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## **ENTRY BY TESTER BILOT MODEL FOR EVALUATION OF SOME KABULI CHICKPEA GENOTYPES BASED ON SEVERAL MULTIPLE TRAITS**

### **SUMMARY**

The aim of investigation was to evaluate the pattern of genetic variation in Kabuli chickpea genotypes through various traits under semi-arid rainfed circumstances. Trial was performed to evaluate the response of 50 Kabuli chickpea genotypes via a randomized complete block layout with three replicates. The entry by tester (genotype by trait) biplot which explained 66% of the variability indicated that the important traits for a favorable genotype in semi-arid environments were seeds' number of pod and pods' number of single plant. The biplot model introduced some desirable chickpea genotypes as good for a trait or a category of traits; genotype 27 for chlorophyll content, genotype 26 for seed yield (SY), SP and PP, and genotype 36 for plant height (PH), days to maturity (DM), pod's weight (PW), hundred seed weight (HSW), plant dry weight (PDW), and plant fresh weight (PFW). Based on an ideal assumptive genotype (entry) position, genotype 1 followed to 2, 10, 16, 17, 23, 26, 33 and 34 were ideal regarding the distinction ability and typical potential. According to an ideal assumptive trait (tester) position, PH, PDW, and PFW were more discriminative and typical traits. The responses of chickpea genotypes regarding SY indicated that genotype 26 following to 3, 17 and 27, were the most desirable and can be advised for commercial cultivar release process.

**Keywords:** distinction potential, discriminative ability, selection, seed yield.

### **INTRODUCTION**

After cereals, legumes are the second source of human food and are considered as a valuable food supplement for cereals. They play an important role in providing human food requirements and regarding their nutritional

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importance, chickpea is cultivated in 49 countries of the world with an area of about 15 million hectares and a production of more than 18 million tons (FAOSTAT, 2022). Chickpea as a diploid ( $2n=2x=16$ ) species belongs to the Fabaceae family, which ranks second in the world among legumes with mean performance of about 1500 kg ha<sup>-1</sup>. Chickpea is a very excellent supply of zinc, iron, and fiber and have about 27% protein, 6% fat and 57% carbohydrates and is important in terms of the calcium content (Gupta *et al.* 2019). This crop stabilizes agricultural systems, especially in rotation with cereals, by improving soil fertility. There are two main types of chickpeas, Desi and Kabuli, the Desi type has small, dark-colored seeds with a hard coating, but the Kabuli type has larger, light-colored seeds and a soft coating. According to FAOSTAT (2022), the harvested area of chickpea, Iran (430 thousand hectares) ranks fifth in the world and ranks ninth in terms of production (176 thousand tons), but in terms of performance per unit area (400 kg ha<sup>-1</sup>), Iran ranks the last locations in the world (45th), which is very low compared to the global average yield and the highest yield performances (China and Jordan with more than 5000 kg ha<sup>-1</sup>). About 90% of the chickpea cultivation area in Iran is rainfed, and due to the occurrence of drought during flowering period, which is the sensitive stage of the crop, this stress has a remarkable impact on reducing the yield.

Despite of the large cultivation area of chickpea in world, the production quantity in most of countries is very low and there is a remarkable gap between production potential and actual production. The important cause for this minimum performance of chickpea is the cultivation of local cultivars, as well as using the old agricultural practices (Sellami *et al.*, 2021). Environment, genetic and their interaction are the main components that determine crop's performance quantity and quality, so the main goal in selecting breeding criteria should be focused on the genetic factors. Therefore, most of the efforts of breeders are directed to discovering ways to increase the genetic potential to select the best genotypes, so the population should have a favorable diversity, and knowledge of this diversity requires germplasm evaluation. In order to estimate genetic diversity, different types of markers including morphological, biochemical and molecular ones are used by breeders. The most important components of chickpea yield include the pods' number, the seeds' number, and the hundred seed weight; so, by improving these characteristics, yield can be improved (Joshi *et al.*, 2018). One of the effective ways to obtain efficient information about genetic diversity is the use of the various statistical multivariate models, which makes it possible to make favorable and suitable identifications suitable genotypes for crossing. Principal components analysis is a powerful method in reducing many numbers of attributes to a restricted number of independent and uncorrelated components.

A restricting factor in the chickpea improvement program is its limited genetic base, which makes it difficult for the breeders to generate new cultivars. Therefore, to improve the effectivity of the chickpea improvement project, it is necessary to expand the genetic base of chickpea. Also, determining the

characteristics of the germplasm in terms of desired traits facilitates the creation of populations that are designed to achieve specific goal. Thus, the knowledge about genetic structure of the target traits, such as heritability and correlations of traits, is important for designing a successful breeding program. High yield performance, earliness, taller plant height and large seed size are key and economically important traits in the chickpea breeding (Roorkiwal et al., 2018). The taller plant height cultivars are suitable for mechanical harvesting and play an effective role in minimizing production costs (Singh et al., 2022). Also, seed size is an important attribute for international trade, so that large types have a higher price in the market. Related traits to yield performance and stress tolerance are controlled by several genes, so the phenotypic expression of the desired characteristics is largely affected by their genotype as well as environmental effects and their interactions. A positively significant correlation was observed for seed yield with the pods' number of plant, the hundred seed weight, the seeds' number of plant and the harvest index, so they had a positive impact on increase of yield performance (Gediya et al., 2019). Also, there is a positively significant association between the seeds' number, the pod's number, the primary branches, the secondary branches and the weight of one hundred seeds with yield performance (Zali et al., 2011).

According to Meena et al. (2010), chickpea yield indicated a positively association with the pods' number, biomass, harvest index and the branches' number, and indicated a negatively relation with the flowering initiation. In another investigation to explore the interrelationships of chickpea yield performance and its main related traits using different statistical methods, plant height, biomass and the pods' number were the major traits affecting chickpea yield; so, by choosing these traits, high performance can be achieved (Kayan and Adak, 2012). Yucel et al. (2006) showed that yield performance, number of primary shoots and harvest index had the most genetic changes among chickpea genotypes. In investigating the genetic variation among 15 chickpea genotypes, the seeds' number and the hundred seed weight showed a positively significant influence on yield performance and justified 96% of the variation in the fitted regression mode. Mardi et al. (2003) in exploring the genetic diversity of chickpea by the morphological traits, showed that the pod weight and the seeds' number have good genetic diversity and their selection leads to the high performance. In another study that was conducted on 104 cultivars of Kabuli chickpea, high diversity in terms of morphological characteristics were found (Fazeli and Cheghamirza, 2011). The aim of present research is to investigate the genetic variation of advanced genotypes of chickpea, to analyze the association between agronomic-morphological characteristics and to select the most superior genotypes for commercial cultivar release as well as use in future genetic improvement projects.

## **MATERIAL AND METHODS**

In this research, 50 Kabuli chickpea genotypes from the breeding program of Iran's Dryland Agricultural Research Institute were examined in terms of different phenological, morphological, yield-related traits based on the chickpea

standard descriptor Biodiversity International. They were selected based on their high performance and previous years. Field operations included manure application and plowing in autumn, as well as adding decomposed manure plowing, disc harrow, and leveling in spring were performed in field located in Gavshaleh, Saqqez, Iran (36°19'N 46°19'E; altitude 1476 m). Planting was carried out on May 3 in the form of a randomized complete block layout in three replicates. Genotypes were cultivated in plots consisting of 4 lines, one meter long, with a distance between rows of 20 25 cm and the distance of seeds on the row approximately 8 cm. The weeding was applied manually in several stages and other operations according to the usual routine of the region. The land was irrigated three times because rainfall was sufficient during growing season. The days to maturity (DM) was recorded. Ten randomly selected were used to measure plant height (PH), days to maturity (DM), chlorophyll content (CHL), number of pods per plant (PP), pod's weight (PW), number of seeds per pod (SP), hundred seed weight (HSW), plant dry weight (PDW) and plant fresh weight (PFW). At physiological maturity, seed yield (SY) was measured from two central rows.

The dataset was analyzed through an entry by tester biplot model via the GGEbiplot application which shows graphic grasp from interaction structure of measured traits (testers) across genotypes (entries) as:

$$\frac{Y_{ij} - \bar{Y}_j}{SD_j} = \sum_{n=1}^2 \Phi_n \Psi_{in} \Omega_{jn} + R_{ij}$$

$Y_{ij}$  is the mean of entry (genotype)  $i$  for tester (trait)  $j$ ,  $\bar{Y}_j$  is the mean of entries for tester  $j$ ,  $SD_j$  is the standard deviation of tester  $j$  for entries,  $\Phi_n$  is the eigenvalue for PC (principal component)  $n$ ,  $\Psi_{in}$  and  $\Omega_{jn}$  are values for entry  $i$  and tester  $j$  on PC  $n$ ,  $R_{ij}$  is the error term of the fitted equation related to entry  $i$  for tester  $j$ . Also, for obtaining symmetrical scales of testers and entries, the eigenvalue is corrected through vectors' absorption, so a normal presentation of testers and entries ( $\Psi_{in}^* = \sqrt{\Phi_n \Psi_{in}}$  and  $\Omega_{jn}^* = \sqrt{\Phi_n \Omega_{jn}}$ ) is happened. The entry by tester interaction biplots are generated by these symmetric scales, and each genotype (entry) or trait (tester) is shown by a special sign. Thus, a graphic interpretation of the relations among genotypes and traits as well as their interaction can be provided.

## RESULTS

The first and second derived PCs, accounted for 66% of the dataset variability (Fig. 1), whereas the first PC contributed 41%, and the second PC contributed 25% to the fitted variance. This fitted variability of the entry by tester interaction indicated the role of non-crossover and crossover types of interactions, so ranks of chickpea genotypes across traits are changing, which is in accordance with the report of Sellami *et al.* (2021) in chickpea and investigation of Kizilgeci *et al.* (2019) in lentil, emphasizing the problem of

getting an indirect reaction to selecting process across genotypes without reading the effect of the entry by tester interaction.

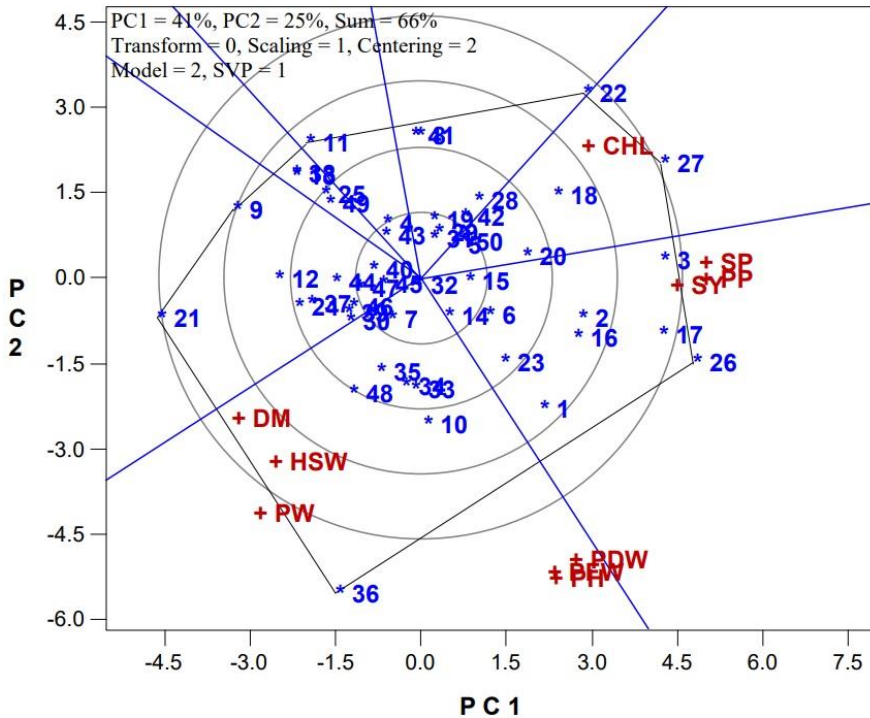


Fig. 1. Which entry (genotype) wins which tester (trait).

Regarding the role of the entry by tester interaction in our chickpea genotypes, this research benefits biplot representation facility, as advised by Yan et al. (2019), as a suitable procedure, because it provide the effective exploration of genotypes and traits. Fig. 1 indicates visual behavior of chickpea genotypes and shows which genotypes were better than others in target traits. Most traits, consist on plant height (PH), days to maturity (DM), pod's weight (PW), hundred seed weight (HSW), plant dry weight (PDW), and plant fresh weight (PFW), were grouped in the section of genotype 36 while seed yield (SY), number of seeds per pod (SP), and number of pods per plant (PP) were located in a distinct section, with the genotype 26 followed by 17 as the winning genotype. Also, genotype 27 was the best genotype for chlorophyll content (CHL), but the other four vertex genotypes (9, 11, 21 and 22) were not the excellent for the chickpea traits (Fig. 1). It seems that yield performance in chickpea is more related to the number of seeds and pods per plant instated the other traits like hundred seed weight. Although, Gediya et al. (2019) reported the positive role of the number of seeds and pods per plant on seed yield, but they found similar positive role for the hundred seed weight while we could not find such relation. However, the

entry by tester biplot method prepared clear insights into the response of genotypes, revealing their potential across measured traits and facilitated the detection of the best genotypes. Thus, for commercial cultivar release, genotype 26 followed by 17 can be considered after their testing under multi-environmental trials for insurance their adaptability and yield stability abilities.

The distinction ability of a genotype for the measured traits and the typical potential for showing the symbolic properties of a genotype based on the traits for chickpea genotypes can be identified by an assumptive genotype as ideal position (Fig. 2), the best genotypes are close to this position; but genotypes of the other side are the worst.

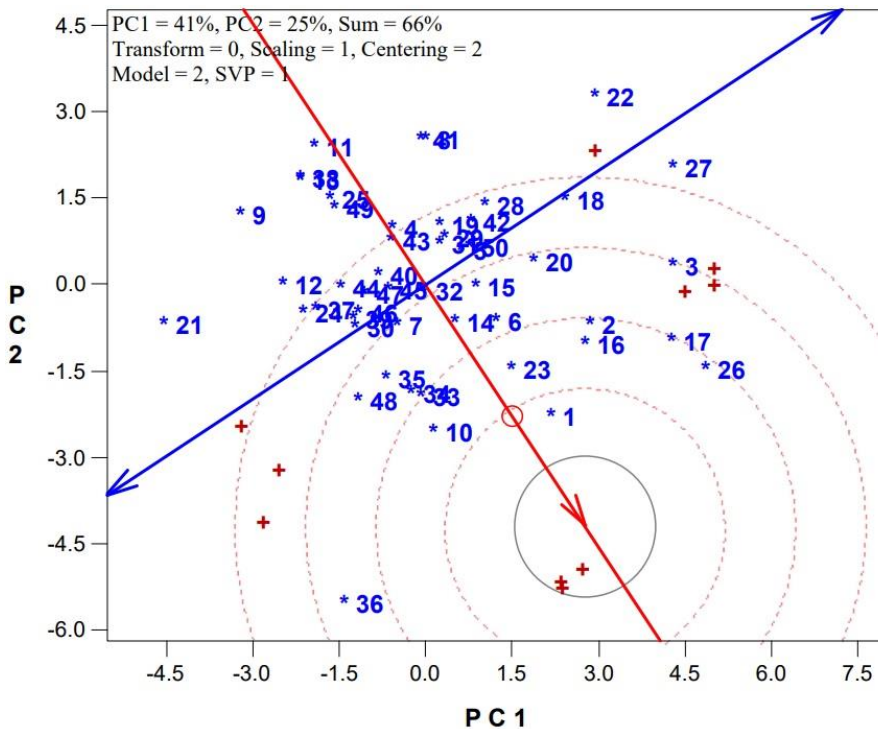


Fig. 2. Ranking entries (genotypes) based on testers (traits).

Based on Fig. 2, genotype 1 followed to 2, 10, 16, 17, 23, 26, 33 and 34 are ideal because they are the closest entries to the ideal position while genotypes 9, 11, 21 and 22 are on the other side and far from this position, so they are the most undesirable genotype regarding the distinction ability and typical potential. The identified ideal genotypes can be assumed as ideotypes which indicated high magnitude of most traits, so the problem appears once the associations of traits are not always significant. Thus, these issues are serious in a chickpea genetic improvement project, in which seed yield and quality characteristics like protein

content or other yield components are important for breeding and usually the association between the seed yield and quality characteristics are low or even negative. finally, for genetic improvement projects, strategies that embrace application of multivariate statistical tools specially with graphic presentations have more importance toward the ideotype determination in chickpea.

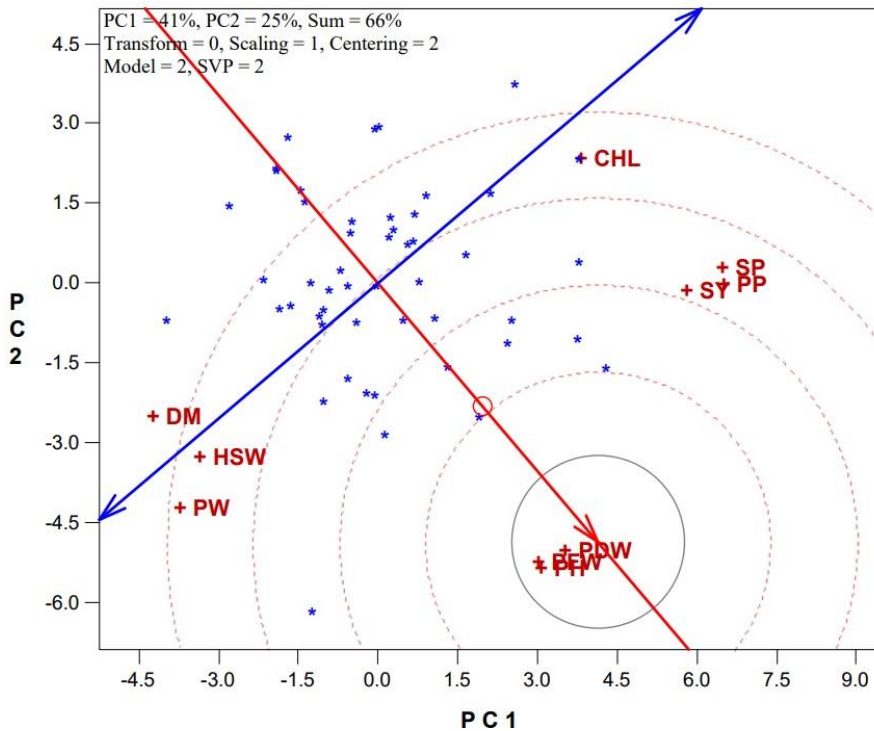


Fig. 3. Ranking testers (traits) based on discriminative and representativeness potentials.

A trait discriminative potential is the magnitude of standard deviation and the larger amount, the higher potential of the trait which is shown an assumptive trait as ideal position of measured traits (Fig. 3), so the best traits are close to this position; but traits of the other side are the worst. Thus, it can be proposed that plant height (PH), plant dry weight (PDW), and plant fresh weight (PFW) are more discriminative traits. However, the discriminative potential of the other remained traits of chickpea except days to maturity (DM) were higher than average of the discriminative potential, so they can discriminate the differences among chickpea genotypes (Fig. 3). Also, the typical potential for indicating the symbolic properties of a trait is measured by the its angle with the axis of the average trait, and the small angle demonstrate the more typical potential of the target trait. Thus, the more desirable traits (PH, PDW and PFW) had a very small angles with this axis and showed more typical potential. In contrast the other

traits (DM, CHL, PP, PW, SP, HSW and SY) had large angles with the axis of the average trait and indicated relatively lower typical potential (Fig. 3)

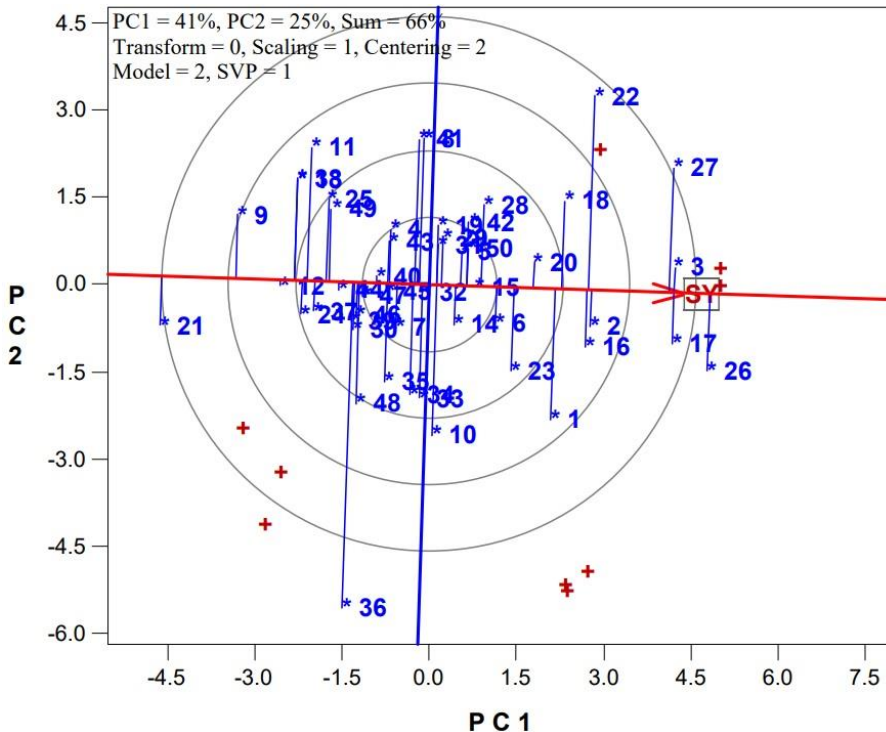


Fig. 4. Examining the performance of/at seed yield (SY).

The responses of chickpea genotypes in the term of seed yield performance as final goal trait are examined in Fig. 4, where a horizontal axis is defined as the line of seed yield and the arrow indicates the axis direction. Therefore, genotype 26 following to 3, 17 and 27, were the most desirable chickpea genotypes considering of the seed yield performance while genotypes 21 and 9 were the most undesirable in this characteristic (Fig. 4). The distance of genotypes from the horizontal axis is the index of standard deviation, so smaller distances are more desirable for selection, thus genotypes 3 and 17 can be advised with low variability. For example, genotype 36 had the low seed yield even lower than average performance (vertical axis) and had more distance from the horizontal axis, so indicated more variability, thus it is one of the most undesirable genotypes.

## DISCUSSION

The genetically background of released chickpea cultivars is relatively narrow, which shows a restriction factor for genetic improvement projects. Thus,



the assessment of chickpea genotypes is important is essential to barricade erosion in plant materials and manage genetic improvement tasks. We observed relatively high variation in the chickpea genotypes, in accordance with the other reports that have confirmed good diversity in chickpea (Joshi *et al.*, 2018; Aswathi *et al.*, 2019). The employed entry by tester interaction biplot model explained relatively sufficient amount of observed variation (about two third) and verified the exitance of both simple (increasable) and complicated (intersecting) types of interaction among chickpea genotypes and measured traits. Such interaction types have been reported for other legumes like dry bean (González *et al.*, 2006) and several *Vicia* L. species (Kökten *et al.*, 2010). The observed simple and complicated interaction types demonstrated different rankings of chickpea genotypes regarding traits, so selection of the best genotypes is relatively difficult for the semi-arid environments. Thus, it would not be easy to obtain an indirect reaction, ignoring the interaction effects because the genotype by trait interaction causes it hard to choose the most superior genotypes. However, various interaction types have major consideration in genetic improvement projects because they decrease the genetic (Rowntree *et al.*, 2013).

Although, genotype 36 was acted better than other genotypes in most traits but genotype 26 was the high yielding genotype with high amounts of seeds' number of pod and pods' number of plant. However, the main yield components of chickpea yield are hundred seed weight, seeds number of pod and pods' number of plant while we could not show the role of hundred seed weight. This may be due to the fact that our chickpeas genotypes were advanced lines and their seed size was almost large for marketable properties, so this trait did not show any remarkable variation in these genotypes. Also, the nine genotypes of section genotype 26 were similar to this genotype but the similarity of genotypes 2, 3, 16 and 17 was more because they indicated low distance from genotype 26, so they can be used for commercial cultivar release propose. Therefore, they must be entered in multi-environmental trials for assessment of adaptability and yield stability potential and then analyzed by statistical methods.

We found that genotype 1 following to genotypes 2, 10, 16, 17, 23, 26, 33 and 34 had high distinction ability of traits as well as showed typical potential for symbolic ability of a chickpea genotype. These genotypes can be used in future investigations for detecting the relationships among traits of chickpea. If the first principal component of the entry by tester biplot model has significant association with effects of genotypes, the ideal position of genotypes shows its higher values to obtain high performance while the low absolute values of the second principal component indicates the low variability in reaction of the ideal position. The efficiency of the ideal position tool for identification of the most favorable genotypes based on multiple traits has been demonstrated by Sabaghnia *et al.* (2016) on spinach (*Spinacia oleracea* L.) and Rahimi *et al.* (2019) on quince (*Cydonia Oblonga* Miller). However, such properties for behavior of the first and the second principal components has been proved in multi-environmental trials while it may be change in other two-way datasets, thus Yan

and Rajcan (2002), for overcoming this problem, another model, which is used in this investigation, was suggested, in which the first principal component is substituted by predication of the linear regression model of the tester-centered data on the genotype effects so that the original scores are the genotype effects and make the model more explicable.

The plant height as well as dry and fresh weight of single plant were identified as the most discriminative traits which can discriminate the differences among chickpea genotypes. Also, their typical potentials for illustrating of the symbolic characteristics of traits were high, so evaluation of chickpea genotypes based on these traits result in more reliable findings and can detect variations among chickpea genotypes. Similar to the ideal position of genotypes, the ideal position of traits indicates the discriminate ability as well as representative potential of traits, so its high values the good discriminate ability of a tester or trait while the low absolute values of the second principal component indicates the better representative potential. The proficiency of the ideal position tool for identification of the most favorable traits has been demonstrated by Baljani *et al.* (2015) on safflower and Porkabiri *et al.* (2019) on tobacco. This option of biplot model is used for our entry by tester dataset based on regression adjustment of the primary biplot model (Yan and Rajcan, 2002). Due to importance of seed yield, the performance of studied genotypes was examined in regards of this final target trait, so genotype 26 following to genotypes 3, 17 and 27, were identified as the most favorable chickpea genotypes. Also, considering the variability, genotypes 3 and 17 were low variable genotypes and so they can be advised for further efforts.

### CONCLUSIONS

Among the ten traits of chickpea used in present investigation, yield is related with seeds' number of pod and pods' number of plant and they could be used in selecting the most favorable genotypes. Regarding the ranks of traits based on discrimination and representative properties, plant height as well as dry and fresh weight of plant are identified as the best traits. Evaluations of several traits aid in detection the best genotypes which will be helpful to breeders to develop new cultivars with the higher yield performance especially in rainfed circumstances of semi-arid environments. Also, genotypes 3 and 17 were the most favorable genotypes so they can be advised for cultivar release.

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