**Scientific Journal of Agricultural Sciences 2 (1): 1-5, 2020**
**Print (ISSN 2535-1796) / Online (ISSN 2535-180X)**

# Genetic variability of some vegetative and flowering growth characteristics of multiflower mutant of *Helianthus annuus* L. plants

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**Received on: 29/4/2020** **Accepted on: 21/5/2020**

## ABSTRACT

Present investigation was conducted to study the genetic variability of some growth and flowering traits of branching mutant of *Helianthus annuus* (sunflower) plants that having many inflorescences per plant. This study was done during two successive seasons at the Nursery of Ornamental Plants, Faculty of Agriculture, South Valley University, Qena, Egypt.

High broad sense heritability with high genetic variance( GCV% and PCV%) were found for number of inflorescences per plant, stem diameter, leave area, fresh weight of vegetative growth and 100 seeds weight. This result refer to the small amount of environmental effects and these traits are under the influence of genetic control. While high heritability in broad sense with moderate genetic variance were found for plant height. Whereas moderate heritability in broad sense with moderate genetic variance were found for number of leaves per plant, inflorescence diameter, number of seeds per mean head. So, Selection is an expected tool to improve branching mutant of *Helianthus annuus* plant characteristics.

**KEYWORDS:** heritability**,** Selection**,** phenotypic coefficient of variation, genotypic coefficient of variation, *Helianthus annuus*

## 1. INTRODUCTION

*Helianthus annuus* plants is belongs to family Asterace. They are commercially grown for different uses: inflorescences as cut flowers, seeds for feed birds, oil extracted from the seeds are used for cooking.

Selection is the most important process which alter the frequencies gene of population (Gvozdenovic *et al*., 2009**)** which may be greater or lesser than the population mean

Selection methods is effective only in the presence of large variability in the population. Consequently, genetic variability is the prerequisite for an effective breeding programme in many crops and it differs from one to other due to its evolutionary process and complexity of genetic system (Datta, 2012).

The variation in a segregating population is divided to both genotypic variance and phenotypic variance Powers (1957) and Panse (1957) further partitioned the genotypic variance into additive and non-additive components. The non-additive one includes dominance and inter allelic interactions. The additive component of genetic variance is highly heritable and the characters are fixable through selection resulting in maximum genetic advance

Improvement of high quality plants requires a knowledge about genetic variation. Genetic improvement of any plant is dependent on the degree of the genetic parameters such as: phenotypic and genotypic variances, phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability and genetic gain; on which the breeding methods are formulated for its further improvement Roychowdhury and Tah (2011).

Therefore, present investigation was conducted to study genetic variability of some growth and flowering traits of branching mutant of sunflower plants that having many inflorescences per plant.

## 2. MATERIALS AND METHODS

The study was investigated at the Nursery of Ornamental Plants, Faculty of Agriculture, South Valley University, Qena, Egypt from 2011 to 2015.

The branching mutant of *Helianthus annuus* that have many inflorescences/ plant was used in this study that obtained from previous study (Mostafa, 2011). The mutant was achieved from previous study using cv. Giza 102 treated with 100 ppm sodium azide in the $M_2$ generation (2). Seeds of the selected mutant as a base population were sown in the field on May 2011 in a non-replicated area. The procedure of three cycles of mass selection was done. After that seeds of unbranched parent (cv. Giza 102), base population (branched mutant), and three cycles of mass selection were sown on 15 May 2014 and 2015, to estimate the genetic parameters.

### 2.1. Recorded data

At flowering stage: plant height(cm), number of leaves, stem diameter(cm), leaf area($cm^2$), fresh weight of vegetative growth(g), flowering date (days from sowing seeds to showing color of the first inflorescence per plant), number of inflorescences per plant, number of ray florets per inflorescence and inflorescence diameter(cm) were recorded. Chlorophyll content (SPAD unit) was estimated as described by Yadava (1986). Number of seeds per main head and twenty seeds weight were recorded at the maturity stage.

### 2.2. Statistical analysis

Data were statistically analyzed using analysis of variance for randomized complete block design (RCBD) for separate analysis as Gomez and Gomez (1984). Moreover, genetic parameters were estimated as follow:

Genotypic variance $\delta^2 g = (MSG - MSE)/r$

Where MSG is mean square of genotype,MSE is mean square of the error, and r is number of replications.

Phenotypic variance $\delta^2 p = \delta^2 g + \delta^2 e$

Where $\delta^2_g$ is genotypic variance and $\delta^2_e$ is the mean square of error

The estimate of phenotypic and genotypic coefficient of variation (PCV%) and (GCV%) were calculated according to Singh and Choudhary(1985) as follow:

PCV%= $(\frac{\sqrt{\delta 2p}}{\overline{X}})$ X100, GCV%=$\frac{\sqrt{\delta 2g}}{\overline{X}}$ X100

Where $\overline{X}$ is the mean of the trait. GCV% and PCV% values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) as described by Sivasubra manian and Madhava Menon (1973).

Heritability in broad sense was calculated according to Falconer 1989 as follows: $h^2B = \delta 2g/\delta 2p$

The heritability percentage was categorized as follow (0-30%), moderate (30-60%), and high (≥60%) as described by Robinson *et al.* 1949

Predicted genetic advance GA% was calculated using the method of Oladosu *et al.*, 2014 as follow: GA%= K x $\sqrt{\delta 2p/}\ \overline{X}$ x $h^2Bx100$, where K is selection intensity which assumed 5% and its value is 2.06. It was categorized as low (0-10%), moderate (10-20%), and high (≥20%)

## 3. RESULTS

The genotypic and phenotypic variance expressed as GCV% and PCV% were moderate for plant height (10.61 and 13.45 for 1st season and 10.29 and 12.93 for 2nd season respectively) as shown in Table 1. Heritability in broad sense was high (62 and 63 for 1st and 2nd seasons respectively)

For stem diameter, GCV percentage and PCV percentage were high for both seasons (24.03, 25.1 for 1st season, 26.4 and 24.7 for 2nd season). High heritability also found (0.91 and 92.0 for both season respectively)

Genotypic coefficient of variance for number of leaves per plant was ranged between low to moderate value (8.20, 18.04 in the 1st and 2nd seasons respectively). While phenotypic coefficient of variance-possessed moderate to high values (11.03, 20.7 for 1st and 2nd seasons respectively). Heritability in broad sense was moderate 0.55 in the 1st season but seems to be high (75) for 2nd season.

Leaf area possess a high phenotypic and genotypic variance in both seasons (46.96, 43.6 for 1st season and 45.59 and 37.63 in the 2nd season). Also high heritability was found in both seasons (91 and 68 for 1st and 2nd seasons respectively

High genotypic and phenotypic variances were found with respect of fresh weight of vegetative growth coupled with high heritability value in both seasons.

Low PCV% and GCV% values were found for chlorophyll content traits (9.47,7.46 in the 1st season and 10.33 and 7.95 in the 2nd one). Heritability in broad sense ranged from moderate (0.59 in the 2nd season) to high (0.62 in the 1st season)

Number of inflorescences per plant presents high values of PCV%, GCV% and heritability in broad sense (25.08, 24.41, 0.94 in the 1st season and 25.5, 21.54 and 71 for 2nd season respectively).

Low phenotypic and genotypic variances were found in number of ray floret/ inflorescence, while a moderate heritability values were found in both seasons.

Regards inflorescence diameter, moderate phenotypic and genotypic variance were found (15.99, 11.90 in the 1st season and 15.80 and 14.92 in the 2nd season). At the same line, high heritability was found (89) in the 2nd season.

Moderate PCV%, GCV% and heritability values were found with respect to number of seed per mean head in both seasons.

On the other hand, high PCV%, GCV% and heritability were found for 100 seeds weight traits (30.14,28.48 and 89 in the 1st season and 30.94, 30.44 and 96 in the 2nd seasons. Predicted genetic advance (GA %) was found to be moderate to high values in most cases in both seasons

## 4. DISCUSSION

Study the genetic variability of some growth and flowering traits of branching mutant of sunflower plants that having many inflorescences per plant. Because that the knowledge about PCV%, GCV% and Heritability enables the plant breeder to decide the method of selection procedure.

**Table 1. Genetic estimates for Plant height (cm), Stem diameter (cm$^2$), No. of leaves, Leaf area (cm$^2$), Fresh weight of vegetative growth (gm), Chlorophyll content (SPAD unit), No.of inflorescence, No. of ray florets, Inflorescence diameter (cm), No. of seeds/mean head, 100seeds weight (gm) for multiflower mutant of *Helianthus annuus* L. plants during two seasons.**

| Genetic parameters | Plant height (cm) | Stem diameter (cm$^2$) | No. of leaves | Leaf area (cm$^2$) | Fresh weight of vegetative growth(gm) | Chlorophyll content (SPAD unit) | No.of inflorescence | No. of ray florets | Inflorescence diameter (cm) | No. of seeds/mean head | 100seeds weight (gm) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | **First season** | | | | | |
| **$\delta^2$g** | 246.05 | 0.11 | 6.61 | 11594.2 | 14488.5 | 4.49 | 15.6 | 2.47 | 0.48 | 1718.29 | 1.19 |
| **$\delta^2$p** | 395.45 | 0.12 | 11.96 | 13448.3 | 15917.28 | 7.23 | 16.48 | 5.89 | 0.86 | 3465.73 | 1.33 |
| **PCV%** | 13.45 | 25.10 | 11.03 | 46.96 | 38.86 | 9.47 | 25.08 | 6.05 | 15.99 | 13.73 | 30.14 |
| **GCV%** | 10.61 | 24.03 | 8.20 | 43.60 | 37.07 | 7.46 | 24.41 | 3.91 | 11.90 | 9.66 | 28.48 |
| **h$^2$B** | 0.62 | 0.91 | 0.55 | 0.86 | 0.91 | 0.62 | 0.94 | 0.41 | 0.55 | 0.49 | 0.89 |
| **GA%** | 17.17 | 0.64 | 12.50 | 83.2 | 72.85 | 12.10 | 48.5 | 5.10 | 18.0 | 13.86 | 55.2 |
| | | | | | | **Second season** | | | | | |
| **$\delta^2$g** | 206.25 | 0.12 | 37.08 | 6527.43 | 14952.51 | 8.47 | 16.06 | 3.47 | 0.77 | 2989.23 | 0.92 |
| **$\delta^2$p** | 325.31 | 0.13 | 48.82 | 9581.4 | 16798.33 | 14.29 | 22.50 | 10.94 | 0.86 | 5179.38 | 0.95 |
| **PCV** | 12.93 | 26.4 | 20.70 | 45.59 | 38.46 | 10.33 | 25.50 | 8.19 | 15.80 | 18.26 | 30.94 |
| **GCV** | 10.29 | 24.7 | 18.04 | 37.63 | 36.28 | 7.95 | 21.54 | 4.61 | 14.92 | 13.87 | 30.44 |
| **h$^2$B** | 0.63 | 0.92 | 0.75 | 0.63 | 0.89 | 0.59 | 0.71 | 0.31 | 0.89 | 0.57 | 0.96 |
| **GA%** | 16.78 | 0.65 | 31.99 | 63.87 | 70.51 | 12.56 | 37.29 | 5.23 | 28.91 | 21.44 | 61.19 |

**$\sigma^2$P:** phenotypic variances**;** **$\sigma^2$G**: Genotypic variances**;** **PCV%:** Phenotypic coefficient of variance**;** **GCV%:** Genotypic coefficient of variance**;** h$^2$B**:** Heritability**;** GA%: predicted genetic advance.

High broad sense heritability with high genetic variance for most studied traits were found. This result refer to the small amount of environmental effects and these traits are under the influence of genetic control (Natikar *et al*., 2013). Therefore, this result suggested the greater effectiveness of selection as expected tool to improve *Helianthus annuus* plant characteristics

These results are in the line with the finding of Roychowdhury and Tah (2011), Mostafa (2016), Mohamed *et al*.(2019)

## 5. Conclusion

Selection is an expected tool to improve branching mutant of *Helianthus annuus* plant characteristics

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## الملخص العربى

# التباين الوراثي لبعض صفات النمو الخضرى و الزهرى لطفرة نبات عباد الشمس متعددة النورات

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تم إجراء البحث الحالي لدراسة التباين الوراثي لبعض صفات النمو والإزهار لطفرة متعددة الازهار لنباتات عباد الشمس والتي تحتوي على العديد من النورات لكل نبات. أجريت هذه الدراسة خلال موسمين متتاليين في مشتل نباتات الزينة ، كلية الزراعة ، جامعة جنوب الوادي ، قنا ، مصر.

أظهرت النتائج أن التباين الوراثى و تباين الشكل المظرى و درجة توريث عالى لعدد من الصفات المدروسة مثل عدد النورات لكل نبات ، وقطر الساق ، والمساحة الورقية، والوزن الطازج للنمو الخضري ووزن ١٠٠ بذرة. تشير هذه النتائج إلى التأثير المنخفض للبيئة و ان هذه الصفات متحكم فيها وراثيا

اتضح من النتائج ان درجة التوريث بمعناه الواسع مرتفعة و التباين الجيني بدرجة متوسطة لصفة ارتفاع النبات. في حين ان التباين الجينى ودرجة التوريث بمعناه الواسع كانت متوسطة لصفات عدد الأوراق لكل نبات ، وقطر النورات ، وعدد البذور لكل قرص زهرى. لذا ، فإن الانتخاب هو وسيلة فعالة متوقعة لتحسين نمو نبات Helianthus annuus ذو الازهار المتعددة