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**FLOWERING IN RELATION TO YIELD,**

**YIELD COMPONENTS AND FIBER PROPERTIES OF FOUR PROMISING EGYPTIAN COTTON GENOTYPES**

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**ABSTRACT**

*Four Egyptian promising cotton genotypes (G. barbadense L.) i.e. (L 97 derived from cross Giza 90 x Aust.), (Giza 90), (L 95 derived from cross [(G.83 x (G.75 x 5844) x G.80] and (Giza 80) and (Giza 80) were tested for their fruiting habit, aiming to evaluate their earliness, yield, its component characters and fiber properties during 2013 and 2014 seasons. The study showed that flowering started slowly and then increased gradually, reached the peak in the fifth week (4 to10 July) after 111 days from planting in all studied genotypes. The line 97 produced higher number of flowers/plant compared to other tested genotypes. The number of flowers/plant significantly different among genotypes. The periods in which each genotype produced 50 % of the total flowers/plant, existed after 31, 32, 33 and 34 days from the initiation of flowering in the four genotypes, respectively. The number of open bolls/plant showed the same trend of flowering in the tested genotypes. The best flowering weeks which produced high number of boll retentions and consequently open bolls/plant was in the fifth week (4-10 July) for all studied genotypes. The first 50 % of flowers produced 67 %, 64 %, 62 % and 59 % of the number of open bolls/plant, determining the yield/plant in the four genotypes, respectively. The obtained mean values of boll weight were not significant, while significant differences were found among the genotypes in seed cotton yield/plant. The genotype line 97 produced better seed cotton yield/plant compared to the other genotypes. The line 97 had the highest lint percentage followed by that of Giza 90. Line 97 showed the longest values for in staple length and strength. The obtained results clarify that L 97 was the earliest compared to the other genotypes. The fifth week showed the best values in the studied characters except micronaire reading.*

**Key words:** *Cotton, Fiber Properties, Flowering, yield.*

2

**GENETIC ANALYSIS OF VARIOUS YIELD CONTRIBUTING AND PHYSIOLOGICAL TRAITS IN BREAD WHEAT UNDER NORMAL AND WATER DEFICIT CONDITIONS**

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**ABSTRACT**

*Seven bread wheat genotypes crossed in a half-diallel model without reciprocals in 2012/13 season to estimate the genetic effects. Parents and F1`s were evaluated in a randomized complete block design (RCBD) with three replicates under normal and water deficit conditions in 2013/2014 at Sakha Agriculture Research Station. Data were recorded on some physiological and agronomic traits. Irrigation mean squares were significant for all studied traits except proline content and 100-kernel weight. General (GCA) and sepecific (SCA) combining ability mean squares**were significant for all studied traits at both conditions, except GCA for chlorophyll A under water deficit condition, chlorophyll B and proline content under normal condition. Also, SCA for days to heading, days to maturity, grain filling period, proline content under water deficit condition and number of spikes plant-1 under both conditions. GCA/SCA ratio were more than unity for days to heading, days to maturity, grain filling period , number of kernels spike-1, 100-kernel weight under normal condition and plant height at both water conditions. Suggesting that additive genetic effects were more important in controlling these traits. The genetic component i.e. additive and dominance were highly significant for most studied traits. Heritability in narrow sense estimates were moderate or high for all traits at both conditions, except chlorophyll B at both water conditions, grain yield plant-1 at normal condition and chlorophyll A at water deficit condition which had low values of heritability in narrow sense. Reflecting the role of additive gene action in governing these traits, Therefore selection for these traits could be applied in early segregating generations. Finally, the results indicated that the parent Vorobey was the best for some traits i.e. grain filling period, grain filling rate, chlorophyll B, plant height , grain yield plant-1. While, line 1 was the best for flag leaf area and proline content. Also, these parents had low values for drought susceptibility index. While, the cross Line 1×Vorobey was the best for grain yield plant-1 and had lowest values for drought susceptibility index. These genotypes could be selected and using in breeding program for drought tolerance to develop the suitable of wheat cultivars under water deficit environmental.*

**Key words:** ***Gene action, wheat, diallel crosses, yield components, physiological indicators, deficient irrigation.***

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##### **GENE ACTION AND HERITABILITY OF FRUIT YIELD AND IT'S COMPONENTS ON MELON** (*Cucumis* *melo*. L)

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**ABSTRACT**

***Six populations; P1, P2, F1, F2, Bc1and Bc2 in two intra-specific crosses of melon (Ananus d'Amerique a Chaire Rouge×Ananas El-Dokki and Top Mark×Ananas El-Dokki) were evaluated in field trial in a randomized complete blocks design with three replication in summer 2012. The study was carried out at the Experimental Farm of the Faculty of Agriculture, Tanta University, Egypt. This work was carried out to study types of gene action, degree of dominance heritability and expected genetic advance for yield and its components and fruit characteristics.*** *Ananas El-Dokki cv. exceeded* ***Ananus d’Amerique a Chair Rouge*** *cv. and Top Mark cv. in all studied traits except number of fruits/plant, flesh firmness, and flesh color.* ***Heterosis relative the better parent was positive and significant or highly significant for fruit yield/plant, fruit weight, flesh thickness, and TSS (Brix) in the two crosses. However, heterosis over the better parent was insignificant or had negative values for the other traits under study. The obtained results encourage producing F1 hybrids for commercial production. In the seconde cross Top Mark×Ananas El-Dokki, heritability estimates, in broad sense were high for all traits under study. Heritability estimates, in narrow sense were high for fruit weight and fruit flesh firmness in the second cross Top Mark×Ananas El-Dokki, and moderate in first one for fruit length, fruit flesh firmness, and flesh color. The genetic advance under selection was high in the first cross, while it was low in the second one for the same traits.***

Keywords*: Six* ***populations, Cucumis melo, Backcross.***

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**UTILIZATION OF TRIPLE TEST CROSS IN BREAD WHEAT F2 POPULATIONS. 2- GENETIC DIVERSITY OF TRIPLE TEST CROSS FAMILIES BASED ON PRINCIPAL COMPONENT AND CLUSTER ANALYSES**

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**ABSTRACT**

 ***Sixty TTC families derived from cross (Gemmeiza 9 x Misr 1 ) were used in a randomized complete block design with three replications at the Experimental Farm of Gemmeiza Agriculture Research Station, Agriculture Research Center, Egypt during four successive growing seasons i.e. 2009 / 2010, 2010 / 2011, 2011 / 2012 and 2012/2013. Highly significant differences were recorded for all the traits studied among triple test cross (T.T.C) families, indicating the presence of high segregations in F2. The results indicated that overall epistasis was found to be highly significant for most traits studied. Partitioning of total epistasis to its component parts revealed that (i) type of epistasis was significant and highly significant for most traits studied. Also, the (J and L type) epistasis was highly significant for most traits studied except main spike length and no. of spikelets per main spike. The mean squares due to sums were found to be significant for most traits studied. Also, the mean square estimates due to differences were found to be highly significant for most traits studied. The first four principal components, PC axes accounted for about 73.2 % of total variance of all traits. PCA1 accounted for about 31.2 % of the variation; PCA2 for 15.7 %; PCA3 for 14.1 % and PCA4 for 12.2 %. The dendrogram for clustering pattern of TTC families were grouped into nineteen clusters. Most members and families of selected clusters exhibited higher values for most agronomic characteristics than TTC families mean. Families (48, 53 and 55) which formed single cell clusters by themselves surpassed all families in the studied cross, having the highest values of all studied characteristics.***

**Key words:** *Wheat, Triple test cross, epistasis, additive, dominance, principal components analysis and cluster analysis.*

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**GENETICAL STUDIES OF YIELD AND ITS COMPONENTS UNDER THREE NITROGEN FERTILIZER LEVELS IN WHEAT**

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**ABSTRACT**

***This investigation aimed to study the potentiality of heterosis expression, potence ratio, heritability, expected genetic advance, nature of gene actions for yield and its components in two wheat crosses, (I) Gemmeiza 9 × C.T 59 and (II) Sakha 93 × C.T 59 under three different levels of nitrogen fertilizer; 25 kg N/fed (N1), 45 kg N/fed (N2) and 65 kg N/fed (N3). Six populations (P1, P2, F1, F2, BC1 and BC2) were used to estimate genetic parameters. These results revealed that genetic parameters values differed under nitrogen fertilizer levels for the two crosses studied. Heterosis relative to mid-parent and better parent was found to be significant positive for most traits studied. Additive (a) and dominance genes effects (d) were highly significant for most traits studied. Epistasis effects were present for most traits studied. F2 deviation (E1) was significant positive for most traits. Back cross deviations (E2) were significant negative for most traits. The magnitude of additive × additive gene effects was high and positive significant except heading date in the two crosses studied, whereas dominance × dominance was negative significant for most of the traits studied. Additive × dominance gene effects were of minor importance in general for most of the traits studied. Heritability estimates in broad and narrow senses were generally moderate to high for most traits studied. Meanwhile, the values of heritability in narrow sense were low for spike length in the first cross under N1. The expected genetic advance from selection estimates in the F2 were low for heading date in the first cross under N1. Based on these results, the first cross; Gemmeiza 9 × C.T 59 could be selected for obtaining plants having high grain yield, no. of spikes per plant, spike length, no. of kernels per spike, no. of tellers per plant and early heading date. Moreover, the second cross; Sakha 93 × C.T 59 is promising for selecting plant height, 1000-kernel weight and biological yield.***

**Key words:** *Wheat, Gene action, Heterosis, Heritability, Genetic advance, Additive, Dominance, Nitrogen fertilizer, Six parameters model.*

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**HETEROSIS, COMBINING ABILITY ANALYSIS FOR BREAD WHEAT UNDER STRESS AND NORMAL IRRIGATION**

**TREATMENTS**

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**ABSTRACT**

Drought is one of the major environmental factors which threaten wheat production worldwide. Nine bread wheat genotypes were crossed in a 9x9 half diallel scheme in 2012/2013. The nine parents Yakora (P1), Sakha 93 (P2), Misr 2 (P3), Sids12 (P4), Gemmiza 11 (P5), Line 150 (P6), Line 116 (P7), Line 145 (P8) and Line 124 (P9) and their thirty-six F1 crosses were evaluated under normal and stress conditions during 2013/2014 in two experiments in a randomized complete block design (RCBD) with three replications at the Experiment Research Station of Moshtohor, Benha University, Kalubia Governorate, Egypt**.** The results of analysis of variance showed significant for all studied traits. Mean squares for genotypes, parents, crosses and parents vs. crosses were significant for all traits except days to heading for parent's mean squares. The highest mean values were detected under combined analysis by parents P5, P7,P1,P4,P4 and p8 for days to heading, plant height, no. of spike/plant, 1000 grain weight, no. of kernels/spike and grain yield, respectively. While, the highest mean values were recorded under combined analysis with crosses P1×P7, P3×P7, P1×P3, P5×P8, P4×P9 and P4×P5 for days to heading, plant height, no. of spike/plant, 1000 grain weight, no. of kernels/spike and grain yield, respectively. Mean squares of both general (GCA) and specific (SCA) combining ability estimates were highly significant for all the studied traits. The ratio of GCA/SCA being more than unity in all cases indicated that the additive gene effects were more important for all of the traits. P8 was a good combiner for days to heading and grain yield. The highest desirable SCA effects were obtained with P6×P8 for days to heading, P1×P4 for plant height and 1000 grain weight, P1×P5 for no. of spike/plant, P1×P3 for no. of kernels/spike, P1×P7 for grain yield under combined analyses. P4 was high tolerant for stress irrigation, for grain yield. The cross P2×P4 had high tolerance to stress irrigation treatment for this trait.

 Key words: Wheat, combining ability, drought, GCA and SCA.

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**Selecting high oil yield stable sunflower (*Helianthus annuus* L.) genotypes for salinity stress using parametric and non parametric stability statistics**

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**ABSTRACT:**

In order to evaluate phenotypic stability, determine stable sunflower genotypes before its commercial release for oil yield/fad. (kg) under a wide range of soil salinity levels and comparison between parametric and non-parametric stability indices, twelve sunflower (*Helianthus annuus* L.) genotypes which obtained from Department of Oil Crop Research, Field Crop Research Institute, Agricultural Research Center, Egypt, were evaluated in eight environments represented in successive 2013 and 2014 summer seasons and two locations (Kafr-El-Hamam located at 30O 58´ N for Latitude and 31o 50´ E for Longitude as control and Tag-El-Ezz located at 31º 36´ N for Latitude and 30º 57´ E for Longitude Agricultural Research Stations with three different salinity levels i.e. S1= 5.0 EC, S2=8.0 EC and S3= 11 EC) in randomized complete block designs with three replications. Genotypes, environments main effects and GEI were significant at (P<0.01). Both parametric (Mean, bi,S2di,Ri2,Wi2,Si2,CVi,δi2,P59, Di,αi,λi,PI,SFi,RDi,RDDi,RDDDi,ASVi,NAi) and non-parametric (Si(1),Si(2),Si(3),Si(6),NPi(1), NPi(2),NPi(3),NPi(4),RSM, YSI, δr, δOY, kr, TOP, Middle, Bottom) stability measures were used to determine stable sunflower genotypes coupled with high oil yield/fad. (kg). Genotypes of L92, L120 and Sakha53 were the most stable ones based on parametric and non-parametric stability measures used. The rank correlation matrix indicated that most non-parametric measures were significantly inter-correlated with parametric ones and therefore can be used as alternatives. To better understand the nature of relationship among the parametric and non parametric measures, a hierarchical cluster analysis based on rank correlation classified them into four groups. One of them has valuable importance for sunflower breeder, being the group 1 which comprised oil yield/fad and non parametric stability measures of Si(3), Si(6), NPi(3), NPi(4), TOP and YSI, were found to be positively and significantly correlated with each other and with oil yield/fad.. Also, evaluated sunflower genotypes classified into three groups based on rank correlation, the preferred being Group 1 included the high yielding genotypes of L120, L770, L885 and Sakha53 which introduced as the most stable ones followed by the moderate yielding sunflower genotypes of L92, L355 and Giza102 which also regarded as stable ones were clustered in group 2.

**Key words:** Sunflower (*Helianthus annuus* L.), Oil yield (kg/fad.), Parametric and non-Parametric stability measures, Spearman’s rank correlation, Cluster analysis

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**GENETICAL ANALYSIS FOR ALLELOPATHIC ACTIVITY IN SOME RICE VARIETIES**

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**ABSTRACT**

This study was carried out at the Experimental Farm of Rice Research and Training Center, Sakha, Kafr ElSheikh, and Plant Pathology and Biotechnology Lab., Faculty of Agriculture, Kafrelsheikh University. The cultivations were carried out in a clay soil type along summer season (May of 2013 and 2014). Allelopathic activity and momilactone B concentration in rice seedlings were increased in the presence of barnyardgrass seedlings by using High performance liquid chromatography (HPLC). These increases were probably caused by nutrient competition between the two species. Up-regulation of the putative genes that encode for Phenylalanine ammonia-lyase (PAL) and cytochrome P450, which are involved in de novo synthesis of phenolic allelochemicals and detoxification of toxic substances, was detected in Giza 179 by Real-time fluorescent quantitative polymerase chain reaction (qRT-PCR) at low nitrogen (0.03 N) concentration. PAL is the first key enzyme in phenylpropanoid metabolism that can be regulated by various biotic and abiotic factors to different extents depending on different plant species and P450 is directly involved in the formation of ρ-coumaric acid. Under decreased N availability, phenolic content and PAL activity in plants may be increased because of decreased demand for proteins required for growth. In this process, ammonium ions released by PAL can be assimilated to increase N cycling. Different genes were up-regulated in Giza 179 when exposed to low N. The results referred to highly genetic effect which controlled these traits since the environmental effect is not significant. The additive and dominance genetic variances might be important in the inheritance of weed control, although the dominance genetic variance played more important role in this case. Rice variety Giza 179 exhibited high allelopathic potential to suppress the growth of accompanying weeds, especially when the culture solution had low N content. Giza 179 also a restorer line because this variety have Restoring Fertility (RF) gene from obvious studies, so, we recommend by using variety Giza 179 as parental line in producing hybrid rice seeds that has high yield and strong allelopathy.

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**Genetic diversity and morphological variability of Manfalouty and some foreign pomegranate cultivars in Egypt.**

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 Abstract

This investigation was carried out to study the genetic diversity of some of pomegranate cultivars. The genetic variability and relationships among Manfalouty as the local cultivar and some imported pomegranate cultivars, namely Wonderful, Sweet, Black and Akka were investigated. The comparison was based on morphological characters such as fruit characteristics (physical and chemical), flowering and ripening dates and RAPD molecular markers. Physical fruit traits were determined (weight, volume and diameter), peel (weight percentage and thickness), arils (weight and percentage) and seeds (weight and softness). The chemical traits such as soluble solid contents (SSC), vitamin C, anthocyanin content and titratable acidity (TA) were assessed. The results revealed wide variations of these traits among the studied cultivars. Depend on the morphological traits the cultivars could be classified as follows; Manfalouty was of hard seeds and sweet-sour cultivar, Wonderful was had hard seeds and sour cultivar, Black was classified as medium-softness and low sour cultivar, Akka was described as medium-softness and sweet-sour cultivar. While, Sweet cultivar can be classified as soft seed and sweet cultivar. Ten RAPD primers generated total of 89 reproducible bands, 46.06% of which were polymorphic. Genetic similarity among cultivars ranged from 0.75 to 0.91. The UPGMA dendrogram of RAPD data showed that ‘Manfalouty’ and ‘Akka’ were very closely related while ‘Wonderful’ is distinct from the other cultivars. This molecular and morphological variability indicated that this germplasm includes rich and valuable plant materials for pomegranate breeding and improvement programs.

Key words: pomegranate, RAPD analysis, genetic variability, morphological characters

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**EFFECT OF GA3 DOSES AND ROW RATIO ON CYTOPLASMIC MALE STERILE LINE IR69625A SEED PRODUCTION IN HYBRID RICE**

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**ABSTRACT**

An experiment was conducted at the Experimental Farm of Rice Research Department at Sakha Agriculture Research Station, Field Crop Research Institute, ARC, Egypt, during 2013 and 2014 rice growing seasons to study the effect of GA3 and row ratio of maintainer and IR69625A cytoplasmic male sterile line (CMS) lines on different characters. Four levels of GA3 doses, zero, 150, 200 and 300 g/ha and three row ratios 2:4, 2:6 and 2:8 for B and A lines, respectively were used. The different doses of GA3 showed highly significantly influence on panicle length, seed set rate, panicle weight, panicle exertion and harvest index when 2:4 row ratio and300g/ha GA3 were used in the first and second seasons. But the highest grain yield was obtained from 2:8 row ratio accompanied with 300g GA3/ha. Germination percentage decreased with increasing doses of GA3, while germination index increased with increasing the doses of GA3. Also, the root and shoot length characters were highly significant affected by the different row ratios and GA3doses, while the tallest root and shoot were obtained with 2:4 row ratio and 300g/ha GA3 dose. The interaction between GA3 and row ratio had highly significant effect on seed yield. The highest seed yield (2.4 t/ha) was obtained when 300 g/ha of GA3 was applied with the row ratio of 2:8. The lowest seed yield (0.6 t/ha) was recorded without application of GA3 (control) at row ratio of 2:4.

**Key words:** Hybrid rice, A line (CMS) , B line, GA3 application, row ratio and grain yield.

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**Screening Cotton Genotypes for Drought Tolerance by Using Non-Enzymatic and Enzymatic Antioxidant Systems**

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**ABSTRACT**

Drought stress is the major environmental factor that negatively impacts cotton yield throughout the world. Thus, there is a need for a protocol to offer new opportunities for improving drought tolerance in cotton. By understanding the correlation between yield andnon-enzymatic (phenolic content, lipid peroxidation and proline) and enzymatic (superoxide dismutase, catalase, peroxidase and ascorbate peroxidase) antioxidants activities, we can develop efficient screening method able to screen large amounts of plant material in the shortest time possible. In the current study, 21 cotton genotypes (6 parents and 15 F1 crosses) were evaluated under two irrigation treatments i.e., 100 % ETc, 1269 mm/season (normal) and 60 % ETc, 761 mm/season (drought). The non-enzymatic and enzymatic antioxidant activities were studied. Also, correlation between yield and antioxidant activities was determined. The results revealed high significant difference among genotypes for all the studied antioxidants under normal and drought treatments (except lipid peroxidation than under drought under normal). Although all antioxidants in all genotypes were significantly affected by drought, Giza 80, Giza 90 and crosses; Giza 80 x Tamcot C. E., Giza 90 x (Giza 90 x Australian), Giza 90 x Tamcot C. E. and Tamcot C. E. x Deltapine maintained the highest activities under drought stress. Yield was correlated with each of the antioxidant activities under drought and not under normal condition. Therefore, it could be concluded that antioxidant systems could be used as selection criteria for high yield under drought stress.

**Key words:** Cotton Genotypes, Drought, Yield, Correlation and Antioxidant enzymes activities.

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**Performance and heterosis for yield, yield components and some physiological traits in barley under rainfed conditions at Maryout.**

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**ABSTRACT**

 Water shortage is one of the major limitations that affect plant growth and cause severe reduction in the crop yield. Such reduction in yield can be compensated throw heterosis breeding. The objectives of this study were to evaluate the performance of barley genotypes for grain yield/plant, no. of spikes/plant, no. of kernels/spike, 100-kernel weight, relative water content (RWC) and free proline content under well watered and rainfed conditions. Also, to estimate heterotic effects for the studied traits under the two irrigation regimes in order to identify the best genotypes which can be grown under drought stress conditions. Six varieties and lines namely: the cv. G126(P1), L Su12303(P2), L 105/20(P3), L105/27(P4), L105/32(P5) and L 105/36(P6) were chosen to achieve the present study. In 2008/09 season, the parents were crossed in a 6**×**6 half diallel matting design. In 2009/10 season, two adjacent field trials each included the 15 F1 hybrids and their respective parents (21 genotypes) were conducted in a randomized complete block design with three replications at the Maryout Agriculture Experiment Station of Desert Research Center (North Western Coast of Egypt). Each experiment was devoted for one of the following to irrigation treatments: a) rainfall treatment (drought stress treatment) and b) rainfall + 2 supplemental irrigations given at sowing date and flowering stage (well watered treatment). Analysis of variance indicated that all traits were significantely affected by soil moisture deficit and presence of sufficient genetic variability among genotypes. Drought stress caused significant reduction in all traits. Such reduction reached 19.24% in no. grains/spikes, 15.68 in no. spikes/plant and grain yield/plant and 7.74% in 100-kernel weight, suggesting that 100- kernel weight is less sensitive to drought stress as compared to the other yield components also, RWC was significantly decreased (30.67%), while proline content was significantly increased (73.39%) when plants were subjected to drought stress.The cross P5xP6 followed by the cross P3xP6 appeared to be the bestthan the other genotypes for grain yield/plant under both irrigation regimes. According to stress susceptibility index (S) the crosses; P1xP3, P1xP4, P2xP6, P3xP4, P3xP5, P4xP5, P4xP6 and P5xP6 were the most tolerant to drought stress for grain yield/plant. Some crosses showed significant desirable better-parent heterosis (heterobeltiosis) for all studied traits under both irrigation treatments. The F1 hybrids; P2xP4, P3xP4, P3xP5, P3xP6 and P5xP6 expressed higher mid and better parent heterosis under rainfed condition than under well watered condition for grain yield/plant, therefore if the hybrids development is feasible in barley these hybrids are considered more desirable to be grown under water shortage conditions for increasing grain yield per unit area and selection could be exercised in segregating generations for developing drought tolerant genotypes. For the physiological traits, the best heterotic effects were recorded by the crosses; P5xP6, P3xP6 and P3xP5 for R.W.C and by P1xP4, P2xP4 and P3xP6 for proline content.

**Key words:** Barley (*Hordeum vulgare*, L.), Rainfed, Supplemental irrigation, Drought stress, Drought tolerant, Drought tolerant, Stress susceptibility index and Heterosis.

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**Molecular Discrimination among Diverse *Vicia faba* L. Genotypes**

**under Thermal Stress Condition Prevailing at the New Valley**

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**Abstract**

Faba bean, (*Vicia* *faba* L.; 2n = 12) is a major food and feed grain legume. A field experiment was conducted to investigate the response of seven divergent faba bean genotypes (Misr-1, Misr-3, Nubaria-2, Sakha-4, NBL (Mar.3), NBL-5, and L3) to thermal stress conditions prevailing at the New Valley during the growing season (2012/2013). For achieved this purpose; yield and its attributes, biochemical and molecular markers and polymorphic information content (PIC) were estimated. Sakha-4 gave the highest level of yielding capacity and could be considered as most tolerant genotype, while Nubaria-2 as least tolerant one. The SDS-PAGE of seed and leaf proteins gave high levels of genetic diversity with polymorphism percentage of 59% and 65.12% respectively. Furthermore, they revealed some important biochemical markers for thermal stress tolerance. A total of 85 amplicons (amplification fragments) were generated by ten ISSR primers (B44, 17898B, 17899B, HB-08, HB-09, HB-10, HB-12, HB-13, HB-14 and HB-15) out of them 75 were polymorphic (88.2 % polymorphism). Among the produced bands, 17 bands could be used as positive molecular markers and 9 ones could be used as negative markers which could be useful in breeding programs of faba bean. The dendrogram based on ISSR-PCR classified the seven genotypes tested into two main clusters. The first cluster comprised four genotypes, while the second cluster included three genotypes. Moreover, the total of polymorphism (PIC) presented values contained among 0.88 to 0.99 attested the existence of a high genetic variability among studied genotypes, which can be efficiently exploited in the breeding programs of faba bean.

**Keywords: Faba bean, Thermal stress, Yield and its attributes, SDS-PAGE, ISSR-PCR markers, polymorphic information content (PIC) and dendrogram.**

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**Genotype - environment interaction for yield in white lupin (*Lupinus albus* L)**

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**ABSTRACT**

The present investigation was performed to analyze the genotype-by-environment (GE) interaction for seed yield of twelve genotypes grown in four locations (Giza, Gemmiza, Mallwy and New valley) during 2013 and 2014 seasons in a randomized complete block design with three replications in each environment. Combined analysis of variance showed highly significant differences for the GE interaction indicating the possibility of selection for stable genotypes. The stability of the assessed genotypes using some stability statistics derived from three types of statistical concepts (variance and regression analyses), AMMI (additive main effect and multiplicative interaction) analysis and GGE biplot (genotype main effects and genotype-by-environment interaction effects) models were applied to obtain good understanding of the interrelationship and overlapping among the used stability statistics. Results showed that Dijon2 (G2), Giza1 (G1), Family 9 (G10) and Mutant 35/2 (G4) scored the greatest seed yield (6.33, 5.59, 5.29 and 5.29 ard fed-1), respectively, over environments. Family 9 (G10) and Giza1 (G1) were the most stable lupin genotypes because they met the assumptions of stable genotype as described by the three types of stability parameters (coefficient of variability, Wricke’s ecovalence and regression coefficient) coupled with high yield. The results of AMMI analysis indicated that the first two IPCA's were highly significant. The partitioning of total sum of squares exhibited that the environment effect was a predominant source of variation (66.66%) followed by GE interaction (22.13%) and genotype effect (11.21%). The GE interaction was ~2 times higher than that of the genotype effect, suggesting the possible existence of different environment groups. AMMI stability value (ASV) discriminated genotypes Giza1 (G1), Dijon2 (G2), Family 9 (G10) and Sohag2 (G11) as the stable accessions, respectively. Based on the YSI (yield stability index) and new rank-sum the most stable genotypes with high yield were the last same genotypes. The GGE biplot analysis result also supported those obtained using AMMI, as well as E5 (Giza) was ideal environment followed by E4 (New valley). The results of this investigation proved that the studied parameters are suitable stability indices for discriminating stable genotypes with high yield. Finally, theperformance of coefficient of variability, Wricke’s ecovalence, regression coefficient, and deviations from regression as well as AMMI analysis and GGE biplot, showed that genotypes Giza1 (G1 and Family 9 (G10) were found to be stable and are adaptable to both tested environments, thus they should be recommended for releasing with wider environmental adaptability.

**Keywords**: Stability parameters, Lupin, GGE biplot, AMMI-additive main effects and multiplicative interaction; ASV–AMMI stability value, Genotype selection index, and rank

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**Genetic Parameters for** **some important characters in alfalfa (*Medicago Sativa* L.) cross by six parameter analysis.**

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**ABSTRACT**

The assessment of gene effect for some vegetative, fertility traits and detection of epistasis in alfalfa was studied in cross between New valley and Ismaelia-94 genotypes involving two parents through six generations mean analysis during three successive generations from 2011/12 till 2013/14 at the Experimental Farm of the Forage Research Department, Field Crops Research Institute, Agriculture Research Center, Giza, Egypt. The nature of gene effects for agronomic and fertility traits were analyzed through six hybrid generations for detecting the gene effects responsible for inheritance.

 Significant differences were detected among generations viz, P1, P2, F1, F2, BC1 and BC2 for most of the studied traits. F2 generation indicated better performance of number of tiller and fresh yield (32.63 and 93.99, respectively) across all generations. Bc1 generation recorded the best values among number of pods tiller-1 and number of seed tiller-1 with (51.87 and 156.73). F2 mean performances were greater than the top parents for all traits except number of inflorescences plant-1 and 1000-seed weight. Bc1 recorded the best average mean across the most of agronomic and fertility traits. Broad sense heritability (H2b) recorded high values of plant height, No tillers and fresh yield (0.941, 0.845 and 0.838, respectively), while leaf stem ratio and dry yield were low values of H2b (0.420 and 0.290, respectively). So, H2b ranged from 0.52 for the number of florets inflorescence to 0.9717 for the number of inflorescencesplant**-**1) respectively, whereas the narrow sense heritability (h2n) illustrated low values across agronomic and fertility traits. The estimated values of additive variance (d) for the most of studied traits recorded highly significant positive sign, it is revealed that both additive and dominance gene effects were important in the performance of these traits. Duplicate epistasis was prevailing for all agronomic traits and number of inflorescence plant-1 except for leaf stem ratio%. Complimentary epistasis of non-allelic gene interaction was showed only for number of pods plant-1.

**Key words:** *Alfalfa, Cross, Inheritance, Genetic parameters, Gen action, Epistasis*

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**EFFECIENCY OF INDEX SELECTION FOR SEED YIELD IN HELALY " BARSEEM CLOVER "*Trifolium alexandrinum*,L."**

**By**

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**ABSTRACT**

A selection index had derived for each barseem family type depending on variance- covariance matrix of seed yield and seed yield components, weighed by the corresponding estimates of heritability. A selection intensity of 20% had practiced, resulting in twenty elite families in each selection scheme. Two synthetics had obtained. These were; a) C1 (H-S); cycle one of half- sib family selection and b) C1 (S1); cycle one of S1 family selection for high seed yield. The two synthetics developed through half- sib and S1- family selection for high seed yield, the base population and three checks namely; Sakha4, Serw1 and Gemmiza1 had evaluated in 2010/2011 winter season.

The obtained results could be summarized in the following; 1) the realized gain in seed yield due to S1 –family selection reached 29.40 percent relative to the base population or 38.19 percent relative to the average of the checks. 2) half-sib family selection gave a realized gain in seed yield reached 14.34 percent relative to the average of the check varieties.3) significant superiority of half-sib family synthetic over the base population in number of inflorescences/plant reached 15.02 percent, mean while, the magnitude of that synthetic superiority over the average of the studied check varieties reached 19.39 percent.4) S1-family selection synthetic significantly gave the highest response to selection in number of inflorescences/plant. That response, reached 23.55% over the base population mean or 25.24% over the average of the check varieties.5) the realized gain in flower density/head due to S1-family selection scheme reached 31.69% over the average of the studied check varieties.6) significantly lower magnitude of realized gain in flowers density/inflorescence due to half-sib family selection scheme reached 22.30% relative to the average of the check varieties had participated.7) the highest number of seeds/inflorescence had expressed by the improved synthetic through S1-family selection scheme (43.79 seeds/head). The second significant seeds/inflorescence was that resulted from the improved synthetic by half-sib family selection (37.62 seeds/head).8).

Commonly, response to selection in seed yield of barseem clover had driven from responses in seed yield component, i.e.; number of inflorescences per plant, number of flowers per inflorescence, number of seeds per inflorescence and percent seed setting. Seed index, that exhibited the least genotypic and phenotypic coefficient of variability whether in half- sib or S1 families and relatively low estimates of expected gain from selecting either from half- sib or S1 families, had not respond to any of the applied selection schemes.

**Key words:**

index selection, gain from selection, seed yield, seed yield components, barseem clover, half- sib family,S1 family.

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**Genotypic variations in Egyptian gene pool of barseem clover ' *Trifolium alexandrinum*,l**

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ABSTRACT

The present study was carried out to detect the prevailing variability within the gene pool of barseem clover “*Trifolium alexandrinum*, L.”. Five random populations of expected variable expressions were included. These were; ''Fahl" a single cut and "Meskawi", "Khadarawi I", "Khadrawi II" and "Saeidi" a multi-cut types. The study period covered two winter seasons of 2005/2006 and 2006/2007.The obtained results could be summsrized in the following: The range of green forage productivity (kg/m2) among the tested barseem populations was 3.5, 1.2 and 4.3 for first, second seasons and combined values. the phenotypic variations among barseem populations were about 180, 70 and 59 percent of the trait grand mean in the first, second seasons and combined yield.Dry forage yield at first cutting of barseem population at first season, showed a wide range of 173 g/m2, while, the corresponding range in second season was only 18.1 g/m2. Over all the two years, the traced range was wider amounting to 197.9 g/m2.Overall the two years of the study, phenotypic variability in dry forage at first cutting yield was about eight percent of the grand mean. The magnitude of genotypic variations was very limited, amounting to about two percentage of the mean.At subsequent cutting the range of variability in green yield was narrower (1.7 kg/m2) at first season than the corresponding value of the second season (3.2 kg/m2).The phenotypic variability in green forage yield of the subsequent cutting amounted to 21.3% of the grand mean over seasons. The corresponding values represented between 17.82% and 8.6% of each of the first and the second seasons grand mean, respectively.Phenotypic variations represented 15.4 and 19.1% of each of the first and second seasons dry forage yield, respectively. Whereas, over the two years of the study, the magnitude of phenotypic variations represented about 28% of the over all mean.Phenotypic differences among barseem populations amounted to 29.7, 12.7 and 4.84 percent of the obtained mean number of heads per plant at first ,second seasons and combined analysis. In the same time, genotypic differences among populations of barseem amounted to 22.95, 6.3 and 10.41% of the populations grand mean over first, second seasons and combined data.As for, number of seeds per head, values of 62.89 and 89 were expressed as a range in the first, second seasons and overall the two seasons. Over the two years, the magnitude of genotypic and phenotypic variations were quite equal and around 20%.

Estimate of heritability for seed yield components varied between the seasons, where, the genotypic variance represented about 60 and 24% of the phenotypic variance of number of heads per plant at the two successive seasons, respectively.Low heritabilities estimates of about 31% and 28% were obtained for number of flowers per head at the two seasons, respectively .Estimates from the combined analysis over seasons, were approaching 96% and 65% for number of seeds per plant and seed weight per plant.The high values of heritability estimates, which were obtained with number of seeds per inflorescence and seed weight per plant, indicate that these two traits might be the main components of seed yield. Furthermore, the low estimates of heritability with number of heads per plant and number of flowers per inflorescence might indicate that these characters are largely affected by environmental factors.

Key words: genotypic variability,clover, heritability,Expected genetic advance.seed yield components, forage yield.

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VARIABILITY IN **BARSEEM CLOVER GENE POOL** *Via* **MOLECULAR MARKERS**

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**ABSTRACT**

Cluster analysis of the five barseem populations, generated by 17 agronomic traits cleary separated into three groups . The first group (A) consisted of Meskawi, Khadarawi (I) and Khadarawi (II).The second group (B) includes only Fahl population. The average genetic similarity among the five barseem population was 0.30, with value ranging from 0.12 to 0.48. The khadarawi (I) and Khadarawi (II) populations showed a very high degree of similarity (0.48) indicating that these two cultivars are closely related genotypic. Concerning the RAPD analysis, atotal of 109 fragments were produced by twenty primers of these 109 amplified fragments (87%) were polymorphic in one or more of such studied population. Similarity matching coefficient based on the RAPD data, ranging from 0.35 to 0.62 , suggested abroad genetic base for barseem populations . The cluster analysis bassed on Jaccard similarity coefficient of these five barseem populations , generated by RAPD markers clearly separate the five barseem populations in to two clusters . The first cluster included two barseem populations, (Khadarawi I and Khadarawi II). The second cluster included the other three populations. This data suggest that RAPD marker was similar to agronomic traits (17 traits) in these different populations comparison of matrices of RAPD and morphological data showed relatively high Correlation coefficient between dendrograms (r= 0.93).

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**A CONVENIENT FIELD PLOT TECHNIQUE TO ENHANCE THE EFFICIENCY OF FABA BEAN YIELD Trials**

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**ABSTRACT**

Field-based agronomic and genetic research is a decision-based process. Many decisions are required to design, conduct, analyze, and complete any field experiment. While these decisions are critical to the success of any research program, their importance is magnified for research on size and shape of the experimental unit, number of replicates, and randomization restrictions. The present investigation aimed toestimate the optimum plot size and shape and to detect the appropriate number of replicates for field research trials on faba bean. A uniformity trial was carried out at the experimental Farm of Sakha Agricultural Research Station during the two growing seasons of 2013/14 and 2014/15 using faba bean cultivar Sakha 1 as plant material. In both seasons, the cultivated area of the uniformity trial was divided into 16 strips; each consisted of 36 ridges of 4.0 m long and 0.6 m apart. Two statistical methods being soil variability index and maximum curvature were used to estimate optimum plot size and shape using the yield data of 576 basic units which were separately harvested, weighted and recorded the seed yield as kg/basic unit (3 m x 0.6 m =1.8 m2). Using soil variability index, results revealed that the net plot size of 2 basic units (3.6 m2) was required for faba bean field trials in the two seasons. According to the maximum curvature method, the optimum plot size was estimated to be 4 (7.2 m2) and 5 (9 m2) basic units in the first and second seasons, respectively. Keeping in view the border effect, the plot consisting of 9 basic units (16.2 m2 as 1/259.26 fed.) would be the optimum size that required to obtain a true comparison among treatment means and at the same time discarding the border effect. On the other hand, the appropriate plot shape, for a specified plot size, depended on the distribution of soil heterogeneity through the experimental field in each growing season. The number of replications required for detecting 15% differences among treatment means would be 3 and 5 at 0.05 and 0.01 probability levels in the first season and their corresponding values in the second season were 6 and 11 replicates, respectively. For detecting 20 % difference among treatment means, it is found that 2 and 3 replications in the first season and 3 and 6 replications in the second would be necessary.

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***STUDIES ON MODE OF GENE ACTION***

***IN CANOLA UNDER DIFFERENT ENVIRONMENTS***

By

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 **ABSTRACT**

 This investigation was carried out at at a private Farm, El-Gharbia Governorate, Tanta, during the two successive winter seasons 2009/10 and 2010/11. using Six parental genotypes or / lines of canola (*Brassica napus,* L.). The parents were kindly obtained from Desert Research Center after crossing between German and Canadian varieties (less than 2% erucic acid in seed oil content) according **(Afiah *et al.,* 1999), (Afiah *et al.*, 2000)** and **(Afiah *et al.,* 2007).** All possible parental combinations without reciprocals were made among the six genotypes, giving 15 crosses. The six parental genotypes and 15 F1's were sown in three sowing dates (Evironments). The first planting date (D1) was sown on 24­th October­. The second (D2) was sown on 12th November and the third one (D3) was sown on 30th November. Each experiment was irrigated three times after sowing irrigation. Each experiment was designated in a randomized complete blocks design with three replicates. The data of six traits i.e. no.of days to first flower open, no.of days to 50%flowering, flowering period,no. of days to physiological maturity, seed filling period andplant height. At first data is analyzed based on the analysis of variance of RCBD, in the case of significant differences between genotypes; The data of each experiment was analyzed using Griffing (1956) method II model I to estimate the general and specific combining abilities.

 The obtained results could be summarized as follows: the crosses; P1 x P6 had significant heterosis relative to better parent and (sˆij) in negative direction for no.of days to first flower open, no.of days to 50% flowering and no.of days to physiological maturity in the first cross and flowering period and no.of days to physiological maturity under all planting dates and their combined data in the second cross, indicating that these two crosses could be used in the breeding programe to improve the earliness of the parent to be used in breeding programe.

**Key words**: Brassica napus, Environments, Genotype x environment, Heterosis, GCA, SCA.

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**nmBREEDING STUDIES ON SOME RAPESEED VARIETIES UNDER DIFFERENT ENVIRONMENTS.**

by

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**ABSTRACT**

The aim of this study was to assess the variations amongeset a half diallel cross using six genotypes or / lines of canola low erucic acid rapeseede oil (LEAR) under different sowing dates, Also; estimating combining ability and heterosis over mid parents and better parent.

 For this obgective, the investigation was carried out at a private Farm, El-Gharbia Governorate, Tanta, during the two successive winter seasons 2009/2010 and 2010/2011. using six diverse canola genotypes/or lines (*Brassica napus*, L.). All possible parental combinations without reciprocals were made among the six genotypes, giving 15 crosses. The six parental genotypes and 15 F1's were planted in three planting dates. The first planting date was sown at 24/10/2010, The second one was sown at 12/11/2010 and the third was sown at 30/11/2010.

 The main results can be summarized as follow : the crosses; P1 x P2 , P1 x P4, P2 x P5, P2 x P6 and P3 x P4 had significant heterosis relative to better parent and (sˆij) in positive direction for seed yield and most of its components under at least the first and second sowing dates, which might be indicated that the possibility to use their crosses as hybrid varieties if it could be overcome the difficults of pollination via discover CMS lines or self incompatibility lines or the use of their progenies to select some pure lines characterized by high yield ability through suitable breeding programme.

 Keywords: *Brassica napus*, Environments, Genotype x environment, Heterosis, GCA, SCA.

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**Studies on Sexual compatibility and or incompatibility in Langra Mango cultivar**

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**ABSTRACT**

 Mango (*Mangifera* *indica* L.) is considered one of the oldest cultivated trees in the world. Low productivity of some mango cultivars is associate with low fruit setting and/or high fruit drop of immature fruits. The self and cross incompatibility has been reported as one of the serious factor affecting fruit set in many mango cultivars. In this respect, five mango cultivars (Alphonse, Ewais, Hindi khassa, Keitt, and Zebda) were used as a pollinizer for Langra cultivar (as a female parent) for exanimated their cross and its self - compatibility / or incompatibility between them. The results of the present study indicated that, microscopic examination for Langra cultivar after self-pollination revealed many deposits of calluse plugs were appeared at a long of the pollen tubes after self-pollination which indicated incompatibility pollen tubes. The number of pollen tubes of Keitt and Zebda c.v. in Langra styles were higher than other combinations and they started to reach the base of the style in 4 days after pollination, this is an indication of high cross compatible between each two cultivars and Langra c.v., while, Alphonse, Ewais and Hindi khassa reached delayed to the base of the style and they gave the lowest percentage of pistils with pollen tubes reaching the base of the style 7 days after cross pollination with Langra styles.

**Key words:** Mango - Langra cultivar - Self-pollination - Compatibility - Pollen tube growth - Pollinizer.

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