

Review Article

Review on Studies on Genetic Variability of Chickpea (*Cicer arietinum* L.) Genotypes for Future Breeding Program in Ethiopia

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Abstract

Genetic variability studies provide basic information concerning genetic properties of population following which breeding methods could be formulated for future improvement of the crop. Components of genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation have an immense importance in detecting the amount of genetic variation exist in the genotypes. Genetic variability study for agronomic traits is a key component of the breeding program for boarding the genetic pool of crop. Once genetic variability of certain crops has been successfully determined crop improvement is easy through the use of appropriate selection methods on yield components hence they are easily inherited than total yield itself. Thus, in this review, studies of genetic variability of chickpea have discussed to help different researchers on their variability studies by providing some important information that will help chickpea improvements.

Keywords: Variability, GCV, PCV, Genotypes, Crop Improvement

Introduction

Chickpea (*Cicer arietinum* L.) is self-pollinated diploid ($2n=2\times=16$) annual leguminous plant belongs to family Fabacea, with a genome size of 738.09 Mbp (Varshney et al., 2013). Chickpea is the third most important pulse crop in the world after faba bean and field pea [1]. Chickpea is one of the first pulse crops domesticated in the Fertile Crescent about 7400 years ago and most probably originated in an area of South-eastern Turkey adjoining Syria [2]. Ethiopia is designated as a secondary center of origin while South-west Asia and the Mediterranean are the two primary center of origin of chickpea according to Vavilov [3].

The achievement of crop improvement through breeding program largely relies on the extent of genetic and phenotypic variability existed among individuals in the population. Selection and development of new variety depends upon the extent of genetic variability in the base population [4] and breeders require existence and extent of interrelationship among important characters for the selection and development of varieties from populations comprising diversified genotypes [5]. The low yields have been attributed to several factors among which include low genetic diversity of cultivated chickpea and several biotic and abiotic stresses [6]. Evaluation and assessment of genetic resources is a pre-requisite for which the future breeding work depends.

Objective

To review Studies on Genetic Variability of Chickpea (*Cicer arietinum* L.) crop for its future Breeding Program in Ethiopia.

Literature Review

Origin and Distribution

Chickpea (*Cicer arietinum* L.) belongs to the family Leguminosae, sub-family Papilionaceae and tribe Cicereae. Chickpea is one of the first pulse crops domesticated in Old World and most probably originated in an area of South-eastern, Turkey adjoining Syria [2,7]. This crop was gradually introduced to the west Mediterranean region, to Eastern and Southern Asia and East Africa. It reached the Indian sub-continent before 2000 BC [8]. Ethiopia is a second center of diversity for chickpea [9]. Chickpea is the only cultivated species within genus *Cicer* and grown in relatively well-drained black soils, in the cool semi-arid areas of the tropics, sub-tropics as well as the temperate areas [10].

Desi and Kabuli are the two chickpea types produced globally. Kabuli types have a larger cream-colored seed with a thin seed coat whereas the Desi types have a smaller, reddish brown-colored seed with a thick seed coat. Their content also vary in carbohydrates content which ranged from 54 - 71% for Kabuli and 51 - 65 % for Desi type; protein from 12.6 - 29% for Kabuli and from 16.7 - 30.6 % for Desi; lipid from 3.4 - 8.8% for Kabuli and from 2.9 - 7.4% for Desi; and energy from 357 - 447 kcal/100g and from 334 - 437 kcal/100g for Kabuli and Desi, respectively [11]. On an average, world production consists of about 75% of Desi and 25% of Kabuli types (EARO, 2004). Although Kabuli types can be profitably adapted in the country, Ethiopia traditionally produces largely the Desi types of chickpea.

Ecology of Chickpea

Chickpea is traditionally grown in the northern hemisphere, mostly at relatively high elevations in India and Ethiopia. However, most of the Desi type chickpea is grown between 20° and 30° N while Kabuli type is grown above 30°N. These environmental conditions give significance difference in photoperiod, temperature and precipitation, all of which have a profound effect on growth and development of the crop. Chickpea requires fertile soil with good drainage system. Any water-logged conditions can severely damage the crop. Chickpeas generally grow on black or red soils and require a soil pH of 6.0 to 7.0. The crop prefers soil with good residual soil moisture content. Chickpeas can be grown on a wide range of soil types provided that the drainage is good and they cannot withstand water logging. For optimum results, clay loams are required. In Ethiopia, chickpea is best adapted to the areas having Vertisols [8].

Economic Importance of Chickpea

Chickpea production has many benefits; first, it fixes atmospheric nitrogen in soils and thus improves soil fertility and saves fertilizer costs in subsequent crops. Second, it improves more intensive and productive use of land, particularly in areas where land is scarce and the crop can be grown as a second crop using residual moisture. Third, it reduces malnutrition and improves human health especially for the poor who cannot afford livestock products. It is an excellent source of protein, fiber, complex carbohydrates, vitamins, and minerals. Fourth, the growing demand in both the domestic and export markets provides a source of cash for small holder producers. Fifth, it increases livestock productivity as the residue is rich in digestible crude protein content compared to cereals [12].

Chickpea Breeding Efforts and Major Achievements in Ethiopia Specifically

According to Asnake et al. [13], the national chickpea and lentil research program came up with 17 superior varieties of chickpea during the decade (2005-2016). The new chickpea varieties have comparative advantages in terms of earliness, Aschochyta blight tolerance, seed size, grain yield, suitability for mechanization and rust resistance among others. The advance in release of chickpea variety for the last decade revealed that 9 Kabili type and 8 Desi type chickpea varieties have been released for production. The release of the chickpea varieties so far was also based on product concepts and market oriented. Despite the release of several improved varieties, however, the variety replacement rate of chickpea is reasonably low. The genetic gains from breeding are also low as compared to the expectation. This calls for improving breeding progress for economic attributes on one hand and effective promotion of the available technologies on the other [13].

In the early phases of chickpea breeding, selections from local landraces were used to develop new varieties. Later the national chickpea improvement program created significant genetic variability for major agro-morphological traits desired by the breeding program through the introduction of diverse germplasm lines from different sources [14]. The major agro-morphological traits prioritized by the breeding program includes productivity, seed size, plant phenology

and resistance to key biotic and abiotic stresses prevalent in the country; particularly resistance to wilt/root rot diseases complex, ascochyta blight, major insect pests, drought, moisture and heat stresses.

In breeding programs, combination of bulk and pedigree methods are mainly used in handling several segregating generation developed from different crossing schemes. In early segregating generations, selection is done for simple traits such as disease resistance and seed traits. Screening of several segregating populations and local germplasm genotypes for resistance/tolerance to Fusarium wilt using an aggressive wilt sick plots at Debre Zeit Agricultural Research Center allowed the identification of sources of disease resistance [14].

Precision in selection for different biotic and abiotic stresses such as disease resistance, drought and heat tolerance can be greatly improved by screening several advanced germplasm line/segregating generation under controlled environmental conditions or at hot spot locations. Genomics assisted breeding (GAB) techniques, particularly marker assisted backcross breeding, marker assisted selection/marker assisted recurrent selection have a great potential to enhance precision and efficiency of chickpea breeding program [6]. These days, several success stories of GAB to develop superior varieties are reported in different pulse and cereal crops [15,16]. Therefore, integration of genomics tools in Ethiopia chickpea breeding program has a great potential to speed up the efficiency of selections in the segregating generations for higher and rapid genetic gains.

Moreover, single seed descent and speed breeding/rapid generation advancement methods are already in use at present and needs to be further strengthened to reduce the time required to reach the desired level of homozygosity and to speed up the release of appropriate varieties with desired traits. Adoption of speed breeding technology by generating 4-6 generations per year will be contributing to accelerate genetic gain in legumes breeding program [17].

Genetic Variation, Heritability and Genetic Advance in Genetic Variability Studies

Genetic variability studies provide basic information concerning genetic properties of population following which breeding methods could be formulated for future improvement of the crop [18]. Genetic variability study for agronomic traits is a key component of the breeding program for boarding the genetic pool of crop [4]. Component of genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation have an immense important in detecting the amount of genetic variation exist in the genotypes.

Scholars like [19,20] reported high PCV and moderate GCV for number of pods per plant. Another scholars, [21] recorded highest phenotypic and genotypic coefficient of variation (PCV and GCV) for number of pods per plant followed by biological yield per plant and 100-grain weight. In relation to this result [22] reported moderate genotypic coefficient of variations were for grain yield per plant (19.73), number of pods per plant (18.90 %), biological yield per plant (13.56%), number of primary branches per plant (12.75%) and 100-grain weight (11.60%).

Ali and Ahsan [23] reported the presence of greatest genotypic and phenotypic coefficient of variation in chickpea for number of seed per plant, number of pods per plant and plant height. Tesfamichael et al. [1] observed the presence of large variation for days to 50% flowering, plant height, days to maturity, number of pod per plant, 100 seed weight, and seed yield. Johnson et al. [24] conducted an experiment to determine genetic variability of thirty-one chickpea genotypes. His study indicated that the mean sum of squares due to genotypes were significant for all characters studied and suggested the existence of sufficient variability among the genotypes for the traits. This report also showed high values of genotypic coefficients of variation for secondary branches per plant, pod per plant, seed yield per plant, biological yield and primary branches per plant.

Chopdar et al. [25] found the highest genotypic coefficients variations for seed yield and 100-seed weight and moderate coefficient of variation for harvest index, number of pods per plant and biomass per plant and plant height in chickpea. And also genotypic coefficients of variations were low for days to maturity, days to 50 per cent flowering, primary branches per plant and number of seeds per pod. Fasil Hailu [20] reported highest phenotypic and genotypic variance for biological yield, harvest index and number of pods per plant while lowest value was recorded for number of seed per pod, primary branches and secondary branches and said selection is effective for high genotypic and phenotypic variability characters. In addition, Awol et al. [26] reported the lowest PCV and GCV (4.2% and 3.91%) for days to maturity, while the highest PCV and GCV values of 28.64% and 27%; respectively, were obtained for grain yield.

Other scholars [27] reported High GCV was recorded for hundred seed weight (36.01), number of secondary branches (20) and harvest index (22.4) and high PCV for hundred seed weight (36.02), number of secondary branches (27.53), harvest index (23.37), grain yield (22.89) and biological yield. And also Moderate GCV and PCV were noted for traits such as grain yield, biological yield, number of primary branches, days to emergence and number of pods per plant, and number of primary branches, days to emergence and number of pods per plant, respectively. Higher phenotypic and genotypic coefficient of variability indicates the existence of wide genetic variation among the genotypes under the study so that genetic improvement could be possible through selection.

Hussain et al. [22] also reported low GCV for days to 50% flowering (2.10%). Traits with low GCV and PCV indicate presence of narrow genetic variability. Traits such as physiological maturity, days to flowering, number of seed per pod, grain filling period and plant height was showed low GCV and PCV value. Thus, improvement for such traits could be possible through hybridization followed by selection.

Dubey and Srivastava [28] also reported high heritability (broad sense) for plant height, number of pods per plant, 100-grain weight and grain yield per plant. Malik et al (2010) reported high broad sense heritability estimates for number of secondary branches, harvest index, hundred seed weight and number of pods per plant and grain yield.

Chand et al. [29] reported that the highest broad sense heritability estimate was obtained for 100 seed weight (80%), number of seeds per pod (77%) and number of primary branch (62%) in chickpea genotypes. Hussain et al. [22] studied genetic variability and mode of inheritance in eight quantitative traits of chickpea and reported that high broad sense heritability for grain yield (96.40%), number of pods per plant (93.19%), 100-grain weight (89.67%), biological yield (83.83%) and plant height (78.83). According to Chopdar et al. [25], 100-seed weight had the highest heritability followed by days to 50% flowering (85.31), seed yield per plant (84.29), days to maturity (78.39), biomass per plant (69.06), number of pods per plant (68.06) and harvest index (67.51) in chickpea.

Parameshwarappa et al. [30] reported high heritability with high genetic advance as percent of mean for pods per plant, 100-seed weight and seed yield per plant, suggesting that these traits could be improved through simple selection. High heritability with high genetic advance as percent of means is the indication for the presence of additive gene action. He also found that high heritability with moderate genetic advance as percent of means for days to 50 percent flowering, and high heritability with low genetic advance as percent of means for plant height, primary branches per plant and secondary branches per plant.

According to Biru et al. [31] hundred seed weight, number of pods per plant, number of seed per pod and grain yield showed high heritability combined with high genetic advance as a percentage of mean. Moreover, low heritability and expected genetic advance were observed for days to maturity and branches per plant.

Joshi et al. [32] observed that high estimates of heritability in broad sense for days to 50% flowering, days to maturity, plant height, biological yield per plant, seed yield, harvest index and 100-seed weight, indicating that these characters were less affected by the environment and the plant breeder may use these characters for selection on the basis of phenotypic expression in the individual material.

Awol et al. [26] reported high broad sense heritability estimate for grain yield, hundred seed weight, biological yield, number of pods per plant, days to flowering, plant height, number of primary branches and number of secondary branches. Also Alemayo et al. [27] in their study on variability of 56 chickpea genotypes, estimate for all thirteen traits showed high (>60%) broad sense heritability. The highest heritability was obtained for hundred seed weight (99.96%) while the lowest was for number of seed per pod (62.96%). Presence of high broad sense heritability indicates selection based on phenotypic expression of individual genotypes for such characters might be easy due to relatively small effects of environment on phenotype.

But Arora and Jeena [33] recorded low value of heritability for days to 50% flowering; Singh and Rao (1991) for number of primary branches per plant. According to Johnson et al. [24] heritability alone might not be effective unless coupled with higher genetic advance as percent of the mean in predicting the effectiveness of selecting the best performing genotypes and he classified estimates of genetic advances as a percentage of the mean excelling 20% as high, ranging from 10 to 20% as moderate and those which showed below 10 as low.

Zali et al. [19] reported that the genetic advance (5% selection intensity) was the highest for number of secondary branches, number of seeds per plant and seed yield. This implies that progress on improving seed yield could be achieved through simple selection of the number of secondary branches and number of seeds per plant. Another scholar [22] reported high heritability coupled with high genetic advance as percent of mean for grain yield per plant (39.91), number of pods per plant (37.59), biological yield per plant (25.58) and 100-grain weight (22.62).

In their research, Alemayo et al. (2021) reported high heritability coupled with high genetic advance as percent of the mean were recorded for hundred seed weight (74.26%), number of secondary branches (54.65%), harvest index (44.34%), grain yield (33.38%), biological yield (32.6%), number of primary branches (28.35%), days to emergence (27.3%) and number of pods per plant (25.8%). High estimate of genetic advance as percent of the mean for these traits indicates that whenever we select the best 5% genotypes as parent for a given trait, genotypic value of the new population for the traits will be improved highly and they are governed by additive gene [34].

In addition, Alemayo et al. [27] reported, for traits like plant height, grain filling period and days to flowering showed high heritability with moderate genetic advance as percent of mean. This shows that, such traits are primarily under genetic control and their selection can be achieved based on their phenotypic performance. In another hand they reported as, Low genetic advance as percent of mean were observed for number of seed per pod and days to physiological maturity. This suggested that the expressions of such traits are controlled by non-additive gene action and their selection might not be satisfactory. So, the appropriate usage of pure line selection may be valuable for improving these characters with moderate or high heritability characters [35].

Conclusion and Future Prospects

For better improvement of a crop study on genetic variability is the crucial that help in getting sufficient information regarding per se performance, variability, heritability, genetic advance and association that may exist among yield and its components - agronomic and phenological traits. Because, without presence of genetic variability among genotypes (in our case, among chickpea genotypes) there is no success for its improvement. So, for successful breeding program [for chickpea] researchers should focus on creating variability among chickpea genotypes.

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