

Factor Analysis of Agronomic Characters in Chickpea Genotypes Under Semi-Arid Circumstances

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Abstract

Chickpea, is a protein supply of human food in many areas and the genetic variation is essential for providing useful genes for genetic improvement projects. To study the genetic variation of 36 genotypes (18 lines from İCARDA, 17 lines from national breeding program and one check cultivar), two yearly experiments were performed in randomized block sachem with three repetitions at semiarid aera of Maragheh, Iran. Some traits like number of the primary and secondary branches; one-grain, two-grain, and empty scabbards of the primary and secondary branches, grain number and husk weight of the primary and secondary scabbards, plant dry weight, ground coverage percent, days to flowering and maturity, grain yield, biomass, and hundred grain weight were measured. The first six and seven factors described 80.7 and 85.1% of observed variability in the first and second years, and were named as yield potential, biological performance, height, scabbard and maturity, canopy, and flowering and grain weight in the first year. In the second year, the identified factors were named as yield and yield components related to the primary branches, the yield components related to the secondary branches, height, biological performance, the number of branches, two-grain scabbards and phenology. Communalities showed that all of the chickpea traits were reliable and in visual analysis, four groups of genotypes were identified while the best genotypes were genotypes of the first classification across both years as 3 (13/A2), 5 (18/A2), 6 (2/A2), and 12 (7/), from ICARDA and 27 (3/3 URCYT-93) from Iran as well as 35 (cultivar Arman) which can be advised for release as cultivars for semiarid areas.

Keywords: Communalities, Multivariate statistics, Seed yield, Yield components

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1. Introduction

Pulses play a crucial role in ensuring global food security, particularly in the face of predicted climate challenges. To address these challenges, international initiatives have been launched to enhance legume production in diverse environmental conditions. Chickpea (*Cicer arietinum* L.), a vital legume crop, is cultivated across most continents, serving as a key source of nutritious food for the growing global population (Maya & Maphosa, 2020). As the second most significant legume globally, chickpea is essential for human nutrition and animal feed. Additionally, its cultivation enhances soil fertility, especially in arid and semi-arid regions (Takıl and Kayan, 2023). When integrated into cereal-legume rotations, it helps break pest and disease cycles, thereby improving the overall productivity of the rotation system (Korbu et al., 2020). In Iran, chickpea covers approximately 430,000 hectares, yielding a total production of 176,000 tons. However, its productivity (410 kg/ha) falls significantly below the global average of 1,222 kg/ha (FAO STAT, 2022). This yield gap is largely attributed to biotic and abiotic stresses that adversely affect production. To address this challenge, developing stress-resilient genotypes is critical to enhance productivity. Genetic diversity among parental lines is a cornerstone for successful breeding programs, as it provides researchers with greater opportunities to design effective strategies. Consequently, evaluating the genetic diversity of chickpea genotypes is essential for advancing breeding initiatives (van Etten et al., 2023).

The patterns and inheritance of genetic diversity vary significantly among genotypes, making the evaluation of these patterns critical for researchers. This process maximizes opportunities to develop plant genotypes best suited to specific environmental conditions. In Mediterranean regions, where moderate-cold weather with autumn rainfall prevail, chickpea is typically produced in the spring. As a result, it often faces hot and water-shortage stress during final stages, leading to low and inconsistent yields (Bouchyoua et al., 2024). However, the development of stress-resistant varieties with enhanced water-use efficiency and stable productivity supports the recommendation of winter sowing in these areas to overcome such challenges. Genetic variation plays a pivotal role in breeding programs and the selection of desirable traits (Atay et al., 2023). The collection and characterization of diverse genetic material are foundational steps for any breeding initiative. Moreover, evaluating genotype-by-environment interactions is crucial for genetic improvement projects, as environmental influences on yield performance are not heritable (Shah et al., 2020). Understanding and utilizing genetic diversity is thus essential for the success of breeding programs. Multivariate analysis has proven to be one of the most effective tools for assessing genetic variation in chickpea genotypes, enabling breeders to identify and select promising traits for crop improvement.

Mahmood et al. (2018) assessed genetic variation of fifteen chickpea genotypes and found three principal components which accounted for 51, 20 and 16% in variation, respectively. They reported higher influences for plant height, yield, harvest index, hundred-seed weight, pods of plant and days to flowering with high most donations to variations among genotypes and can be utilized for breeding programs. Sharifi et al. (2018) evaluated 25 genotypes of chickpea via factor analysis and found that three factors explained 70% of the variation and named as phenology, morphology and yield properties while yield indicated high relations with harvest index, canopy, pods of plant, and biomass, so above information can be used for planning proper strategy for next crossbreeding programs for increasing yield. Kumar et al. (2019) studied forty chickpea genotypes using principal component analysis, and three components with eigen value more than 1.0, described 92% of variability. They reported that the first component contributed 60% of the variation and related negatively with hundred-seed weight; the second component contributed 25% of the variation and involved to hundred-seed weight and days to flowering; and the third component contributed 7% of the variation and related to pods of plant. Jain et al. (2023) used principal component analysis for evaluating of 40 chickpea genotypes and found that only three components had large eigenvalue whereas the first one contributed 29% of the variability and involved with seeds of pod, pods of plant, days to flowering and maturity, as well as height of plant and the first pod. Also, they found that the second component explained 21% of the variance and related to yield performance, the first pod height and plant height while the third component described only 13% of the variability and associated with main branches. For achieving sustainability targets, plant breeders require to merge adaptability as a focus in cultivar release process. Current production of chickpea is not sufficient to achieve the market demands which emphasizes the choose of best performing individuals regarding of yield components. The sufficient knowledge on genetic diversity and relationship among grain yield performance and components is needed for next breeding efforts. The purpose of current research was scheduled to assessment genetic variation among improved genotypes and their utilization in chickpea genetic improvement program.

2. Materials and Methods

2.1. Experiments

Thirty-five advanced chickpea genotypes, sourced from Iran's national legume breeding program and the International Center for Agricultural Research in the Dry Areas (ICARDA), were tested, alongside a control cultivar, Arman, which was developed in Iran (Table 1). These genotypes were chosen for their potential in improving chickpea yield and adaptation to semi-arid environments. The study was conducted over two growing seasons, 2022 and 2023, in a semi-arid region at the research field of the University of Maragheh, Iran. The field trials were set up using a randomized complete block design with three replications, ensuring reliable statistical analysis and results. Each genotype was planted in four rows, with each row measuring 2 meters in length and spaced 50 cm apart. This setup allowed for a planting density of 20 plants per square meter, which is a typical density for chickpea cultivation. Prior to planting, essential fertilizers were applied to ensure optimal growth. Specifically, 50 kg/ha of nitrogen and 60 kg/ha of phosphorus pentoxide were used to meet the crop's nutritional needs. These fertilizers were chosen to support healthy plant development and boost yield potential under the study's challenging environmental conditions. The soil in the research field had a depth of 20 to 40 cm, which is adequate for growing chickpeas but may limit root growth under dry conditions. Soil chemical analysis showed a pH of 7.7, which is slightly alkaline but still within the range suitable for legume growth. The phosphorus content was measured at 48 kg/ha, which is relatively high, indicating good nutrient availability. The organic matter content was 0.7%, which is moderate and provides essential nutrients and microbial activity to the soil, contributing to soil fertility. Maragheh, located in a semi-arid region, experiences a Mediterranean climate, characterized by hot, dry summers and cold, wet winters. The long-term climate data for the area revealed an annual average precipitation of 1225 mm, though much of this rainfall occurs during the winter months, with 330 mm typically falling during the growing season. The mean annual temperature is 18.1°C, which supports the growth of chickpeas, a crop well-suited to warm climates. These climatic conditions, combined with the relatively low rainfall during the growing season, create a semi-arid environment, which challenges crop productivity and highlights the importance of selecting drought-resistant genotypes. By conducting this research under these specific climatic and soil conditions, the study aimed to evaluate how different chickpea genotypes perform under stress, particularly with respect to water availability.

Table 1. Code, name and origin of 36 chickpea (*Cicer arietinum* L.) genotypes

Code	Name	Origin	Code	Name	Origin
G1	8/A2	ICARDA	G19	4/3 URCYT-93	Iran
G2	6/A2	ICARDA	G20	15/3 URCYT-93	Iran
G3	13/A2	ICARDA	G21	10/3 URCYT-93	Iran
G4	15/A2	ICARDA	G22	5/3 URCYT-93	Iran
G5	18/A2	ICARDA	G23	6/3 URCYT-93	Iran
G6	2/A2	ICARDA	G24	12/3 URCYT-93	Iran
G7	7/A2	ICARDA	G25	17/3 URCYT-93	Iran
G8	16/A2	ICARDA	G26	7/3 URCYT-93	Iran
G9	2/A1	ICARDA	G27	3/3 URCYT-93	Iran
G10	17/A1	ICARDA	G28	1/3 URCYT-93	Iran
G11	13/A1	ICARDA	G29	8/3 URCYT-93	Iran
G12	7/A1	ICARDA	G30	2/3 URCYT-93	Iran
G13	4/A1	ICARDA	G31	18/3 URCYT-93	Iran
G14	11/A1	ICARDA	G32	13/3 URCYT-93	Iran
G15	10/A1	ICARDA	G33	11/3 URCYT-93	Iran
G16	8/A1	ICARDA	G34	9/3 URCYT-93	Iran
G17	14/A1	ICARDA	G35	Arman	Iran
G18	14/3 URCYT-93	Iran	G36	FLIP 99-6C	ICARDA

The findings from this study will help in selecting the most resilient genotypes for future breeding programs, particularly those aimed at improving productivity in semi-arid regions where water scarcity is a major concern

2.2. Characteristics

Observations for each genotype were recorded regarding ten random samples in plant height (PH), first branch height (FBH), first scabbard height (FSH), number of the primary branches (NPB), number of the secondary branches (NSB), one-grain scabbard of the primary branches (OSPB), one-grain scabbard of the secondary branches (OSSB), two-grain scabbard of the primary branches (TSPB), two-grain scabbard of the secondary branches (TSSB), empty scabbard of the primary branches (ESPB), empty scabbard of the secondary branches (ESSB), grain number of the primary scabbard (GNPS), grain number of the secondary scabbard (GNSS), grain weight of the primary scabbard (GWPS), grain weight of the secondary scabbard (GWSS), plant dry weight (PDW), husk weight of the primary scabbard (HWPS), and husk weight of the secondary scabbard (HWSS). The magnitude of canopy range of plant (CRP), and ground coverage percent (GCP) were estimated for each plot. Also, days number to flowering (DNF), and days number to maturity (DNM) were recorded for each repetition. Finally, grain yield performance (GYP) in each plot as well as biomass yield performance (BYP) were measured. From some random grain samples, hundred grain weight (HGW) was obtained.

2.3. Data analysis

The normality of the obtained dataset and the uniform distribution of model residuals were assessed using Minitab 23.0 software. To identify the most influential traits and genotypes, factor analysis was conducted, and the resulting factor loadings were rotated using the varimax method. Only factors with eigenvalues greater than 1.0 were retained as significant factors. Factor analysis was performed using Statistica 14.1.0 software, and two-dimensional plots were generated to visualize the relationships between variables. To evaluate the suitability of factor analysis, the Kaiser-Meyer-Olkin (KMO) test was applied to assess the adequacy of the sample size, while Bartlett's test of sphericity was used to determine the appropriateness of the correlation matrix for factor analysis. Additionally, the communality was calculated to indicate the proportion of variance explained by the common factors, reflecting the extent to which each variable is influenced by the extracted factors. This helps in understanding how much of the variability in each trait is attributable to the identified factors.

Table 2. The KMO statistic and Bartlett's test

Statistics		First year	Second year
KMO	Statistic	0.620	0.619
Bartlett's Test			
	χ^2	1053	1113
	Degrees of freedom	300	300
	Probability level	0.00	0.00

3. Results

The evaluation of the expedience of the dataset for factor analysis (*Table 2*), indicated that KMO index was greater than 0.50 (0.620 and 0.619 for the first and second years, respectively), therefore the existing associations among the traits were enough for valid factor analysis. Also, the Bartlett test for sphericity was significant across both years (*Table 2*), which demonstrated the existence of good amounts of relationships among the studied traits, thus current data was proper for factor analysis. The factor analysis showed that the first six eigenvalue of factors were greater than unity in the first year and accounted 80.7% of the observed variance (*Table 3*). The first factor accounted 40.8% of variation and included one-grain scabbard of the primary branches (OSPB), one-grain scabbard of the secondary branches (OSSB), two-grain scabbard of the secondary branches (TSSB), empty scabbard of the primary branches (ESPB), grain number of the primary scabbard (GNPS), grain number of the secondary scabbard (GNSS), grain weight of the primary scabbard (GWPS), grain weight of the secondary scabbard (GWSS), husk weight of the primary scabbard (HWPS), husk weight of the secondary scabbard (HWSS), and grain yield performance (GYP), so the yield potential was suggested for the first factor.

Table 3. The scores of factors with eigen-values (EV) greater than unity with varimax rotation and communalities (Comm.).

	First year							Second year							
Traits†	F1	F2	F3	F4	F5	F6	Comm.	F1	F2	F3	F4	F5	F6	F7	Comm.
PH	0.44	0.19	0.72	-0.06	0.34	-0.02	0.87	0.37	0.21	0.75	0.24	0.03	0.02	0.11	0.82
FBH	0.22	-0.06	0.83	0.00	0.10	0.18	0.78	0.22	0.06	0.84	0.07	0.01	-0.13	0.06	0.79
FSH	0.07	0.04	0.80	0.27	-0.14	0.00	0.74	0.25	0.01	0.75	0.41	0.08	0.11	0.00	0.81
CRP	0.14	0.21	0.06	0.01	0.90	0.06	0.88	0.43	0.03	0.38	0.11	0.40	-0.18	-0.47	0.75
GCP	0.07	0.83	0.09	-0.14	0.06	0.04	0.73	0.29	0.05	0.24	0.83	0.11	-0.05	0.03	0.85
NPB	0.37	0.45	-0.41	0.14	0.31	0.33	0.73	0.27	0.01	-0.11	0.03	0.81	-0.09	0.12	0.77
NSB	0.04	0.58	-0.07	0.48	0.13	-0.09	0.59	0.07	0.13	0.19	0.37	0.75	0.28	0.01	0.84
OSPB	0.90	0.24	0.13	0.06	0.16	0.03	0.91	0.81	0.17	0.24	0.35	0.09	-0.03	-0.06	0.89
OSSB	0.89	0.02	0.23	0.16	0.00	-0.14	0.89	0.50	0.65	0.28	0.31	0.06	0.10	-0.08	0.88
TSPB	0.46	0.18	-0.06	0.55	0.33	-0.36	0.79	0.49	0.21	-0.12	0.07	0.35	0.54	0.19	0.86
TSSB	0.73	-0.24	0.23	-0.16	0.02	-0.14	0.69	-0.06	0.49	0.55	-0.12	-0.15	0.06	-0.36	0.72
ESPB	0.77	0.20	-0.28	-0.12	-0.27	-0.03	0.80	0.34	0.71	-0.10	0.01	0.18	0.25	0.11	0.74
ESSB	0.40	0.20	-0.10	-0.60	0.01	-0.30	0.66	-0.05	0.72	-0.07	0.30	0.04	-0.19	-0.07	0.66
GNPS	0.88	0.27	0.05	0.18	0.16	-0.08	0.92	0.85	0.24	0.10	0.22	0.17	0.25	0.04	0.93
GNSS	0.93	-0.05	0.19	0.09	0.00	-0.12	0.93	0.46	0.73	0.23	0.13	0.03	0.06	-0.07	0.93
GWPS	0.92	0.06	0.03	0.02	0.12	0.12	0.88	0.88	0.23	0.20	0.19	0.16	0.02	0.01	0.93
GWSS	0.90	-0.19	0.07	-0.01	0.02	0.09	0.86	0.45	0.71	0.25	0.01	0.01	-0.08	-0.07	0.89
PDW	0.15	0.70	0.15	-0.08	0.29	-0.29	0.71	0.33	0.25	0.10	0.84	0.10	0.06	0.03	0.90
HWPS	0.89	0.25	0.06	0.00	0.25	-0.01	0.92	0.84	0.18	0.33	0.24	0.13	-0.07	-0.15	0.94
HWSS	0.95	-0.02	0.18	-0.02	0.06	-0.07	0.94	0.43	0.71	0.31	0.14	-0.01	-0.10	-0.17	0.95
DNF	0.04	0.47	0.34	0.26	-0.25	0.44	0.65	0.01	-0.08	0.05	0.11	0.09	-0.08	0.87	0.80
DNM	0.21	0.01	0.21	0.82	-0.09	-0.17	0.80	-0.03	-0.13	0.40	-0.20	0.33	0.48	0.52	0.83
HGW	-0.09	-0.30	0.12	-0.21	0.12	0.79	0.79	-0.06	0.04	0.05	-0.07	0.03	-0.93	0.09	0.88
GYP	0.90	0.32	0.02	0.12	0.05	0.00	0.92	0.77	0.31	0.20	0.42	0.11	0.13	0.10	0.95
BYP	0.01	0.86	-0.10	0.07	0.01	-0.13	0.78	0.47	0.25	0.14	0.72	0.17	0.12	0.05	0.97
EV	10.20	3.32	2.46	1.77	1.25	1.19		11.31	2.69	2.14	1.64	1.26	1.17	1.06	
Var.	40.8	13.3	9.8	7.1	5.0	4.7		45.3	10.7	8.5	6.6	5.0	4.7	4.2	
Cum.	40.8	54.1	63.9	70.9	75.9	80.7		45.3	56.0	64.6	71.1	76.2	80.9	85.1	

†For traits' abbreviations refer to text. Var. % of explained variance; Cum. cumulative variance %.

Tiwari et al. (2019) used factor analysis in chickpea for assessment of yield potential and found number of number of branches per plant, days to maturity, seed weight, and number of pods plant as the main influencing traits. In the first year, the second factor had the high values for ground coverage percent (GCP), plant dry weight (PDW), number of the primary and secondary branches (NPB and NSB), biomass yield performance (BYP), which is accounted 13.1% of observed variation; thus, the biological performance is suggested for this factor (*Table 3*). The third factor accounted 9.8% of variability and consist on first branch height (FBH), plant height (PH), and first scabbard height (FSH), so the name height was selected for this factor (*Table 3*). The fourth factor accounted 7.1% of variation and consist of two-grain scabbard of the primary branches (TSPB) and days number to maturity (DNM) with positive scores, while empty scabbard of the secondary branches (ESSB) had negative value, so the scabbard and maturity characteristics was suggested for the fourth factor in the first year. Relatively the same reports were found in chickpea by Ghorbani et al. (2013) who identified five factors as seed size, yield, morphology, harvest index and filled pods which described 81% of the observed variation. The fifth factor had the high values for canopy range of plant (CRP), which is accounted 5.0% of variability; thus, the canopy name is suitable for this factor (*Table 3*). The sixth factor accounted only 4.7% of variation and consist on days number to flowering (DNF), and hundred grain weight (HGW), so name the flowering and grain weight is chosen for this factor (*Table 3*). Regarding magnitudes of communalities in the first year, almost all of the chickpea traits had good reliability and showed high amount of similar of genetically issue.

In the second year, the factor analysis identified first seven eigenvalues greater than 1.0 which accounted 85.1% of the variation (*Table 3*). The first factor explained 45.3% of variance and included OSPB, GNPS, GWPS, HWPS and GYP, so the yield and yield components related to the primary branches was suggested for the first factor. The second factor had the high values for OSSB, TSSB, ESPB, ESSB, GNSS, HWSS, which is accounted 10.7% of variation; thus, the yield components related to the secondary branches is suggested for this factor (*Table 3*). Similar to the first year, the third factor consist on PH, FBH, and FSH, so the name height was selected for this factor while it accounted 8.5% of variability (*Table 3*). The fourth factor accounted 6.6% of variance and consist of GCP, PDW, and BYP so the biological performance was suggested for this factor in the second year.

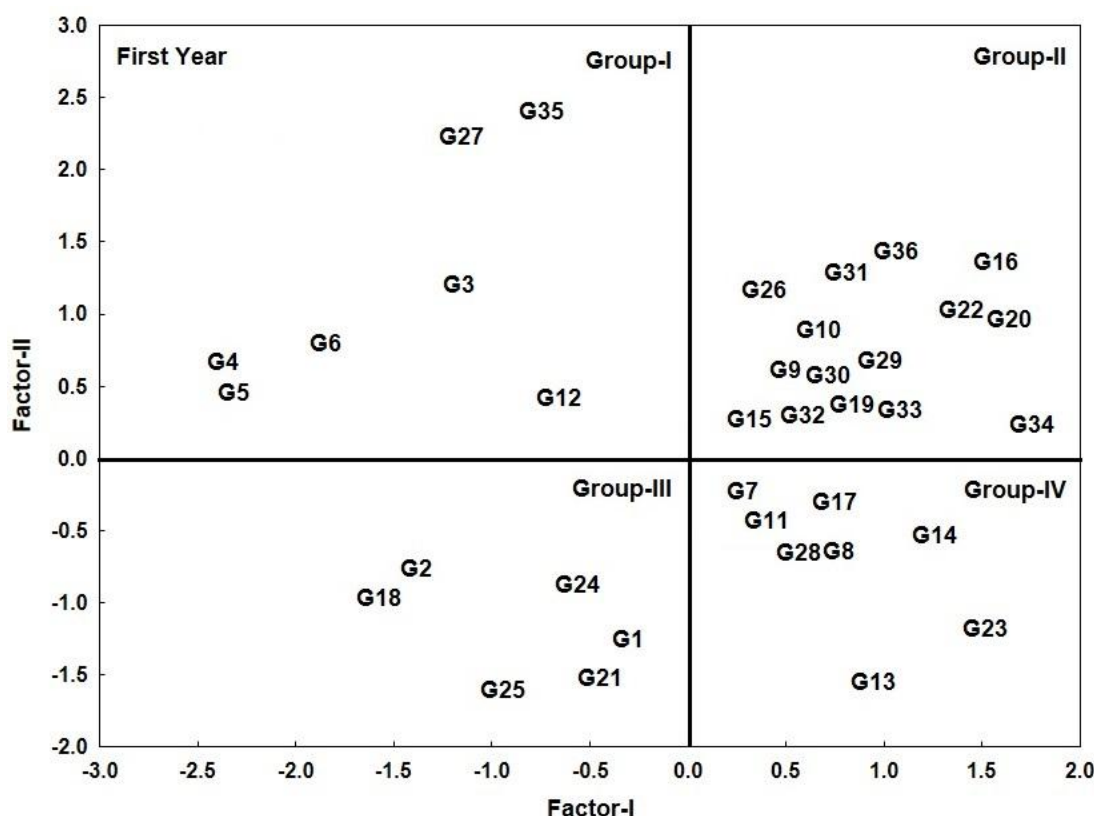


Figure 1- Tow-dimensional plot based on first two factors for classifying of chickpea genotypes in the first year

The fifth factor had the high values for NPB and NSB, which is accounted 5.0% of variability; thus, the number of branches is suitable for this factor (*Table 3*). The sixth factor described 4.7% of variability and consist on positive score for TSPB, and negative value for HGW, so name two-grain scabbards is chosen for sixth factor. The seventh factor explained only 4.2% of observed variance and consist on DNF and DNM, and negative amount of CRP, so name the phenology is chosen for this factor in the second year (*Table 3*). Similar to the first year, the amounts of communalities in the second year indicated that almost all of the chickpea traits had high reliability values and demonstrated high amount of similar of genetically issue. Also, these high amounts of communalities across both years shows that the six or seven extracted factors described more variability of traits (more than 70 to near 100%), and have to be well-described traits variabilities. Toker and Ilhan-Cagiran (2004) and Sharifi et al. (2018), identified three main factors as phonologic, morphologic and the seed yield related characteristics. We could identify these components as well as other properties which is named as biological performance or yield and yield components related to the primary and secondary branches

For grouping and visual understanding of the relationships among the genotypes, they were displayed as a two-dimensional plot, whereas the first two factors accounted for 54 and 56% of the variation in the first and second years, respectively. This amount of genotype by trait interaction implies that both linear and non-linear interactions in chickpea dataset, indicating differential rankings of measured traits across genotypes. This finding aligns with similar observations in chickpea (Getachew et al., 2015) and other crop investigations like rye (Yari et al. 2018) and safflower (Sabaghnia et al. 2024), highlighting the challenge of achieving an indirect response to selection overall genotypes without considering the genotype by trait interaction. At the first year, four genotypic groups were identified (*Figure 1*): Group-I consisting of seven genotypes 3, 4, 5, 6, 12, 27, and 35; Group-II comprising fifteen genotypes (9, 10, 15, 16, 19, 20, 22, 26, 29, 30, 31, 32, 33, 34, and 36); Group-III consisting of six genotypes 1, 2, 18, 21, 24, and 25; and Group-IV comprising eight genotypes (7, 8, 11, 13, 14, 17, 23, and 28).

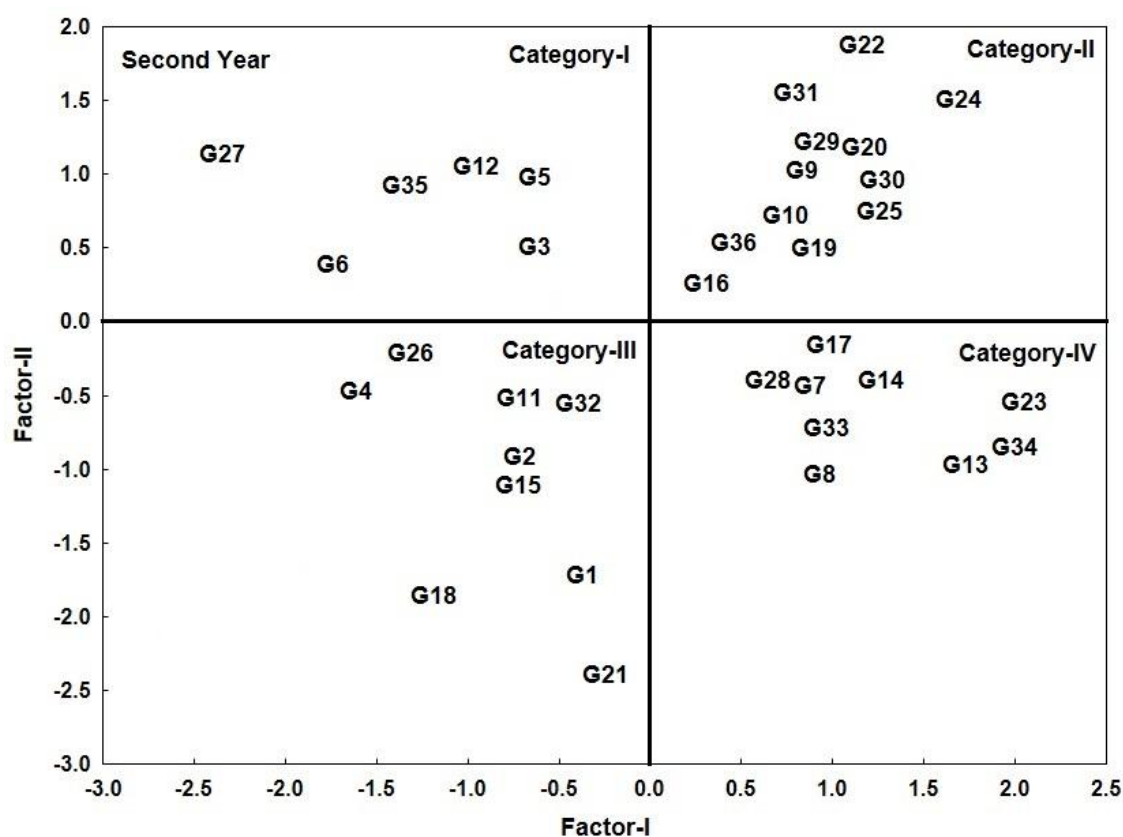


Figure 2- Tow-dimensional plot based on first two factors for classifying of chickpea genotypes in the second year.

Also, in the plot of the second year (*Figure 2*), the genotypic categories were observed as: Category-I included six genotypes 3, 5, 6, 12, 27, and 35; Category-II containing of twelve genotypes (9, 10, 16, 19, 20, 22, 24, 25, 29, 30, 31, and 36); Category-III containing of nine genotypes (1, 2, 4, 11, 15, 18, 21, 26, and 32); and Category-IV included nine genotypes 7, 8, 13, 14, 17, 23, 28, 33, and 34 (*Figure 2*). Comparison of the results of classifying across both years indicated six common genotypes between the Group-I and Category-I (3, 5, 6, 12, 27, and 35); ten common genotypes between the Group-II and Category-II (9, 10, 16, 19, 20, 22, 29, 30, 31, and 36); four common genotypes between the Group-III and Category-III (1, 2, 18, and 21); and seven common genotypes between the Group-IV and Category-IV (7, 8, 13, 14, 17, 23, and 28). Thus, 27 from 36 genotypes (75%) were classified similarly across two years, so the behavior of these genotypes is reliable and did not indicate serious genotype by year (or environment) interaction

Table 4 indicates the averages of the chickpea traits for each of the four classifications across both years. In the first year, genotypes in Group-I indicated high magnitudes for all measured traits especially in seed yield and yield components, except hundred grain weight. Also, genotypes in Group-II indicated lower amounts for all measured traits, except high magnitudes of number of the primary and secondary branches; and moderate values for ground coverage percent, plant dry weight, days number to maturity biomass yield performance and hundred grain weight (*Table 4*). The obtained findings were in good agreement with the investigation of Alemayo et al. (2021), who report the positively relation between phenologic traits and pod characteristics of chickpea.

Table 4. The averages of chickpea traits for four genotypic classes in both years.

	First year				Second year			
	Group-I	Group-II	Group-III	Group-IV	Cat-I	Cat-II	Cat-III	Cat-IV
PH	33.79	32.36	33.32	32.37	29.44	28.00	29.22	26.54
FBH	28.20	27.50	28.17	27.68	22.68	21.44	22.26	21.07
FSH	24.60	23.82	24.28	24.07	20.93	19.19	20.00	18.66
CRP	21.16	20.44	20.61	20.40	22.34	20.60	21.76	20.41
GCP	84.40	77.75	71.52	72.42	68.33	54.48	55.54	48.77
NPB	1.91	1.84	1.79	1.78	2.61	2.61	2.52	2.45
NSB	2.84	2.71	2.55	2.41	5.30	4.95	4.72	4.10
OSPB	6.21	4.42	5.38	4.36	8.20	6.17	7.10	5.55
OSSB	4.65	3.37	4.73	3.31	4.74	3.27	4.80	2.84
TSPB	1.08	0.81	0.90	0.66	1.75	1.29	1.10	0.93
TSSB	0.67	0.46	0.76	0.56	0.61	0.43	0.72	0.54
ESPB	0.51	0.38	0.48	0.40	0.38	0.30	0.37	0.25
ESSB	0.49	0.45	0.49	0.46	0.43	0.39	0.54	0.44
GNPS	8.47	5.94	7.31	5.72	11.94	8.84	9.67	7.57
GNSS	5.85	4.23	6.16	4.30	5.52	3.99	5.99	3.52
GWPS	3.82	2.53	3.42	2.74	4.05	3.08	3.51	2.71
GWSS	2.86	1.98	3.05	2.25	2.01	1.48	2.21	1.35
PDW	208.7	176.3	140.8	145.3	602.5	486.8	526.1	387.9
HWPS	0.91	0.63	0.78	0.62	1.17	0.83	1.01	0.76
HWSS	0.64	0.46	0.66	0.48	0.55	0.38	0.61	0.36
DNF	51.84	51.28	51.21	51.50	51.44	51.46	50.94	51.02
DNM	78.67	78.40	78.60	78.21	79.19	79.14	78.56	78.52
HGW	34.06	35.11	35.83	35.60	33.95	34.94	36.23	35.64
GYP	2124.1	1201.9	1674.1	1001.3	2111.3	1305.3	1619.1	917.5
BYP	4524.1	4024.5	3184.1	3066.0	4925.9	3696.0	3993.1	2863.4

Genotypes in Group-III demonstrated high amounts for first branch height, one-grain scabbard of the secondary branches, two-grain scabbard of the secondary branches, empty scabbard of the primary branches, empty scabbard

of the secondary branches, husk weight of the secondary scabbard days number to maturity and hundred grain weight while this group had moderate performance in grain yield performance as well as plant height, first scabbard height, one-grain scabbard of the primary branches, husk weight of the primary scabbard, two-grain scabbard of the primary branches and grain number of the primary scabbard. Finally, genotypes in Group-IV indicated lower magnitudes for all traits, except days number to maturity in the first year.

Relatively similar results were obtained for the second year with minor differences. In the second year (*Table 4*), genotypes in Category-I (Cat-I) indicated higher values for all traits, except moderate values of empty scabbard of the secondary branches and low amounts of hundred grain weight, so these genotypes are excellent for improving seed yield and yield components. Genotypes of Category-II (Cat-II) showed high values for number of the primary and secondary branches, days number to flowering, and days number to maturity; moderate values for plant height, two-grain scabbard of the primary branches, empty scabbard of the primary branches, plant dry weight, biomass yield performance, and hundred grain weight; and low magnitudes for the other remained traits. Also, genotypes in Category-III (Cat-III) demonstrated high or moderate amounts for all traits except two-grain scabbard of the primary branches and phenologic traits (days number to flowering and maturity). Finally, genotypes in Category-IV (Cat-IV) indicated lower magnitudes for all traits, except high values for empty scabbard of the primary branches and hundred grain weight; and moderate values for two-grain scabbard of the secondary branches and empty scabbard of the secondary branches. Thus, the most superior genotypes of Group-I and Category-I; 3 (13/A2 from ICARDA), 5 (18/A2 from ICARDA), 6 (2/A2 from ICARDA), 12 (7/A1 from ICARDA), 27 (3/3 URCYT-93 from Iran), and 35 (Arman from Iran) can be advised for commercial release as improved cultivars for rainfed condition of cool upland semiarid areas after multi-environmental trials.

This investigation benefited factor analysis as an effective multivariate statistical tool to explore the pattern of genetic diversity in some morphologic characteristics of chickpea and could distinguish an overall grasp into the measured traits as well as genotypes, which is main primary section for effective use of chickpea germplasm. Such as similar results were reported by Nogay and Azabağaoğlu (2024) on factor analysis of corn. According to KMO measure and the Bartlett's test, the factor analysis was suitable statistical tool for this chickpea dataset and identified six and seven factors for the first and second years, respectively. They were identified as seed yield, biologic yield, phenology, and yield components across both years. Also, the communality magnitudes indicated that all of the chickpea traits had high accuracy. Graphic analysis of chickpea dataset via two-dimensional plot demonstrated that four distinct genotypic groups for 36 genotypes of chickpea whereas the most favorable classification were Group-I of the first year and Category-I of the second year (3, 5, 6, 12, 27, and 35) which had the high yield performance and yield components. Although, previous researches have mentioned the hundred grain weight as one of the yield components in chickpea, this research could not reach this issue. Current observations were consistent with the study of Sharifi et al. (2018), who found the positively relation between seed yield of chickpea with the pod and seeds numbers. It seems that the used genotypes, which were from improved breeding lines, did not differ much in this respect, and therefore they could not show the role of weight of one hundred grains.

5. Conclusions

The results can be utilized in the genetic improvement programs for future high-yielding cultivar release as well as classification of genetic variation among chickpea genotypes. The seed yield, biologic yield, phenology, and yield components related to the primary and secondary branches were identified as the main influencing traits on yield performance, and hence can enhance the genetic gain of the genetic improvement efforts of chickpea in the rainfed condition of cool upland semiarid regions. Finally, the most desirable genotypes of Group-I of the first year and Category-I of the second year; 3 (13/A2), 5 (18/A2), 6 (2/A2), and 12 (7/), from ICARDA and 27 (3/3 URCYT-93) from Iran can be released as improved cultivars for rainfed condition of cool upland semiarid areas. Also, cultivar Arman from Iran was classified with above mentioned genotypes and its superiority is verified among newly bred genotypes.

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Ethical Statement

There is no need to obtain permission from the ethics committee for this research.

Conflicts of Interest

There is no conflict of interest between the article authors.

Authorship Contribution Statement

Concept: Sabaghnia, N., Design: Sabaghnia, N., Nouraein, M., Data Collection or Processing: Nouraein, M., Janmohammadi, M., Statistical Analyses: Sabaghnia, N.; Literature Search: Nasiri, Y., Writing, Review and Editing: Sabaghnia, N.

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