.7692	70.7371	2.088	67.058	74.4805	67.8748	0.902	0.9761	0.902	0.9761	18.0194
RDW	0.434	0.264	0.018	0.014	0.1068	59.74	0.1864	68.7737	66.359	76.606	0.8105	0.806	0.8105	0.806	74.5318
SDW	0.635	0.739	0.044	0.069	0.3284	64.6938	0.2875	61.2855	66.9902	66.9966	0.9326	0.8368	0.9326	0.8368	-12.4543
TDW	0.94	0.964	0.062	0.083	0.4352	59.0423	0.473	61.4812	62.1762	67.3023	0.9017	0.8345	0.9017	0.8345	8.6857
RMR	0.6493	0.4664	0.0238	0.1146	0.2347	26.28	0.3899	27.2816	31.6193	31.598	0.6908	0.7455	0.6908	0.7455	66.127
PCON	6.2033	9.2825	1.3004	2.9895	5.4966	24.8703	3.1525	24.1528	27.9669	25.2744	0.7908	0.9132	0.7908	0.9132	-42.6464
TPU	4.454	5.8785	0.2132	0.3995	2.2314	70.7853	1.566	62.3073	73.6427	67.5949	0.9239	0.8497	0.9239	0.8497	-29.8198
PUE	19.7078	55.5727	4.0747	9.0949	27.1506	42.0473	8.8517	36.4874	45.2661	37.4351	0.8628	0.95	0.8628	0.95	-67.3978
PUE	40.8625	24.9968	1.8034	1.7237	9.0771	60.509	15.2394	72.309	67.3663	78.3057	0.8068	0.8527	0.8068	0.8527	67.8884

PRL, Primary root length (cm/plant); TRL, Total root length (cm/plant); TSA, Total surface area (cm²/plant); AVD, Average root diameter (mm); RVL, Root volume (cm³/plant); RDW, Root dry weight (g/plant); SDW, Shoot dry weight (g/plant); TDW, Total dry weight (g/plant); RMR, Root mass ratio; PCON, Phosphorus concentration (mg P/g dry matter); TPU, Total phosphorus uptake (mg P/plant); PUE, Phosphorus uptake efficiency (mg P/root dry weight); PUE, Phosphorus utilization efficiency under LP-Low Phosphorus; AP, Adequate Phosphorus conditions.

Table 2 Categorization of genotypes into efficient, moderate, and inefficient based on the PUE index scores of all the studied traits

Genotype	PRL	TRL	TSA	AVD	RVL	SDW	RDW	TDW	RMR	PCON	TPU	PUpE	PUE	Category
													index	
IG5860	2.6431	5.4951	6.1317	1.0153	5.9337	2.6018	6.0374	3.3941	1.9181	0.4321	1.6884	0.1765	6.0948	43.5621 Efficient
ILC0 (Moldova)	1.3852	3.6479	3.6851	0.9158	3.8076	2.7308	4.1522	3.0545	1.4914	0.5346	1.8821	0.2822	4.3397	31.9092 Efficient
ILC1906	0.8373	2.4667	2.6382	1.0605	2.6547	3.3307	3.7438	3.4348	1.2151	0.4492	1.7615	0.2741	5.8742	29.7408 Efficient
ILC0 (Russia)	0.8692	3.3725	2.9169	0.8587	2.3766	2.5523	4.2775	2.9381	1.5974	1.2596	4.2808	0.6037	1.7828	29.6862 Moderate
IG5889	1.6489	4.5827	4.0493	0.795	3.2102	1.2788	3.3488	2.123	1.7712	0.29	0.7085	0.1167	5.5647	29.4879 Moderate
IG5858	1.9787	2.7205	3.015	0.9583	3.2296	1.8963	3.965	2.4449	1.7141	0.3776	1.044	0.2053	5.0661	28.6156 Moderate
IG5848	0.7496	1.9759	2.4646	1.2335	2.8919	3.1307	3.3218	3.1948	1.1391	0.9245	3.3881	0.6033	2.636	27.6539 Moderate
IG5985	0.9602	2.6886	1.9763	0.7208	1.3733	0.8542	7.5166	1.9058	4.2972	0.3894	0.8444	0.078	3.8831	27.4879 Moderate
IG5876	2.0829	1.3946	2.1847	0.9572	3.7654	2.3533	3.8696	2.747	1.4412	0.6914	2.149	0.4118	3.0846	27.1328 Moderate
IG5862	2.6833	3.2616	2.8854	0.7662	3.0893	1.5969	3.1159	2.0045	1.4669	0.2586	0.7477	0.2022	4.9144	26.9929 Moderate
ILC11889	0.8561	0.2138	0.2423	1.1343	0.2603	0.2516	0.3183	0.2695	1.4126	0.4866	0.1474	0.2854	0.4327	6.3108 Moderate
ILC180	0.7212	0.1511	0.1632	1.0955	0.1518	0.1815	0.4324	0.3106	1.5133	0.5982	0.213	0.3236	0.3964	6.2519 Moderate
ILC238	0.4648	0.156	0.1716	1.1033	0.1792	0.3286	0.4046	0.3899	1.1553	0.5835	0.2619	0.428	0.5078	6.1345 Moderate
ILC11913	0.4945	0.1552	0.155	0.9889	0.1361	0.0859	0.2978	0.1302	2.498	0.5735	0.0857	0.1918	0.1731	5.9658 Moderate
ILC10771	0.7515	0.1176	0.1443	1.2234	0.1679	0.1024	0.212	0.1285	1.842	0.6283	0.0931	0.3051	0.1564	5.8726 Moderate
ILC10729	0.7771	0.1145	0.149	1.3101	0.1826	0.215	0.3462	0.2227	1.0592	0.7021	0.1793	0.3433	0.2427	5.8437 Moderate
ILC1932	0.4571	0.1269	0.1467	1.1773	0.1622	0.2111	0.3181	0.2452	1.4214	0.6522	0.1857	0.3591	0.2849	5.748 Moderate
ILC595	0.6602	0.1082	0.1307	1.196	0.1487	0.0873	0.1734	0.1077	1.7242	0.5633	0.0688	0.2433	0.1508	5.3627 Inefficient
ILC12022	0.5404	0.0823	0.1025	0.9455	0.09	0.0844	0.1426	0.1106	1.4021	0.5626	0.071	0.3121	0.1512	4.5974 Inefficient
ILC0(CR)	0.5114	0.0871	0.089	0.8676	0.0728	0.0769	0.0403	0.0676	0.6891	0.5652	0.0435	0.6263	0.0923	3.829 Inefficient

PRL, Primary root length (cm/plant); TRL, Total root length (cm/plant); TSA, Total surface area (cm²/plant); AVD, Average root diameter (mm), RVL, Root volume (cm³/plant); RDW, Root dry weight (g/plant); SDW, Shoot dry weight (g/plant); TDW, Total dry weight (g/plant); RMR, Root mass ratio; PCON, Phosphorus concentration (mg P/g dry matter); TPU, Total phosphorus uptake (mg P/plant); PUpE, Phosphorus uptake efficiency (mg P/root dry weight); PUE, Phosphorus utilization efficiency.

respectively) and were classified as efficient genotypes. Conversely, ILC0 (CR), ILC12022, ILC595 recorded the lowest indices (3.829, 4.5974 and 5.3627, respectively) and were classified as inefficient. The remaining 14 genotypes were moderate performers, with PUE indices ranging from 29.6862 to 5.748 (Table 2). This approach employs raw low P and adequate P values normalized by adequate P means, avoids arbitrary weighting and multicollinearity, and yields robust genotype classifications.

Selection of genotypes based on MGIDI: The MGIDI was used to select the best-performing genotypes, evaluated based on multiple investigated traits under both low P and adequate P conditions, with a selection intensity of 15%. MGIDI is a robust method designed to identify genotypes with both high overall performance and preferred specific traits. This approach upholds the datasets natural correlation structure, enabling the identification of outstanding genotypes across multiple traits. In addition to its statistical strengths, MGIDI serves as a valuable visual aid by highlighting strengths and weaknesses of each genotype and pinpointing traits that require improvement. Compared to other multivariate selection indices such as FAI-BLUP (Factor Analysis and Ideotype-design with Best Linear Unbiased Prediction) and SH (Smith-Hazel), MGIDI offers greater selection accuracy, particularly when trait correlations are low. It is also computationally more efficient and easier to interpret, making it a preferred choice for multi-trait selection in contemporary plant breeding programmes. The genotypes that showed the lowest MGIDI values are the closest to the ideotype. Under low P condition the genotypes IG5876, ILC0 (Moldova) and ILC1906 were selected as the best performing genotypes close to the performance of ideotype and under adequate P condition, the genotypes ILC0 (Russia), IG5848, and ILC0 (Moldova) were identified as the superior genotypes. It was found that under both the conditions ILC0 (Moldova) was identified as a superior genotype.

Loadings and factor descriptions for MGIDI: The analytical results from a factor analysis that evaluated the 13 studied traits were compiled in Supplementary Table 3 for low P and adequate P. The final loadings derived from the principal component analysis followed by exploratory factor analysis revealed three factors with eigenvalues greater than 1, explaining a cumulative variance of 93.4% and 90.1% under low P and adequate P conditions, respectively. The traits retained in each factor are presented in Supplementary Tables 4 and 5 for low P and adequate P conditions, respectively. For instance, under low P conditions, the lower contribution of FA1 to ILC0 (Moldova) reflected its strong performance for the traits retained in FA1 namely, PRL, TRL, TSA, RVL, RDW, SDW, TDW, TPU, and PUE, but a high contribution of FA2 indicated its low performance in traits RMR, PCON, and PUE. Similarly, the lower contribution of FA3 and FA2 to IG5876 demonstrated its superior performance in the traits AVD and RMR, PCON, and PUE in the respective factors. Thus, MGIDI served to reduce the complexity of the data while preserving its robust explanatory power. The mean communality values

were 0.9338 and 0.901 after varimax rotation under low P and adequate P conditions, respectively, demonstrating that the high proportion of each variable's variance was explained by the factors. The uniquenesses of individual traits explain

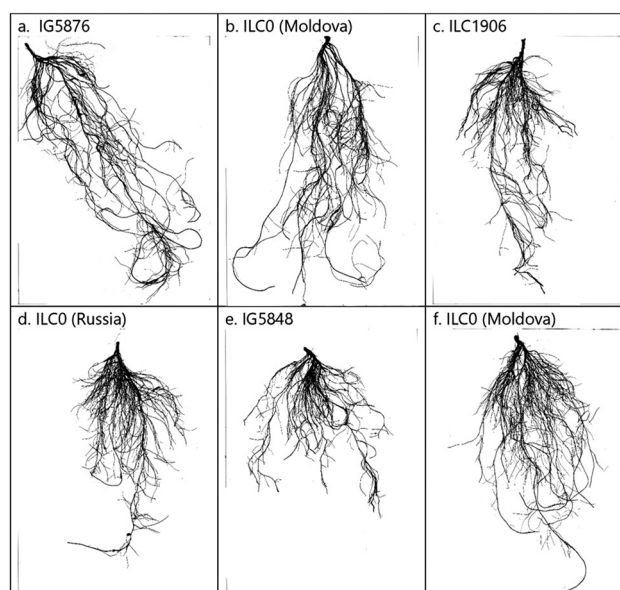


Fig. 1 The scanned root images of the selected genotypes based on MGIDI under low P conditions (a, b and c) vs the scanned root images of the selected genotypes based on MGIDI under adequate P conditions (d, e and f).

Table 3 MGIDI scores of the genotypes under low P and adequate P conditions.

Low P		Adequate P	
Genotype	MGIDI	Genotype	MGIDI
IG5876	1.18	ILC0 (Russia)	1.48
ILC0 (Moldova)	1.44	IG5848	1.52
ILC1906	1.56	ILC0 (Moldova)	2.72
IG5848	1.92	ILC1906	2.86
IG5858	2.22	IG5860	3.17
ILC0 (Russia)	2.35	IG5876	3.19
IG5862	2.37	ILC10771	3.32
IG5860	2.43	ILC10729	3.79
IG5985	2.62	ILC1932	3.82
IG5889	2.78	ILC238	4.04
ILC238	2.98	ILC595	4.1
ILC11889	3.05	ILC11889	4.15
ILC1932	3.25	ILC180	4.16
ILC12022	3.34	IG5858	4.21
ILC0(CR)	3.36	ILC11913	4.44
ILC11913	3.42	IG5889	4.73
ILC180	3.43	ILC12022	4.81
ILC595	3.59	ILC0(CR)	4.88
ILC10771	3.67	IG5862	5.24
ILC10729	3.76	IG5985	5.35

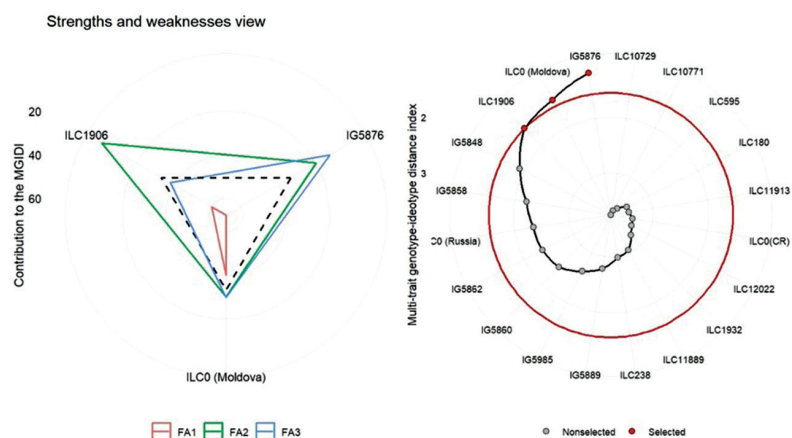


Fig. 2 Under low P condition, left plot- indicates the strength and weakness view of the selected genotypes, shown as the proportion of each factor on the computed MGIDI. Right plot - Genotype ranking in ascending order for the MGIDI index. The selected genotypes are shown in red and the circle represents the cutpoint according to the selection pressure.

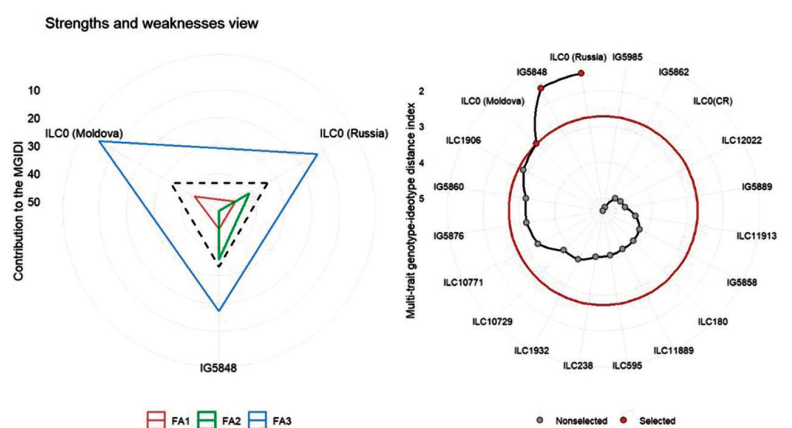


Fig. 3 Under adequate P condition, left plot-indicates the strength and weakness view of the selected genotypes, shown as the proportion of each factor on the computed MGIDI. Right plot- Genotype ranking in ascending order for the MGIDI index. The selected genotypes are shown in red and the circle represents the cutpoint according to the selection pressure.

the proportion of variance unique to the variable, where the lower values indicate more shared variance, suggesting strong relationship among the variables.

MGIDI values and selection gains: Under each of the testing conditions three genotypes were selected based on the selection intensity of 15%. The lower the MGIDI value, the closer the genotype is to the ideotype. IG5876, ILC0 (Moldova), and ILC1906 scored 1.18, 1.44, and 1.56 under low P conditions, respectively, whereas ILC0 (Russia), IG5848, and ILC0 (Moldova) scored 1.48, 1.52, and 2.72, respectively, under adequate P conditions. The MGIDI scores of all the tested genotypes were presented in Table 3. The root images of selected genotypes under low P and adequate P conditions are presented in Fig. 1. The mean of the original population, the mean of the selected genotypes, selection differential, selection differential (%), heritability, selection gain, and selection gain (%) of low P and adequate P were presented in the Supplementary Tables 4 and 5, respectively. The selection gains were negative for

the traits RMR and AVD under low P conditions and PRL and PUE under adequate P conditions, and the remaining traits exhibited positive selection gains. The highest genetic gains were observed for SDW under low P and TPU under adequate P, highlighting their significant role in enhancing the PUE.

Strength and weaknesses view of selected genotypes: The strength and weaknesses plot served as a graphical tool for evaluating and choosing genotypes that exhibit desirable traits. A smaller proportion explained by a factor that is nearer to the external edge, representing the strengths, indicates that the traits within that factor are more aligned with the ideotype. The smaller the contribution of the factor, the higher the value for the traits in that factor. The dashed line represents the theoretical value assuming equal contribution from all the factors (Fig. 2 and Fig. 3). Under low P conditions, FA1 had the smallest contribution to the genotypes ILC0 (Moldova) followed by ILC1906 and higher contribution to the genotypes IG5876; FA2 had the smallest contribution for the genotypes ILC1906 followed by IG5876 and higher contribution to the genotype ILC0 (Moldova); FA3 had the smallest contribution to the genotypes IG5876 followed by ILC0 (Moldova), and higher contribution to the genotypes ILC1906 (Fig. 2). Whereas under adequate P conditions FA1 and FA3 had the smallest contribution to the genotypes ILC0 (Moldova), followed by ILC0 (Russia) and higher contribution to the genotype IG5848; FA2 had the smallest contribution for IG5848 followed by ILC0 (Russia) and higher contribution for the genotype ILC0 (Moldova) (Fig. 3). According to the desired selection intensity, the cut point score

is 1.56 (ILC1906) and 2.72 (ILC0 (Moldova)) for low P and adequate P conditions, respectively. Singamsetti *et al.* (2023) described MGIDI as a valuable selection approach in shaping breeding strategies in developing maize hybrids with climate resilience by testing their adaptability across multiple moisture regimes. Similarly, Silva *et al.* (2023) proposed MGIDI as an efficient method for refining the selection process of wheat lines under drought conditions. Comparable findings were reported in maize (Yue *et al.* 2022), rice (Olivoto and Nardino 2021), upland cotton (Raj *et al.* 2024), and chickpea (Jorben *et al.* 2022). Likewise, MGIDI was also leveraged to evaluate and select high-ranking genotypes across different traits in lentil (Amin *et al.* 2024), black bean (Klein *et al.* 2023), and oats (Ambrósio *et al.* 2024).

The results from the present investigation reported the existence of enormous variability among the 20 chickpea landraces and revealed the adaptive response of the genotypes under low P and adequate P conditions. PUE

index served as the best approach to classify the genotypes into efficient and inefficient ones and these can be used to develop mapping populations to map the genomic regions responsible for enhanced PUE. While hydroponics does not capture the full complexity of field conditions, it enables precise isolation of P effects, which is not possible in soil. Following field evaluation, the genotypes selected based on MGIDI can be used for allele mining and SNP detection, and subsequently incorporated into the chickpea breeding programmes to develop varieties with improved PUE.

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