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PHENOTYPIC VARIATION AMONG FIFTY *CICER ARIETINUM* L. GENOTYPES CULTIVATED UNDER UPLAND, COOL SEMI-ARID CONDITIONS

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Abstract: Chickpea (*Cicer arietinum* L.) is a significant source of protein for people in various regions. To investigate the phenotypic variation among 50 chickpea genotypes, a trial was conducted in the upland, cool, semi-arid region of Gavshaleh, Saqqez, Iran, utilizing a randomized complete block scheme with three replicates. The number of days from seeding to flowering and maturity (NDF, NDM), plant height (PH), chlorophyll content (CHL), ground cover (GC), number of subsidiary branches (NSB), height of first pod from ground (HFB), number of pods per plant (NPP), weight of pod per plant (WPP), weight of shuck per plant (WSP), plant dry weight (PDW), number of seeds per pod (NSP), number of unfilled pods per plant (NUP), plant fresh weight (PFW), protein content (PC), seed yield (SY) and hundred seed weight (HSW) were measured. The analysis revealed that the primary six factors accounted for 80% of the observed variability, representing key aspects such as yield potential, plant stature, biochemical composition, pod and seed weight, flowering time, and plant morphology. Communalities indicated the reliability of all chickpea traits, ranging from 0.53 for NUP to 0.98 for NSP. In the visual analysis, four distinct trait groups were identified based on the first three factors, which explained 60% of the variability. Furthermore, a three-dimensional plot unveiled eight genotypic groups with varying characteristics. Notably, one cluster comprising three genotypes displayed exceptionally high mean yield performance. Ultimately, the top-performing genotypes were categorized into four groups, showcasing their potential for release as cultivars tailored for upland cool semi-arid regions.

Keywords: communality, multivariate statistics, seed performance yield, yield components

Introduction

Legume crops serve as a vital secondary food source after cereals, offering valuable nutritional supplements. They excel in providing both quality and quantity of food, particularly in Latin American, Asian, and African regions. Additionally, chickpeas - in particular - play a crucial role in enhancing soil fertility through nitrogen fixation. Despite some legumes thriving in rainfed conditions, the overall performance of many legume crops remains modest. Chickpea (*Cicer arietinum* L.) holds significant global importance, being cultivated in approximately 50 countries worldwide. Globally, it is as the third most cultivated legume. Iran stands out as a key player in chickpea cultivation, ranking first in terms of both harvested area and production

quantity. The crop dominates in many semi-arid regions across the country, underscoring its pivotal role in Iranian agriculture. Despite the widespread cultivation of chickpeas in numerous countries, its overall production remains relatively low, highlighting a significant gap between its potential yield and actual output. In Iran specifically, over 90% of chickpea cultivation occurs under rainfed conditions, resulting in lower yield performance, averaging around 400 kg per hectare. In contrast, under irrigated conditions, chickpea yields can reach as high as 1100 kg per hectare [2].

Iran serves as a significant hub of chickpea diversity, yet progress in increasing yields has been minimal. Given the rising global population and food scarcity concerns, boosting crop yields emerges as a fundamental strategy to address this challenge. Aside from management issues requiring attention, the primary obstacle to enhancing chickpea yield is the shortage of high-yielding varieties [9]. By selecting desired genotypes and understanding trait relationships, breeders can effectively choose the optimal combination of components that lead to high yields. Morphological and genetic markers provide invaluable tools for studying genetic diversity and evaluating the performance of superior genotypes. The insights gleaned from genetic diversity studies play a crucial role in selecting appropriate parent plants for crossbreeding, thereby avoiding unproductive crossings. Consequently, plant breeders commonly rely on morphological traits as selection criteria to enhance yield performance and other desired traits [3]. Thus, to advance chickpea cultivation, it is imperative to thoroughly investigate genotype diversity and diligently maintain and preserve genetic accessions.

Toker and Ilhan-Cagirgan [16] discovered three key factors that accounted for 93% of the total variance in chickpea traits. Among these factors, yield was strongly linked with biomass, plant height, branch number, and pod number per plant, suggesting their suitability for constructing a selection index. Additionally, Toker [16] identified four factors for assessing yield components in chickpea, explaining 78% of the observed variance in traits, so these findings enable breeders to group germplasm efficiently, minimizing the need for resampling from populations. Also, they categorized yield performance, biomass, and the number of pods per plant as the primary factor, emphasizing their importance. Phenological traits constituted the second factor, distinguishing characteristics related to plant growth stages. Height-related properties emerged as the third factor, indicating their significance in plant structure and development. Finally, hundred seed weight was grouped as the fourth factor, highlighting its role in seed quality and quantity.

Yücel et al. [18] investigated genetic variability in chickpea and identified promising heritable potential for traits such as seed number per plant, seed weight, and number of full pods. They also observed a positive correlation between yield performance and height properties, number of branches, pods, full pods, and seeds per plant. Notably, the contribution of full pods and seeds to yield was found to be particularly significant compared to other traits. Sharifi et al. [11] employed factor analysis on 25 chickpea genotypes and identified three key factors explaining 70% of the observed variation. The first factor encompassed phenological traits, while the second factor comprised morphological characteristics. Interestingly, the third factor was

associated with seed yield-related traits. These findings suggest that such characteristics could prove valuable in future breeding projects aimed at increasing yield. Moreover, they offer a suitable framework for categorizing the genetic variation present in chickpea populations.

The primary objective of the present study was to assess the genetic diversity among 50 chickpea genotypes and to identify key traits influencing seed yield through factor analysis. The aim is to leverage these findings in future chickpea breeding programs, thereby enhancing the crop's yield potential and overall performance.

Materials and Methods

Plant cultivation

The plant materials comprised 50 chickpea genotypes from the International Center for Agricultural Research in Dry Areas (ICARDA) or from Turkey, as detailed in Table 1, which were evaluated in a randomized complete block design with three replicates at the research farm in Gavshaleh, Saqqez, Iran. Situated at an elevation of 1476 meters, the farm is positioned at 36°19’ North latitude and 46°19’ East longitude, lying within a semi-arid cool upland region. Field preparation commenced with plowing to a depth of 25 cm during autumn and continued with spring plowing before planting. Based on the soil analysis findings, the fertilizer requirement was determined, leading to the application of approximately 25 kg ha^{-1} of nitrogen and phosphorus fertilizers before planting. The seeds were then sown in four 1-meter rows, with a line spacing of 25 cm and a plant spacing of 8 cm, beginning in early March. Throughout the growing period, standard crop management practices were implemented as needed, with one irrigation performed during this time. Additionally, the amount of rainfall during the crop season was deemed sufficient for two complete irrigations, considering the field's soil texture, classified as clay loam. Manual weeding was conducted twice before flowering, and phenological traits such as the number of days to flowering and maturity (NDF, NDM) were meticulously recorded for each plot.

Plant traits collection

Once approximately 90% of the plants had reached the physiological maturity stage, the harvesting process commenced. Subsequently, after eliminating the marginal effects of plots, ten plants were randomly chosen from the remaining two rows of each plot for measuring plant height (PH), chlorophyll content (CHL), ground coverage (GC), number of the subsidiary branches (NSB), height of first pod from ground (HFB), number of pods per plant (NPP), weight of pod per plant (WPP), weight of shuck per plant (WSP), plant fresh weight (PFW), number of seeds per pod (NSP), number of unfilled pods per plant (NUP), plant dry weight (PDW), and protein content (PC). The SPAD-502 chlorophyll meter (Konica Minolta, Japan) was employed to measure chlorophyll content and the Zeltex ZX-50 (Zeltex Inc. USA) portable grain analyzer was used to determine protein content. The ground coverage as percentage of soil covering by the canopy was assessed visually based on method of Janmohammadi (2015). To determine seed yield (SY) at physiological maturity, an area equal to 0.25 square meters from the two central rows was sampled in each repetition. The calculated value was then extrapolated to represent the

yield per square meter. Additionally, the hundred seed weight (HSW) was measured using three subsamples from each experimental plot.

Table 1: Name and origin of 50 chickpea genotypes.

Code	Source	Origin		Code	Source	Origin
G1	CIEN-2015-22	ICARDA		G26	PRCYT2-93−92	Turkey
G2	PRCYT2-93−43	Turkey		G27	PRCYT2-93−57	Turkey
G3	CIEN-2015-7	ICARDA		G28	CIEN-2015-16	ICARDA
G4	PRCYT2-93−25	Turkey		G29	PRCYT2-93−17	Turkey
G5	PRCYT2-93−36	Turkey		G30	CIEN-2015-2	ICARDA
G6	PRCYT2-93−37	Turkey		G31	PRCYT2-93−33	Turkey
G7	PRCYT2-93−2	Turkey		G32	CIEN-2015-17	ICARDA
G8	CHECK	IRAN		G33	PRCYT2-93−97	Turkey
G9	PRCYT2-93−83	Turkey		G34	PRCYT2-93−39	Turkey
G10	PRCYT2-93−21	Turkey		G35	PRCYT2-93−27	Turkey
G11	CIEN-2015-20	ICARDA		G36	PRCYT2-93−15	Turkey
G12	CIEN-2015-30	ICARDA		G37	PRCYT2-93−18	Turkey
G13	PRCYT2-93−85	Turkey		G38	PRCYT2-93−20	Turkey
G14	PRCYT2-93−32	Turkey		G39	CIEN-2015-18	ICARDA
G15	PRCYT2-93−74	Turkey		G40	PRCYT2-93−52	Turkey
G16	PRCYT2-93−79	Turkey		G41	PRCYT2-93−100	Turkey
G17	PRCYT2-93−7	Turkey		G42	CIEN-2015-12	ICARDA
G18	PRCYT2-93−35	Turkey		G43	PRCYT2-93−9	Turkey
G19	CIEN-2015-11	ICARDA		G44	PRCYT2-93−12	Turkey
G20	PRCYT2-93−94	Turkey		G45	CIEN-2015-14	ICARDA
G21	PRCYT2-93−69	Turkey		G46	PRCYT2-93−47	Turkey
G22	PRCYT2-93−14	Turkey		G47	CIEN-2015-28	ICARDA
G23	PRCYT2-93−23	Turkey		G48	CIEN-2015-34	ICARDA
G24	PRCYT2-93−4	Turkey		G49	PRCYT2-93−24	Turkey
G25	PRCYT2-93−102	Turkey		G50	PRCYT2-93−34	Turkey

Numerical analyses

The normality of the data and the uniformity of error variances were assessed using Minitab 16.0 software. ANOVA and Tukey's HSD (honestly significant difference) test was used to comparison of final detected genotypic groups. While there are various methods for measuring genetic diversity, some may not effectively demonstrate the relationships among different traits. Multivariate statistical methods, on the other hand, enable the simultaneous evaluation of genotypes based on multiple characteristics. By employing these methods, important and effective traits contributing to performance can be identified, allowing for the determination of their useful and efficient contributions to overall performance [10]. Among these methods, factor analysis stands out as a powerful technique for reducing numerous correlated traits to a smaller set of independent factors, thereby elucidating the correlations between variables. By utilizing

the rotated coefficients of the factors, particularly with varimax rotation, factors with eigenvalues exceeding unity were identified and analyzed as the most significant influencing factors. The factor analysis was conducted using Statistica 10.0 [13]. To evaluate the appropriateness of factor analysis, two statistical indices were utilized: the Kaiser-Meyer-Olkin (KMO) index, which assesses the sampling adequacy, and the Bartlett sphericity test. Additionally, the magnitudes of common factors or communality were calculated to determine the extent to which each trait contributed to the variation observed in the data. A three-dimensional plot, makes easy visualization of the relations among the traits, and if the used factors describe a proper magnitude of the variability, the traits' associations can be grasped graphically.

Results and Discussion

The KMO value obtained was greater than 0.50 (0.63), indicating sufficient correlation among the traits for factor analysis. Additionally, the Bartlett sphericity test yielded a statistically significant result (χ^2= 790.3, P<0.01), indicating ample association among the variables (traits). Therefore, the dataset was deemed ideal for factor analysis, suggesting that environmental conditions could effectively influence the importance and grouping of traits.

The factor analysis revealed that the first six eigenvalues of the main factors exceeded unity, collectively explaining 80% of the total variance (Table 2). The first factor, which explained 29% of the variability, encompassed important yield components such as the number of pods per plant (NPP) and the number of seeds per pod (NSP), along with seed yield (SY), suggesting a focus on yield potential. Conversely, the second factor, which accounted for 20% of the observed variation, displayed high negative values for traits such as plant dry weight (PDW), plant height (PH), number of subsidiary branches (NSB), plant fresh weight (PFW), and canopy width (CW). This indicates a preference for smaller plant stature within this factor (Table 2). Tiwari and Saxena [15] identified the number of days to maturity, number of branches per plant, number of pods per plant, and seed weight as the primary influencing traits.

The third factor, explaining 12% of the variance, comprised traits such as chlorophyll content (CHL) and protein content (PC), leading to the designation of 'biochemical compounds' for this factor (Table 2). Meanwhile, the fourth factor, which accounted for 8% of the variability, included traits like weight of pod per plant (WPP) and hundred seed weight (HSW), hence it was labeled as the 'pod and seed weight' factor. The fifth factor, explaining 7% of the observed variance, exhibited high negative values for phenological traits (number of days to flowering and maturity, NDF and NDM) as well as weight of shuck per plant (WSP). As such, it was aptly labeled as 'earliness' (Table 2). On the other hand, the sixth factor, which accounted for 6% of the variance, primarily comprised traits such as height of first pod (HFB) and ground coverage (GC), albeit indicating a relatively high negative value for number of unfilled pods per plant (NUP). Hence, 'plant morphology' was deemed suitable for this factor (Table 2). In terms of communalities, most of the chickpea traits demonstrated good reliability, underscoring their genetic consistency.

Table 2: The varimax rotated scores of first six factors and amounts of communalities.

Traits	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Communality
PH	0.11	-0.91	0.05	0.08	0.04	0.13	0.87
NDF	-0.23	0.21	-0.35	-0.08	-0.69	0.02	0.70
NDM	-0.34	-0.03	-0.42	0.27	-0.58	0.02	0.70
CHL	0.17	-0.01	0.84	-0.24	0.26	0.01	0.87
GC	0.28	-0.13	0.01	0.31	0.51	0.54	0.75
NSB	0.44	-0.50	-0.42	-0.21	-0.01	-0.15	0.68
HFB	0.02	-0.30	-0.13	0.10	0.01	0.84	0.82
NPP	0.92	-0.19	0.08	-0.18	0.15	0.10	0.96
WPP	-0.27	-0.15	-0.22	0.81	-0.11	0.02	0.81
WSP	0.08	0.00	0.07	0.57	-0.69	0.01	0.81
NSP	0.94	-0.14	0.07	-0.21	0.12	0.10	0.98
NUP	-0.15	0.09	-0.25	0.29	0.07	-0.59	0.53
HSW	-0.12	0.00	-0.19	0.89	-0.02	-0.02	0.85
PDW	0.15	-0.79	0.20	0.07	-0.02	0.29	0.78
PFW	0.06	-0.87	0.01	0.00	0.09	0.19	0.80
CW	0.13	-0.63	-0.53	0.08	0.17	-0.14	0.76
PC	0.02	-0.11	0.86	-0.16	0.12	0.02	0.79
SY	0.97	-0.08	0.05	0.02	0.09	0.10	0.97
Eigenvalue	5.15	3.51	2.00	1.51	1.20	1.03	
Proportion	0.29	0.20	0.12	0.08	0.07	0.06	
Cumulative	0.29	0.48	0.60	0.68	0.74	0.80	

Abbreviations: PH, plant height; NDF, number of days to flowering; NDM, number of days to maturity; CHL, chlorophyll content; GC, ground coverage; NSB, number of the subsidiary branches; HFB, height of first pod; NPP, number of pods per plant; WPP, weight of pod per plant; WSP, weight of shuck per plant; NSP, number of seeds per pod; NUP, number of unfilled pods per plant; HSW, hundred seed weight; PDW, plant dry weight; PFW, plant fresh weight; CW, canopy width; PC, protein content; and SY, seed yield.

The values of communalities ranged from 0.53 for number of unfilled pods per plant (NUP) to 0.98 for number of seeds per pod (NSP). However, most of the measured traits exhibited communalities of around 0.70 or higher, indicating high accuracy (Table 2). These high communalities suggest that the six extracted factors effectively described the variability of traits, accounting for more than 70% to nearly 100% of the variability. Hence, they provide a comprehensive description of trait variabilities. Similarly, Ghorbani et al. [6] reported findings in chickpea, identifying five factors: seed size, yield, morphology, harvest index, and filled pods, which collectively explained 81% of the observed variation. Conversely, Toker and Ilhan-Cagirgan [17], as well as Sharifi et al. [11], identified three main factors encompassing phenological, morphological, and seed yield-related characteristics. We were able to identify similar components, including negative values for plant properties, which we categorized as the 'small plant' factor, suggesting caution in selection to avoid favoring larger plants. Furthermore, the measured biochemical compounds (CHL and PC) emerged as an independent factor, while the weight of pods and seeds formed another independent factor.

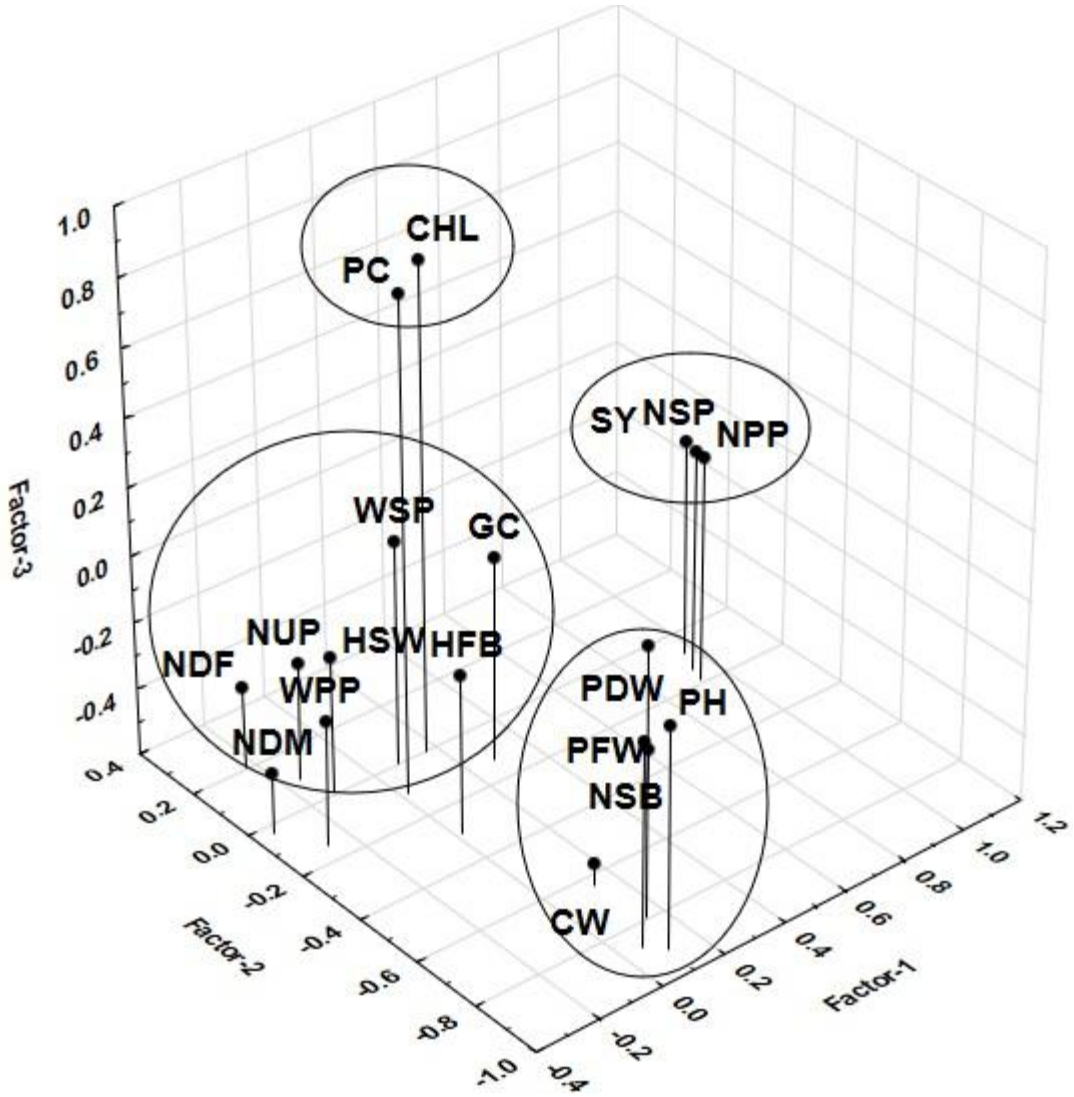

Fig. 1: Three-dimensional plot based on first three factors for grouping traits of chickpea.

Abbreviations: PH, plant height; NDF, number of days to flowering; NDM, number of days to maturity; CHL, chlorophyll content; GC, ground coverage; NSB, number of the subsidiary branches; HFB, height of first pod; NPP, number of pods per plant; WPP, weight of pod per plant; WSP, weight of shuck per plant; NSP, number of seeds per pod; NUP, number of unfilled pods per plant; HSW, hundred seed weight; PDW, plant dry weight; PFW, plant fresh weight; CW, canopy width; PC, protein content; and SY, seed yield.

The first three factors collectively accounted for 60% of the variability in the dataset (Table 2); whereas, this amount of genotype by trait interaction implies that both additive and crossover interactions in chickpea dataset, indicating differential rankings of measured traits across genotypes. This finding resonates with similar observations in chickpea studies [5] and other crop investigations [4 and 12], underscoring the challenge of achieving an indirect response to selection across all genotypes without considering genotype-by-trait interactions. As depicted in Fig. 1, chlorophyll content (CHL) and protein content (PC) are grouped within Category-1, consistent with the third factor, while number of pods per plant (NPP), number of seeds per pod

(NSP), and seed yield (SY) are grouped within Category-2, aligning with the first factor. These results are consistent with the findings of Sharifi et al. [11], who observed a positive relationship between seed yield of chickpea and pod and seed numbers. Furthermore, plant height (PH), number of subsidiary branches (NSB), plant dry weight (PDW), plant fresh weight (PFW), and canopy width (CW) are grouped within Category-3, consistent with the second factor (Fig. 1). Guptha et al. [7] reported a positive correlation between plant height and plant dry weight in chickpea. Finally, the remaining traits are grouped within Category-4, consistent with the fourth, fifth, and sixth factors. These traits include weight of pod per plant (WPP), hundred seed weight (HSW), number of days to flowering and maturity (NDF, NDM), weight of shuck per plant (WSP), height of first pod (HFB), ground coverage (GC), and number of unfilled pods per plant (NUP). These findings align well with the investigation of Alemayo et al. [1], who observed a positive relationship between phonological traits and pod characteristics in chickpea.

Table 3: The scores of three first factors for 50 chickpea genotypes.

	F1	F2	F3	GG†		F1	F2	F3	GG
G1	-2.90	**1.99**	**0.73**	5	G26	-6.30	**2.44**	-1.38	6
G2	-2.60	**1.95**	-2.95	6	G27	-4.49	-1.84	-2.55	8
G3	-3.44	-0.16	-3.19	8	G28	-0.91	-1.58	-1.43	8
G4	-0.14	-1.65	**1.36**	7	G29	-0.57	-0.87	**0.64**	7
G5	-0.22	**0.04**	-0.23	6	G30	**1.93**	**1.29**	-0.95	2
G6	-1.06	**0.90**	**0.01**	5	G31	**0.16**	-1.27	-0.73	4
G7	0.42	**1.63**	**0.26**	5	G32	-0.01	**0.49**	-0.08	6
G8	-0.28	-2.66	**1.57**	7	G33	**0.85**	**2.31**	-1.23	2
G9	**4.70**	-1.14	-1.03	4	G34	-0.27	**2.03**	**0.11**	5
G10	-0.52	**3.77**	**0.98**	5	G35	-0.12	**2.46**	**0.01**	5
G11	**3.33**	-2.10	-0.83	4	G36	**0.19**	**6.00**	**3.03**	1
G12	**2.84**	**0.47**	**0.54**	1	G37	**1.98**	**1.56**	-1.77	2
G13	**2.85**	-2.43	**0.30**	3	G38	**2.79**	-1.69	-1.24	4
G14	-0.83	-0.14	**1.43**	7	G39	**1.01**	**0.91**	**0.21**	1
G15	-1.37	-1.74	**3.28**	7	G40	**0.62**	**0.89**	-0.07	2
G16	-3.25	-1.00	**2.77**	7	G41	**0.63**	-2.62	-0.42	4
G17	-3.49	-0.75	**0.97**	7	G42	-1.04	-0.95	-0.28	8
G18	-2.45	-2.75	**1.62**	7	G43	**1.75**	-1.00	-0.11	4
G19	-0.57	-2.82	**2.59**	7	G44	**0.82**	**0.09**	**1.16**	1
G20	-2.30	-1.28	**0.94**	7	G45	**1.45**	**1.00**	-1.25	2
G21	**5.03**	**1.06**	**0.35**	1	G46	**0.85**	**1.03**	-0.52	2
G22	-1.97	-2.67	-2.26	8	G47	**1.37**	**1.01**	-0.94	2
G23	-1.45	**0.81**	**0.75**	5	G48	**1.45**	**1.96**	**0.40**	1
G24	**2.54**	**0.39**	**0.69**	1	G49	**2.07**	-1.24	-0.77	4
G25	**1.90**	-1.23	**0.02**	3	G50	-1.00	-0.93	-0.48	8

†GG, genotypic groups. There are eight genotypes' groups based on positive (bold scores) and negative scores (regular scores) of first three factors; GG1, +F1+F2+F3; GG2, +F1+F2-F3; GG3, +F1-F2+F3; GG4, +F1-F2-F3; GG5, -F1+F2+F3; GG6, -F1+F2-F3; GG7, -F1-F2+F3; and GG8, -F1-F2-F3.

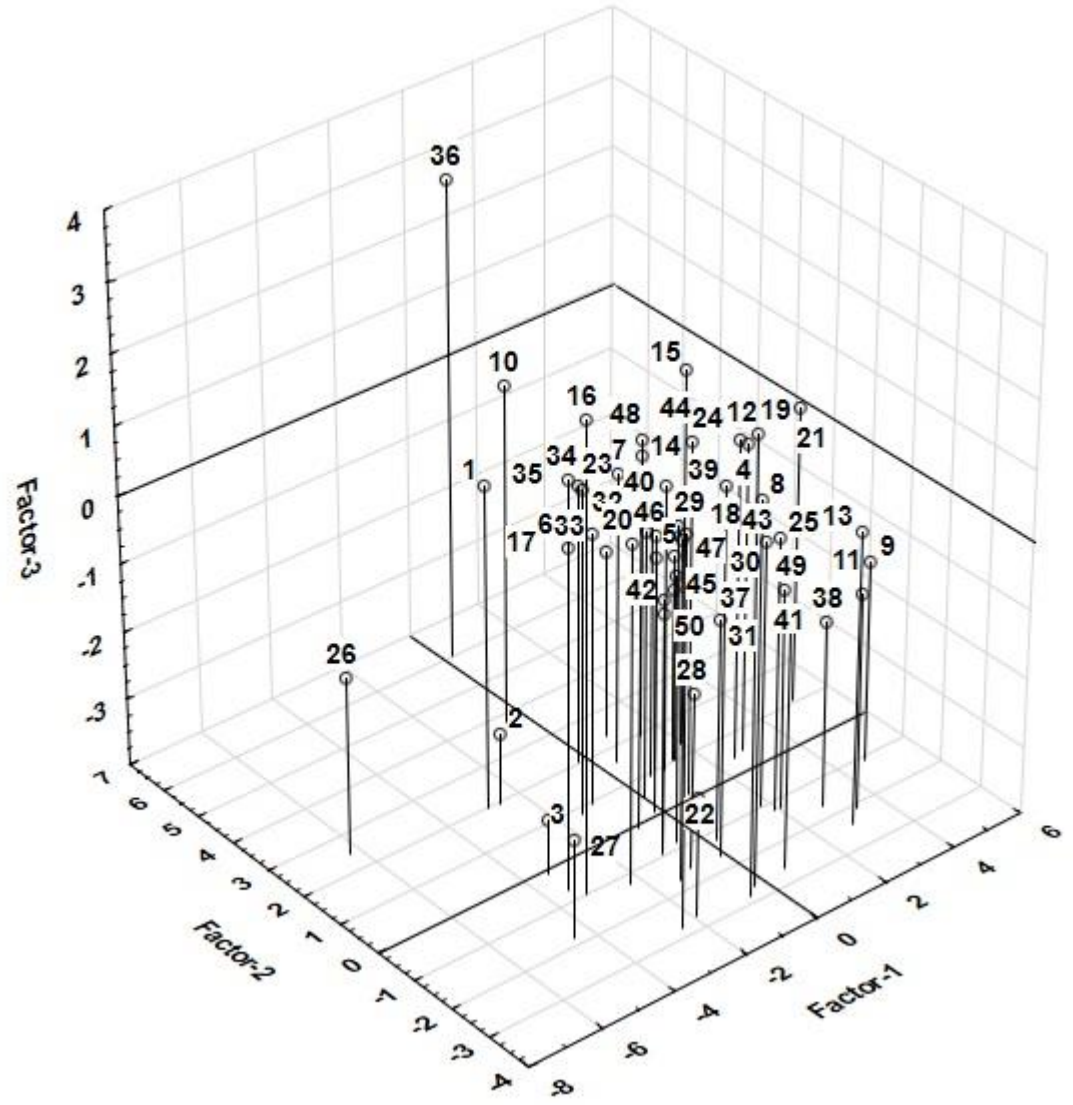

Fig. 2: Three-dimensional plot based on first three factors for grouping chickpea genotypes. For more details, refer to e Table 9.

Eight distinct genotypic clusters were identified (Table 3) and showed in Fig. 2 as: Group-1: comprising three genotypes (1, 10, and 23); Group-2: consisting of eleven genotypes (2, 5, 6, 26, 32, 34, and 35); Group-3: including four genotypes (3, 22, 27, and 28); and Group-4: comprised of ten genotypes (4, 8, 14, 15, 16, 17, 18, 19, 20, and 29). Additionally, other similar genotypic clusters observed in the plot were: Group-5: encompassing eleven genotypes (7, 12, 21, 33, 37, 39, 40, 45, 46, 47, and 48); Group-6: consisting of ten genotypes (9, 11, 13, 25, 30, 31, 38, 41, 43, and 49); Group-7: containing three genotypes (24, 36, and 44) and Group-8: including two genotypes (42 and 50). Table 4 presents the averages of chickpea traits for each of the eight groups. Genotypes in Group-3 exhibited higher values for seed yield and yield components such as number of subsidiary branches (NSB), number of pods per plant (NPP), and

number of seeds per pod (NSP), while these genotypes showed lower or moderate values for other traits. Following Group-3, genotypes in Group-5 displayed higher values for seed yield along with ground coverage (GC), NSB, height of first pod (HFB), weight of pod per plant (WPP), plant fresh weight (PFW), and canopy width (CW), suggesting that the high values in these traits could compensate for the moderate amounts of NPP and NSP (Table 4). Genotypes in Group-1, Group-4, and Group-8 exhibited moderate values for seed yield, high ground coverage (GC), and moderate NPP and NSP, indicating favorable properties in terms of early flowering and maturity (Table 4). Genotypes in Group-5, Group-6, and Group-7 displayed low values for seed yield, along with low or moderate values for most traits, but exhibited favorable properties in terms of hundred seed weight. These genotypes could be considered for the breeding of cultivars with larger seed sizes, which could potentially enhance marketability (Table 4). Therefore, the best genotypes identified in Group-3, namely G3 (CIEN-2015-7 from ICARDA), G22 (PRCYT2-93-14 from Turkey), G27 (PRCYT2-93-57 from Turkey), and G28 (CIEN-2015-16 from ICARDA), are recommended for commercial release as improved cultivars suitable for rainfed conditions in cool upland semi-arid areas, following multi-environmental trials.

Conclusions

The six latent factors identified (yield potential, small plant, biochemical compounds, pod and seed weight, earliness, and plant morphology) offer valuable insights into the underlying structure of genetic diversity in chickpea and facilitate targeted breeding efforts to enhance desired traits. Despite previous research mentioning hundred seed weight as a yield component in chickpea, this study did not delve into this aspect extensively. It appears that the utilized genotypes, sourced from improved breeding lines, did not significantly differ in this regard, thus limiting the ability to discern the role of hundred seed weight.

These findings hold significant implications for genetic improvement programs aimed at releasing high-yielding chickpea cultivars and classifying genetic variation among genotypes. The number of pods and seeds emerged as crucial influencing traits for seed yield, suggesting their potential to enhance the genetic gain in chickpea improvement efforts, particularly in rainfed conditions of cool upland semiarid regions. Consequently, the most desirable genotypes identified in Group-3, namely CIEN-2015-7 (ICARDA), G22 PRCYT2-93-14 (Turkey), PRCYT2-93-57 (Turkey), and CIEN-2015-16 (ICARDA), can be recommended for release as improved cultivars tailored to the rainfed conditions of cool upland semiarid areas. These genotypes exhibit promising traits that could contribute significantly to enhancing chickpea productivity and resilience under challenging environmental conditions.

Table 4: Mean ± SE of chickpea traits corresponding to the eight genotypic groups distinguished in Fig. 2 and Table 3.

	Group-1	Group-2	Group-3	Group-4	Group-5	Group-6	Group-7	Group-8	HSD†
PH	31.22±4.86	26.52±3.94	23.08±2.13	26.17±3.90	24.70±2.33	21.80±2.54	28.56±8.70	23.67±2.83	2.22
NDF	53.00±1.86	53.05±1.57	53.58±0.83	52.80±1.02	54.15±0.91	54.07±0.84	53.78±1.02	53.00±0.47	0.334
NDM	87.67±1.050	87.24±1.150	87.17±0.577	86.80±0.984	88.52±1.158	87.97±0.949	88.56±1.503	87.17±0.707	0.385
CHL	29.56±10.67	25.90±6.64	36.58±6.66	49.23±8.16	24.79±5.98	27.07±6.63	25.78±5.06	35.83±1.18	6.94
GC	54.44±13.47	54.76±9.64	46.67±3.85	52.67±8.32	47.58±9.20	33.00±13.00	46.11±5.85	50.00±0.00	3.46
NSB	5.33±1.45	5.67±1.99	5.67±1.12	4.13±0.77	5.09±0.86	4.23±0.90	4.78±1.26	5.67±0.00	0.290
HFB	16.78±5.10	15.00±1.74	11.75±1.32	13.57±2.48	12.48±2.36	11.03±1.72	15.44±5.43	12.33±0.94	2.12
NPP	17.11±2.17	19.90±6.31	26.08±5.36	16.30±4.37	12.48±3.50	11.53±2.64	10.56±0.38	18.00±3.30	2.38
WPP	0.48±0.051	0.48±0.044	0.32±0.103	0.42±0.048	0.52±0.038	0.45±0.073	0.55±0.048	0.43±0.072	0.012
WSP	0.12±0.011	0.11±0.024	0.10±0.028	0.10±0.015	0.12±0.012	0.12±0.032	0.12±0.011	0.09±0.025	0.003
NSP	18.89±2.04	21.62±6.08	28.17±5.42	18.13±3.60	14.55±3.15	14.07±2.41	11.78±0.84	19.50±2.59	3.20
NUP	1.44±0.192	1.52±0.262	1.42±0.319	1.50±0.393	1.97±0.505	1.67±0.385	1.56±0.192	1.50±0.236	0.127
HSW	35.64±4.10	36.91±3.37	31.21±6.10	32.77±4.51	39.78±3.98	33.73±5.60	42.03±3.37	33.68±4.74	1.37
PDW	15.11±0.694	13.62±0.826	12.42±0.957	13.60±1.131	12.76±1.165	11.80±0.789	14.33±1.453	12.50±0.236	0.913
PFW	21.89±0.839	20.86±1.103	19.33±1.414	20.20±1.219	19.76±1.484	18.20±1.009	20.33±2.887	19.67±0.000	0.672
CW	24.89±1.68	27.62±5.08	24.17±1.67	20.00±2.61	26.36±4.58	19.50±3.15	27.78±5.09	23.33±4.71	2.19
PC	17.29±1.51	17.70±0.57	19.20±1.19	21.36±0.90	17.61±1.16	17.76±1.21	19.22±0.73	19.53±0.82	1.89
SY	1340.2±173.4	1515.8±319.7	1838.7±289.6	1247.6±205.9	1127.6±212.9	1031.3±185.6	922.8±74.0	1338.9±257.5	254.0

Abbreviations: PH, plant height; NDF, number of days to flowering; NDM, number of days to maturity; CHL, chlorophyll content; GC, ground coverage; NSB, number of the subsidiary branches; HFB, height of first pod; NPP, number of pods per plant; WPP, weight of pod per plant; WSP, weight of shuck per plant; NSP, number of seeds per pod; NUP, number of unfilled pods per plant; HSW, hundred seed weight; PDW, plant dry weight; PFW, plant fresh weight; CW, canopy width; PC, protein content; and SY, seed yield.

†HSD, Tukey's HSD (honestly significant difference.

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VARIAȚIA FENOTIPICĂ A CINCIZECI DE GENOTIPURI DE *CICER ARIETINUM* L. CULTIVATE ÎN CONDIȚII ALTITUDINALE SEMI-ARIDE

(Rezumat)

Năutul (*Cicer arietinum*L.) este o sursă importantă de proteine pentru oamenii din diverse regiuni. Pentru a investiga variația fenotipică a 50 de genotipuri de năut, a fost efectuat un studiu în regiunea montană, rece și semi-aridă din Gavshaleh, Saqqez, Iran, utilizând o schemă completă randomizată, cu trei repetiții. Astfel, au fost estimate: numărul de zile de la semănare până la înflorire și maturitate (NDF, NDM), înălțimea plantei (PH), conținutul de clorofilă (CHL), acoperirea solului (GC), numărul ramurilor subsidiare (NSB), înălțimea primei păstăi de la sol (HFB), numărul de păstăi per plantă (NPP), greutatea păstaie per plantă (WPP), greutatea cojilor per plantă (WSP), greutatea uscată a plantei (PDW), numărul de semințe per păstaie (NSP), numărul de păstăi fără semințe per plantă (NUP), greutatea proaspătă a plantei (PFW), conținutul de proteine (PC), randamentul semințelor (SY) și greutatea a o sută de semințe (HSW). Analiza a subliniat că cei șase factori primari au explicat 80% din variabilitatea observată, reprezentând aspecte cheie precum potențialul de producție, statura plantei, compoziția biochimică, greutatea păstăilor și semințelor, timpul de înflorire și morfologia plantei. Comunitățile au indicat fiabilitatea tuturor caracterelor năutului, variind de la 0,53 pentru NUP la 0,98 pentru NSP. În analiza vizuală, au fost identificate patru grupuri de caractere distincte pe baza primilor trei factori, care au explicat 60% din variabilitate. În plus, o diagramă tridimensională a dezvăluit opt grupuri genotipice cu caracteristici diferite. În special, un grup care cuprinde trei genotipuri a prezentat un randament de productivitate foarte ridicat. În cele din urmă, genotipurile cu cele mai bune performanțe au fost clasificate în patru grupuri, care le recomandă ca soiuri adaptate pentru regiunile semiaride răcoroase.

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