

Genetic components and heterotic effect in 3x3 diallel crossing experiment on egg production and hatching traits in chickens

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Abstract: Three genotypes of chickens [one local strain named Mandarah (MM) and two exotic parental commercial meat type strains [Saso (SS) and Italian (II)] were crossed in a 3 x 3 diallel mating (nine combinations) throughout two successive years to evaluate crossbreeding effects, combining ability, general (GCA) and specific (SCA), percentage of heterotic effect (H%), reciprocal effect R_E , maternal effect M_E (and, direct additive effect) D_A (for egg production and hatching traits in purebred parental and their crosses. Moreover, using GCA and SCA to predict the hybrid performance, breeding (BV) and genetic (GVFM) values for purebred parental and their crosses. There were highly significant differences among the different genotypes for body weight (BWSM) and age (ASM) at 50 % egg production, egg number per hen-housed at the first 90 days (EN_1), the first 180 days (EN_2) of production, egg weight at the mentioned periods (EW_1 and EW_2 , respectively), egg production rate (ER%) and egg mass (g / hen /180 days) (EM), feed intake (g / hen / day) (FI_1), feed intake (g / egg) (FI_2), feed efficiency (g feed / egg) (FC), in addition to hatch traits [fertility percentage (F%), hatchability percentage of fertile eggs (HFE%), hatchability percentage of total eggs (HTE%), embryonic mortality (EM%), egg pip (EP%) and total egg loss (TEL%)]. The pure strain MM had the highest significant values of EN_1 (65eggs), EN_2 (120 eggs), ER% (67eggs), F% (91.7%), HFE% (89.1%) and THE% (81.7%), moreover, the best values for FC and M% compared to the other pure strains, followed by Italian II strain. No significant difference between S x I cross and it's reciprocal I x S were found for BWSM, ASM, EN_2 , ER, EW_1 , EW_2 , FI_1 , M%, F% and EP% traits. Moreover, the reciprocal crosses (I x M and M x I) had statistically the highest values for ER%, EM, FC, HFE%, HTE% and EM% compared to the other genotypes, while no significant difference were found between the two crosses for the rest studied traits. Fortunately, MM strain and both of its reciprocal crosses with II strain (I x M and M x I) had the highest values for EN_1 , EN_2 , ER, EM, FC, M%, HFE%, HTE% and EP% traits compared to the other genotypes. The MM strain had positive significant values of GCA for BWSM, EN_1 and ER traits. The II strain had positive significant GCA estimates of BWSM and EM. Both of the reciprocal crosses (I x M and M x I) had the highest positive significant estimates of SCA for EN_1 , FI_2 and M% traits, while, M x S and M x I had significantly the highest positive estimates for EN_1 , EW_1 , EW_2 and EM traits compared to the other genotypes. Reciprocal crosses (S x I and I x S) had significantly the highest values of SCA for BWSM, While, I x S hens had significantly positive values for EN_2 , ER, F%, HFE% and THE% traits followed by M x S cross for the former traits. Heterotic percentages (H %) of both of the reciprocal crosses S x I and I x S had positive and significant values of H% for BWSM, EN_2 and EM traits were found. Cross S x M had significant and positive estimates for EN_2 , ER, EW_1 , EW_2 and EM traits were observed. Moreover, I x M cross and it's reciprocal M x I had positive significant values for BWSM, EN_1 , EN_2 , ER %, EW_1 , EW_2 , EM and M%. On the other hand, the three crosses (S x I, S x M and M x I) and their reciprocal crosses had positive significant values of H% for F% and hatchability traits (except M x I for F %). Both of S x M and I x M crosses had positive significant values of reciprocal effect (R_E) (for BWSM and EM. The MM strain had positive significant values of maternal effect (M_E) for BWSM and negative significant estimates for EM. The SS strain had positive significant estimates of M_E for EN_1 , EN_2 , ER, EM FI_2 , and F% and hatchability traits. Positive significant estimates of M_E were found for MM strain concerning PE% and TEL% traits. The MM strain had positive significant values of (D_A) for EN_1 , EN_2 , ER, EM traits. Both of the SS and II strains had positive significant values of D_A for BWSM, ASM and EW_2 . On the other hand, II strain had positive values for EN_2 , ER%, EW_1 , EW_2 and EM traits. Both of MM strain and I x M cross had the highest expected breeding values for EN_1 , EN_2 , ER, EM, HFE%, and HTE % traits. Both of SS strain and I x S cross had the highest breeding values for BWSM, ASM, EW_1 , EW_2 , FI_1 , FI_2 , FC, M %, EM %, PE % and TEL% traits. Moreover, S x I cross had the highest estimates of GVFM for BWSM, ASM, FI_1 , FI_2 , FC, PE % and TEL% traits, while, M x I cross had the highest values of GVFM for EN_1 , EN_2 , ER, EM, and hatchability traits.

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1. Introduction

The genetic resource base of the indigenous chickens could form the basis for genetic improvement and diversification to produce breeds adapted to local conditions. However, breeding programs for local chicken will be difficult to set-up because of the competition with commercial breeding companies which have access to technology advantages and economics of scale (Hoffmann, 2005). Poultry industry has a history of using diallel crossing to establish broad genetic basis for the development of new breeds or lines and to find superior crossbreds. Crossbreeding can be used as a tool that allows manipulating genetic variation to change the populations in a fashion that attempts to optimize desired phenotype. The main purpose of crossing is to produce superior crosses to improve performance of local chickens and to combine different characteristics in which the crossed breeds were valuable for growth or egg production traits (Shebl *et al.*, 1990; Nawar and Abdou, 1999; Aly *et al.*, 2005; Amin, 2007 and 2008; Saadey *et al.*, 2008; Lalev *et al.*, 2014). According to some researchers (Fairfull and Gowe, 1990 and Abou El-Ghar *et al.*, 2003), the anticipated dominant effect is high for egg production traits, while others affirm that the additive effect is markedly higher than the dominant effect. Many reports showed that general combining ability (additive genetic effects) was high and important as well as specific combining ability (non-additive effects that involve dominance and epistasis) (Mohamed *et al.*, 2005; Aly *et al.*, 2005; Amin, 2007). Shebl *et al.* (1990) found highly estimates of non-additive gene effects for native breeds. The estimation of crossbreeding effects (combining ability, general and specific, direct genetic effect and heterotic, maternal and reciprocal effects) is therefore of major importance. Many reports showed that

general combining ability was high and important as well as specific combining ability for body weight at different ages (Mohamed *et al.*, 2005; Amin, 2007; Saadey *et al.*, 2008; El-Bayomi *et al.*, 2009; Razuki and Sajida, 2011; Abou El-Ghar *et al.*, 2012 and Lalev *et al.*, 2014).

The objectives of the present study were to evaluate crossbreeding effects, combining ability, general (GCA) and specific (SCA), percentage of heterotic effect (H%), reciprocal effect) R_E (maternal effect) M_E (and, direct additive effect) D_E (for egg production and hatching traits in purebred parental and their crosses. Moreover, using GCA and SCA to predict the hybrid performance and breeding (BV) and genetic (GVFM) values for purebred parental and their crosses in 3x3 diallel mating system among one local strain (Mandarah, MM) and two exotic parental commercial meat types breed) Saso (SS) and Italian (II) chickens.

2. Materials and Methods

This experiment was conducted at Maryout Experimental Station, belonging to the Desert Research Center, Ministry of Agriculture, through the period from two successive years. One local breed (Mandarah, MM) and two exotic parental commercial meat types' strains, Saso (SS) and Italian (II) chickens were used. The local strain was obtained from the Poultry Improvement Project (Ferhash, Behaira Governorate), while the commercial two exotic ones were obtained from the General Poultry Company, Cairo, Egypt. Birds were apparently healthy, vaccinated and medicated against the common diseases (according to the vaccination program, in the corresponding centers). The mating design was made in 3 x 3 full diallel and all possible combinations (nine crosses) among these genotypes had been done (3 purebreds and 6 crossbreds), Table 1.

Table1: Mating design

Females \ Males*	SS	II	MM
Saso, SS	S×S	I×S	M×S
Italian, II	S×I	I×I	M×I
Mandarah, MM	S×M	I×M	M×M

* Male parent was given the first letter.

All chicks tested in this experiment originated from parents were divided into 3 groups in sire and dam position. Each group included 756 hens from the three genotypes (252 hens from each strain) and 108 cocks (7 females and one male each). The eggs were collected for 7 days, marked with combination mating (cross type) and set in incubator. The hatched chicks, 2160 (240 chicks per combination cross) were reared

on floor pens with wood shavings. Each cross was allocated on 4 pens (replicates) with 60 chicks per pen (3.2 x 3.5 m²). The chicks were provided with heat and light program according to the recommendations of growing management. At 28 days of age, males and females were sexed phenotypically via external characteristics at hatch all chicks were weighed using electronic scale within 0.1 g precision and reared

according to each cross in floor pens till 135 days of age.

All chicks were fed *ad libitum* basis on commercial starting diet (up to 4 wks) of 22% protein and 2770 kcal/kg, grower (4-12 wks) diet of 18% protein and 2750 kcal/kg, and a layer (16 wks-up) diet of 16% protein and 2700 kcal/kg. At 135 days of age, pullets of each of the three strains and their crosses were divided at random into nine groups (3 purebreds and 6 crossbreds). Each group is composed of 4 pens and all pens containing 14 pullets each. Feed consumption by pen was recorded weekly.

Egg production traits:

Age in days (ASM) and body weight in grams (BWSM) were recorded for each individual pullets in each pen reached 50 % of egg production. Egg production was recorded daily through the first 90 and 180 days of laying for each breeding pen. Egg weight was recorded in grams during both of the two intervals. Egg mass was calculated in grams by multiplying the numbers of eggs per hen housed by the average of egg weight for the two studied intervals. Feed consumption was recorded for each pen weekly and recorded in gram per hen per day and gram per egg and feed efficiency was estimated for the two traits for the 180 days of laying. In addition, mortality percentage was estimated for the interval studied.

Hatch traits:

Settable eggs were sanitized and stored in a cooler at approximately 10°C and 70% RH. Eggs were incubated for 18 day at 37.5°C and 55 % RH and then transferred into a hatch operating at 37.2°C and 70 % RH. Fertility was calculated by the number of fertile eggs as a percentage of total number of eggs set. Hatchability was calculated by the number of hatched healthy chicks as a percentage of fertile eggs. All unhatched eggs were broken to calculate embryonic mortality rate during the period of 7- 18 days of incubation as a percentage of fertile eggs. All non-hatched eggs were categorized to early embryonic mortality (the embryos dead during the first week of incubation), mid embryonic mortality (the embryos dead during the second week of incubation), and late embryonic mortality (internal and external pip embryos) and embryonic mortality included early embryonic and mid embryonic mortality.

Statistical analysis:

All percentages of the hatch traits were transferred to arcsine values before analysis. Data of all studied traits were analyzed using fixed models SAS Institute, SAS User's Guide (2000). Differences which considered significant were compared by Duncan Test (Duncan, 1955). Data was analyzed using the following linear model.

$$Y_{ij} = \mu + G_i + e_{ij}$$

Where

Y_{ij} = the observed value of the ij^{th} pullet,

μ = the overall mean,

G_i = the effect of the i^{th} genotype,

e_{ij} = the effect of random error.

CBE program package (Wolf, 1996) was used to estimate the genetic parameters.

1-General Combining Ability (GCA):-

The GCA values were calculated as the deviation of specific genotype means from overall mean for given trait estimated for nine diallel crosses [i.e., $GCA_i = (\sum y_i/n) - \mu$], where GCA_i = the GCA for strain (SS, II and MM Genotypes), y_i = trait for a progeny with either one of his or her parents or both parents from line i , and μ = overall mean for given trait estimated from all nine diallel crosses.

The GCA for (S×S) calculated from formula as:-

$$GCA \text{ for } (S \times S) = \{0.2 * [(SS) + (S \times I) + (S \times M) + (I \times S) + (M \times S)] - 0.11 * [(SS) + (II) + (MM) + (S \times I) + (S \times M) + (I \times M) + (I \times S) + (M \times S) + (M \times I)]\}$$

2- Specific Combining Ability (SCA):-

The SCA was calculated as follows:

SCA_{ij} = cross effect- ($GCA_i + GCA_j$), where the cross effect = certain trait mean of given cross-overall mean of certain trait, GCA_j = the GCA for line j (SS, II and MM Genotypes) (Odeh *et al.*, 2003).

The SCA for (S×I) calculated from formula as:-

$$SCA \text{ for } (S \times I) = \{[(S \times I) - 0.11 * [(SS) + (II) + (MM) + (S \times I) + (S \times M) + (I \times M) + (I \times S) + (M \times S) + (M \times I)]] - [(GCA \text{ for } S \times S + GCA \text{ for } II)]\}$$

3-Heterosis and Reciprocal Heterosis Percentages:-

Heterosis was calculated on percentage of midparents: $\{F_1 - [(P_1 + P_2)/2] / [(P_1 + P_2) / 2] \times 100\}$ using mean, where F_1 = the first cross and P_1 or P_2 is a parent in diallel and reciprocal crosses (Williams *et al.*, 2002).

Heterosis % for crosses (S×I) = $\{(S \times I) - [(S \times S + I \times I)/2] / [(SS + II) / 2] \times 100\}$

4-Reciprocal Effect (R_E) and Maternal Effect (M_E):-

Reciprocal effect for the combination $i \times j$ was calculated as $r_{ij} = (y_{ij} - y_{ji})/2$.

Reciprocal effect for (S×I) = $[(S \times I) - (I \times S)] / 2$.

Maternal effect was calculated as the mean deviation of progeny for a particular dam from mean estimated from a particular sire line (i.e. $m_j = (y_{i.j} - y_{i.})$), where $y_{i.j}$ = mean of dam line and $y_{i.}$ = mean of sire line.

Maternal effect for S×S = $1/3[(SS) + (I \times S) + (M \times S)] - 1/3[(SS) + (S \times I) + (S \times M)]$

5-Direct Additive Effect (D_E) (i.e. line group of sire differences):-

D_E for (SS) = $1/3[(SS) + (S \times I) + (S \times M)] - 1/4 [(II) + (M \times M) + (I \times S) + (M \times S)]$

D_E for (II) = $1/3[(II) + (I \times S) + (I \times M)] - 1/4 [(SS)$

+ (M M) + (S x I) + (M x I)]
 D_E for (MM) = $1/3[(MM) + (M x S) + (M x I)] - 1/4 [(SS) + (I I) + (S x M) + (I x M)]$

7- Expected of Hybrid Performances

The expected full-sib family (cross) mean is the sum of four components were μ = overall mean for given trait estimated from all nine diallel crosses, GCA for male, and for female, and SCA for male and female (Gowda *et al.*, 2012). Hybrid mean for (S x I) calculated from formula as:-

$\bar{x}_{s \times i} = \mu + GCA \text{ for } (S \times S) + GCA \text{ for } (I \times I) + SCA \text{ for } (S \times I)$

8-Expected Breeding values (BV) and Genetic values (GV)

Breeding value of a parent or half-sib family is 2 times of its general combining ability. $BV = 2GCA$.

Any cross between two parents has an expected breeding value, which is the sum of the GCA of male and female. $BV_{FM} = GCAF + GCAM$

The expected full-sib family (cross) mean may deviate from above sum. This deviation is called specific combining ability (SCA) of two parents. The sum of three components is called genetic value of the cross:

$$GV = GCAF + GCAM + SCA_{FM}$$

Where, GCAF, GCAM, and SCA_{FM} are general combining ability of female, male and the specific combining ability of the cross between both sexes. (Isik, 2009).

3. Results and Discussion

Egg production traits:-

The results of Tables 2 and 3 showed that highly significant ($p < 0.001$) differences among the different genotypes for pullets body weight (BWSM) and age (ASM) at 50 % egg production, egg number per hen-housed at both of the first 90 day (EN_1) and at the first 180 day of production (EN_2). Saso (SS) pullets and both its reciprocal crosses with the Italian cross were the heaviest at sexual maturity and had significantly ($P < 0.001$) the highest values of ASM while the same three genotypes had significantly the lowest averages of EN_1 and EN_2 . Also, high significant differences among the different genotypes were found concerning egg production rate (ER%), egg weight at the two aforementioned intervals of laying (EW_1) and (EW_2), egg mass (g/hen/180day) (EM), where the MM strain and its reciprocal crosses with the Italian strain had the highest rate of laying and SS strain and its reciprocal crosses with the Italian strains and M x S reciprocal cross had the heaviest eggs at the 1st 90 d. Eggs laid by pullets of SS strain, S x M and I x M crosses and the three reciprocal crosses at the 1st 180 d were significantly the heaviest. On the other hand I x M cross and both of M x S and M x I reciprocal crosses had the highest egg mass production. Results at Table

4 showed highly significant differences among the different genotypes concerning feed intake (g/hen/d) (FI_1), feed intake (g/egg) (FI_2), feed efficiency (g feed/egg) (FC) and mortality percentage (M%) MM strain and its reciprocal crosses with the Italian strain had the lowest means for the former traits compared to the other genotypes.

The former results showed clearly that MM local strain was considered to be fitting parental lines that play an important role in improving egg production traits and mortality throughout the studied laying interval. These results were confirmed with **Annual book of Egyptian strains of chicken (2009)**, who reported that Egyptian local chicken had averages ranged from 190 to 215 eggs per hen for annual egg number, from 50 to 58 g for egg weight and from 9.5 to 12.5 Kg for the total egg mass ranged. Moreover, this finding agreed with those reported by Amin (2007), Kosba and Abd El-Halim (2008); Razuki and AL-Shaheen (2011), Iraqi *et al.* (2012) and Lalev *et al.* (2014). Also Abou El-Ghar *et al.* (2010, 2012 and 2014) Similar results were obtained by Razuki and Al-Shaheen (2011) crossed in a 3 x 3 diallel mating using three breeds of chickens (and they found significant differences among the different genotypes forage at sexual maturity and egg number were purebred was earlier in sexual maturity while their reciprocal crosses exhibited higher egg number than purebred. El-Diebshany *et al.* (2013) crossed in a 2 x 2 diallel mating using two local strains selected from Alexandria chickens (Egg line E and Meat line M) and two crosses, they found that body weight at sexual maturity of crossbred was higher than the purebred with no significant differences. Taha and Abd El-Ghany (2013) found that cross of El-Salam x Mandarah recorded the highest significant averages for at 90 days, 42 weeks of age, egg mass at 90 days, 42 weeks and 65 weeks of age, feed conversion ratio for egg production at 90 days, 42 weeks and 65 weeks of age.

General and specific combining ability for egg production traits:-

The general (GCA) and specific (SCA) combining ability for egg production traits are presented in Tables 2, 3 and 4. The GCA of BWSM, ASM, EW_1 , EW_2 , FI_1 , FI_2 , FC and M% for SS strains were positive and highly significant, in addition, it had the highest values compared to the other genotypes. It had highly significant negative GCA for EN_2 and EM traits. The MM had the highest positive values and highly significant for EN_1 , EN_2 , ER% and EM traits and it had highly negative significant for BWSM, FI_1 , FI_2 and M% traits. The II chicks had positive significant values for BWSM, and EM traits. Sands *et al.* (1995) noticed that the GCA for ASM ranged from 1.35 for WL to -16.35 for White Plymouth Rock

and for hen housed egg production from 0.90 for Rhode Island Red to -9.20 for Araucona. Most of the previous studies (**Eisen et al., 1967 and Fairfull et al., 1987**) concluded that the GCA was important. **Saadey et al. (2008)** found that the Sinai hens gave the highest values of GCA for EW compared to Fayoumi (F) hens which had the lowest values of GCA for EW. However, RIR and WL hens had intermediate values. However, Sinai hens had the lowest values of GCA for egg production. The F and RIR hens had intermediate value and RIR, WL and F hens achieved the highest values of GCA for egg number followed by Sinai hens. **Razuki and Al-Shaheen (2011)** found that significantly negative GCA for ASM, egg production and egg weight.

Specific combining ability (SCA) was significant source of egg production among cross-bred groups for egg production traits during the tested periods. Estimates of SCA for egg production traits indicated that I x M and M x I hens gave significantly positive estimates of SCA for EN₁, FI₂ and M% traits. However, MxS and M x I gave significantly positive estimates for EN₁, EN₂, EW₁, EW₂ and EM traits. These results indicate that non-additive genetic effects (e.g. dominance, over-dominance and epistasis) of these crossbreds were high on former traits. Cross of IxS recorded the highest values of SCA for BWSM (234.7g) followed by I x M cross (42.7g) while SxI and IxS hens had significantly the highest values of SCA for BWSM (225.6g), moreover, IxS hens had significantly the highest values for EN₂(3.8) and ER (4.84) followed by M x S cross (3.6) and (1.44) for EN₂ and ER, respectively. Contrary, MxS cross had significantly the highest values for EM (414.9g) followed by M x I cross (237.5g), moreover, M x I cross had the highest significant values for EN₁ (3.56), EW₁ (1.3) EW₂ (1.6) and FI₂ (4.6). It could be concluded that non – additive genetic effects of those crossbreds were high on egg weight and egg number. **Saadey et al. (2008)** found that Sinai x RIR, F x Sinai and WL x RIR hens gave positive estimates of SCA for egg weight, while F x RIR, F x WL and Sinai x WL hens had the lowest estimates of SCA for egg weight. The WL x RIR, F x Sinai, F x WL and Sinai x WL crosses revealed positive estimates of SCA for egg production rate. Moreover, Sinai x RIR recorded the lowest values of SCA for ER. The F x Sinai and WL x RIR hens recorded positive estimates of SCA for egg number in first 105 days of laying. **Razuki and Al-Shaheen (2011)** found that estimations of SCA of BW, ASM, egg production and egg weight varied from positive to negative depended on cross type. **Abou El-Ghar et al. (2012)** found that SCA variance was evident from mean squares, indicating that egg production traits had been controlled by non-additive genes. However, among the four male lines,

Silver Montazah showed maximum GCA effects for number of eggs at 90 d and at 180 d of laying.

Specific and reciprocal heterosis for egg production traits:-

Heterosis percentage estimates for egg production traits are presented in Tables 2, 3 and 4. The estimates of individual heterosis percentages (H%) within crosses revealed that I×S cross had positive and high heterosis percentage (H%) for BWSM (14.6%), EN₂ (34.1%), and ER (16.5%) followed by M x I cross for BWSM (8.2%), I x M cross for EN₂ (34.1%) and M x S for ER (14.0%). The I×M cross had positive and high H% for BWSM (8.2%). Fortunately, all genotypes had positive and high significantly heterotic percentages (specific and reciprocal heterosis) for EN₃, ER (except S×I cross had non-significant value), EW₁, EW₂ (except S×I and I×S crosses which had non- significant and negative values) and EM that ranged from 1.6% to 24.3%. In contrary, specific and reciprocal heterosis estimates for all genotypes were negative. Estimates were significant for FI₁, FI₂, FC and M% (except I×M cross had positive estimate (12.3%) and ranged from zero to- 43.2%. The previous results find in the literatures are in good agreement with this result, **Fairfull et al. (1987)** found an average heterosis of 11.9% for hen housed egg production to 497 days of age in a 4 x 4 diallel of unrelated WL strains. **Vitek et al. (1994)** revealed that an average heterosis was 10.8% for 274 days of production in an 8 x 8 full diallel of WL lines. **Merat et al. (1994)** noticed that the average heterosis for egg number recorded for seven months period was 7.5% and 10.5% for normal and dwarf genotype lines, respectively. With respect of egg weight, the values of heterosis measured at different ages that given by these authors didn't exceeded 2.55% when it measured at different ages at production periods, also, heterosis was 4.7% and 5.2% for normal and dwarf genotype lines, respectively. Generally, it seemed from the previous results, the highest heterosis is observed in egg production and the lowest in egg weight. Heterosis is usually greater for reproductive traits than for growth traits **Fairfull, (1990)**, which influenced by maternal and dietary effects. In this respect, **Khalil et al. (2004)**, **Abou El-Ghar et al. (2007)** and **Ghanem et al. (2008)** reported negative heterosis estimates for Matrouh (MT), Silver Montazah (SM), Inshas (IN) and Mandarah. The same findings were reported by **Udeh and Omeje (2005)**, and **Santosh and Deepak (2006)**. On the other hand, **Khalil et al. (2004)** found a positive H% for (EN₉₀). **Saadey et al. (2008)** found that F x S and S x RIR crosses and their reciprocals recorded positive and high heterotic effects on EW. Utilize WL dams with F, S and RIR sires achieved positive and high heterosis percentage for ER (5.48, 3.69 and 4.55%,

respectively). The same trend was observed for crossing between S dams and WL and F sires. The cross of S dams with F sires scored positive heterosis percentage for ER (2.7%). The F x S cross and its reciprocal SxF achieved the highest H% for egg number (12.49% and 8.12%, respectively). However, utilize WL dams with F, S and RIR sires gave high and positive H% for egg number (4.71, 5.81 and 1.72%, respectively). **Razuki and Al-Shaheen (2011)** found that all combinations (crosses or reciprocals) showed a positive heterosis in egg production ranged from 2.77 to 8.75% with significant average heterosis (3.20%). All combinations (crosses or reciprocals) showed a negative heterosis in egg weight from -0.15 to -3.66 with significant average heterosis (-1.21). Reciprocal effects were significant for BWSM and ASM and not in egg production or in egg weight. **El-Dlebhshany et al. (2013)** found that estimates of heterosis were -0.53 and -14.34 for ASM and BWSM, respectively, with no significant difference for these traits. Heterosis estimate for a cross (ML x EL) of ASM was -0.35, while heterosis for the reciprocal cross was -0.72. The negative results were indicated that the pure progenies have late ASM than the cross (EL x ML). The estimate of direct heterosis was 0.14 for (EN₉₀) while no significant differences were found for all egg productive traits.

Reciprocal, maternal and direct additive effects for egg production traits:-

Reciprocal effects were positive and significant for S×M and I×M crosses concerning BWSM, also for FI₁ and FI₂ in S×I cross while, negative significant values were found for EM in the three crosses (S×I, S×M and I×M.) (Tables 2, 3 and 4). Significant reciprocal effects for BW were found by **Jakubec et al. (1987)** and **Vitek et al. (1994)**, for egg production and egg weight were found by **Vitek et al. (1994)**. **Razuki and Al-Shaheen (2011)** found that reciprocal effects were found in ASM and not in egg production or in egg weight. Concerning maternal effect, the results obtained in Tables 2, 3 and 4 revealed that SS strain had positive significant (P<0.05) values for EN₂ (3.7 eggs), ER (3.33) and EM (295.3 g) traits, also, II strains for FI₁ (1.6) and FI₂ (7.0) and MM strains had positive significant values for BWSM (71.7g). **Saadey et al. (2008)** found that most crosses gave positive estimates of maternal effect for EW while the other crosses achieved positive and high estimates of maternal effect for egg production. **Razuki and Al-Shaheen (2011)** found that significant maternal effect on ASM was found in some crosses which they studied, while there were non-significant in egg production and egg weight due to maternal effect.

Regarding direct additive effect, results in Tables 2, 3 and 4 showed that MM strain had significantly (P<0.01) the highest values for EN₁ (10.7egg), ER (10.25) and EM (771.9g) followed by II strain for EN₂ (4.5egg), ER (2.92) and EM (435.0 g) and negative for EN₂ (16.7egg), while it had the lowest significant values for both of EW₁, EW₂ (which had equal estimates) and FI₁, FI₂ and M%. The SS strain had the highest significant (p<0.01) values for BWSM (423.3g), ASM (p<0.05) (6.5d), EW₁ (2.3g), EW₂ (2.3), FI₁ (8.2), FI₂ (53.2), FC (0.8) and M% (3.8). The results presented in this study for the direct additive effect and maternal effect indicating that using MM toms realized the best estimates compared to both of SS or II toms, this result suggested that the use of MM strain as a terminal sire breed in crossbreeding programs including SS or II dams would be beneficial for improving EN₁, EN₂, ER, EM, ASM, FI₁, FI₂, FC and M% traits.. Using SS toms in diallel crossing surpassed both of MM and II toms concerning BWSM, EW₁ and EW₂ traits. **Razuki and Al-Shaheen (2011)** found varied estimates negative or positive of the direct genetic effect among the different studied crosses for BW. Direct genetic effects on ASM and egg production traits were non-significant, while it was significant on egg weight. **El-Dlebhshany et al. (2013)** used a 2 x 2 diallel mating between two local strains (Egg line E and Meat line M) and two crosses and found that estimate of direct additive was 1.18 for ASM. The corresponding value for direct maternal genetic effect was 1.1 for the same trait. In addition, estimates of direct additive effect were positive for both of ASM and EN₉₀ they indicated that meat line was better as a sire than the egg line for the former traits. Estimate of direct maternal effect was positive for EN₉₀.

Using general and specific combining ability to expect of hybrid performances, breeding and genetic values for egg production traits:-

The expected of hybrid performance for egg production traits and the difference between both of the actual and the expected traits and the percentage of the difference are presented in Tables 5, 6 and 7. The differences (g and %) for the actual and the expected values and in relation to actual (Y) % for all genotypes were generally equal zero. It could be observed that the small difference may be due to figures rounded entering in the prediction equations, it is mean the sum of four components were μ = overall mean for given trait estimated from all nine diallel crosses, general combining ability for male, general combining ability for female and specific combining ability SCA for male and female (**Gowda et al., 2012**).

Table (2): Means \pm SE for actual (Y) body weight and age at sexual maturity, egg number per hen- housed at two intervals of laying, general and specific combining ability, heterosis% and reciprocal effect, maternal and direct effects at the diallel crossing of Saso (SS), Italian (II) and Mandarrah (MM) chickens strains

Genotypes	Body weight at 50 % egg production	Age at 50 % egg production	Egg number per hen- housed at	
			First 90 days	First 180 days
Purebreds				
SS	2550 ^a \pm 490	200 ^a \pm 19.0	43 ^f \pm 6.3	73 ^e \pm 10
II	1950 ^b \pm 250	195 ^b \pm 17.2	45 ^e \pm 9.2	100 ^d \pm 11
MM	1200 ^c \pm 220	175 ^c \pm 19.2	65 ^a \pm 11	120 ^a \pm 15
Crosses				
S \times I	2550 ^a \pm 250	195 ^b \pm 25.0	42 ^f \pm 7.1	94 ^d \pm 111
S \times M	1620 ^e \pm 300	190 ^c \pm 23.2	50 ^d \pm 10	107 ^c \pm 13.
I \times M	1800 ^c \pm 210	185 ^d \pm 18.3	59 ^b \pm 10	113 ^b \pm 13.
Reciprocal				
I \times S	2550 ^a \pm 320	192 ^b \pm 21.2	45 ^e \pm 7.8	102 ^d \pm 12
M \times S	1500 ^f \pm 200	192 ^b \pm 22.1	55 ^c \pm 9.9	110 ^b \pm 12
M \times I	1705 ^d \pm 310	182 ^d \pm 25.0	60 ^b \pm 12	115 ^a \pm 13
Overall mean	1930.6	189.0	51.60	103.8
Significance	***	***	***	**
General Combining Ability (GCA)				
SS	213.4 \pm 30**	4.8 \pm 0.9**	-4.5 \pm 0.8 ns	-6.6 \pm 1.1**
II	180.4 \pm 22**	-0.2 \pm 0.01ns	-1.3 \pm 0.1 ns	1.0 \pm 0.1ns
MM	-365.5 \pm 36**	-5.2 \pm 1.01ns	6.2 \pm 1.8**	9.2 \pm 1.7**
Specific Combining Ability(SCA)				
S \times I	225.6 \pm 55**	1.4 \pm 0.2*	-3.6 \pm 0.5*	-4.2 \pm 1.0 ns
S \times M	-158.5 \pm 23 ns	1.4 \pm 0.2 ns	-3.2 \pm 0.6 ns	0.6 \pm 0.1 ns
I \times M	54.5 \pm 11*	-3.6 \pm 0.3 ns	2.6 \pm 0.6*	-1.0 \pm 0.1 ns
I \times S	225.6 \pm 32**	-1.6 \pm 0.2 ns	-0.6 \pm 0.1 ns	3.8 \pm 0.2*
M \times S	-278.5 \pm 30**	3.4 \pm 0.7*	1.76 \pm 0.2*	3.6 \pm 0.7*
M \times I	-40.5 \pm 7.0*	-1.6 \pm 0.3	3.56 \pm 0.7*	1.0 \pm 0.1*
Specific heterosis				
S \times I	14.6 \pm 1.60**	-1.3 \pm 0.07*	-4.5 \pm 0.7*	8.7 \pm 1.1**
S \times M	-12.4 \pm 1.3 ns	1.3 \pm 0.07 ns	-7.4 \pm 0.5 ns	10.9 \pm 1.4**
I \times M	14.3 \pm 1.45**	-2.7 \pm 0.09 ns	7.3 \pm 0.72**	2.7 \pm 0.11**
Reciprocal heterosis				
I \times S	14.6 \pm 1.8**	-2.8 \pm 0.08*	2.3 \pm 0.2*	17.9 \pm 2.9**
M \times S	-18.9 \pm 1.9**	2.4 \pm 0.10*	1.8 \pm 0.2*	14.0 \pm 2.1**
M \times I	8.2 \pm 0.95*	-1.6 \pm 0.01 ns	9.0 \pm 0.10**	4.6 \pm 0.90**
Reciprocal effect				
S \times I	0.0 \pm 0.00 ns	1.5 \pm 0.08 ns	-1.5 \pm 1.0 ns	-4.0 \pm 0.8 ns
S \times M	60.0 \pm 7.20*	-1.0 \pm 0.05 ns	-2.5 \pm 0.9 ns	-1.5 \pm 0.05 ns
I \times M	47.5 \pm 4.9*	-1.0 \pm 0.01 ns	-0.5 \pm 0.2 ns	-1.0 \pm 0.02 ns
Maternal effect				
SS	-40.0 \pm 5.6*	-0.3 \pm 0.00 ns	2.7 \pm 0.3*	3.7 \pm 0.4*
II	-31.7 \pm 4.5*	1.7 \pm 0.07 ns	-0.7 \pm 0.0 ns	-2.0 \pm 0.2 ns
MM	71.7 \pm 9.3*	-1.3 \pm 0.20 ns	-2.0 \pm 0.2 ns	-1.7 \pm 0.3 ns
Direct additive effect				
SS	423.3 \pm 50**	6.5 \pm 0.65*	-7.5 \pm 0.7*	-16.7 \pm 1.2 ns
II	111.2 \pm 12**	2.7 \pm 0.3*	-2.8 \pm 0.2	4.5 \pm 0.45*
MM	-499.2 \pm 40**	-8.0 \pm 0.7 ns	ns10.7 \pm 0.9*	16.7 \pm 0.2*

(a-h)= Means within a column with no common superscripts differ significantly ($p < 0.01$),* $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, ns: not significant.

Concerning breeding values for the pure line (2GCA) the MM strain had the highest breeding values for EN₁ (12.49), EN₂ (18.44), ER (9.91) and EM (983.02) followed by II strain while, SS strain had the lowest values for the aforementioned traits. Contrarily, the pure line SS had the highest breeding values for BWSM (426.89g), ASM (9.60d), EW₁ (3.3), EW₂ (3.31), FI₁ (7.06), FI₂ (38.9), FC (0.52) and M % (2.30) followed by II strain while, MM strain had the lowest values for the aforementioned traits. As for breeding value for the crosses, results obtained in Tables 5, 6 and 7 revealed that SS had the highest and positive estimates of breeding values concerning BWSM, ASM, egg weight, feed intake, feed conversion and mortality percentage traits. The estimates of the rest traits were negative. The three crosses had the same trend (value and sign) for

breeding values of the pure lines. Considering the genetic values for crosses (GVFM), the S×I cross had the highest estimates for BWSM (619.40), ASM (6.00), FI₁ (1.09), FI₂ (15.35), and FC (0.28) followed by its reciprocal cross I×S, while M×I cross had the highest and positive values of GVFM for EN₁ (8.4), EN₂ (11.2), ER (5.56) and EM (808.11) while I×M cross were 7.40, 9.20, 4.56 and 571.11 for the former traits, respectively. The values of genetic values showed that the offspring of the M×I cross had better performance than those of its reciprocal cross I×M for the former traits. The superiority of MM as sires or dam suggest that the use of this strain as a terminal sire breed or dam breed in crossbreeding programs including II and SS strains would be beneficial for improving most of the egg production traits.

Table (3): Means± SE for actual (Y) egg production rate at first 180 days, egg weight at 90 days, egg weight at 180 days, egg mass at 180 days, general and specific combining ability, heterosis%, reciprocal effect, maternal and direct effects at the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chickens strains

Genotypes	Egg production rate		Egg weight, g at the 1 st 90 days.	Egg weight, g at the 1 st 180 days	Egg mass, g at the 1 st 180 days)
	Actual	Corrected			
Purebreds					
SS	41 ^d	39.8±4.5	60.5 ^a ±8.1	64.0 ^a ±8.5	4672 ^c ±520.2
II	56 ^c	48.4±4.9	58.2 ^b ±7.8	61.0 ^b ±7.4	6100 ^c ±670.8
MM	67 ^a	54.9±6.5	50.7 ^d ±7.1	54.0 ^c ±6.1	6480 ^b ±750.9
Crosses					
S×I	52 ^c	46.1±4.9	59.0 ^a ±6.3	61.0 ^b ±7.5	5734 ^d ±620.8
S×M	59 ^b	50.2±6.2	58.8 ^b ±6.2	62.0 ^a ±7.3	6634 ^b ±710.2
I×M	63 ^a	52.5±6.9	56.7 ^c ±6.2	61.0 ^b ±7.6	6893 ^a ±800.8
Reciprocal					
I×S	56 ^c	48.4±4.8	60.3 ^a ±7.9	62.0 ^a ±6.5	6324 ^c ±740.3
M×S	61 ^b	51.4±6.3	59.4 ^a ±6.8	63.0 ^a ±6.3	6930 ^a ±800.8
M×I	64 ^a	53.1±6.7	58.6 ^b ±7.1	62.0 ^a ±7.2	7130 ^a ±820.4
Overall mean	58		58	61	6278
Significance	**		*	**	**
General Combining Ability (GCA)					
SS	-3.80±0.5**	1.7±0.070**	1.7±0.50**		-219.0±22.5**
II	0.59±0.09ns	0.6±0.010 ns	0.7±0.01 ns		158.3±17.9**
MM	4.96±0.90**	-1.2±0.07 ns	-1.0±0.05 ns		456.3±50.1**
Specific Combining Ability (SCA)					
S×I	-3.10±0.55 ns	-1.2±0.10**	-2.0±0.20**		-483.1±50.5**
S×M	-0.56±0.05 ns	0.44±0.01ns	0.6±0.07 ns		118.9±12.4**
I×M	-0.96±0.05 ns	-0.68±0.07 ns	0.3±0.01 ns		-34.7±3.90**
I×S	4.84±0.80**	0.08±0.01 ns	-1.0±0.04 ns		106.9±10.9**
M×S	1.44±0.02**	1.04±0.09**	1.6±0.01**		414.9±45.3**
M×I	0.04±0.00 ns	1.3±0.200**	1.6±0.02**		237.5±25.7**
Specific heterosis					
S×I	8.7±0.90 ns	-0.6±0.01 ns	-2.4±0.26 ns		6.5±0.90**
S×M	10.9±1.9**	5.8±0.42**	5.1±0.80**		19.0±2.6**
I×M	2.7±0.38**	4.1±0.50**	6.1±0.75**		9.6±1.20**
Reciprocal heterosis					
I×S	16.5±2.2**	1.6±0.25 ns	-0.8±0.07 ns		17.4±2.30**
M×S	14.0±1.9**	6.8±0.88**	6.8±0.78**		24.3±3.0**
M×I	4.5±0.60**	7.6±1.00**	7.8±0.90**		13.4±1.80**

Reciprocal effect				
S×I	-4.00±0.30**	-0.7±0.01 ns	-0.50±0.04 ns	-295.0±35.20**
S×M	-1.00±0.09 ns	-0.3±0.00 ns	-0.50±0.04 ns	-148.0±22.50**
I×M	-0.50±0.05 ns	-1.0±0.01*	-0.50±0.03 ns	-118.5±14.20**
Maternal effect				
SS	3.33±0.20*	0.6±0.01 ns	0.67±0.08 ns	295.3±32.50**
II	-2.33±0.25 ns	0.2±0.01 ns	0.00±0.00 ns	-117.7±18.21**
MM	-1.00±0.01 ns	-0.8±0.01 ns	-0.67±0.07 ns	-177.7±20.1**
Direct additive effect				
SS	-11.08±1.80 ns	2.3±0.03**	2.3±0.20**	-778.5±80.50**
II	2.92±0.35**	1.2±0.10*	1.0±0.10*	435.0±45.90**
MM	10.25±1.53**	-2.3±0.25**	-2.3±0.21**	771.9±780.21**

(a-e)= Means within a column with no common superscripts differ significantly (p<0.01)

* P ≤ 0.05, ** P ≤ 0.01, *** P ≤ 0.001, ns: not significant.

Table (4): Means± SE for actual (Y) feed intake, feed efficiency, mortality percentage (%), general and specific combining ability, heterosis%, reciprocal effect, maternal and direct effects at the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chickens strains

Genotypes	Feed intake		Feed efficiency	Mortality (%)	
	g/hen/d	g/egg		Actual	Corrected
Purebreds					
SS	120.1 ^a ±15.1	295.9 ^a ±35.9	4.6 ^d ±0.56	15.5 ^a	3.93±0.4
II	110.0 ^b ±12.3	198.0 ^b ±20.5	3.2 ^c ±0.45	7.3 ^b	2.70±0.3
MM	90.2 ^f ±10.2	135.0 ^d ±15.6	2.5 ^a ±0.4	5.2 ^c	2.28±0.2
Crosses					
S×I	105.1 ^c ±11.2	201.1 ^b ±22.3	3.3 ^c ±0.42	7.5 ^b	2.73±0.7
S×M	105.0 ^c ±11.3	176.6 ^c ±20.8	2.85 ^b ±0.3	8.2 ^b	2.86±0.3
I×M	98.2 ^e ±10.20	156.1 ^d ±18.6	2.56 ^a ±0.3	7.1 ^{b c}	2.66±0.3
Reciprocal					
I×S	102.0 ^c ±10.9	180.4 ^c ±23.5	2.91 ^b ±0.3	7.5 ^b	2.73±0.3
M×S	105.1 ^c ±10.8	171.8 ^c ±19.2	2.73 ^b ±0.3	6.5 ^{b c}	2.54±0.3
M×I	100.3 ^d ±11.0	156.1 ^d ±17.5	2.52 ^a ±0.3	6.2 ^{b c}	2.48±0.3
Overall mean	103.9	185.7	3.0	7.9	
Significance	**	***	**	***	
General Combining Ability (GCA)					
SS	3.5±0.42 **	19.4±2.50**	0.3±0.08**	1.2±0.20*	
II	-0.9±0.07ns	-7.3±0.91 ns	-0.1±0.01 ns	-0.8±0.09 ns	
MM	-4.3±0.95**	-26.5±3.50**	-0.4±0.07 ns	-1.3±0.30**	
Specific Combining Ability (SCA)					
S×I	-1.6±0.21 ns	3.2±0.35**	0.14±0.01**	-0.8±0.09 ns	
S×M	1.9±0.23**	-2.0±0.21 ns	-0.0±0.00 ns	0.4±0.01 ns	
I×M	-0.7±0.07**	4.2±0.60**	0.0±0.00 ns	1.2±0.20**	
I×S	-4.4±0.45 ns	-17.5±1.5 ns	-0.3±0.02 ns	-0.8±0.08 ns	
M×S	1.9±0.21**	-6.9±0.89 ns	-0.2±0.01 ns	-1.3±0.20 ns	
M×I	1.3±0.13**	4.6±0.70**	0.0±0.00 ns	0.3±0.01**	
Specific heterosis					
S×I	-8.7±1.12 ns	-18.6±2.10**	-15.5±1.24	-34.2±4.50**	
S×M	0.0±0.00 ns	-18.0±2.20**	-19.7±2.26**	-20.8±2.90**	
I×M	-2.0±0.09 ns	-6.2±1.00 ns	-11.5±1.12	12.3±1.95**	
Reciprocal heterosis					
I×S	-11.2±1.50**	-27.0±3.25 ns	-25.4±2.32**	-34.2±4.20**	
M×S	0.0±0.00 ns	-20.3±3.00 ns	-23.2±2.29**	-43.0±4.98**	
M×I	0.0±0.00 ns	-0.0±0.00 ns	-10.2±1.90	-0.8±0.080 ns	

Reciprocal effect				
S×I	1.4±0.12*	10.4±1.20*	0.2±0.01 ns	0.3±0.01 ns
S×M	0.0±0.00 ns	2.4±0.25*	0.0±0.00 ns	0.9±0.08 ns
I×M	-1.0±0.01 ns	-0.2±0.04 ns	0.0±0.00 ns	0.5±0.04 ns
Maternal effect				
SS	-0.9±0.04 ns	-8.5±0.90*	-0.2±0.01 ns	-0.6±0.02 ns
II	1.6±0.08*	7.0±0.89*	0.1±0.01 ns	-0.3±0.01 ns
MM	-0.7±0.07 ns	1.5±0.12 ns	0.0±0.00 ns	0.9±0.07 ns
Direct additive effect				
SS	8.2±1.20**	53.2±6.30**	0.8±0.07*	3.8±0.40**
II	-0.3±0.05 ns	-19.0±2.21*	-0.4±0.07 ns	-1.3±0.20 ns
MM	-9.9±1.10*	-52.2±6.6*	-0.7±0.08 ns	-3.6±0.39*

(a-d)= Means within a column with no common superscripts differ significantly ($p < 0.01$),

* $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, ns: not significant.

Table (5): Prediction traits for body weight and age at sexual maturity, egg number per hen- housed at two intervals of laying, breeding value, genetic value and differences and percent between actual (Y) and predicted (\tilde{Y}_i) from the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chickens strains

Prediction traits	Genotypes	Body weight at 50 % egg production	Age at 50 % egg production	Egg number per hen- housed	
				First 90 days	First 180 days
Hybrid (\tilde{Y}_i)	S×I	2550.00	195.00	42.00	94.00
	S×M	1620.00	190.00	50.00	107.00
	I×M	1800.00	185.00	59.00	113.00
	I×S	2550.00	192.00	45.00	102.00
	M×S	1500.00	192.00	55.00	110.00
	M×I	1705.00	182.00	60.00	115.00
Breeding values	SS	426.89	9.60	-9.11	-13.16
	II	360.89	0.49	-2.71	2.04
	MM	-731.11	-9.51	12.49	18.44
	S×I	393.90	4.60	-5.90	0.40
	S×M	-152.10	-0.40	1.70	2.70
	I×M	-185.10	-5.40	4.90	10.20
Genetic values	S×I	619.40	6.00	-9.60	-9.80
	S×M	-310.60	1.00	-1.60	3.20
	I×M	-130.60	-9.00	7.40	9.20
	I×S	618.00	3.00	-6.60	-1.80
	M×S	-430.60	3.00	3.40	6.20
	M×I	-225.60	-7.60	8.40	11.20

-The differences (g and %) for the actual and expected and in relation to actual (Y) % for all genotypes were approximately equal zero.

Table (6): Prediction traits for egg production rate at first 180 day, egg weight at the 1st 90 d, egg weight at the 1st 180 day, egg mass at the 1st180 day, breeding value, genetic value and differences and percent between actual (Y) and predicted (\tilde{Y}_i) from the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chicken strains

Prediction traits	Genotypes	Egg production rate	Egg weight, g at the 1 st 90 days	Egg weight, g at the 1 st 180 days	Egg mass, g at the 1 st 180 days
Hybrid (\tilde{Y}_i)	S×I	52.00	59.00	61.00	5734.00
	S×M	59.00	58.80	62.00	6634.00
	I×M	63.00	56.70	61.00	6893.00
	I×S	56.00	60.30	62.00	6324.00
	M×S	61.00	59.40	63.00	6930.00
	M×I	61.00	58.60	62.00	7130.00

Breeding values	SS	-7.69	3.30	3.31	-438.20
	II	1.11	1.00	0.58	228.62
	MM	9.91	-2.40	-1.42	983.02
	S×I	-3.29	2.12	1.58	-148.78
	S×M	1.11	0.40	0.58	228.42
	I×M	5.51	-0.64	-0.42	605.82
Genetic values	S×I	-6.44	0.98	-0.11	-587.89
	S×M	0.56	0.78	0.89	312.11
	I×M	4.56	-1.32	-0.11	571.11
	I×S	1.56	2.28	0.89	2.11
	M×S	2.56	1.38	1.89	608.11
	M×I	5.56	0.58	0.89	808.11

-The differences (g and %) for the actual and expected and in relation to actual (Y) % for all genotypes were approximately equal zero.

Table (7): Prediction for feed intake, feed efficiency, mortality percentage (%), breeding value, genetic value and differences and percent between actual (Y) and predicted (\bar{Y}_i) from the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chicken strains

Prediction traits	Genotypes	feed intake		Feed efficiency	Mortality percentage (%)
		g/hen/d	g/egg		
Hybrid (\bar{Y}_i)	S×I	105.10	201.10	3.30	7.50
	S×M	105.00	176.60	2.85	8.20
	I×M	98.20	156.10	2.56	7.10
	I×S	102.00	180.30	2.91	7.50
	M×S	105.10	171.80	2.73	6.50
	M×I	100.30	156.50	2.52	6.20
Breeding values	SS	7.06	38.90	0.52	2.30
	II	-1.74	-14.60	-0.24	-1.54
	MM	-8.62	-53.00	-0.77	-2.30
	S×I	2.66	12.14	0.14	0.38
	S×M	-0.78	-7.05	-0.13	-0.10
	I×M	-5.18	-33.79	-0.51	-2.02
Genetic values	S×I	1.09	15.35	0.28	-0.39
	S×M	1.09	-9.07	-0.17	0.31
	I×M	-5.91	-29.60	-0.46	-0.79
	I×S	-1.71	-5.36	-0.11	-0.39
	M×S	1.09	-13.89	-0.29	-1.39
	M×I	-3.91	-29.19	-0.49	-1.69

-The differences (g and %) for the actual and expected and in relation to actual (Y) % for all genotypes were approximately equal zero.

Hatching traits

There were highly significant differences among the different genotypes for fertility percentage (F %), hatchability percentages of fertile eggs (HFE %), hatchability percentages of total eggs (HTE %), and embryonic mortality (EM %), egg pip mortality (EP %) and total egg loss (TEL %) percentages, Tables (8 and 9). The pure line MM had the highest significant values of F%, HFE% and HTE% (91.7%, 89.09% and 81.7%, respectively) compared to the other pure lines followed by II strain. While MM had the lowest significant values for EP% (3.0%) and TEL % (18.3%). No significant differences among the MM strain and both of its reciprocal crosses with II strain were found. On the other hand, eggs laid by both of S×M and M×S pullets had the lowest values for the

same traits. No significant differences were found among the three pure strains, S x I, I x M and M x I crosses concerning EM% trait. On the other hand, MM pure strain and its reciprocal crosses with II strain had significantly the lowest values of PE%; also, the three aforementioned genotypes and IxS cross had the lowest estimates of TEL%. Crossbreds were found to have higher fertility percentage than their parental pure strains (**Gad et al., 1991**). Significant differences between strains, lines and crossbreds in hatchability traits were reported by **Mostafa and Younis (2001)**, **Amin (2008)**, **El-Diebshany et al. (2013)** and **Taha and Abd El-Ghany (2013)** in chickens and **Hulet et al. (1992)**, **Nestor and Noble (1995)** and **Amin (2014a and 2014b)** in turkeys. **Taha and Abd El-Ghany (2013)**

found that cross of El-Salam x Mandarah strains recorded the highest significant averages for fertility and hatchability for total eggs percentages compared to the pure strains.

General (GCA) and specific (SCA) combining ability for hatch traits:-

The GCA and SCA for hatch traits are presented in Tables 8 and 9. The MM strain had the highest positive significant values of GCA for HFE% (3.57) and HTE% (3.65) traits, while SS strain had the lowest negative significant values of GCA and II strain had intermediate estimates. On the other hand, the SS strain had the highest positive significant values of GCA for EP% and TEL%, while MM strain had the lowest negative significant values of GCA for the aforementioned traits. The SCA was significant source of hatch traits among cross-bred groups for hatch traits. Estimates of SCA showed that I×S reciprocal cross had the highest positive significant values of SCA for F% (2.21), HFE % (1.95) and THE% (3.35) followed by M×S cross (0.31, 1.41 and 1.75, respectively) while M x I had the lowest significant values of GCA (0.17, 0.75 and 0.83, respectively), for the same traits. However, I x S gave significantly positive estimates for EM%, EP%, and TEL%. Working on turkeys, **Amin (2008)** found that GCA for the local Black Baladi (B) strain was superior to those for the White Nicholas strain (W) for F%, H%, and EM%. Moreover, the SCA for BW cross was positive and higher than that for its reciprocal cross WB for fertility. Also, the results indicated that the SCA effect for BW cross was better than its reciprocal cross WB for embryonic mortality percentage.

Specific and reciprocal heterosis for hatch traits:-

Results of Tables 8 and 9 showed that I×S reciprocal cross had the highest positive significant values of heterosis (H%) for F% (7.0%), HFE% (11.3%) and THE% (18.2%) traits followed by I x S cross for F% (5.30%) and M×S cross for HFE% (9.20%) and THE% (13.04%) traits, while I x M cross had the lowest significant values of H% for F%, HFE% and THE% traits (-2.14%, 3.58% and 1.28%, respectively). Generally, crosses and reciprocal crosses had positive significant values of heterosis (H %) for F% (except IxM and M x I crosses which were negative). On the other hand, HFE% and THE% had negative significant values of heterosis H% for EM% (except M x I was positive), EP% and TEL% traits. Similar results were found by **Hossari and Dorgham (2000)** who found positive heterotic effects on hatchability. In addition, **Amin (2008)** found that in turkeys BW cross had superior heterotic effect than the WB reciprocal cross for fertility, hatchability, embryonic mortality percentages. Moreover, crossing enhanced early embryonic mortality percentage of

both the reciprocal crosses, the range of H% was -3.18 % to -4.28% and for mid embryonic mortality percentages (-36.38% - 18.58%). The pure BB variety had significantly the lowest late embryonic mortality percentage and the crossing improved this trait, H% estimates were positive and ranged from 4.06% to 19.48%. Also, crossing improved total egg loss percentages of the two reciprocal crosses compared to the WW parent. The H% estimates ranged from -3.6% to 0.85%. **El-Dlebhany et al. (2013)** found that the estimate of direct heterosis for hatchability percentage was (1.07), individual heterosis estimate for reciprocal crosses was positive and the negative direct heterosis in the third generation (-5.87) for hatchability was found. Moreover, found that individual heterosis (H₂) for a cross (ML X EL) of hatchability was 0.33, while heterosis for the reciprocal cross for TEL% was 1.8%, for F% was 0.877%. **Taha and Abd El-Ghany (2013)** found that positive estimates and percentages of heterosis were recorded for most of egg production traits. It was concluded that using of SS strain as a sire line and MM strain as a dam line resulting in best new commercial egg line (SM) which is of great concern for poultry breeder in Egypt.

Reciprocal, maternal and direct additive effect for hatch traits:-

There were negative reciprocal effect and non significant values of F%, HFE% and HTE% traits for S×I cross (except THE% was significant) and for S×M and I×M crosses, in contrary, positive and non significant values of EM%, EP% and TEL% were found for crosses S×I and S×M, moreover, I×M had significant reciprocal effect for the former traits. The SS strain had the highest positive significant values of maternal effect for F% (0.63%), HFE% (1.51%) and THE% (2.0%), while both of MM and II strains had non significant values of maternal effect for the former traits. Contrarily, the MM strain had the highest positive significant values for EP% and TEL% traits.

Regarding direct additive effect, the MM strain had the highest significant values for F%, HFE% and HTE% (3.52, 6.32 and 8.62, respectively), followed by II strain (2.11, 1.90 and 3.81, respectively), while strains had the lowest significant values of direct additive effect for the former traits. In contrast, the SS strain had the highest positive significant values for EM%, EP % and TEL% traits (0.49, 2.17 and 8.32, respectively). The values of direct additive effect and maternal effect indicating that using MM toms surpassed the SS ones for F%, HFE%, HTE%, EM%, EP% and TEL%. The superiority of MM as sires suggest that the use of this strain as a terminal sire breed in crossbreeding programs including SS or II dams would be beneficial for improving the former traits. Negative estimates of maternal additive showed

that pullets sired by egg line were superior in fertility. On the other hand, **Nawar and Abdou (1999)**, and **Hossari and Dorgham (2000)** found positive maternal additive effects on fertility. In contrast, **El-Delebshani et al. (2013)** found negative estimates of direct additive effect for fertility and HFE %. Moreover, **Khalil et al. (2004)** found that using White Leghorn as sired hens had higher values of direct additive effects than Baladi Saudi-sired hens. **Taha and Abd El-Ghany (2013)** found that cross of (El-Salam x Mandarah) recorded positive direct additive effect for fertility, HFE% and HTE%, but estimates of maternal heterosis were negative for HFE%.

Using general and specific combining ability to expect hybrid performances, breeding and genetic values for hatch traits:-

Prediction for F%, HFE%, HTE%, EM%, PE%, TEL%, breeding value(BV), breeding value for

crosses (BVC), genetic value for crosses (GVFM) and differences and percent between actual (Y) and predicted (\bar{Y}_i) from the diallel crossing in the three studied strains are presented at Table10. Results indicated that the differences (g and %) for the actual and expected and in relation to actual (Y) %for all genotypes were approximately equal zero. The small difference may be due to figures rounded entering in the prediction equations (**Gowda et al., 2012**). Concerning breeding values for pure line (2GCA), the MM strain had the highest and the same BVC for HFE% and HTE% (7.02) followed by II strain for the former traits while SS strain had the lowest values for aforementioned estimates. Contrary, the pure SS strain had the highest BVC for EM%, PE% and TEL%, followed by II strain, while MM strain had the lowest values for the aforementioned estimates.

Table (8):Means± SE for actual (Y) and corrected fertility percentage (F%),hatchability percentage from fertility eggs (HFE%) and hatchability percentage from total eggs (HTE%), general and specific combining ability, heterosis %, reciprocal effect, maternal effect and direct effect at the diallel crossing of Saso (SS), Italian (II) and Mandarah (MM) chickens strains

Genotypes	F%		HFE%		HTE%	
	Actual	Corrected	Actual	Corrected	Actual	Corrected
Purebreds						
SS	80.5 ^c	63.5±7.90	71.42 ^d	57.4±6.2	57.5 ^d	49.0±5.50
II	90.6 ^a	72.5±9.90	82.33 ^c	64.9±7.3	74.6 ^c	59.3±6.59
MM	91.7 ^a	73.6±10.8	89.09 ^a	70.6±7.9	81.7 ^a	64.9±7.87
Crosses						
S×I	90.1 ^a	71.6±9.80	82.24 ^c	64.9±6.5	74.1 ^c	58.7±8.91
S×M	88.5 ^b	69.7±7.50	86.44 ^b	68.0±8.9	76.5 ^c	60.7±7.54
I×M	89.2 ^a	70.6±11.1	88.78 ^a	69.7±8.7	79.2 ^a	62.7±7.89
Reciprocal						
I×S	91.5 ^a	72.5±9.40	85.57 ^b	67.2±8.4	78.5 ^b	62.1±8.25
M×S	89.0 ^b	70.6±8.80	87.64 ^{a,b}	68.9±8.7	78.0 ^b	62.0±8.00
M×I	91.1 ^a	72.5±10.1	90.12 ^a	71.6±9.7	82.1 ^a	64.9±9.12
Overall mean	89.13		84.8		75.57	
Significance	**		**		**	
General Combining Ability (GCA)						
SS	-1.21±0.21*		-2.19±0.30*		-2.97±0.35**	
II	1.37±0.25**		0.96±0.11*		2.05±0.45**	
MM	0.77±0.10*		3.57±0.45**		3.65±0.85**	
Specific Combining Ability (SCA)						
S×I	0.81±0.71 ns		-1.38±0.10 ns		-0.65±0.01 ns	
S×M	-0.19±0.04 ns		0.21±0.05 ns		-0.25±0.02 ns	
I×M	-2.07±0.25 ns		-0.59±0.03 ns		-2.27±0.25 ns	
I×S	2.21±0.23*		1.95±0.25*		3.35±0.35**	
M×S	0.31±0.04*		1.41±0.16*		1.75±0.120*	
M×I	0.17±0.02*		0.75±0.09*		0.83±0.08*	
Specific heterosis						
S×I	5.30±0.61**		7.00±1.0**		12.10±1.80**	
S×M	2.79±0.32*		7.71±0.99**		10.14±1.20*	
I×M	-2.14±0.29*		3.58±0.80*		1.28±0.50*	
Reciprocal heterosis						
I×S	7.00±0.95*		11.3±1.2*		18.20±2.24**	
M×S	3.37±0.51*		9.20±1.9*		13.04±1.98**	
M×I	-0.05±0.00 ns		5.15±0.45*		5.26±0.89*	

Reciprocal effect			
S×I	-0.70±0.08 ns	-1.67±0.09 ns	-2.00±0.21 *
S×M	-0.25±0.02 ns	-0.60±0.08 ns	-1.00±0.11 ns
I×M	-0.95±0.09 ns	-0.67±0.08 ns	-1.55±0.11 ns
Maternal effect			
SS	0.63±0.09*	1.51±0.09*	2.00±0.21*
II	0.17±0.01 ns	-0.66±0.05 ns	-0.30±0.05 ns
MM	-0.80±0.05 ns	-0.85±0.80 ns	-1.70±0.49 ns
Direct additive effect			
SS	-4.53±0.50*	-5.02±0.98*	-9.00±1.99*
II	2.11±0.23**	1.90±0.21**	3.81±0.77**
MM	3.52±0.39**	6.32±0.98**	8.62±1.27**

(a-d)= Means within a column with no common superscripts differ significantly ($p < 0.01$),

* $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, ns: not significant.

As for breeding value for crosses (BVC) results obtained in Table (10) revealed that the three crosses had the same trend for the breeding values for pure line, I x M cross had the highest breeding values for F%, HFE% and HTE%, followed by II strain, while SS strain had the lowest values for the aforementioned traits. The I x M cross had the highest breeding values for F%, HFE% and HTE%, followed by S x M cross while I x S cross had the lowest values for the aforementioned estimates. Contrary, the pure line and I x S cross had the highest breeding values for EM%, PE% and TEL%, followed by S x M cross while IxM cross had the lowest values for the three aforementioned estimates.

Considering genetic values (GVFM), the I x S cross had the highest value for fertility and the M×I

cross had the highest estimates for HFE%, HTE% and EM% traits, followed by its reciprocal cross I×M for the same traits except for EM% trait which S×I cross had the highest value. The M×I cross achieved the lowest values for PE% and TEL% traits. The S×I cross had the highest values of GVFM for the aforementioned hatch traits. The estimates of genetic values showed that the offspring of M×I cross had better performance than those of I×M cross for the former traits. The superiority of MM as sires or dam suggest that the use of this strain as a terminal sire breed or dam breed in crossbreeding programs including II and SS strains would be beneficial for improving most of hatch traits.

Table (9): Means± SE for actual (Y) and corrected embryonic mortality percentage (EM %), Pipe eggs percentage (PE %), total egg loss percentage (TEL%), general and specific combining ability, heterosis %, reciprocal effect, maternal effect and direct effect at the diallel crossing of Saso (SS), Italian (II) and Mandarrah (MM) chickens strains

Genotypes	Embryonic mortality%		Pipe eggs%		Total egg loss%	
	Actual	Corrected	Actual	Corrected	Actual	Corrected
Purebreds						
SS	7.4 ^a	2.72±0.35	15.6 ^a	3.94±0.64	42.5 ^a	6.51±1.01
II	6.5 ^a	2.54±0.31	9.5 ^b	3.08±0.42	24.4 ^b	4.93±0.72
MM	7.0 ^a	2.64±0.33	3.0 ^d	1.73±0.11	18.3 ^c	4.27±0.61
Crosses						
S×I	6.2 ^a	2.48±0.45	9.8 ^b	3.13±0.39	25.9 ^b	5.08±0.95
S×M	4.7 ^b	2.16±0.22	7.3 ^c	2.70±0.29	23.5 ^b	4.84±0.63
I×M	6.8 ^a	2.60±0.29	3.2 ^d	1.78±0.12	20.8 ^{b,c}	4.56±0.65
Reciprocal						
I×S	4.8 ^b	2.19±0.23	8.2 ^{b,c}	2.86±0.31	21.5 ^c	4.63±0.46
M×S	4.9 ^b	2.21±0.22	6.1 ^c	2.46±0.45	22.0 ^b	4.69±0.48
M×I	6.9 ^a	2.62±0.30	3.1 ^d	1.76±0.50	17.9 ^c	4.23±0.51
Overall mean	5.3		7.7		24.4	
Significance	**		***		***	
General Combining Ability (GCA)						
SS	-0.2±0.01 ns		0.8±0.12*		2.8±0.25*	
II	0.05±0.01 ns		-0.8±0.13 ns		-1.8±0.18 ns	
MM	-0.3±0.02*		-1.9±0.19*		-3.8±0.35*	
Specific Combining Ability (SCA)						

S×I	0.60±0.08 *	1.40±0.21*	0.90±0.80*
S×M	-0.45±0.01 ns	-1.12±0.01 ns	-1.19±0.18
I×M	-0.83±0.08 ns	1.66±0.50 ns	2.45±0.25*
I×S	-0.79±0.09 ns	-0.18±0.01 ns	-3.07±0.35*
M×S	-0.45±0.01 ns	-1.12±0.02 ns	-1.19±0.12 ns
M×I	1.37±0.15 ns	-2.54±0.25*	-0.65±0.35 ns
Specific heterosis			
S×I	-10.79±2.20*	-21.91±3.56*	-22.6±2.90*
S×M	-34.72±15.20**	-21.50±18.50**	-22.6±2.82*
I×M	-27.70±3.50	-23.2±4.21*	-4.5±0.84*
Reciprocal heterosis			
I×S	-30.9±4.56**	-34.7±4.25**	-35.3±0.45*
M×S	-29.5±3.95**	-51.4±6.25*	-29.0±0.29*
M×I	2.22±1.20**	-67.4±8.35**	-18.6±2.50*
Reciprocal effect			
S×I	0.70±0.09 ns	0.80±0.10 ns	2.00±0.21 ns
S×M	0.00±0.00 ns	0.00±0.00 ns	0.00±0.00 ns
I×M	-1.10±0.23*	2.10±0.21*	1.55±0.21*
Maternal effect			
SS	-0.47±0.21 ns	-0.53±0.08 ns	-1.33±0.01 ns
II	1.20±0.08 ns	-0.87±0.05 ns	0.30±0.03 ns
MM	-0.73±0.12 ns	1.40±0.11*	1.03±0.02*
Direct additive effect			
SS	0.49±0.25*	2.17±0.22*	8.32±1.02*
II	-1.42±0.60 ns	-1.17±0.21 ns	-3.88±0.42*
MM	0.22±0.01 ns	-3.39±0.35*	-7.84±0.95*

(a-g)= Means within a column with no common superscripts differ significantly ($p < 0.01$),

* $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, ns: not significant.

Table (10): Prediction for fertility % (F %), hatchability% from fertility eggs (HFE %), hatchability % from total eggs (HTE %), embryonic mortality% (EM %), Pipe eggs %(PE %), total egg loss %(TEL%),breeding value, genetic value and differences and percent between actual (Y) and predicted (\tilde{Y}_i) from the diallel crossing of Saso (SS), Italian(II) and Mandarah (MM) chickens strains

Prediction traits	Genotypes	F%	HFE%	HTE%	EM %	PE%	TEL %
Hybrid(\tilde{Y}_i)	S×I					9.80	25.90
	S×M	90.10	82.24	74.10	6.20	6.10	23.30
	I×M	88.50	86.44	76.50	4.70	7.30	20.80
	I×S	89.20	88.78	79.20	6.80	8.20	21.50
	M×S	91.50	85.57	78.50	4.80	6.10	22.00
	M×I	89.00	87.64	78.00	4.90	3.10	17.90
			91.10	90.12	82.10	6.90	
Breeding values	SS	-2.43	-4.37	-5.93	-0.50	1.60	5.60
	II	2.73	1.92	4.11	-0.10	-1.60	-3.70
	MM	1.47	7.02	7.31	-0.60	-3.90	-7.70
Breeding values	S×I	0.15	-1.23	-0.91	-0.27	0.03	0.98
	S×M	-0.45	1.38	0.69	-0.51	-1.13	-0.90
	I×M	2.13	4.53	5.71	-0.33	-2.71	-5.54
Genetic values	S×I	0.97	-2.61	-1.57	0.33	1.44	1.91
	S×M	-0.63	1.59	0.43	-0.97	-2.26	-2.09
	I×M	0.07	3.93	3.43	-1.17	-1.06	-3.09
	I×S	2.37	0.72	2.43	-1.07	-0.16	-2.09
	M×S	-0.13	2.79	2.43	-0.97	-2.26	-2.09
	M×I	1.97	5.27	6.53	1.03	-5.26	-6.19

-The differences (g and %) for the actual and expected and in relation to actual (Y) % for all genotypes were approximately equal zero.

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