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Genetic Variability and Morphological Characterization of Oil-type Sunflower (*Helianthus annuus* L.) for Economically Important Traits: An Overview

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Abstract

Genetic variability among plants of a population is a precondition for a successful crop improvement strategy. Sunflower is an important oil crop to humans primarily for edible oil, and other purposes. Sunflower improvement showed a significant change from the past to the present to become one of the most significant oil crops. Considerable improvement has been made in oil-type sunflower from domestication to sophisticated research findings in its breeding, and genetics. Recently sunflower research has advanced to biotechnological tools of CRISPR-Cas9 techniques with different approaches contributing to modern breeding and genetics to change the genetic constitution and phenotypic structure of sunflower. So far sunflower improvement work and evaluating the genetic variability and associated studies are the basis for sunflower breeding for future improvement works. A review of studies done by scholars on genetic variability and morphological characterization of cultivated oil-type sunflower for economically important traits is the target and motivation of this paper.

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CRISPR-Cas9, edible-oil, Genetic Variability, phenotypic, oil-type.

Introduction

The fourth important oilseed crop, sunflower, belongs to the Asteraceae family (Heiser, 1978; Hu *et al.,* 2010). Sunflower is a high-quality and nutritional edible premium oil adopted and accepted worldwide. Genetic variability is a prerequisite to embarking on any breeding program and the presence of basic information on genetic variability is important to plan breeding strategy and make effective selection for desirable traits. Variations are very precious for any breeding program (Hussain *et al.,* 2015) as the success of a breeding program mainly relies upon the extent of variation present in a genotype for yield and its contributing traits (Qamar *et al.,* 2015). According to Sowmya *et al.,* (2010), genetic variability present in a population can be used effectively as the gene pool of breeding programs managed well. Thus, during selection for yield, more consideration has to be given to those attributes with low environmental variability. Yield being a complex character is collectively influenced by various component traits that are polygenically inherited (Cooper *et al.,* 2005; Falconer, 1989; Falconer, 1996). Heritability estimations are key to determining the relative heritable portion in variation and thus help plant breeders in selecting the elite inbred from a diverse population. During selection, it's important to consider heritability, genetic gain, and also genetic advance for the total existing genetic variability in a population (Allard, 1999). It's important to show the real correlation of economic yield with other related traits to support the selection efficiency using association. Path coefficient analysis facilitates the partitioning of correlation coefficients into the direct and indirect effects of economic traits on achene yield. So, the coefficients of variation expressed at phenotypic and genotypic levels are used to compare the variability observed among different characters. A significant source of variation has been reported by different scholars for achene yield and the number of seeds per head and yield components (Virupakshappa and Sindagi, 1988; Zain, 2015). Therefore, improvement in yield cannot be achieved through simple phenotypic selection because of its polygenic nature and low heritability estimates. High heritability is needed to execute an effective selection scheme for the trait of interest. Heritability along with genetic advance is more reliable than heritability alone (Johnson *et al.,* 1955). Understanding the association of traits and variability among genotypes helps the breeders formulate effective selection procedures and identify traits that may help for the indirect selection of grain and oil yield. So, Genetic improvement of existing cultivars cannot be made without access to new germplasms for introgression. The success story of any breeding program shows the existence of sufficient genetic variability and divergent genotypes to work effectively in selection or hybridization. So, the objective of this paper is to review important scholarly works about these aspects of sunflower has been discussed here under the following heads.

Literature Review

Sunflower Genetic Variability

Multivariate analysis has been considered an important means of measuring the degree of genetic divergence (Rao, 1952). Genotypes from different localities are generally included in the hybridization programs assuming genetic diversity and greater likelihood of recovering promising segregates. However, according to Murthy and Anand's (1966) report, there is no parallelism between geographical and genetic diversity. Genetic variability is the most important feature of any base population. Genetic variability is the tendency of individual genetic characteristics in a population to vary from one another and the potential of a genotype to change or deviate when exposed to environmental or genetic factors. Genetic variability in population is the prerequisite for response to selection in any crop improvement program. Hence the estimates of genetic variability are of immense value in identifying the superior genotypes. The magnitude of variability present in a gene pool of a crop species is of utmost importance to plant breeders for starting a sensible plant breeding program. Researchers globally collect germplasm from various Agro-climatic regions and evaluate and characterize them to generate genetic variability. Both genetic and environmental factors contribute to variation among individuals (George, 2002). According to Siva Subramanian and Menon (1973), genotypic coefficients of variance (GCV) and phenotypic coefficients of variance (PCV) Values of any genetic variability study greater than 20% are high, less than 10% are low and between 10 % and 20 % are medium.

According to Sujatha *et al.,* (2002), fifty-one inbreed lines with three sunflower genotypes showed significant variation for quantitative traits. Similarly, Seneviratne *et al.,* (2003) studied 200 sunflower lines and reported a high PCV and GCV for plant height, head diameter, number of days to 50 % flowering, number of days to maturity, 100-seed weight, seed yield, and oil yield. According to Rajeswari (2004), 16 sunflower genotypes were evaluated using 10 morphological characters that showed significant differences and also had high PCV and GCV for major traits of interest. Also, a genetic variability study done by Khan *et al.,* (2007) for important agro-morphological characters using 32 genotypes showed a significant difference in all characters except days to maturity and GCV was low in all the studied characters but high heritability coupled with genetic advance of mean were recorded for Seed yield per plant. Inversely, Arshad *et al.,* (2007) reported high heritability for days to flower initiation, completion, and plant height, while head diameter and seed yield had low heritability.

According to Khan *et al.,* (2007), PCV was higher than the genotypic coefficient of variation for all the traits of interest. High heritability estimates were observed for oil content, 1000-seed weight, days to maturity, and plant height, while seed yield, number of seeds per head, and days to flowering depicted low heritability values. High genetic advance was recorded on plant height, number of seeds per head, seed yield, and oil yield as well. A similar study done by Arshad *et al.,* (2010) revealed high heritability associated with high genetic advance for days to flower initiation, days to maturity, plant height, and seed yield while the characters having low heritability were head diameter and seed yield. A similar study done by two scholars reported genetic variability studies in 27 sunflower genotypes, 26 germplasm lines and one check, high heritability with high genetic advance was recorded for the number of unfilled seeds per head, seed yield per plant, plant height, and 100-seed weight, while high heritability along with low genetic advance was observed for oil content, days to 50%flowering, hull content and days to maturity. Also, high values of PCV and GCV were observed for the number of unfilled seeds per head, seed yield per plant, plant height, 100-seed weight, and number of filled seeds per head (Kalukhe *et al.,* 2010; Khoufi *et al.,* 2013).

Tyagi *et al.,* (2010) evaluated twenty-two sunflower genotypes for different quantitative traits of interest and highly significant differences were observed among the genotypes for all traits considered. A slight increase of genotypic correlation coefficients over the corresponding phenotypic correlation coefficients was observed for all the character combinations. Similarly, Makane *et al.,* (2011) evaluated 79 recombinant lines of, Morden and EC-68415, sunflower varieties for nine quantitative traits, and considerable variability was noticed for days to maturity, plant height, test weight, and seed yield per plant. Also, high GCV was observed for hull content, seed yield per plant, plant height, test weight, and oil content. The genetic advance expressed as a percent of mean was high for hull content, seed yield per plant, and plant height, whereas it was moderate for test weight, oil content, and head diameter and low for days to maturity and days to 50% flowering. High heritability was recorded for plant height and hull content, followed by seed yield per plant, oil content, and test weight, and moderate for head diameter and days to maturity. Also, this study confirmed high genotypic and phenotypic variances for seed yield, plant height, and oil content. High heritability and genetic advance were recorded for oil content and seed yield whereas plant height and capitulum diameter exhibited low genetic advance.

Ten genotypes of sunflower evaluated for different agronomical and seed quality characters showed highly significant differences observed for all the characters. Plant height, oil content, protein content, and seed yield per head showed high heritability with moderate genetic advance (Hassan *et al.,* 2012). This study was also confirmed by Iqbal *et al.,* (2013). A diversity study done using 18 sunflower inbred lines involving alloplasmic CMS lines, conventional CMS, and restorer lines using twenty traits showed significant variability among the germplasm lines (Tyagi *et al.,* 2013; Madhavilatha *et al.,* 2017). Recently similar findings also reported by Abu (2019) and Lagiso *et al.,* (2021), 25 sunflower genotypes, were evaluated for Agro-morphological traits of interest and reported highly significant to significant differences for all characters except petiole length, stem diameter, and ray floret number. Additionally, the authors reported high GCV and PCV values were recorded for oil yield and seed yield per hectare and also GCV was low for all traits except oil yield and number of seeds per plant which showed medium GCV.

Heritability (H^2), Genetic Advance, and Genetic Advance of Mean

Heritability represents the ratio between genetic and all factors (including non-genetic ones) that influence the variability (Bernardo, 2002). Heritability estimates aid in determining the relative amount of heritable portion in variation and thus help plant breeders in selecting the elite inbreds from a diverse population. Phenotypic and genotypic variance, heritability along genetic advance have been used to assess the magnitude of variance in sunflower breeding material. Heritability percentage estimates from total genetic variance without taking into consideration the components of genetic variance are referred to as heritability in the broad sense because it estimate heritability based on all genetic effects. Heritability expressed as a percentage of the additive component of variance is referred to as narrow sense heritability. It indicates the effectiveness with which the selection of phenotypes can be based on phenotypic performance. If heritability were 100% then phenotypic performance would be a perfect indication of genotypic value. The response of selection for qualitative characteristics is directly proportional to the function of its heritability and its genetic variance Johnson *et al.,* (1955). To start an efficient breeding program heritability estimation and genetic advances are core and basic (Atta *et al.,* 2008). Genetic advance alone also has some gaps to show the expected selection impact because it indicates the magnitude of genetic gain from a selection (Hamdi *et al.,* 2003). Heritability value alone may not give a clue of breeding value but heritability with genetic advance is more effective and reliable in depicting the cumulative effect of selection (Ramanjinappa *et al.,* 2011).

Heritable variation cannot be determined with the high genetic coefficient of variation alone and for greater heritability, the heritability estimates as well as the genetic advance are essential. At the gene level, broad sense heritability is the proportion of the total variance that is attributable to the average effects of genes and this is what determines the degree of resemblance between relatives. Heritability of a trait does not depend only on genetic factors; it also depends on the environmental effects to which an individual is subjected (Falconer, 1996). Less genetic gain is expected through selection in characters depicting high heritability estimates with low genetic advance while considerable genetic gain is expected through selection for traits possessing high GCV, moderate heritability, and high genetic advance (Patil *et al.,* 1996).

According to Johnson *et al.,* (1955), heritability values of more than 60% are regarded as high whereas, values less than 30% are considered to be low and values between 30% and 60% are to be moderate. Johnson *et al.,* (1955) also predicted genetic advance as the percent of the mean (GAM) was categorized as high (>20%), moderate (10-20%) and low (0-10).

Taking into consideration the importance of heritability, different workers estimated heritability in sunflower. Hassan *et al.,* (2012) conducted heritability studies on 10 genotypes of sunflower and reported high heritability with moderate genetic advance for plant height, oil content, protein content, and achene weight per head. Similarly, Iqbal *et al.,* (2013) estimated the heritability and genetic advance in 10 genotypes of sunflower and reported moderate heritability with high genetic advance as a percent of the mean for total leaf area and achene weight. Premnath *et al.,* (2014) reported high heritability and high genetic advance as a percent of the mean for plant height, head diameter, and seed yield per plant in two back cross populations of sunflower.

Correlation and Path Analysis

In plants, the dynamics of many important physiological and biochemical processes are often influenced by multiple interacting factors. To resolve the biological complexity, plant geneticists need to estimate the relative strengths of competing causes of biological phenomena. The advantage of path analysis in plant breeding was demonstrated by Dewey and Lu (1959) which allows partitioning of the correlation coefficient into its components.

One component of the path coefficient analysis is the standardized partial regression coefficient that measures the direct influence of an independent variable upon its dependent variable whereas another component is the indirect effects of an independent variable on the dependent variable through the independent variables. If the correlation between dependent and independent variables is due to the direct effects of the character, it reflects a true relationship between them, and selection can be practiced for such a character to improve the dependent variable. But if the association is mainly through indirect effects of the characters via another component characters, the breeder has to select for the later one through which the indirect effect is exerted on the ultimate dependent character such as seed yield.

Rao *et al.,* (1952) found a positive correlation between seed yield per plant with head diameter and the number of achenes per head. Subsequently, path coefficient analysis revealed that achenes per head had the greatest direct effect on achene yield. On the other hand, the author reported that harvest index had the greatest positive direct effect on achene yield, through plant height and total dry-matter content and concluded that early selection for days to maturity could be based on days to flower bud appearance and days to 50%-*disc floret* opening. Similar results were reported on the maximum direct effect of the number of seeds per head, 100-seed weight, seed yield per plant, oil yield, plant height, head diameter, and seed filling percentage (Nehru *et al.,* 2003; Sridhar *et al.,* 2005; Vidhyavathi *et al.,* 2005).

Farhatullah *et al.,* (2006) investigated the inter-relationships among studied traits at both genotypic as well phenotypic levels and showed that seed yield was positively correlated with plant height, head diameter, and oil content. The number of seeds per head showed a significant and positive association with seed yield. Days to maturity, plant height, head diameter, number of seeds per head, 1000-seed weight, and oil content showed a positive direct effect on seed yield whereas the number of leaves per plant and days to flowering had negative direct effects on seed yield. According to Arshad *et al.,* (2007), the positive direct effects on seed yield through days to flower initiation, plant height, and head diameter, and the other traits of interest exhibited negative direct effects. Days to flower initiation and plant height on seed yield showed the highest direct effect. Similarly, Amorim *et al.,* (2008) studied 14 genotypes and reported significant positive correlations were observed between seed yield, head diameter, and weight of 1000 seeds. The head diameter and weight of 1000 seeds showed positive direct effects on seed yield.

Based on the study results obtained from 118 sunflower hybrids conducted in dry and rainy seasons, Kaya *et al.,* (2008) concluded that 1000-seed weight had the maximum contribution towards higher yield followed by head diameter and plant height. Similarly, Iqbal *et al.,* (2009) reported that stem diameter exerted a positive direct effect on oil content under restricted water conditions. Similarly, Sowmya *et al.,* (2010) also reported that days to 50% flowering, days to maturity, plant height, head diameter, seed filling percentage, 100-seed weight, and oil content were positively and significantly correlated with seed yield per plant. Yasin *et al.,* (2010) computed correlation and path coefficient analysis for 24 genotypes of sunflower, and found that yield per plant had a highly significant and positive correlation with the number of seeds per head, head diameter, and 1000-seed weight at both genotypic and phenotypic level. Path coefficient analysis revealed that the number of seeds per head, thousand seed weight, and head diameter had high positive direct effects on seed yield per plant. But Darvishzadeh *et al.,* (2011) reported that only head diameter was positively associated with seed yield per plant under well-watered, and water-stressed conditions and interestingly, head diameter and number of seeds per head had also positive direct effects on seed yield per plant in both the conditions. Similar findings also reported that seed yield was positively and significantly linked to hundred-seed weight, seeds per head, head diameter, stem diameter, and plant height, and the results of path coefficient analysis depicted that hundred-seed weight, head diameter, and seed number per head had positive direct effects on seed yield (Kholghi *et al.,* 2011 & Patil, 2011).

Another study was done by Neelima *et al.,* (2012) correlation between seed yield and its component traits revealed that the number of seeds per head, hundred seed weight, head diameter, and seed filling percentage had a highly significant positive effect on seed yield and component traits. The number of seeds per head, seed filling percentage, hull content, and plant height influenced the seed yield directly whereas hundred seed weight influence was indirectly through the number of seeds per head and seed filling percentage. The maximum indirect contribution for most of the studied traits was through the number of seeds per head. Similarly, Iqbal *et al.,* (2013) noted that the number of leaves, stem diameter, head diameter, and oil content showed a positive direct effect on seed yield and head diameter. Also, Rao (2013) revealed a higher magnitude of a positive direct effect of number of filled seeds per head, followed by hundred seed weight and plant height on seed yield. Interestingly, days to maturity showed a direct positive effect on seed yield, but an indirect effect through plant height, number of filled seeds, and hundred seed weight was also noticed. In contrast, days to 50% flowering and oil content showed negative direct effects on seed yield. Similar findings also reported by Zia *et al.,* (2013) showed that harvest index, hundred seed weight, and head diameter had significant positive correlations with seed yield per plant. The highest direct effects were recorded for head diameter, hundred seed weight, and harvest index, respectively. The highest indirect effects were recorded for filled seed percentage and 100-seed weight *via* harvest index.

According to Tyagi *et al.,* (2013), grain yield showed a highly significant positive correlation with days to 50% flowering, days to maturity, plant height, chlorophyll content, oil content, and biological yield at both genotypic and phenotypic levels. Path coefficient analysis revealed the direct positive effect of the number of leaves per plant, hundred seed weight, chlorophyll content, leaf area, leaf area index, oil content, biomass yield, and harvest index on grain yield. Chander *et al.,* (2014) reported that days to 50%flowering, days to maturity, plant height, head diameter, hundred seed weight, and oil content had significant positive correlations with seed yield. The maximum positive direct effect on seed yield was exhibited by head diameter, whereas plant height showed maximum indirect effect. However, Maria *et al.,* (2018) reported that a study done on genetic variability and association of economic traits with seed yield using fifteen lines of sunflower showed high significance for all traits of interest. In addition to those genotypic correlations were higher than phenotypic correlations and also hundred seed weight, leaf number, leaf area, and head diameter had positive and highly significant genotypic correlations with seed yield per plot. However, the genotypic correlation of seed yield per plot was significantly negative with plant height, days to flowering, and oil contents. Leaf area, leaf number, hundred seed weight, and Oil Content showed a direct positive effect on seed yield per plot. Days to flowering, plant height, head diameter, and fatty acid profile had a negative direct effect on seed yield per plot.

Furthermore, a recent study done by Abu (2019) and Lagiso *et al.,* (2021), a genetic variability study between 25 sunflower genotypes depicted seed yield had positive and significant genotypic and phenotypic correlation with the number of seeds per plant, yield per plant, head diameter and seed filling percentage. Positive and significant phenotypic associations were also observed for petiole length, plant height, and hundred seed weight. Positive phenotypic direct effects on seed yield per hectare were observed for oil yield, hundred seed weight, seed filling percentage, and seed yield per plant. Oil yield, seed filling percentage, and seed yield per plant gave the highest positive direct effect on seed yield genotypically.

Genetic Divergence and Cluster Analysis

Genetic divergence is the relative contribution of different characters to differentiate among genotypes based on genetic distance (D^2). D^2 statistic helps in the identification of genetically divergent genotypes that facilitate grouping and characterization using Agro-morphological, and molecular data. Genetic diversity studies have an important contribution to plant breeding because crosses between diverse parental lines show greater heterosis than crosses of closely related parents. Hence, it is important to identify the best parents with wide genetic divergence for traits of interest to obtain better heterotic progeny. According to Mahalanobis (1936); a statistical procedure 'D^2 statistic' is useful to measure the genetic divergence in a given population. It is a powerful tool for quantifying the degree of genetic divergence among parents (Sujatha *et al.,* 2002; Punitha *et al.,* 2010).

A study done by Subrahmanyam *et al.,* (2003) grouped 85 sunflower genotypes into fifteen clusters based on their genetic distance. The result of this study revealed maximum genetic divergence exhibited by the number of filled seeds per head followed by hundred seed weight, kernel-to-hull ratio, and seed yield per plant. Similarly study done by Komuraiah *et al.,* (2004) grouped the 101 sunflower genotypes into ten clusters by basing genetic distance among genotypes and traits like the number of filled seeds, hundred seed weight, and plant height contributed maximum genetic divergence. Reddy *et al.,* (2005) also assessed genetic divergence among 102 genotypes and grouped them into twelve clusters based on genetic distances. The author also showed the maximum contribution was by seed yield per plant followed by number of leaves per plant and hundred seed weight. Mahalakshmi *et al.,* (2006) reported a genetic divergence study using 29 sunflower genotypes that were grouped into seven clusters and the maximum contribution was by days to first flowering. Binodh *et al.,* (2007) also reported genetic divergence in addition to cluster analysis for 24 breeding lines, which were grouped into ten clusters. And 13 genotypes were categorized under Cluster I, 3 genotypes under Cluster IV. The maximum contribution was by Plant height followed by seed yield per plant and oil content, and the genotypes were selected as best parents from traits of interest that could be intercrossed to obtain high heterosis.

According to Kumar *et al.,* (2008), 32 parental lines were clustered into eleven distinct groups. Oil content was the maximum contributor to genetic divergence followed by days to 50% flowering and days to maturity. Even though the number of genotypes is not satisfiable for a diversity study, Camarano *et al.,* (2010) investigated genotypic divergence among 10 sunflower genotypes to identify similar and divergent groups and reported similar results as Kumar *et al.,* (2008). Likewise, Punitha *et al.,* (2010) reported genetic variability among sunflower genotypes using a few traits of interest and depicted the presence of considerable genetic divergence by grouping the genotypes into four major clusters. Among the investigated characters, seed yield, plant height, oil content, and oil yield exhibited high genetic divergence and identified genotypes for future breeding programs that could result in the development of superior sunflower variety. Per the above two studies, Dan *et al.,* (2012) also did genetic divergence of 79 inbred lines of sunflower and showed the presence of substantial genetic diversity among studied genotypes. The maximum contributor for genetic divergence was oil yield per plant followed by plant height, hundred seed weight, head diameter, and seed yield per plant accordingly. Recently, similar results have also been reported by Reddy *et al.,* (2012); Tyagi *et al.,* (2013); Chandira *et al.,* (2014); Pandya *et al.,* (2014); Hussain *et al.,* (2017); Abu (2019) and Lagiso *et al.,* (2021) on genetic divergence of sunflower genotypes from different parts of the world based on their traits of interest and they recommended their best fitting clusters to get heterotic progeny for future breeding work.

Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate analysis methods, is used to identify the most significant variables in the data set and is also an important tool to assess and evaluate genetic diversity in a population. Plant breeders usually apply this tool to investigate clear patterns of diversity in existing genotypes. According to Shanker *et al.,* (2004), the potential use of PCA in a variety development programsis for the selection of superior genotypes or parents based on the most significant characters or traits, and exploit it in the planning and execution of the future breeding program (Pecetti and Damania, 1996; Nazir *et al.,* 2013; Mustafa *et al.,* 2015; Venujayakanth *et al.,* 2017).

Taking into account the importance of PCA, different scholars have done different sunflower genetic variability studies. Arshad *et al.,* (2010) carried out a multivariate analysis of 37 sunflower hybrids for eight agronomic characters and observed that days to flower initiation, days to flower completion, days to maturity, plant height and oil content contributed to PC1 while hundred seed weight alone contributed to PC2, and the first three PC accounted cumulatively 74.53% and separately 47.29%, 14.23% and 13.01% respectively to the total genetic divergence. Similarly, Kholghi *et al.,* (2011) reported a study on 36 confectionary sunflower populations using PCA and noted a relative contribution of 78% of total variation by the first four components. Furthermore, PC1 displayed 40.2% of total variation and was found to be negatively associated with head diameter, seed yield, harvest index, stem diameter, and number of leaves indicating genotypes with high values of PC1 were noted for lower seed yield and vice versa. Similarly, a study done on genetic diversity using seventy sunflower genotypes and the results of PCA revealed that plant height, head diameter, hundred seed weight, number of seeds per head, volume weight, and leaf area index were the highest contributors to the variability and can be utilized as selection criterion (Zeinalzadeh-Tabrizi & Nabipour, 2005; Madhavilatha *et al.,* 2017).

Recently, a genetic variability study done by Hussain *et al.,* (2017) showed that twenty-eight sunflower hybrids were grouped into two PCs with 73.7% total variability observed. Additionally, PC1 was the maximum contributor (59.7%) towards diversity, and surprisingly all the traits in PC1 showed positive factor loading except plant height, stem diameter, and days to 50% flowering being the most important characters in PC2. However, another study reported by Abu (2019) and Lagiso *et al.,* (2021) with a limited number of genotypes, 25, shows that the genotypes were grouped into five and four clusters which makes them moderately divergent. The first five and four PCs showed a contribution of 84.72 % and 80.2 % of total variability respectively. Additionally, the authors suggested that during selection considering Oil content, thousand seed weight, seed filling percentage, head diameter, and seed yield as selection criteria is beneficial.

Conclusion

The edible oil scenario in Ethiopia is a major headache for the country. Importing oil to stabilize markets is the current solution, but the gap is still there. The demand for sunflower oil has been increasing for the last five years and it's mainly due to the health benefit of the oil quality. The limited number and low Productivity of released sunflower varieties are uncovered facts in the production system. Consequently, it becomes a challenge for domestic oil factories to function at their full potential due to raw material shortages, especially sunflowers. This scenario shows the need for a highly adapted and stable variety for wider or specific adaptation. So, to combat and give solution-intensive breeding works like genetic variability and multivariate analysis and GxE works highly needed from the research system since a pilar and starting point to develop the required variety and equipped well with knowledge of Genetic variability and character association, GxE, and characterization of breeding materials to best-suited traits of interest. Thus, why this work was initiated to give clues and compile work done by scholars so far on sunflowers, so, this review paper compiled efforts of research work on sunflower. Genetic variability and character association were reviewed and useful information that could be used in future development endeavors was organized. Finally, I would like to recommend the importance of Genetic variability and character association study in sunflower as an important pillar for future breeding strategy and variety development and also for the sunflower variety extension and demonstration work as a whole it’s not an option but mandatory to incorporate and penetrate the current cereal-cereal cropping pattern and meet the edible oil demand of upcoming the country population growth.

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Conflict of interest

The author declares no conflict of interest.

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