# Allelopathy, genetic parameters and cluster analysis of some rice (*Oryza sativa* L.) genotypes

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## ABSTRACT

The present investigation was conducted at Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt during 2012 and 2013 seasons to evaluate twenty-one rice genotypes for allelopathic activity. The selected genotypes were classified into three categories, eight entries as Japonica type, nine entries as Indica and four entries as Indica/Japonica type. The results showed that some rice genotypes showed allelopathic activity against *Echinochloa crus-galli* L. (barnyard grass) in the field after planting. These varieties showed biologically active suppression of *E. crus-galli* L. by 80-90 % in the field. These genotypes are important and suitable for direct seeded rice; also it could be utilized in breeding programs to transfer this trait to commercial varieties. For agronomic traits, the most of traits under study had a wide range of variability. This range was reflected differences among these genotypes. Four genotypes namely; Giza 177, Milyang 97, Giza 181 and Suweon 339 were very early. Five genotypes namely; Giza 178, Giza 177, Milyang 97, Giza 181 and IET 1444 scored high values for harvest index. Giza 177 and Giza 178 are cultivated in more than 50% of the cultivated area with rice in Egypt. Clustering varieties, based on similarity of quantitative characteristics, produced two large groups. The first one included seven rice genotypes, *i.e.*; Giza 171, Giza 176, Suweon 339, IET 1444, IR 65598, Giza 178 and Giza 181. This group divided into two sub-groups, the first one included Giza 178 and Giza 181, which were similar in plant height, No. of tillers plant$^{-1}$, Flag leaf area, grain yield plant$^{-1}$, No. of spikelets panicle$^{-1}$ and blast reaction. The phenotypic coefficient of variability (PCV %) was higher than genotypic coefficient variability (GCV %) for all genotypes, indicating that the most portion of PCV% was more contributed by environmental conditions and cultural practices. Relatively, high genetic coefficient of variability was found to be higher for all traits, indicating that these traits might be more genetically predominant, and it would be possible to achieve further improvement in both traits. The genetic coefficient of variability refers to the additive and non-additive genetic variance which played an important role in the inheritance of these traits.

**Key words: Rice (*Oryza sativa* L.), allelopathy, cluster analysis, genetic parameters.**

## INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important cereal crops all over the world, and represents a staple food for more than half of the global population (FAO, 2009). In Egypt, rice is the second food crop after wheat, and also is the second one for cash money (Badawi, 1999).

Rice productivity has remarkably increased year after year according to the percentage replacement of the rice area with the modern varieties to realize a maximum yield average (10t ha$^{-1}$) in the year 2014 against (5.7 t ha$^{-1}$) for the period 1986-1998. Because of adopting of the new short duration rice varieties, about 30% of the irrigation water consumption was saved every year (Aidy and Maximos, 2006). However, the weeds grown in rice fields are the main suppressor of rice growth and significantly affecting rice grain yield. Also the chemical treatments or herbicides for weed control are very dangerous due to the pollution and high production costs. Allelopathy is the result of biochemical interactions between plants and represents an economic way to control weeds in rice fields. It is caused by toxic chemicals released by the plant through volatilization, leaching, and root exudation or produced during decomposition of plant residues in the soil (Chou, 1995). Allelopathic rice varieties suppress weed emergence, root and shoot development, tillering capacity and the plant canopy (Hassan and Rao, 1996). Allelopathic compounds for some weeds may be produced by other plant species. The genes responsible for such allelochemicals could be cloned and introduced through genetic transformation, leading to the development of rice cultivars with a broad spectrum of allelopathic properties against rice weeds. It should be remembered, however, that over time, weeds develop resistance to allelopathic chemicals (Khush, 1996). Success of breeding programs depends on the magnitude of genetic variability and the extent to which the advantageous characteristics are heritable (Mruthunjaya and Mahadevappa, 1993). Therefore, the study of genetic variability in rice is not only essential for selecting valuable genotypes and predicting the effect of selecting best genotypes but it will also aid breeders in simultaneous improvement of characteristics through selection (Patil *et al.*, 1993). Using quantitative traits in genetic relationships has valuable advantages, especially in rice: (i) rice has many quantitative traits with high heritability values that can be easily scored (ii) rice databases are available that can be used (Dingkhun and Asch, 1999), and (iii) computer analyses for quantitative traits are available. The study of genetic relationships is important in selection and prediction of progeny as well as for the conservation and characterization of restrained germplasm (Fahmi *et al.*, 2005).

In this study, twenty-one rice genotypes were studied for nineteen agronomic characteristics to explore their genetic variability by determining the magnitude of mean performance to calculate heritability, genotypic coefficient variability, phenotypic coefficient variability and genetic advance. Also, averages of two years of quantitative characteristics were used for constructing genetic relationships among studied rice genotypes. The genetic relationships among individuals and populations could be constructed using similarity values of some quantitative characteristics (Souza and Sorrells (1991), Zhang *et al.*, (1995), Dinghuhn and Asch (1999), Bahrman *et al.*, (1999) and El-Malky (2004).

The aims of this investigation were to evaluate twenty-one rice genotypes for allelopatic activity against *E. crus-galli* L. and study the genetic parameters and phylogenetic relationships using nineteen quantitative characteristics for the studied rice genotypes.

## MATERIALS AND METHODS

Twenty-one rice genotypes were selected to conduct this study, and were classify into three categories, eight entries as Japonica type, nine entries as Indica type and four entries as Indica/Japonica type (Table 1). All genotypes were evaluated at the experimental farm of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt, during the two rice growing seasons; 2012 and 2013.

### Studied characteristics

Nineteen quantitative characteristics were studied as following:

**Allelopathic activity:** Rice genotypes were screened in two field experiments, in 2012, 2013 to identify genotypes possessing allelopathic properties around *Echinochloa crus-galli* L. at RRTC, Sakha, Kafr Elsheikh. Pre-germinated seeds of each genotype were planted in five rows with 20cm space in 1m$^2$ plots in randomized complete block design with three replicates. Each plot was infested with the selected weed before seeding rice. Other weeds were controlled with specific herbicide applications followed by hand weeding. Plots were drained 5 days after seeding, flooded every 3-4 days, and permanently flooded 30 days after seeding. Allelopathic activity was recorded 30-40 days after seeding based on reduction in dry weight of the weeds between rows.

**Vegetative characteristics:** included days to heading, plant height (cm), No. of tillers plant$^{-1}$, flag leaf area (cm$^2$), total chlorophyll content (mg/ds$^2$); measured by using chlorophyll analytical apparatus as amount of total chlorophyll per square decimeter (chlorophyll meter 5 PAD-502 Minolta camera Co. Ltd., Japan), and blast reaction which evaluated according to the Standard Evaluation System (SES) for rice, International Rice Research Institute (IRRI, 1996).

**Yield and its component characteristics:** included No. of panicles plant$^{-1}$, grain yield plant$^{-1}$ (g), panicle weight (g), 1000-grain weight (g), No. of filled grain panicle$^{-1}$, No. of unfilled grain panicle$^{-1}$, panicle length (cm) and harvest index %.

**Grain quality characteristics:** which were hulling percentage, milling percentage, gel consistency which was determined based on the consistency of milled rice paste that has been gelatinized by boiling in dilute alkali and then cooled to room temperature, then tubes were laid horizontally on a table lined with millimeter graph paper and total length of the gel measured in millimeters, and amylose percentage. All these characteristics were calculated according to the Standard Evaluation System (SES) for rice (IRRI, 1980). Each studied genotype was grown in 10m$^2$ in a randomized complete block design (RCBD) experiment with three replicates. Weeds were chemically controlled by Saturn 50% using recommended dose. Monthly temperature and relative humidity are shown in Table (2) according to Sakha Meteorological Station.

### Cluster analysis

Genetic relationships among studied genotypes were measured by similarity of studied quantitative characteristics as reported by Zhang *et al.*, (1995), Dinghuhn and Asch (1999) and El-Malky (2004). Analysis for clustering was conducted using the Numerical Taxonomy and Multivariate Analysis system, Ver. 2.1 (NTSYS-PC; Rolhf, 2000). The output was analyzed using an agglomerative hierarchical clustering method with complete linkage strategy. Firstly, a matrix of dissimilarity values was produced and the phenotypic distance between each pair of lines was estimated as Euclidean distance. Secondly, cluster analysis was then conducted on the Euclidean distance matrix with un-weighed pair-group method based on arithmetic average (UPGMA) to develop a dendogram.

**Table 1: The studied twenty-one rice genotypes with their parentage, origin and types.**

| No. | Entries | Parentage | Origin | Types |
|---|---|---|---|---|
| 1 | Giza 177 | Giza 171 / Yamji No.1 //PiNo.4 | Egypt | Japonica |
| 2 | Giza 178 | Giza 175 / Milyang 49 | Egypt | Indica/Japonica |
| 3 | Dular | Dumai / Larkoch | IRRI | Indica |
| 4 | TKY 1014 | J692153X / Fukunishi // Taichung | China | Japonica |
| 5 | Giza 181 | IR 28 / IR 22 | Egypt | Indica |
| 6 | IET 1444 | TN1 / Co29 | India | Indica/Japonica |
| 7 | IET 11754 | na* | India | Indica/Japonica |
| 8 | Suweon 339 | SR 9373-71-3 / Pungsan Byeo | Korea | Japonica |
| 9 | IR 65598 | na | IRRI | Indica |
| 10 | IR 65603 | na | IRRI | Indica |
| 11 | IR 31775-30-3-2-2 | IR 10154-23-3-3 / IR 9129-209-2-2 | IRRI | Indica |
| 12 | IR 2037-93-1-3-1-1 | IR 1697-47-2-2 / IR 1818-2 | IRRI | Indica |
| 13 | IR 62155-138-3-3-2 | na | IRRI | Indica |
| 14 | IR 29 | IR833-6-1-1/IR1561-149-1//IR1737 | IRRI | Indica |
| 15 | Giza 171 | Nahda / Calady 40 | Egypt | Japonica |
| 16 | Giza 176 | Calrose 76 / Giza 172 // GZ 14 | Egypt | Japonica |
| 17 | Giza 159 | Giza 14 / Agami M1 | Egypt | Japonica |
| 18 | Agami | Pure line selection | Egypt | Japonica |
| 19 | Milyang 97 | na | Korea | Japonica |
| 20 | GZ 1368-S-5-4 | IR 1615-31-3 / BG 94-2 | Egypt | Indica/Japonica |
| 21 | IR 65829-28-H-P | GZ 2175 / GYEHWA 7 | IRRI | Indica |

* na, not available.

**Table 2: Monthly average temperature and relative humidity at RRTC, Sakha, Kafr Elsheikh for the two rice growing seasons 2012 and 2013.**

| Month | Temperature (°c) | | | | Relative humidity (%) | |
|---|---|---|---|---|---|---|
| | 2012 | | 2013 | | 2012 | 2013 |
| | Max. | Min. | Max. | Min. | | |
| April | 26.04 | 15.87 | 27.50 | 16.40 | 43.90 | 42.85 |
| May | 31.43 | 21.81 | 30.47 | 19.57 | 45.78 | 48.60 |
| June | 32.44 | 23.97 | 32.65 | 20.60 | 51.27 | 52.30 |
| July | 32.32 | 24.31 | 33.15 | 23.64 | 54.70 | 55.11 |
| August | 33.79 | 24.76 | 34.10 | 21.80 | 60.63 | 53.50 |
| September | 32.50 | 22.93 | 32.49 | 20.67 | 56.60 | 52.20 |
| October | 27.79 | 19.42 | 29.75 | 18.75 | 57.36 | 53.39 |
| November | 27.34 | 18.91 | 28.43 | 18.20 | 55.34 | 52.67 |

**Statistical analysis and Genetic parameters**

The analysis of variance was computed using IRRISTAT for Windows statistical program Ver. 5 (IRRI, 2005). Estimation of genotypic variance ($б^2$ g), environmental variance ($б^2$ e), phenotypic variance ($б^2$ ph) and percentage of genotypic (GCV %) and phenotypic (PCV%) coefficients of variability were computed according to the formula suggested by Burton (1952). Genetic advance upon selection ($\Delta G$) as percentage of the mean ($\Delta G$ %) was computed according to Johanson *et al.*, (1955). All recommended agricultural practices were applied for the permanent rice field.

## RESULTS AND DISCUSSION.

In this study twenty-one rice genotypes (Tables 1 and 3) originating from different sources were evaluated for allelopathic activity against *E. crus-galli* L. and also eighteen quantitative characteristics in direct seeded rice experiment.

**1- Allelopathic activity**

The obtained results showed that some rice genotypes had allelopathic activity against *E. crus-galli* L. at the field after planting (Table 3). These genotypes had the biological capability to suppress germination and growth of *E. crus-galli* L. by 65-90 % at the field. The most of these genotypes are indica and indica/japonica types and demonstrate their allelopathic properties at 3-4 leaf stage. The mechanism is to inhibit the root development and emergence at first or second leaf stage of the weed. So, it could be suggested and recommended that these genotypes are very useful as allelopathic rice genotypes suitable for direct seeded rice.

The highest activity was recorded for IR 62155-138-3-3-2 (90%) followed by TKY 1014 (89%), IR 31775-30-3-2 (88%), GZ 1368-S-5-4 (88%), IR 65829-28-H-P (85%), IET 1444 (80%) and IR 2037-93-1-3-1-1 (80%). Moreover, incorporating residues of some of these genotypes in the soil reduced soil seed bank of *E. crus-galli* L. These genotypes could be utilized in breeding programs as donors of this trait. On the other hand, five genotypes namely; Dular, IET 11754, IR 65598, Giza 159 and Giza 181 scored allelopathic activity ranged from 70% to 78%. The rest of the studied genotypes were non-allelopathic and that was very clearly for Giza 176, which scored zero allelopathic activity. Similar results were obtained by Hassan and Rao, (1996) and Hassan and Abou El-Darag, (2000).

**2- Vegetative characteristics**

Twenty-one rice genotypes were evaluated in two seasons under Egyptian conditions and the mean performances of these genotypes for vegetative characteristics are presented in Table (4). Results showed that, the most of the characteristics under study had a wide range of variability. This range was reflected that four genotypes namely; Giza 171, Giza 176, Giza 159 and Agami were highly susceptible to blast reaction and these varieties are old Egyptian varieties, the other genotypes were resistant to blast reaction. As for short duration, varieties Giza 177, Milyang 97, Giza 181 and Suweon 339 were very early and scored 93, 95, 97 and 98 days to heading, respectively, and could be utilized in breeding programs for earliness. For plant height, the results showed that eight genotypes (IR65603, Giza 181, IR 65598, Giza 178, Suweon 339, Milyang 97, Giza 177 and IR 29) were short stature and could be utilized as donors for this trait.

For No. of tillers plant$^{-1}$ both genotypes Giza 178 and Giza 181 recorded the highest values and also were resistant to blast. Generally, the varieties Giza 177, Giza 178 and Giza 181 were the best varieties for all studied vegetative characteristics and could be utilized as donors for transfer these characteristics in breeding programs. Similar results were obtained for most studied traits by El-Abd and Abdalla (2004); Babu *et al.*, (2006); Hammoud, (2005); Hammoud *et al.*, (2006 and 2008), and Mohapatra and Mohanty, (2008).

**3- Yield and its component characteristics**

Eight characteristics were investigated for the twenty-one rice genotypes and the results are presented in Table (5). The genotypes Giza 178, Giza 181, IET 11754 and Dular scored the highest values for No. of panicle plant$^{-1}$ (24 panicles), panicle weight (3.84 g), No. of filled grains panicle$^{-1}$ (200 grains) and panicle length (28 cm), respectively. These genotypes could be utilized as donors for these characteristics.

**Table 3: Twenty-one rice genotypes with origin, types and weed control percentage.**

| No. | Entries | Origin | Types | Weed Control % |
|---|---|---|---|---|
| 1 | Giza 177 | Egypt | Japonica | 40 |
| 2 | Giza 178 | Egypt | Indica -Japonica | 66 |
| 3 | Dular | IRRI | Indica | 70 |
| 4 | TKY 1014 | Japan | Japonica | 89 |
| 5 | Giza 181 | Egypt | Indica | 78 |
| 6 | IET 1444 | Indian | Indica -Japonica | 80 |
| 7 | IET 11754 | India | Indica -Japonica | 70 |
| 8 | Suweon 339 | Korea | Japonica | 27 |
| 9 | IR 65598 | IRRI | Indica | 73 |
| 10 | IR 65603 | IRRI | Indica | 65 |
| 11 | IR 31775-30-3-2-2 | IRRI | Indica | 88 |
| 12 | IR 2037-93-1-3-1-1 | IRRI | Indica | 80 |
| 13 | IR 62155-138-3-3-2-2 | IRRI | Indica | 90 |
| 14 | IR 29 | IRRI | Indica | 45 |
| 15 | Giza 171 | Egypt | Japonica | 39 |
| 16 | Giza 176 | Egypt | Japonica | 0 |
| 17 | Giza 159 | Egypt | Japonica | 74 |
| 18 | Agami | Egypt | Japonica | 30 |
| 19 | Milyang 97 | Korea | Japonica | 35 |
| 20 | GZ 1368-S-5-4 | Egypt | Indica -Japonica | 88 |
| 21 | IR 65829-28-H-P | IRRI | Indica | 85 |
| L.S.D. | 0.05 | | | 0.80 |
| | 0.01 | | | 1.15 |

**Table 4: Mean performance of 21 rice genotypes for six vegetative morphological characteristics.**

| Entries | | BR | DH | Ht | TiP | FLA | Chl |
|---|---|---|---|---|---|---|---|
| Giza 177 | | 2 | 93 | 99 | 21 | 34 | 29 |
| Giza 178 | | 2 | 105 | 97 | 26 | 38 | 37 |
| Dular | | 1 | 115 | 120 | 19 | 37 | 32 |
| TKY 1014 | | 2 | 118 | 112 | 24 | 42 | 37 |
| Giza 181 | | 1 | 97 | 95 | 26 | 43 | 27 |
| IET 1444 | | 2 | 107 | 108 | 25 | 38 | 28 |
| IET 11754 | | 2 | 109 | 107 | 24 | 37 | 29 |
| Suweon 339 | | 2 | 98 | 97 | 24 | 30 | 33 |
| IR 65598 | | 2 | 107 | 96 | 18 | 52 | 40 |
| IR 65603 | | 2 | 108 | 89 | 21 | 41 | 35 |
| IR 31775-30-3-2-2 | | 2 | 107 | 85 | 22 | 39 | 34 |
| IR 2037-93-1-3-1-1 | | 2 | 119 | 112 | 21 | 46 | 33 |
| IR 62155-138-3-3-2-2 | | 2 | 117 | 107 | 22 | 42 | 36 |
| IR 29 | | 1 | 104 | 100 | 20 | 49 | 34 |
| Giza 171 | | 7 | 122 | 134 | 23 | 32 | 33 |
| Giza 176 | | 6 | 112 | 104 | 25 | 31 | 34 |
| Giza 159 | | 7 | 115 | 113 | 24 | 37 | 41 |
| Agami | | 6 | 110 | 108 | 19 | 32 | 40 |
| Milyang 97 | | 2 | 95 | 98 | 19 | 25 | 33 |
| GZ 1368-S-5-4 | | 2 | 110 | 104 | 22 | 38 | 39 |
| IR 65829-28-H-P | | 2 | 112 | 94 | 23 | 45 | 37 |
| L.S.D. | 0.05 | 0.37 | 0.48 | 0.61 | 2.68 | 2.68 | 3.47 |
| | 0.01 | 0.53 | 0.69 | 0.87 | 3.85 | 3.85 | 5.00 |

Abbreviations: BR, Blast Reaction; DH, Days to Heading; Ht, Plant Height (cm); TiP, No. Tillers Plant$^{-1}$; FLA, Flag Leaf Area (cm$^2$); Chl, Chlorophyll content (mg/ds$^2$).

**Table 5: Mean performances of 21 rice genotypes for yield and its component characteristics.**

| Genotypes | | PaP$^{-1}$ | PnL | PaW | NFG | NUG | TGW | GYP$^{-1}$ | HI% |
|---|---|---|---|---|---|---|---|---|---|
| Giza 177 | | 19 | 20 | 3.30 | 120 | 5.41 | 27.3 | 39 | 50 |
| Giza 178 | | 24 | 24 | 3.58 | 198 | 6.18 | 22.1 | 41 | 55 |
| Dular | | 17 | 28 | 2.70 | 156 | 17.0 | 30.0 | 41 | 33 |
| TKY 1014 | | 22 | 24 | 3.30 | 184 | 5.10 | 32.0 | 35 | 45 |
| Giza 181 | | 23 | 25 | 3.84 | 176 | 8.71 | 26.5 | 46 | 49 |
| IET 1444 | | 22 | 25 | 3.56 | 181 | 3.80 | 23.7 | 36 | 47 |
| IET 11754 | | 21 | 21 | 2.97 | 200 | 3.60 | 24.0 | 43 | 44 |
| Suweon 339 | | 19 | 19 | 3.61 | 152 | 13.6 | 22.2 | 44 | 44 |
| IR 65598 | | 17 | 24 | 3.75 | 145 | 28.1 | 22.5 | 32 | 33 |
| IR 65603 | | 19 | 24 | 3.44 | 121 | 5.78 | 27.3 | 33 | 41 |
| IR 31775-30-3-2-2 | | 20 | 23 | 3.50 | 168 | 4.90 | 30.0 | 32 | 42 |
| IR 2037-93-1-3-1-1 | | 21 | 27 | 2.70 | 139 | 17.0 | 28.0 | 39 | 39 |
| IR 62155-138-3-3-2 | | 20 | 25 | 2.90 | 188 | 21.0 | 24.0 | 47 | 31 |
| IR 29 | | 18 | 22 | 2.19 | 99 | 13.5 | 22.7 | 45 | 41 |
| Giza 171 | | 21 | 23 | 3.40 | 158 | 6.34 | 26.7 | 42 | 38 |
| Giza 176 | | 23 | 24 | 3.48 | 156 | 9.66 | 27.1 | 40 | 40 |
| Giza 159 | | 20 | 24 | 2.81 | 112 | 9.80 | 26.5 | 39 | 40 |
| Agami | | 17 | 16 | 2.26 | 119 | 12.6 | 23.7 | 34 | 38 |
| Milyang 97 | | 18 | 24 | 3.03 | 115 | 8.21 | 25.4 | 33 | 50 |
| GZ 1368-S-5-4 | | 20 | 21 | 2.49 | 110 | 11.4 | 21.6 | 42 | 43 |
| IR 65829-28-H-P | | 22 | 25 | 3.70 | 144 | 5.65 | 29.0 | 32 | 43 |
| L.S.D. | 0.05 | 2.22 | 1.38 | 0.79 | 7.32 | 3.76 | 0.68 | 3.55 | 3.18 |
| | 0.01 | 3.19 | 1.99 | 1.13 | 10.53 | 5.42 | 0.98 | 5.11 | 4.57 |

Abbreviations: PaP$^{-1}$, No. of panicles plant$^{-1}$; PaW, panicle weight (g); NFG, No. of filled grains panicle$^{-1}$; NUG, No. of unfilled grains panicle$^{-1}$; PnL, panicle length (cm); TGW, 1000-grain weight (g); GYP$^{-1}$, grain yield plant$^{-1}$ (g); HI%, harvest index %.

The lowest value for No. of unfilled grains panicle$^{-1}$ was recorded with IET 11754 (3.6 grains). For 1000-grain weight, six genotypes recorded high values and the highest was TKY 1014 (32.0 g). For grain yield plant$^{-1}$, nine genotypes yielded more than 40g plant$^{-1}$ and the highest values recorded for IR 62155-138-3-3-2 (47 g), and Giza 181 (46 g). For harvest index %, five genotypes namely; Giza 178, Giza 177, Milyang 97, Giza 181 and IET 1444 scored the highest values. The highest varieties were Giza 178 (55) and Giza 177 (50) which cultivated at about 50% of the total rice area in Egypt. Same results were obtained for most studied characteristics by El-Abd and Abdalla (2004), Babu *et al* (2006), Hammoud (2005), Hammud *et al* (2006 and 2008), and Mohapatra and Mohanty (2008).

**4- Grain quality characteristics**

Four grain quality characteristics were investigated; the results are presented in Table (6). For hulling percentage, the results showed that the percentage of hulling was ranged from 74% to 81% and the highest value was for Giza 177, while the lowest values were for Agami and GZ 1368. Also, Giza 177 scored the highest value for milling percentage (74%). For gel consistency, if it is hard, then cooked rice tends to be less sticky. Harder gel consistency is associated with harder cooked rices and this feature is particularly evident in high-amylose rice. While, if gel consistency is soft, then cooked rice has a higher degree of tenderness. This is a preferred characteristic. The trend of classification is hard ranged from 27-35, medium hard 36-40, medium 41-60 and soft 61-100 length of gel (mm). The results in Table (6) showed that the three genotypes; *i.e.*, Giza 181, IR 65603 and IR 29 were belonged to medium gel consistency and ranged from 45 to 49 (mm) length of the gel. While, the other genotypes belonged to soft categories are ranged from 62 to 93 (mm) length of the gel.

The amylose content % for the studied genotypes is presented in Table (6). The results showed that the amylose % was ranged from 17 to 28%, with a mean value of 17%. Both genotypes Giza 171 and IR 65598 had the highest percentages of amylose %, followed by IR 29, IR 65603, IET 1444 and Giza 181. Generally, the amylose % of starches usually ranges from 15 to 35%. High amylose content rice has high volume expansion (not necessarily elongation) and high degree of flakiness. The cooked grains are dry, less tender and become hard upon cooling. In contrast, low-amylose cooked rice is moist and sticky. Intermediate amylose rice is preferred in most rice-growing areas. Similar results were obtained by Magdy *et al.*, (2010) and Oko *et al.*, (2012).

**5-Cluster analysis for studied genotypes based on quantitative characteristics**

The characteristics used for this analysis were the same agronomic quantitative characteristics. Normality was checked for all traits, which indicated that all traits had good approximations of normal distributions (Fahmi *et al.*, 2005 and El-Malky *et al.*, 2013).

**Table 6: Mean performance of 21 rice genotypes for grain quality characters.**

| Genotypes | | Hulling% | Milling% | Gel Consistency | Amylose% |
|---|---|---|---|---|---|
| Giza 177 | | 81 | 74 | 79 | 18 |
| Giza 178 | | 77 | 71 | 64 | 21 |
| Dular | | 76 | 63 | 44 | 24 |
| TKY 1014 | | 79 | 72 | 71 | 19 |
| Giza 181 | | 78 | 71 | 49 | 23 |
| IET 1444 | | 79 | 72 | 92 | 24 |
| IET 11754 | | 78 | 71 | 61 | 23 |
| Suweon 339 | | 76 | 68 | 93 | 20 |
| IR 65598 | | 76 | 67 | 48 | 28 |
| IR 65603 | | 77 | 71 | 64 | 26 |
| IR 31775-30-3-2-2 | | 77 | 71 | 64 | 28 |
| IR 2037-93-1-3-1-1 | | 77 | 65 | 41 | 27 |
| IR 62155-138-3-3-2 | | 79 | 65 | 44 | 28 |
| IR 29 | | 75 | 68 | 45 | 27 |
| Giza 171 | | 80 | 73 | 68 | 17 |
| Giza 176 | | 79 | 71 | 71 | 19 |
| Giza 159 | | 78 | 70 | 72 | 18 |
| Agami | | 74 | 69 | 62 | 22 |
| Milyang 97 | | 77 | 69 | 72 | 21 |
| GZ 1368-S-5-4 | | 74 | 71 | 70 | 20 |
| IR 65829-28-H-P | | 78 | 70 | 63 | 26 |
| L.S.D. | 0.05 | 2.48 | 2.62 | 0.54 | 0.25 |
| | 0.01 | 3.57 | 3.76 | 0.78 | 0.36 |

Clustering genotypes, based on similarity of quantitative characteristics, produced two large groups (Figure 1). The first one included almost Japonica genotypes and divided into two sub-groups, the first sub-group included three rice genotypes; *i.e.*,Giza 177, Milyang 97 and Agmi which were similare in non allolopathy, No. of tillers plant$^{-1}$, No. of panicles plant$^{-1}$, No. of filled grains panicle$^{-1}$ and harvest index %. While, the second sub-group included three genotypes; *i.e.*, Suweon 339, Giza 176 and Giza 171 in one branch, these genotypes had the highest stature.

The second large group divided into two sub-groups, the first one included Dular, IR 2037-93-1-3-1-1 and IR 65598 these genotypes were similare in allolopathy, resistance to blast, days to heading, No. of tillers plant$^{-1}$, hulling percentage, milling percentage, gel consistency and amylose percentage, while the second sub-group divided into two sub-sub groups the first one included two indica genotypes; *i.e.*, IR 65598 and IR 65603 which were similare in allolopathy, days to heading, plant height, flage leaf area, grain yield plant$^{-1}$, panicle weight, gel consistency and amylose percentage, while the second sub-sub group included Giza 159 and GZ 1368 these two genotypes are belnoged to Japonica and Indica/Japonica types and similare in allolopathy, plant height, flage leaf area, chlorophll content, No. of panicles plant$^{-1}$, panicle weight, No. of filled grains panicle$^{-1}$, No. of unfilled grains panicle$^{-1}$ and amylose percentage. Meanwhile, the second sub-group divided into two sub-sub groups the first one included IR 62155 and IR 29 which were indica type and similar in blast reaction, days to heading, flage leaf area, chlorphll content, grain yield plant$^{-1}$, hulling percentage, milling percentage, gel consistency and amylose percentage. While, the second one incuded TKY 1014 and IET 1444 in one branch this is due to the similarity in allolopathy, blast reaction, No. of tillers plant$^{-1}$, No. of panicles plant$^{-1}$, grain yield plant$^{-1}$, panicle weight, No. of filled grains panicle$^{-1}$, harvest index %, hulling percentage and milling percentage. Also, the genotypes Giza 178 and IET 11754 were in one branch because these two genotypes are belonged to Indica/Japonica type and were similar in allolopathy, blast resistant, days to heading, plant height, flage leaf area, panicle weight, 1000-grain weight, No. of filled grains panicle$^{-1}$ and amylose percentage. The last branch included Giza 181 and IR 31775, which were Indica type and similar in allolopathy, blast resistant, plant height, panicle weight and milling percentage.

**6- Genetic parameters for yield characteristics**

The results of genotypic variance, phenotypic and genotypic coefficient of variability percentages, heritability and genetic advance percentage for all characteristics are presented in Table (7). The studied twenty-one rice genotypes showed a wide range of mean performances. Mean square estimates for all studied characteristics of all genotypes were highly significant, thus the selection for these characteristics among these genotypes would be effective to improve the performance of these genotypes. Similar results were obtained by Han *et al.,* (1995), Tang (1995); Veillet *et al.,* (1996); Hammoud *et al.,* (2012) and El-Malky *et al.,* (2013).

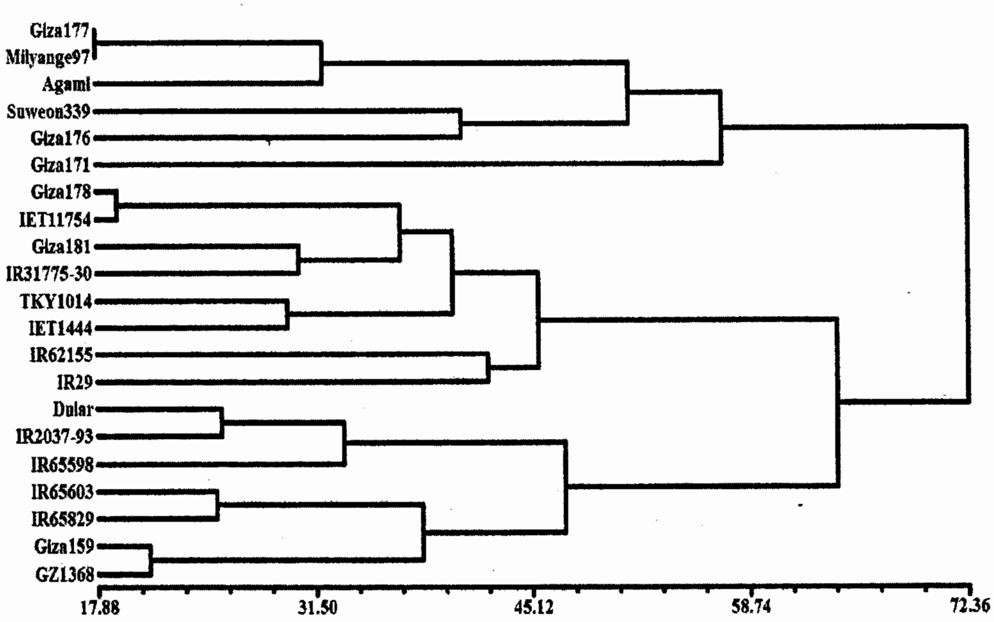


**Figure 1: Cluster diagram for the studied 21 rice genotypes classified by nineteen quantitative characteristics.**

**Table 7: Estimates of genetic parameters for nineteen quantitative characteristics for the studied rice genotypes.**

| Traits | MS | (MSe) | Grand Mean | GV | PV | GCV | PCV | $H_{bs}$ | GA | GA% |
|---|---|---|---|---|---|---|---|---|---|---|
| Blast reaction | 10.6 | 0.07 | 3 | 3.5 | 3.6 | 71.6 | 72.3 | 97.9 | 3.8 | 116.3 |
| Days to heading | 186.3 | 0.12 | 109 | 62.1 | 62.2 | 7.2 | 7.2 | 99.8 | 16.2 | 56.9 |
| Plant height (cm) | 357.2 | 0.19 | 104 | 119.0 | 119.2 | 10.5 | 10.5 | 99.8 | 22.5 | 114.4 |
| No. of tillers plant$^{-1}$ | 17.3 | 3.79 | 22 | 4.5 | 8.3 | 9.5 | 12.9 | 54.3 | 3.2 | 20.4 |
| Flag leaf area (cm$^2$) | 130.3 | 3.80 | 39 | 42.2 | 45.9 | 16.8 | 17.5 | 91.8 | 12.8 | 108.1 |
| Chlorophyll content | 44.9 | 6.38 | 34 | 12.8 | 19.2 | 10.4 | 12.7 | 66.8 | 6.0 | 37.8 |
| No. of panicles plant$^{-1}$ | 12.9 | 2.60 | 20 | 3.5 | 6.1 | 9.3 | 12.3 | 57.0 | 2.9 | 17.3 |
| Grain yield plant$^{-1}$ | 73.1 | 6.67 | 39 | 22.2 | 28.8 | 12.1 | 13.8 | 76.9 | 8.5 | 56.8 |
| Panicle weight(g) | 0.4 | 0.33 | 4 | 0.02 | 0.4 | 4.4 | 17.6 | 6.4 | 0.1 | 0.6 |
| 1000-grain weight(g) | 26.6 | 0.25 | 26 | 8.8 | 9.0 | 11.5 | 11.6 | 97.3 | 6.0 | 33.9 |
| Filled grains panicle$^{-1}$ | 2871.1 | 28.37 | 151 | 947.8 | 976.2 | 20.4 | 20.7 | 97.1 | 62.5 | 627.7 |
| Unfilled grains panicle$^{-1}$ | 120.0 | 7.51 | 10 | 37.5 | 45.0 | 58.5 | 64.1 | 83.3 | 11.5 | 375.1 |
| Panicle Length (cm) | 24.2 | 1.01 | 23 | 7.7 | 8.7 | 12.3 | 13.0 | 88.4 | 5.4 | 34.0 |
| Harvest index % | 109.9 | 5.33 | 42 | 34.9 | 40.2 | 13.9 | 15.0 | 86.7 | 11.3 | 82.5 |
| Hulling % | 9.8 | 3.25 | 78 | 2.2 | 5.4 | 1.9 | 3.0 | 40.1 | 1.9 | 2.8 |
| Milling % | 14.7 | 3.62 | 69 | 3.7 | 7.3 | 2.8 | 3.9 | 50.6 | 2.8 | 5.3 |
| Gel consistency | 643.7 | 0.16 | 64 | 214.5 | 214.7 | 23.0 | 23.0 | 99.9 | 30.2 | 337.3 |
| Amylose % | 40.2 | 0.03 | 23 | 13.4 | 13.4 | 16.1 | 16.2 | 99.8 | 7.5 | 58.9 |
| Weed control % | 1683.7 | 0.34 | 61 | 561.1 | 561.5 | 39.2 | 39.2 | 99.9 | 48.8 | 927.5 |

Abbreviations: MS, Mean squares; GV, Genotypic variance; PV, Phenotypic variance; GCV, Genotypic coefficient of variability; PCV, Phenotypic coefficient of variability; $H_{bs}$, Heritability (broad sense); GA, Genetic advance; GA%, Genetic advance %.

The phenotypic coefficient of variability (PCV %) was higher than genotypic coefficient of variability (GCV %) for all genotypes, indicating that the most portion of PCV % was more contributed to environmental conditions and cultural practices. Relatively, genetic coefficient of variability was found to be higher for all studied characteristics, indicating that these characteristics might be more genotypically predominant, and it would be possible to achieve further improvements. The genetic coefficient of variability refers to the additive and non-additive genetic variance which played an important role in the inheritance of these characteristics. These results are in agreement with those obtained by Han *et al.,* (1995); Tang (1995); Veillet *et al.,* (1996); Hammoud *et al.,* (2012) and El-Malky *et al.,* (2013).

Heritability and genetic advance under selection were computed and the obtained results are illustrated in Table (7). High estimates of heritability were found in all characteristics except for panicle weight. These results indicated that the presence of both additive and non additive genetic variance in the inheritance of most traits except panicle weight and also these traits were stable under different conditions and culture practices. Therefore, it could be concluded that selection procedures could be successful to improve the most of studied characteristics. Same results were previously obtained by Han *et al.,* (1995); Tang (1995); Veillet *et al.,* (1996); Hammoud *et al.,* (2012) and El-Malky *et al.,* (2013).

Genetic advance under selection which presented in (Table 7) showed the possible gain from selection when the most desirable 5% of the plants are selected. Relatively, moderate genetic gains were obtained for grain yield, which scored more than 20%. Low genetic advance were found in remaining characteristics which were less than 10%. Johnson *et al* (1955) revealed that heritability estimates along with genetic gain upon selection were more valuable than the former alone in predicting the effect of selection. On the other hand, Dixit *et al.* (1970) pointed out that high heritability is not always associated with high genetic gain, but in order to make effective selection, high heritability should be associated with high genetic gain. In this investigation, high genetic gain was found to be associated with high heritability estimates. Consequently, selection for these traits should be effective and satisfactory for successful breeding purposes. Moderate estimates of both heritability and genetic advance were obtained for plant height and grain yield. Therefore, selection for these two characteristics using these two genetic parameters will be effective, but probably with less success than for the former characteristics. Low genetic gain was associated with low heritability values for the rest of the characteristics studied. Hence, selection for these traits would be of less effectiveness. Similar results were obtained by Han *et al.,* (1995); Tang (1995); Veillet *et al.,* (1996); Hammoud *et al.,* (2012) and El-Malky *et al.,* (2013).

## REFERENCES

Aidy, I. R. and M. A. Maximos (**2006**). Rice varietal improvement in Egypt during the last two decades: achievements and future strategies. Egypt, J. Agric. Res., **83**(5A): 23-30.

FAO (**2009**). Food and Agriculture Organization of the United Nations. The state of food security in the world. pp. 1-30.

Babu, V. R.; S. Kishore; N. Shobha Rani and Ravichandran (**2006**). Genetic divergence analysis using quality traits in rice genotypes (*Oryza sativa* L.). Oryza, **43** (**4**): 260-263.

Badawi, A.T. (**1999**). The final report of the national campaign of rice in Egypt (**1998** season). Ministry of Agriculture and the Academy of Scientific Research and Technology, Cairo, Egypt (*In Arabic*).

Bahraman, N.; J.L. Gouis; D. Hariri; L. Guilbaud and L. Jestin (**1999**). Genetic diversity of old French six-rowed winter barley cultivars assessed with molecular, biochemical and morphological markers and its relation to BaMMV resistance. Heredity, **83**: 568-574.

Burton, G.W. (**1952**). Quantitatative inheritance in grasses. Proc 6th Int. Grassid Congr. **1**: 277-283.

Chou, C.H. (**1995**). Allelopathic compounds as naturally occurring herbicides. Proceedings of the 15th Asian-Pacific Weeds Control Conference, Tsukuba, Japan, pp. 154-159.

Dingkhun, M. and F. Asch (**1999**). Phenological responses of *Oryza sativa* L., *O. glaberrima* and inter-specific rice varieties on a top sequence in West Africa. Euphytica, **110**: 109-126.

Dixit, P.K.; P.D. Saxena and L.K. Bhatia (**1970**). Estimation of genotypic variability of some quantitative characters in groundnut. Indian J. Agric. Sci. **40**: 192-201.

El-Abd, A. B. and A. A. Abd Allah (**2004**). Genetic behavior of some grain quality characters in rice (*Oryza sativa* L.). Egyptian Journal of Agricultural Research, **82**(**1**): 167-182.

El-Malky, M.M. (2004). Genetic studies on blast disease resistance in rice (*Oryza sativa* L.). *Ph.D.* Thesis, Fac. of Agric. Menofiya Univ., Egypt.

El-Malky, M.M.; M.M. El-Habashy; S.A.A. Hammoud and M.R. Shreif (**2013**). Genetic studies of some rice varieties for rice stem borer (*Chilo agamemnon* Bles.) and agronomic characters under Egyptian condition. Egypt. J. Plant breeding, **17**(**2**): 196-212.

Fahmi, A. I.; I. R. Aidy; H. H. Nagaty and M. M. El-Malky (**2005**). Studies on combining ability and genetic relationship among some Egyptian and exotic rice varieties. Egypt. J. Agric. Res., **83** (**5A**): 204-231.

Hammoud, S. A. A. (**2005**). Genetic behavior of some agronomic characters in two rice crosses. Egypt. J. Agric. Res. **83**(**5B**): 305-321.

Hammoud, S.A.A.; A.B. Khattab; S.E.M. Sedeek and A.B. El-Abd (**2006**). Genetic Analysis of grain yield, panicle traits and some grain quality in rice (*Oryza Sativa* L.). Proceedings of the 1st Field Crops Conference. Field Crops Research Institute, Egypt, pp. 157-170.

Hammoud, S.A.A; I.S.M. El-Degwy; S.E.M. Sedeek and B.A. Zayed (**2008**). Line x Tester analysis for some quantitative traits in rice. Proceedings of the 2nd Field Crops Conference. Field Crops Research Institute, Egypt, pp 121-140.

Hammoud, S.A.A; S.E.M. Sedeek; I.O.A. Rewaniy and R.A. El-Namaky (**2012**). Genetic behavior of some agronomic traits, blast disease and stem borer resistance in two N levels. J. Agric. Res., Kafr Elsheikh Univ., Egypt, **38**(**1**): 83-105.

Han, Q.L.; P. Zhuang; Z.H. Tang; Q.F. Han; P.J. Zhuang and Z.H. Tang (**1995**). Estimation of realized heritability of resistance to penetration rice stem borer *Chilo suppressalis*. Acta. Entomology. Academia Sinca, **38** (**4**): 402-406, (*In Chines*).

Hassan, S.M. and A.N. Rao (**1996**). Weed management in rice in the Near East. *In* Weed Management in Rice. A.B. Auld and K.U. Kim, *eds*. FAO Plant Prod. Prot. **139**: 141-156.

Hassan, S.M. and I.H. Abou El-Darag (**2000**). Weed management in rice. Annual report for **1999**. *In* proceedings of the 4th National Rice Research and Development Program Workshop. Rice Research and Training Center, Sakha, Kafr El-Sheikh, Egypt.

IRRI (**1980**). Alkali digestion, *In* Standard Evaluation System for rice: International Rice Testing Program, 2nd *Ed.*, IRRI, Manila, Philippine, pp: 43-44.

IRRI (**1996**). Standard Evaluation System (SES) for rice. 3rd *ed.* International Rice Research Institute (IRRI), Los Banos, Philippines.

IRRI (**2005**). IRRISTAT for Windows, version 5. International Rice Research Institute, Los Banos, Philippines.

Johnson, H.W.; H.F. Robinson and R.E. Comstock (**1955**). Estimates of genetic and environmental variability in soybean. Agron. J. 47: 314-318.

Khush, G.S. (**1996**). Genetic improvement of rice for weed management. Pages 201-207 *in* Herbicides in Asian rice: transitions in weed management. R. Naylor, ed. Institute for International Studies, Stanford University, California and International Rice Research Institute, Philippines.

Magdy, S.A.; E.A. Beltagi; S. Hossam; A.M. Mona; T.M. Amera and N.A. Sohir (**2010**). Effect of amylose content and pre-germinated brown rice on serum blood glucose and lipids in experimental animals. Australian Journal of Basic and Applied Sciences **4**:114–121.

Mohapatra, K.C. and H.K. Mohanty (**2008**). Inheritance of some quantitative characters including heterosis in rice by combining ability analysis. Rice Genetics **1**: 579-591.

Mruthunjaya, C.W. and M. Mahadevappa (**1993**). Genetic variability, heritability and genetic advance for yield and its contributing characters in ratoon crop of rice (*Oryza sativa* L.). Mansore J Agric. Sci., **29**: 285-288.

Oko, A.O.; B.E. Ubi.; A.A. Efisue and N. Dambaba (**2012**). Comparative analysis of the chemical nutrient composition of selected local and newly introduced rice varieties grown in Ebonyi State of Nigeria. International Journal of Agriculture and Forestry. **2(2)**: 16-23

Patil, P.A.; C.R. Mahajan; S.S. Mehetre and D.N. Hajare (**1993**). Analysis of variability and heritability in upland rice. Oryza, **30**: 154-156.

Rohlf, F.J. (**2000**). NTSYS-PC manual Exeter Software, Setauket, New York.

Souza, E. and M.E. Sorrells (**1991**). Relationships among 70 North American Oat germplasms: 1. Cluster analysis using quantitative characters. Crop Sci. **31**: 599-605.

Tang, Z.H. (**1995**). Estimation of realized heritability of resistance to penetration in rice stem borer *Chilo suppressalies*. Entomology. Science. **38(1)**: 233-235.

Veillet, S.; M.C. Filippi and A. Gallais (1996). Combined genetic analysis of partial blast resistance in an upland rice population and recurrent selection for line and hybrid values. Appli. Genet. 92: 644-653.

Zhang, Q.; Y.J. Gao; M.A. Saghai Maroof; S.H. Yang and J. X. Li (**1995**). Molecular divergence and hybrid performance in rice. Molecular Breeding, **11**: 133-142.

## الملخص العربى

# الأليلوباثي، المكونات الوراثية وتحليل القرابة الوراثية لبعض التراكيب الوراثية من الأرز

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أجري هذا البحث بمركز البحوث والتدريب في الأرز، سخا، كفرالشيخ، مصر خلال موسمي الزراعة ٢٠١٢ و٢٠١٣ لتقييم واحد وعشرون تركيباً وراثياً من الأرز لصفة الأليلوباثي وعدد من الصفات الوراثية الأخرى. وقد تم تقسيم التراكيب الوراثية المنتخبة للدراسة الي ثلاث أقسام؛ ثمانية تتبع الطراز الياباني، تسعه تتبع الطراز الهندي وأربعة تتبع الطراز الهندي/الياباني. وقد أوضحت النتائج المتحصل عليها أن بعض التراكيب الوراثية المدروسة أظهرت نشاط أليلوباثي لمقاومة حشيشة الدنيبة *E. crus-galli* L. في الحقل بعد الزراعة. وأظهرت هذه الأصناف تثبيطاً بيولوجياً لهذه الحشيشة يقدر بـــ ٨٠ – ٩٠% في الحقل. وتعتبر هذه الأصناف مهمة ومناسبة لطريقة الزراعة بالبذرة مباشرةً وكذلك يمكن إستخدامها في برامج التربية لنقل هذه الصفة للأصناف التجارية. كما أوضحت أغلب الصفات المدروسة مدي واسع من التباين. ويعكس هذا المدي درجة الإختلافات بين هذه التراكيب الوراثية. وكانت أربعة أصناف مبكرة جداً ألا وهي؛ جيزة ١٧٧، ميليانج ٩٧، جيزة ١٨١ وسيون ٣٣٩. بينما أعطت خمسة أصناف تقديرات عالية لدليل المحصول وهي؛ جيزة ١٧٧، جيزة ١٧٨، ميليانج ٩٧، جيزة ١٨١ وأي إي تي ١٤٤٤. وقد أظهرت دراسة درجة القرابة بين الأصناف المدروسة من خلال التشابة بين الصفات الكمية انقسامها الى مجموعتين أساسيتين. إشتملت المجموعة الأولى على سبعة أصناف هي؛ جيزة ١٧١، جيزة ١٧٦، سيون ٣٣٩، أي إي تي ١٤٤٤، أي أر ٦٥٥٩٨، جيزة ١٧٨ وجيزة ١٨١. وقد إنقسمت هذه المجموعة لتحت مجموعتين، أحتوت الأولى على الصنفين جيزة ١٧٨ وجيزة ١٨١ والمتشابهين في طول النبات، عدد الفروع، مساحة الورقة العلم، محصول الحبوب، عدد السنيبلات وتفاعل اللفحة. وكان معمل التباين المظهري أعلى من معامل التباين الوراثي في كل التراكيب الوراثية المدروسة وهو مايدل على أن الجزء الأغلب من معامل التباين المظهري يعود للظروف البيئية والمعاملات الزراعية. في حين كانت تقديرات معامل التباين الوراثي عالياً لكل الصفات المدروسة، مما يشير الى أن هذه الصفات ربما تكون سائدة وراثياً ويمكن التحسين الوراثي فيها. حيث يشير معامل التباين الوراثي الى كلا من التباين المضيف والتباين الغير مضيف ويلعب دوراً مهماً في توارث هذه الصفات.