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Field Evaluation and Diversity of 238 Global Chickpea (*Cicer arietinum* L.) Genotypes Grown in South-East Kazakhstan

A three-year field evaluation was conducted to assess the agronomic performance, trait associations, and diversity of 238 chickpea (*Cicer arietinum* L.) genotypes from a global collection cultivated under the semi-arid conditions of South-East Kazakhstan. The trials, carried out across three growing seasons, recorded significant variation for plant height (PH), height to lowest pod (HLP), number of lateral branches (NLB), number of seeds per plant (NSP), yield per plant (YP), and thousand-seed weight (TSW). Analysis of variance revealed significant effects of genotype origin, seed type, and year for several traits, with strong genotype × environment interactions. Correlation analysis showed that YP was strongly and positively associated with TSW ($r = 0.605$) and moderately with NSP ($r = 0.530$), while NSP and TSW were negatively correlated, indicating a trade-off between seed size and seed number. Principal component analysis (PCA) revealed that the genotypes originating from the Middle East and Africa were primarily grouped with higher values for yield per plant (YP) and thousand-seed weight (TSW), whereas South Asian germplasm showed wide phenotypic dispersion, reflecting their broad variability. Kabulitype of chickpea seeds showed a strong association with yield-related traits, while Desi types revealed greater variability and a weaker association with seed size. A total of 24 perspective genotypes, such as ICC456, ICC637, ICC1392, ICC2065, ICC3362, and ICC3410, were identified as valuable candidates for breeding aimed at improving productivity and adaptability of chickpea in South-East Kazakhstan. Overall, these results enhance understanding of the diversity and interrelationships of agronomic traits in global chickpea germplasm and emphasize the breeding potential of selected genotypes for semi-arid regions.

Keywords: chickpea, global collection, agronomic traits, semi-arid Kazakhstan.

Introduction

Chickpea (*Cicer arietinum* L.) is one of the important legume crop, widely grown in arid and semi-arid regions due to its adaptability, nutritional value, and contribution to sustainable agriculture. Globally, chickpea occupies approximately 14.8 million hectares, with an annual production exceeding 15 million tons and an average yield of 1.01 t ha^{-1} in 2020 — considerably below the potential yield of up to 6 t ha^{-1} under optimal conditions [1]. As a member of the founder crops of the Fertile Crescent, chickpea was domesticated together with lentil (*Lens culinaris*) and pea (*Pisum sativum*) and has since spread across South Asia, the Middle East, Africa, and the Mediterranean basin, where it remains a crucial dietary protein source [2, 3].

Kazakhstan encompasses diverse agroecological zones, many of which are characterized by arid or semi-arid climates, low and variable precipitation, and temperature extremes. Agricultural production in these environments is constrained by drought stress, short growing seasons in the north, and high summer temperatures in the south [4]. Chickpea, with its deep root system, moderate water requirement, and ability to fix atmospheric nitrogen through symbiosis with *Rhizobium* spp., is well suited to these conditions and has the potential to enhance the resilience of cropping systems [5].

From an agronomic perspective, chickpea serves as a valuable rotational crop in cereal-based systems, improving soil fertility, disrupting pest and disease cycles, and enhancing sustainability [6, 7]. Economically, the rising global demand for both desi and kabuli types, particularly in South Asia, the Middle East, and expanding European markets, presents opportunities for Kazakhstan to strengthen its domestic production and explore export potential [1]. Nutritionally, chickpeas provide 18–24 % protein, complex carbohydrates, essential amino acids, minerals such as iron and zinc, and vitamins, making them a key crop for addressing food and nutrition security challenges [8, 9].

Although chickpea is a relatively recent introduction into Kazakhstan's cropping systems, research efforts over the past decade have advanced understanding of its adaptability and genetic potential under local conditions. For example, Khasanova et al. (2021) [10] identified high-performing genotypes such as ICC-456, ICC-15697, and ICC-7272 under northern Kazakhstan environments, while Khasanova et al. (2022) [11] highlighted drought-tolerant accessions with favorable yield components. Molecular studies have also begun to support breeding programs: Mazkirat et al. (2023) [12] applied SSR (simple sequence repeat) markers to identify marker–trait associations for yield-related traits, while Ansabayeva and Akhmetbekova (2023) [13] demonstrated that biological inoculants (e.g., Baikal EM-1) enhanced yield stability under continental climatic conditions. Recent multi-location trials have identified elite cultivars with yields up to 5.94 t ha^{-1} under favorable management, underscoring the untapped potential of chickpea for Kazakhstan [14].

Despite these advances, comprehensive multi-year evaluations of large, diverse chickpea germplasm sets under Kazakhstan's heterogeneous agroclimatic conditions remain limited. Most existing studies have focused on northern environments, whereas the south-east region, characterized by warmer temperatures and distinct rainfall patterns, has received less attention. Identifying genotypes with superior yield performance, stable expression of key traits, and adaptability to such conditions is essential to broaden the genetic base of breeding materials and accelerate cultivar development.

The present study was undertaken to address this gap. Specifically, we aimed to evaluate the agronomic performance of 238 global chickpea genotypes across three consecutive growing seasons (2022–2024) in South-East Kazakhstan, assess correlations among yield and yield-related traits, and identify superior genotypes with potential utility in breeding programs targeting resilience and productivity under Kazakhstan's semi-arid agroecological conditions.

Experimental

A total of 238 chickpea (Cicer arietinum L.) genotypes were evaluated, representing diverse geographic origins including Africa (n = 26), Europe (n = 5), Latin America (n = 5), the Middle East (n = 94), and South Asia (n = 108). The collection comprised accessions of different seed types, including kabuli, desi, and pea-shaped forms, consistent with earlier global chickpea diversity assessments [15–17].Whole collection accessions were evaluated over three growing seasons (2022, 2023, and 2024)at the experimental site of LLP "Kazakh Research Institute of Agriculture and Plant Growing" (KRIAPG). Each trial was conducted in a randomized complete block design with three replications. Standard agronomic practices were followed for chickpea cultivation in each season. Traits measured: PH — Plant height (cm); HLP — Height to lowest pod (cm); NLB — Number of lateral branches (count); NSP — Number of seeds per plant (count); YP — Yield per plant (g); TSW — Thousand-seed weight (g).

Descriptive statistics (mean, maximum, minimum, standard deviation, and coefficient of variation) were calculated to assess the extent of phenotypic variation within and across geographic groups. Trait correlations were estimated using Pearson's correlation coefficient, and significance levels were determined at $p < 0.05$, $p < 0.01$, and $p < 0.001$ [18].

Analysis of variance (ANOVA) was performed using a mixed linear model to partition the effects of origin, seed type, and year, as well as their interactions, on each trait. Significance was assessed using F-tests, and post hoc comparisons were conducted where appropriate.

Multivariate analysis of trait variation was carried out using principal component analysis (PCA) to reduce dimensionality and detect patterns among traits and accessions [19]. PCA biplots were generated to visualize relationships among traits and the distribution of accessions by geographic origin and seed type, following approaches previously applied in chickpea germplasm studies.

All statistical analyses were conducted in R softwarep [20], using packages *stats*, *ggplot2*, and *factoextra* for data analysis and visualization.

Results and Discussion

Trait Variability Across Growing Seasons

The evaluation of 238 global chickpea genotypes revealed substantial variation in agronomic traits across different regions of origin (Table 1). Mean PH ranged from 29.05 cm in European accessions to 32.91 cm in those from the Middle East, with the tallest individual plant recorded in the Middle East group (46.02 cm). The HLP varied between 16.68 cm (Europe) and 18.41 cm (Middle East), with coefficients of variation (CV) generally exceeding 15 %, indicating moderate variability. The NLB per plant was highest in Middle Eastern accessions (mean 2.25) and lowest in Europe (mean 2.01), while the NSP ranged from 17.08 in European lines to 21.05 in Latin American lines, with the maximum value (32.48) also observed in Middle

Eastern germplasm. YP showed a similar trend, with the highest mean recorded in Latin America (4.43 g) and the highest individual yield in Middle Eastern lines (7.75 g).

Table 1

Descriptive statistics for agronomic traits of 238 global chickpea genotypes from five geographic origins

Traits	Max	Min	Mean	SD	CV (%)
Africa					
Plant height (cm)	36.167	25.090	30.790	3.069	9.969
Height to lowest pod (cm)	23.623	12.300	17.020	2.929	17.211
NLB — Number of lateral branches (count)	2.533	1.523	2.078	0.275	13.228
Number of seeds per plant (count)	28.667	13.450	19.043	3.377	17.734
YP — Yield per plant (g)	6.412	2.225	3.720	1.129	30.338
TSW — Thousand-seed weight (g)					
Europe					
Plant height (cm)	39.943	23.067	29.053	6.479	22.299
Height to lowest pod (cm)	21.023	14.133	16.677	2.599	15.585
NLB — Number of lateral branches (count)	2.577	1.523	2.007	0.477	23.789
Number of seeds per plant (count)	20.710	13.610	17.075	2.778	16.268
YP — Yield per plant (g)	4.661	2.161	3.202	1.077	33.640
TSW — Thousand-seed weight (g)	268.033	110.667	155.500	65.086	41.856
Latin America					
Plant height (cm)	39.477	25.333	30.189	6.344	21.014
Height to lowest pod (cm)	23.210	13.100	17.024	4.537	26.650
NLB — Number of lateral branches (count)	2.777	2.123	2.431	0.260	10.692
Number of seeds per plant (count)	24.800	17.683	21.045	2.555	12.142
YP — Yield per plant (g)	5.727	3.587	4.425	0.974	22.007
TSW — Thousand-seed weight (g)	272.050	119.983	166.637	60.715	36.436
Middle East					
Plant height (cm)	46.022	20.300	32.906	4.577	13.910
Height to lowest pod (cm)	26.743	11.567	18.410	3.269	17.758
NLB — Number of lateral branches (count)	3.357	1.410	2.250	0.346	15.382
Number of seeds per plant (count)	32.477	11.543	19.025	4.384	23.044
YP — Yield per plant (g)	7.753	1.892	4.074	1.086	26.646
TSW — Thousand-seed weight (g)	329.433	98.017	168.612	56.273	33.374
SouthAsia					
Plant height (cm)	42.007	20.500	30.574	4.438	14.515
Height to lowest pod (cm)	27.067	11.800	17.503	3.077	17.580
NLB — Number of lateral branches (count)	3.057	1.333	2.174	0.316	14.534
Number of seeds per plant (count)	31.823	11.065	19.438	4.760	24.487
YP — Yield per plant (g)	7.550	1.713	3.963	1.014	25.591
TSW — Thousand-seed weight (g)	309.350	98.767	161.850	45.121	27.878
Total					
Plant height (cm)	46.022	20.300	31.479	4.570	14.518
Height to lowest pod (cm)	27.067	11.567	17.781	3.183	17.898
NLB — Number of lateral branches (count)	3.357	1.333	2.196	0.331	15.097
Number of seeds per plant (count)	32.477	11.065	19.216	4.407	22.934
YP — Yield per plant (g)	7.753	1.713	3.974	1.061	26.686
TSW — Thousand-seed weight (g)	329.433	98.017	163.895	51.071	31.161

Note. Max — maximum observed value; Min — minimum observed value; Mean — arithmetic average; SD — standard deviation; CV — coefficient of variation

TSW exhibited the largest variability among traits, with values ranging from 98.02 g to 329.43 g. The heaviest seeds were found in Middle Eastern genotypes (mean 168.61 g), followed by Latin American lines (166.64 g), whereas European accessions had the lowest mean TSW (155.50 g). Overall, the combined dataset across all origins showed a mean plant height of 31.48 cm, height to the lowest pod of 17.78 cm, two lateral branches per plant on average, and a yield per plant of 3.97 g. These results highlight that Middle Eastern and Latin American germplasm tend to possess superior yield-related traits, whereas European and

African lines may contribute to diversity in plant architecture. The observed variability suggests ample opportunities for selecting promising genotypes for breeding programs targeting high yield and desirable morphological attributes under South-East Kazakhstan's agro-climatic conditions.

Pearson correlation analysis explored relationships among traits, averaged across years (Fig. 3). A strong, highly significant positive correlation was observed between PH and HLP (r = 0.866; p<0.001), indicating a very close association where an increase in one trait is strongly linked to an increase in the other. Another strong positive correlation was observed between TSW and YP (r = 0.605; p<0.001), indicating that plants with larger seeds tend to produce higher yields.

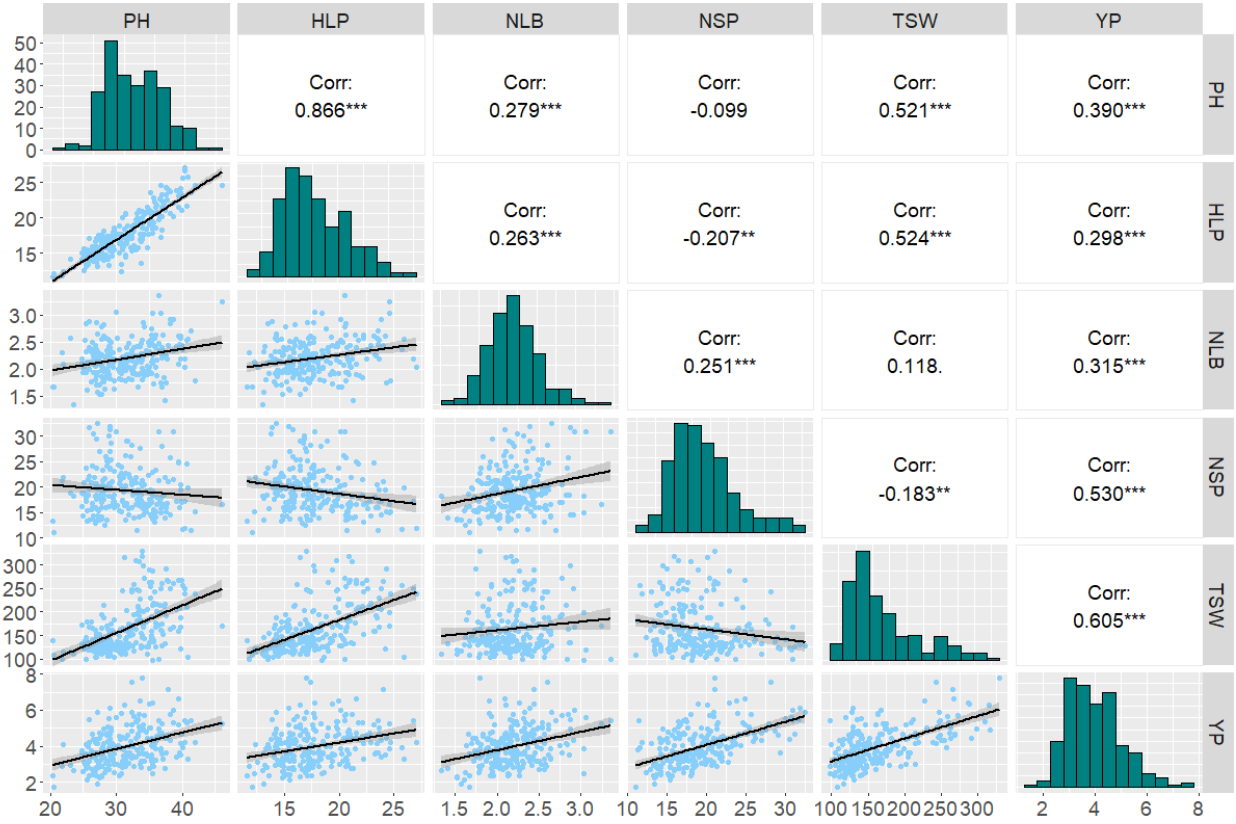

Figure 1. Correlation analysis of agronomic traits.
PH — plant height; HLP — height to lowest pod; NLB — number of lateral branches;
NSP — number of seeds per plant; YP — yield per plant; TSW — thousand seed weight

Moderate positive correlations were identified between NSP and YP (r = 0.530; p<0.001) and between PH and YP (r = 0.390; p<0.001). These suggest that while the number of seeds per pod and plant height are significantly associated with yield, their influence is less pronounced than that of thousand seed weight.

A weak but statistically significant positive correlation was noted for HLP and NLB (r = 0.263; p<0.001) and HLP and YP (r = 0.298; p<0.001). The weak negative correlation between NSP and TSW (r = -0.183; p<0.01) is also statistically significant, suggesting that there is a slight, inverse relationship between the number of seeds and their weight.

Multivariate Analysis of Accession Diversity

The analysis of variance revealed distinct effects of origin, type, and year, as well as their interactions, on several agronomic traits of the 238 chickpea genotypes evaluated (Table 2). For plant height (PH), significant main effects were detected for origin (F = 4.291, p = 0.00195), type (F = 5.203, p = 0.00572), and year (F = 16.538, p < 0.001), along with a significant origin × type interaction (F = 3.363, p = 0.00522). Other interaction terms were not significant. Similarly, height to lowest pod (HLP) was significantly influenced by origin (F = 2.575, p = 0.03657), type (F = 5.720, p = 0.00344), and origin × type interaction (F = 2.449, p = 0.03262), whereas year and higher-order interactions were not significant.

Table 2

ANOVA for agronomic traits of 238 global chickpea genotypes evaluated in South-East Kazakhstan

Traits	*Df*	*SS*	*MS*	*F*	*P value*
PH					
Origin	4	990	247,5	4,291	0,00195**
Type	2	600	300,1	5,203	0,00572**
Year	1	954	953,8	16,538	5,32E-05***
Origin: Type	5	970	193,9	3,363	0,00522**
Origin: Year	4	39	9,9	0,171	0,95317
Type: Year	2	30	14,8	0,257	0,77374
Origin: Type: Year	5	137	27,4	0,474	0,79556
Residuals	690	39794	57,7		
HLP					
Origin	4	209	52,13	2,575	0,03657*
Type	2	232	115,78	5,72	0,00344**
Year	1	5	5,34	0,264	0,60779
Origin: Type	5	248	49,56	2,449	0,03262*
Origin: Year	4	21	5,17	0,255	0,90638
Type: Year	2	12	5,81	0,287	0,75045
Origin: Type: Year	5	19	3,77	0,186	0,96775
Residuals	690	13966	20,24		
NLB					
Origin	4	3,34	0,83	2,064	0,0839
Type	2	0,57	0,28	0,7	0,4969
Year	1	173,97	173,97	430,116	<2e-16***
Origin: Type	5	2,75	0,55	1,362	0,2367
Origin: Year	4	1,01	0,25	0,625	0,6445
Type: Year	2	0,34	0,17	0,421	0,6565
Origin: Type: Year	5	2,59	0,52	1,281	0,2701
Residuals	686	277,47	0,4		
NSP					
Origin	4	154	38,6	0,474	0,755
Type	2	111	55,5	0,681	0,507
Year	1	2401	2401,1	29,465	7,92E-08***
Origin: Type	5	187	37,5	0,46	0,806
Origin: Year	4	206	51,4	0,631	0,641
Type: Year	2	319	159,4	1,956	0,142
Origin: Type: Year	5	148	29,5	0,362	0,874
Residuals	683	55659	81,5		
YP					
Origin	4	18,5	4,634	1,214	0,30367
Type	2	41,1	20,54	5,379	0,00481**
Year	1	0	0,022	0,006	0,93982
Origin: Type	5	18,2	3,641	0,953	0,4457
Origin: Year	4	12	2,99	0,783	0,53635
Type: Year	2	14,9	7,436	1,947	0,14344
Origin: Type: Year	5	10,1	2,012	0,527	0,75607
Residuals	683	2607,9	3,818		
TSW					
Origin	4	12956	3239	1,197	0,3109
Type	2	223030	111515	41,201	2,00E-16***
Year	1	102627	102627	37,918	1,26E-09***
Origin: Type	5	30225	6045	2,233	0,0494*
Origin: Year	4	1121	280	0,104	0,9813
Type: Year	2	12157	6079	2,246	0,1066
Origin: Type: Year	5	1919	384	0,142	0,9824
Residuals	686	1856715	2707		

Note. PH — plant height; HLP — height to lowest pod; NLB — number of lateral branches; NSP — number of seeds per plant; YP — yield per plant; TSW — thousand seed weight. *Df* — degrees of freedom; *SS* — sum of squares; *MS* — mean square; *F* — F-statistic; *P value* — significance level. * — $P< 0.05$, ** — $P< 0.01$, *** — $P < 0.001$

For the number of lateral branches (NLB), year exerted a highly significant effect (F = 430.116, p < 0.001), but origin and type had no significant main or interaction effects. A similar pattern was observed for the number of seeds per plant (NSP), with year showing a strong effect (F = 29.465, p < 0.001), while origin, type, and their interactions were non-significant.

In terms of grain yield per plant (YP), type was the only factor with a significant main effect (F = 5.379, p = 0.00481), whereas origin, year, and all interaction terms were non-significant. In contrast, thousand seed weight (TSW) showed highly significant effects of type (F = 41.201, p < 0.001) and year (F = 37.918, p < 0.001), as well as a weaker but significant origin × type interaction (F = 2.233, p = 0.0494). No other interactions were significant for TSW.

Differences by Origin and Type

Principal component analysis (PCA) with origin groups revealed that the first two principal components (PC1 and PC2) collectively explained 72.1 % of the total phenotypic variation among chickpea genotypes (Fig. 2). PC1 accounted for 45.7 % of the variance and was positively associated with YP, TSW, and PH, whereas PC2, explaining 26.4 % of the variance, was positively correlated with NSP and NLB.

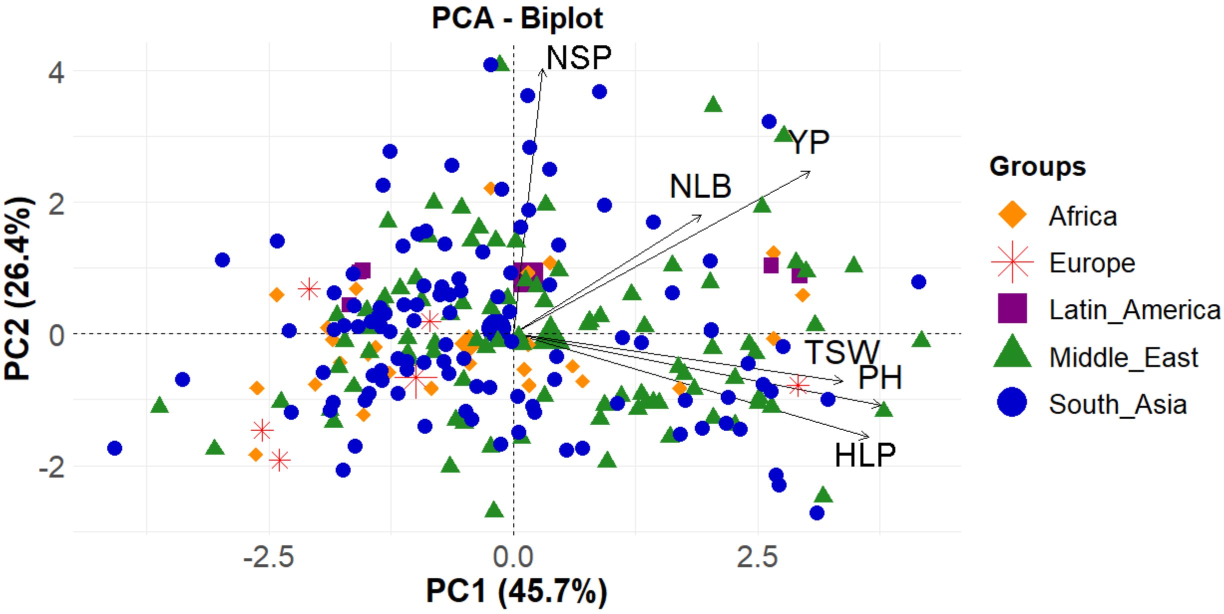

Figure 2. PCA showing the distribution of accessions from different origin groups based on six agronomic traits.
PH — plant height; HLP — height to lowest pod; NLB — number of lateral branches;
NSP — number of seeds per plant; YP — yield per plant; TSW — thousand seed weight

The PCA showed that chickpea accessions were partly separated by their origin. Genotypes from Africa and the Middle East were mainly grouped on the positive side of PC1, reflecting their higher YPand TSW. European genotypes clustered on the negative side of PC1, corresponding to lower performance for these traits. Latin American accessions occupied an intermediate position, representing average trait values, while South Asian accessions were widely scattered across both components, highlighting their high genetic and phenotypic diversity. Analysis of trait relationships further indicated that YP, TSW, and PH were positively associated, whereas HLP was negatively correlated with these yield components.

Principal component analysis (PCA) indicated that the first two principal components (PC1 and PC2) together explained 72.1 % of the total phenotypic variation among chickpea accessions (Fig. 3). PC1, which accounted for 45.7 % of the variance, was positively associated with yield potential (YP), thousand-seed weight (TSW), and plant height (PH).

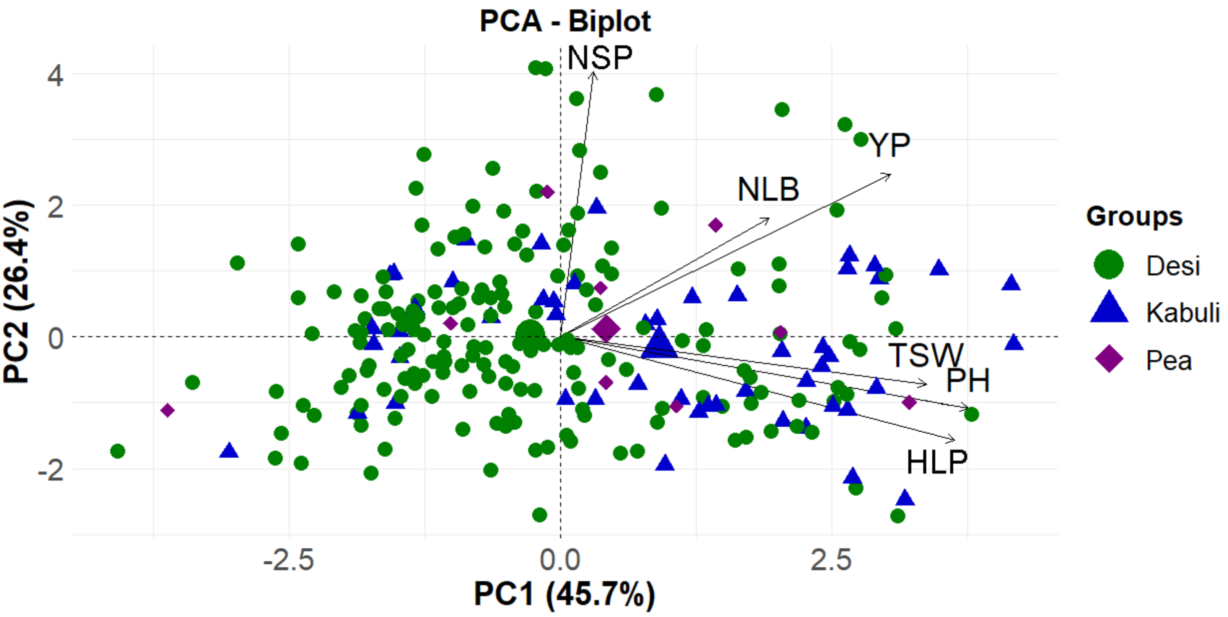

Figure 2. PCA showing the distribution of accessions from different seed types based on six agronomic traits.
PH — plant height; HLP — height to lowest pod; NLB — number of lateral branches;
NSP — number of seeds per plant; YP — yield per plant; TSW — thousand seed weight

PC2, explaining 26.4 % of the variance, was positively correlated with the number of pods per plant (NSP) and number of lateral branches (NLB). The PCA biplot revealed a distinct separation among the three seed types. Kabuli accessions (blue triangles) were predominantly located on the positive side of PC1, reflecting higher YP and TSW values. Desi accessions (green circles) were more widely dispersed, occupying mainly the negative and central regions of PC1, suggesting lower association with yield-related traits and greater genetic variability. Pea-shaped accessions (purple diamonds) were sparsely distributed without a clear clustering pattern, likely due to the limited number of samples.

Discussion

The present multi-year evaluation of 238 chickpea genotypes from diverse global origins under South-East Kazakhstan's semi-arid conditions revealed substantial variability in agronomic traits, emphasizing the richness of genetic diversity within the tested collection. Such diversity is critical for broadening the genetic base of local chickpea breeding programs, which remain relatively narrow compared to major chickpea-growing regions [21, 22]. The significant main effects of genotype origin and seed type on PH, HLP and TSW demonstrate that both genetic background and seed morphology strongly influence performance under local environments. Conversely, strong year effects for NLB and NSP highlight the impact of annual climatic variation on yield-related traits, a finding consistent with other multi-environment studies in chickpea [23, 24].

The strong positive association between YP and TSW (r = 0.605) indicates that larger-seeded genotypes, particularly kabuli types, represent promising candidates for yield improvement in South-East Kazakhstan. This is in line with earlier findings that seed size is one of the primary determinants of market-preferred yield gains [25, 26]. The moderate correlation between YP and NSP (r = 0.530) suggests that increasing seed number can also contribute to yield gains, although the negative correlation between NSP and TSW reflects a well-known trade-off between seed size and seed number in grain legumes [27]. Thus, breeding strategies should seek to optimize both traits, potentially through ideotype-based selection or marker-assisted introgression of favorable alleles.

PCAprovided further insights into the structuring of diversity. Accessions from the Middle East and Africa clustered toward higher yield-related traits, supporting their utility as donor parents for productivity improvement. This agrees with the historical role of the Fertile Crescent and surrounding regions as hotspots of chickpea diversity [17]. In contrast, European accessions generally exhibited lower yield potential but may serve as sources of unique alleles for plant architecture or phenology. Latin American genotypes showed intermediate performance, whereas South Asian lines displayed wide dispersion, reflecting both the high genetic variability and broad adaptation of germplasm from this major chickpea-growing region [28]. The differentiation of kabuli and desi types in the PCA biplot underscores their distinct breeding potential, with kabuli types aligning more strongly with yield-related traits.

Importantly, the identification of 24 superior genotypes across years, including ICC456, ICC637, ICC1392, ICC2065, ICC3362, and ICC3410, provides valuable immediate resources for chickpea improvement in Kazakhstan. Their consistent performance under variable seasonal conditions suggests they possess both yield potential and adaptability. Integrating these genotypes into local breeding programs can enhance productivity and stability under semi-arid environments, where water limitation and temperature stress are key challenges [29].

Conclusion

This study demonstrated that substantial genetic variation exists among 238 chickpea genotypes when cultivated under South-East Kazakhstan conditions. Yield potential was strongly linked to seed size and moderately to seed number, indicating that these traits should be key targets in future breeding programs. PCA and ANOVA analyses confirmed that geographic origin and seed type play an important role in improving agronomic traits, while strong year-to-year variation underlines the need for multi-season testing of genotypes.

Identified high-yielding and stable genotypes from the Middle East and Africa, offering valuable sources to expand the genetic base of local breeding programs. Kabuli types stood out for their close association with yield components, making them especially promising for yield improvement. The 24 perpective lines identified in this study represent an important resource for developing chickpea cultivars with improved productivity and resilience in the semi-arid regions of Kazakhstan.

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Conflict of Interest

Authors declare no conflict of interest.

Author contribution

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript. **Zatybekov A.K.** – Investigation, Methodology, Writing-original draft preparation, Writing-review & Editing; **Yeshengaliyeva A.N.** – Writing-review & Editing; **Anuarbek Sh.N.** – Funding acquisition, Writing-review & Editing; **Kudaibergenov M.S.** – Resources, Data curation; **Turuspekov Y.K.** – Cconceptualization, Plant material collection; **Abugalieva S.I. —** Conceptualization, Writing-review & Editing.

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Қазақстанның оңтүстік-шығысында өсірілген 238 әлемдік ноқат (*Cicer arietinum* L.) генотиптерін далалық бағалау және әртүрлілігі

Қазақстанның оңтүстік-шығысының жартылай шөлейтті жағдайында өсірілетін әлемдік коллекциядан 238 ноқат генотипінің (Cicer arietinum L.) агрономиялық көрсеткіштеріне, сипаттамаларының байланысына және әртүрлілігін бағалау үшін үш жылдық дала зерттеуі жүргізілді. Үш вегетациялық маусымда жүргізілген сынақтар өсімдіктің биіктігі (ӨБ), төменгі бұршақтың бекітілу биіктігі (ТБББ), бүйірлік бұтақтардың саны (ББС), өсімдіктегі бұршақ саны (ӨБС), өсімдік өнімділігі (ӨӨ) және 1000 тұқымның салмағы (МТС) бойынша айтарлықтай өзгергіштікті анықтады. Дисперсиялық талдау бірнеше белгілер бойынша генотиптің шығу тегінің, дән түрінің және жылдың маңыздылығын көрсетті, сондай-ақ генотип × қоршаған орта ықпалдарының күшті әсерін анықтады. Корреляциялық талдау ӨӨ мен МТС арасында күшті және оң корреляция (r = 0,605) және ӨБС мен МТС арасында орташа оң корреляция (r = 0,530) бар екенін көрсетті, ал ӨБС-де теріс корреляция анықталды, бұл дәннің көлемі мен саны арасында ерекшеліктер бар екенін көрсетеді. Негізгі компоненттерді талдауда алғашқы екі компоненттің жалпы вариацияның 72,1%-ын түсіндіретінін көрсетті: Таяу Шығыс пен Африка елдерінен алынған үлгілер жоғары ӨӨ және МТС мәндеріне топтастырылды, ал оңтүстік Азиядан келген генотиптер кең фенотиптік дисперсиямен сипатталды. Кабули типі жалпы өнімділік белгілерімен байланысты болды, ал дези-типі тұқым өлшемінің үлкен өзгергіштігімен әлсіз байланысты көрсетті. Қазақстанның оңтүстік-шығысы жағдайында ноқаттың өнімділігі мен бейімделуін арттыру үшін перспективалы селекциялық материалды ұсынатын ICC456, ICC637, ICC1392, ICC2065, ICC3362 және ICC3410 сияқты 24 жоғары өнімді желі анықталды. Алынған нәтижелер ноқаттың әлемдік гермоплазмасы белгілерінің генетикалық әртүрлілігі мен өзара байланысы туралы құнды ақпарат береді және жартылай шөлейт аймақтарға бағытталған селекциялық бағдарламаларда пайдалану үшін таңдалған генотиптердің әлеуетін көрсетеді.

Кілт сөздер: ноқат, әлемдік үлгілер, агрономиялық белгілер, жартылай шөлейтті Қазақстан.

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Полевая оценка и разнообразие 238 мировых генотипов нут (*Cicerarietinum* L.), выращенных в Юго-Восточном Казахстане

Проведена трёхлетняя полевая оценка агрономических признаков, их взаимосвязей и разнообразия 238 генотипов нута (*Cicerarietinum* L.) из мировой коллекции, возделываемых в полузасушливых условиях юго-востока Казахстана. Испытания, проведённые в течение трёх вегетационных сезонов, выявили значительную вариабельность по высоте растения (ВР), высоте прикрепления нижнего боба (ВПНБ), числу боковых ветвей (ЧБВ), числу бобов с растения (ЧБР), урожайности с растения (УР) и массе 1000 семян (МТС). Дисперсионный анализ показал достоверное влияние происхождения образца, типа семян и года на ряд признаков, а также выявил выраженные взаимодействия генотип × среда. Корреляционный анализ продемонстрировал сильную положительную связь УР с МТС (r = 0,605) и умеренную — с ЧБР (r = 0,530), тогда как между ЧБР и МТС выявлена отрицательная корреляция, отражающая известный компромисс между размером семян и их количеством. Анализ главных компонент показал, что первые две компоненты объясняют 72,1 % общей вариации: образцы из стран Ближнего Востока и Африки группировались в сторону высоких значений УР и МТС, тогда как генотипы из Южной Азии характеризовались широкой фенотипической дисперсией. Кабули-тип в целом был ассоциирован с урожайными признаками, тогда как дези-тип демонстрировал большую изменчивость и слабую связь с размером семян. Выделены 24 высокопродуктивные линии, включая ICC456, ICC637, ICC1392, ICC2065, ICC3362 и ICC3410, представляющие перспективный селекционный материал для повышения урожайности и адаптации нута в условиях юго-востока Казахстана. Полученные результаты предоставляют ценную информацию о генетическом разнообразии и взаимосвязи признаков мировой гермоплазмы нута, а также подчёркивают потенциал отобранных генотипов для использования в селекционных программах, ориентированных на полузасушливые регионы.

Ключевые слова: нут, мировая коллекция, сельскохозяйственные признаки, полузасушливый Казахстан.

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