

## Carcass Characteristics in Three Lines of Quail (*Coturnix coturnix spp*) and Their Crosses II- The Percentages

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### Abstract

A total of 54 quail birds aged 42 days from both sexes within nine genotypes (WW, LL, DD, WL, WD, LD, LW, DW and DL) - that resulted from full diallel cross of three lines (White, Light brown and Dark brown) - were used in this research. The trial was conducted at Dept. of Animal production, college of Agricultural Engineering Sciences, University of Duhok, KR-Iraq, 2016. The live birds were weighed (LBW) and then slaughtered to be dissected into four major parts after eviscerating; the giblets part, the whole slaughtered birds (carcass), both legs and finally the rest body (included breast and back of both sides). These major parts were weighed and calculated as ratio to LBW to be percentage (%). The findings showed that the effect of genotype, sex and their interaction were significant on all studied characteristics, except the effect of sex on giblets %. The WD cross recorded the highest carcass and body %, while the WW line achieved the highest giblets % and DL reciprocal cross resulted in the highest leg %. The males surpassed females in carcass, leg and body %; in spite of superiority of females in LBW than males. The crosses resulted from D dam, appeared the highest interaction with males for carcass, body and leg percentages; while the same line as sire was combined well with L line as dam, and interacted positively with males for giblets %. Carcass percent correlated significantly and negatively with LBW, and regression analysis illustrated a good dependency of carcass % on LBW.

**Key words:** Quail, Crosses, Carcass dissection percentages.

### Introduction:

As it is known, the quail bird (*Coturnix coturnix spp*) is the smallest poultry species reared for meat and egg yield, in addition to the assumption that considering it as an important laboratory animal (Minville, 2004). The quail bird also has different advantages to be used in genetic studies. Such advantages involve small size; rearing a large number of birds in a limited available space; early sexual maturity (35 days old); and has short generation interval (Kul and Seker, 2004).

In a study conducted by Alkan *et al.*, (2010), on meat production and carcass characteristics of three lines of quail (High body weight (HL) or Low body weight (LL) Japanese quail lines and their random bred control line (C). They found as expected that HL surpassed significantly both LL and C counter

parts in live body weight; and females recorded significantly higher body weight than males. But they mentioned that carcass percentage didn't differ significantly among the studied lines, where their carcass percentages were ranged (from 66 to 67.8 %); whereas males surpassed females in carcass % (71.2 vs. 63.1%, respectively). These results may confirm that the higher live body weight of quail, didn't necessary resulted in a higher carcass %. The same authors reported that all of breast (with bones) %, wing %, neck % and back %, also didn't affect significantly by line; while just thigh (with bones) % was affected significantly by line (22.9, 22.1 and 22.8 % for HL, LL and C, respectively). They added that the same trend was true for sex effect, except breast %. They found also that the correlation coefficients were just significant between carcass% with left wing % (0.38); and between breast percent with both back percent (-0.63) and thigh percent (-0.38).

Also, Vali *et al.*, (2005) stated that breast percent was differed significantly between females and males (41.55 vs. 39.98 %, respectively). According to Bonos *et al.*, (2010), the average of different carcass dissections in Japanese quail birds at 42 days old were (74.52, 34.23, 27.33 and 22.34 % for carcass, breast, back and leg percent, respectively). However, Kosshak *et al.*, (2014), reported that the percentages of dressing carcass, breast back, and thigh were (78.4, 41.88, 26.68 and 25.72 %, respectively). A significant variation in live body weight at 42 days old, among four quail stains (Major, Kaleem, Saadat and Zahid) as difference (23 gm.) was found by Jatoi *et al.*, (2015); such variation was explained by Vali *et al.* (2005), as genetic makeup differences. Moreover, Inci *et al.*, (2015) studied the carcass characteristics of four quail lines (White, Dark brown, Golden and Wild-type), and demonstrated that differences among them for (carcass yield % and breast yield %) were highly significant ( $p < 0.01$ ); they mentioned that the highest carcass % was recorded 71.1 % for wild-type female birds, and 43.1 % for wild-type male birds; in addition they stated that females had significantly higher percent than males for breast %. On the contrary to the previous findings, Tarhyel *et al.* (2012) mentioned that white-colored quail surpassed insignificantly the wild-type ones in average of both breast and thigh.

Anyway, the data about quail production and feather color is insufficient to decide whether using it in commercial farms or not, but many research workers studied different quail lines across generations to illustrate their genetic gain. Hussen *et al.*, (2016) mentioned that live body weight of Japanese quail was responded to selection and increased across three generations by about 15.7 % at 42 days old. But another study conducted by Hussen and Salih (2018), illustrated that heritability estimate of quail's live body weight at 6 weeks of age was ranged between (0.19-0.23). However, Hussen and Saleh, (2019) indicated insignificant differences ( $P > 0.05$ ) among nine genotypes of quail for body weight trait at slaughter age, which ranged from 156.8 – 171.2 gm.

This study aimed to investigate the percentages of carcass dissections of nine quail genotypes resulted from full diallel crossing and its interaction with the sex.

### **Material and Methods:**

This study was conducted at Animal Production department, College of Agricultural Engineering Sciences, University of Duhok, KR-Iraq. The trial was designed as full diallel cross within CRD, and included three lines of quail (White, Light brown and Dark brown) which were producing nine genotypes according to sire and dam mating (Table 1); where when the same line mated with its own sire and dam resulted in a pure lines as their parents (WW, LL and DD); while when the mating done according to the probability of mating (sire and dam, respectively) according to the order of the

previous lines resulted in crosses (WL, WD and LD); whether when the vice versa of previous mating system (location of both parents were reversed) was done, the reciprocal crosses were obtained (LW, DW and DL).

A total of 54 quail birds aged 42 days from both sexes (equally) within the nine studied genotypes were used in this research (6 birds / genotype), its data was measured at the same day. The live birds were weighed (LBW) using a sensitive balance in grams and then slaughtered using knife to be dissected into four major parts. After eviscerating, the giblets parts (gizzard, heart and liver) were separated, weighed as pooling mass (gm.) and divided by LBW in order to calculate their percentage (%); then the whole slaughtered birds were weighed as carcass records and changed into ratio (percentage %) relative to the LBW; while the both legs (involving thigh and drumsticks) of each bird were weighed as leg measure and relatively to LBW, its percentage was computed; and finally the rest body (including breast and back of both sides) was weighed as body mass and also modified to be ratio or percentage (%) relative to the LBW.

Regarding to managing the studied genotypes, the slaughtered birds were obtained as *F2* generation from full diallel cross trial. During the experiment, birds were reared in cages; water and feed submitted *ad libitum* and the rations were composed according to (NRC, 1994) which contained; starter (2850 K. cal. ME/ kg & 26 % CP, from 0-4 weeks old) and grower (2850 K. cal. ME/ kg & 21% CP, from 4-6 weeks old). The light program was applied as 15 hours/day to the flock for all experimental periods (except the first day which was 23 hours).

#### Statistical analysis:

The data was analyzed as quantitative numeric using SAS software (SAS, institute, 2016) via GLM procedure and according to the following model:

$$Y_{ijk} = \mu + G_i + S_j + (G*S)_{ij} + e_{ijk}$$

Where:

$Y_{ijk}$  = the observations of the studied character.

$\mu$  = overall mean;

$G_i$  = the effect of genotype;

$S_j$  = the effect of sex;

$(G*S)_{ij}$  = interaction between genotype and sex.

$e_{ijk}$  = random error.

The differences among different means were tested using Duncan multiple range test (Duncan, 1955).

Within the same previous software, simple correlation analysis was carried out on the data of studied characteristics irrespective to the genotype and sex. The simple regression analysis was done also within the same software, for carcass percent characteristic depending on LBW.

**Table 1. Genotypes resulted according to mating design**

Pure lines	Genotypes		
	WW	LL	DD
Crosses	WL	WD*	LD
Reciprocal crosses	LW	DW	DL

\*The first letter refers to the sire and the second indicates to the dam.

## Results and Discussion:

### Effect of genotype:

The effect of genotypes on carcass dissections are presented in Table (2). It could be noticed that all studied parts % are differ significantly ( $p < 0.05$ ) among studied genotypes.

In respect to dressing carcass part, there was no obvious trend according to pure, crosses and reciprocal crosses; but the highest percentage was achieved by WD cross (66.16 %), while the lowest percentage was recorded for reciprocal cross DL (61.93%) and the rest genotypes were intermediate between the mentioned two percentages. These results may confirm the main role of D line and it possible interaction (positively or negatively) with the other line, where the D dam interacted positively with W sire and negatively with L dam (Figure 2).

Regarding to leg part (thigh and drumsticks), the highest and lowest percent were recorded for reciprocal crosses (16.06 and 14.39 % for LW and DW, respectively). Here W line play an active role when used as dam and crossed to L line as sire, while the same dam interacted negatively with the sire D for leg % character. So, diallel cross design illustrating the best combination of different lines, in order to select the best line as sire and other best one as dam.

In regard to giblet (gizzard, heart and liver), the reciprocal cross DL resulted in the highest percent (5.27 %), while the lowest one was pure line WW (4.33 %) and the crosses were intermediate. These results may reflect the metabolism action of each genotype, because the live body weight of WW line was the lightest (Figure 1).

In respect to body (breast and back), the highest percent was achieved by the cross WD (40.23 %), while the lowest one was recorded for WW (36.83 %), and the rest genotypes were intermediate. This result confirm that low body weight line resulted in low breast percent (WW), unless mate and interact with heavier line (DD), to obtain a new cross (WD), having a considerable breast and then body.

However, the present results are disagreement with the findings of (Alkan *et al.*, 2010; and Bonos *et al.*, 2010), in respect to dressing carcass %; while the results of Kosshak *et al.*, (2014), were disagreement with the present finding regarding to leg and body percentages. It could be concluded from (Table 2), that the most active line was DD in combining ability. Moreover, findings of some research workers reported that white line quail had in general less body weight then the brown one (Petek *et al.*, 2004; Minvielle *et al.*, 2005; Yilmaz and Çağlayan, 2008); but on contrary, Tarhyel *et al.* (2012) indicated that the white line quail had significantly higher breast and thigh percent than the brown one, and differences between the dressing carcass of white and brown lines were not significant.

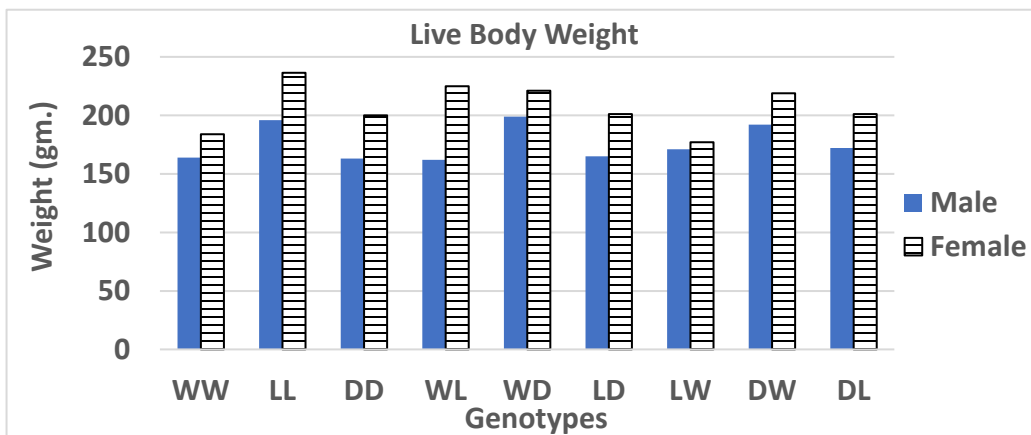
**Table 2. Effect of genotypes on some carcass dissections percentages in quail**

Crosses	Genotype	Carcass %	Leg %	Giblet %	Body %
		Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
Pure n=18	WW	63.89 ± 1.24 abc	15.73 ± 0.55 a	4.33 ± 0.12 c	36.83 ± 0.61 c
	LL	64.28 ± 1.16 ab	15.12 ± 0.27 ab	5.07 ± 0.37 ab	38.52 ± 0.68 abc
	DD	63.10 ± 1.64 bc	15.22 ± 0.65 ab	4.64 ± 0.19 bc	38.35 ± 0.76 abc
Crosses n=18	WL	64.34 ± 2.07 ab	15.85 ± 0.30 a	4.98 ± 0.27 ab	38.51 ± 1.66 abc
	WD	66.16 ± 2.04 a	15.40 ± 0.60 ab	4.53 ± 0.07 bc	40.23 ± 1.10 a
	LD	64.08 ± 1.66 abc	15.23 ± 0.63 ab	4.79 ± 0.20 abc	38.68 ± 0.95 abc
Reciprocal crosses n=18	LW	64.71 ± 1.33 ab	16.06 ± 0.28 a	4.50 ± 0.13 bc	37.34 ± 0.80 bc
	DW	63.91 ± 0.99 abc	14.39 ± 0.77 b	4.79 ± 0.14 abc	39.33 ± 0.60 ab
	DL	61.93 ± 1.14 c	14.43 ± 0.63 b	5.27 ± 0.25 a	37.48 ± 0.92 bc
Genotype $p > F$ (Sig.)		0.021*	0.015*	0.029*	0.014*

Means with different letters within columns are differed significantly; \* = significant at 0.05 level; \*\* = significant at 0.01 level

**Effect of sex:**

The effect of sex on carcass parts percentages are presented in Table (3). It could be noticed that all studied parts are differ significantly ( $p < 0.01$ ) between both sexes, except giblet, which may due to its small values. However, males surpassed females, in spite of reverse results of live body weight (Figure 1). This results are in agreement with findings of Alkan *et al.*, (2010) in respect to carcass %; and disagree with the findings of Inci *et al.*, (2015) regarding to body percent. However, Yalçın *et al.* (1995) mentioned that the breast percent of males was (32.1%) and of females was (30.6%) with no significant difference; also, Akşit *et al.* (2003) and Genchev *et al.* (2008) found that the difference between both sexes of quail regarding to breast percentage was not significant.



**Figure 1. Live body weight as affected by genotypes and sex of quail**

**Table 3. Effect of sex on some carcass dissections percentages in quail**

Gender		Carcass %	Leg %	Giblet %	Body %
Gender n=27/sex	Sex	Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
	Male	66.94 ± 0.40 a	16.16 ± 0.14 a	4.70 ± 0.12	39.67 ± 0.39 a
	Female	61.15 ± 0.42 b	14.38 ± 0.24 b	4.84 ± 0.10	37.05 ± 0.37 b
	Sex P>F (Sig.)	0.001 **	0.001 **	0.29 NS	0.001 **

Means with different letters within columns are differed significantly; \*= significant at 0.05 level; \*\*= significant at 0.01 level

**Interaction between genotype and sex:**

The interaction between genotype and sex for carcass characteristics percentages is illustrated in Table (4) and Figures (2, 3, 4 and 5). It could be noticed from Table (4) that the interaction between genotype and sex for all studied characters are significant ( $p < 0.05$ ), except for body %, which is highly significant ( $p < 0.01$ ).

**Table 4. Interaction between genotype and sex for some carcass dissections percentages in quail**

Interaction		Carcass %	Leg %	Giblet %	Body %
n= 54	Genotype*Sex P>F (Sig.)	Fig. 2	Fig. 3	Fig. 4	Fig. 5
		0.017 *	0.041 *	0.042 *	0.002 **

\*= significant at 0.05 level; \*\*= significant at 0.01 level

Regarding to the interaction between genotype and sex, for dressing carcass %, it could be observed from Figure (2), that WD cross interacted significantly and positively with males in order to give the highest carcass %; while on the contrary DD pure line interacted negatively with females and resulted

in the lowest carcass %. As mentioned in genotype effect, the line D is active and its interaction with the sex dependent on the combination of specific sex with a specific genotype. Unfortunately, the review on the interaction between genotype and sex is seem to be very rare in quail.

In respect to the interaction between genotype and sex, for leg %, it could be observed from Figure (3), that the highest interaction was achieved when DD line interacted with the males; and the lowest one was recorded when DW reciprocal interacted with females. Also, it could be concluded that D line is active in its combination.

Regarding to the interaction between genotype and sex, for giblets %, it could be observed from Figure (4), that the highest interaction was achieved when DL reciprocal interacted with males; and lowest value of interaction was recorded when WW line interacted with males too.

In respect to the interaction between genotype and sex, for body %, it could be observed from Figure (5), that the highest interaction was achieved when WD cross interacted with males; while the lowest one was recorded when WL cross interacted with females. This result gave an idea about the positive combination between W sire and D dam, for the male progeny; while the same sire combined negatively with L line, for females' progeny.

However, it appeared there was no unique trend for the effect of interaction between genotype and sex on the four studied characters, but in general it could be concluded that D line involved the most active birds that had combining ability either as sire or as dam.

#### Correlation between carcass dissections percentages:

Table (5) shows the correlation coefficients between different carcass dissection percentages. It could be noticed that LBW correlated significantly with all studied characters, and all coefficients were negative except that between LBW with giblets which was positive (0.34); this findings confirm that when LBW increased the percent of carcass, leg and body decreased.

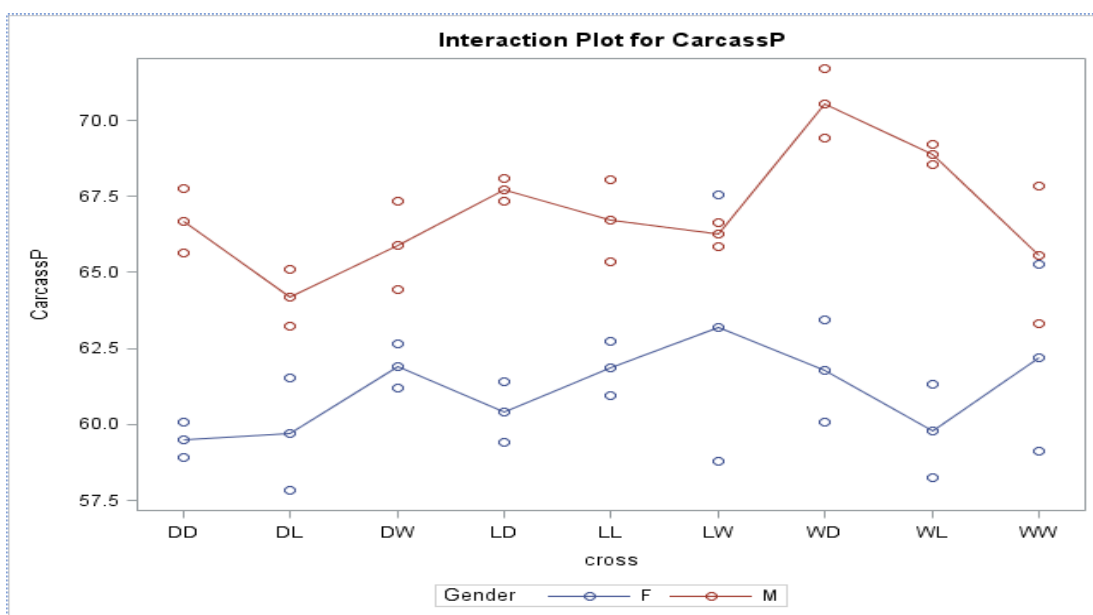
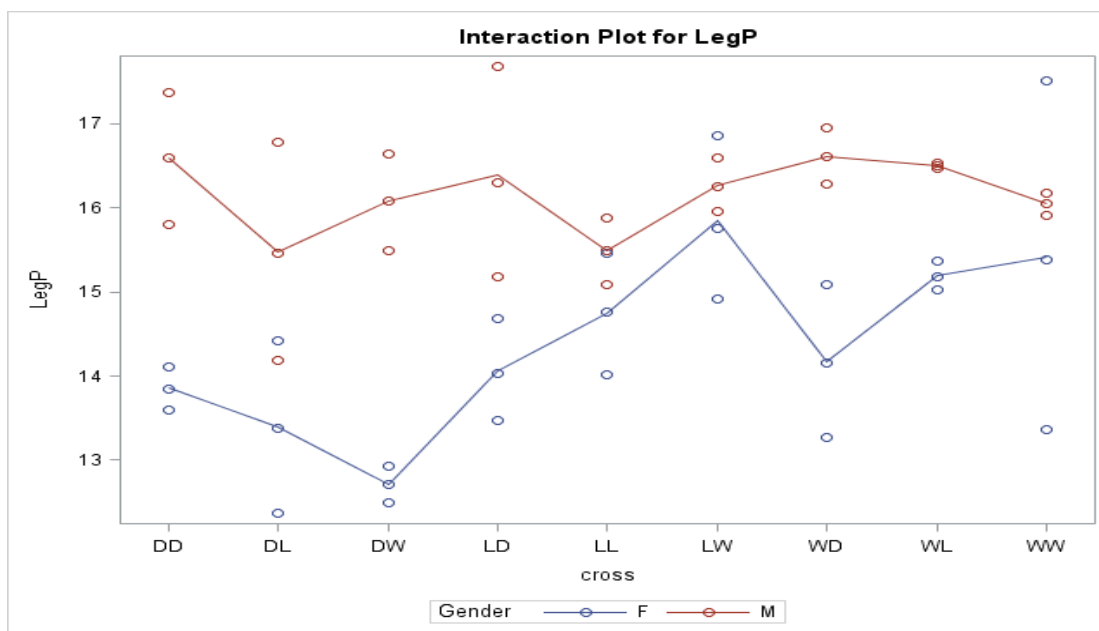
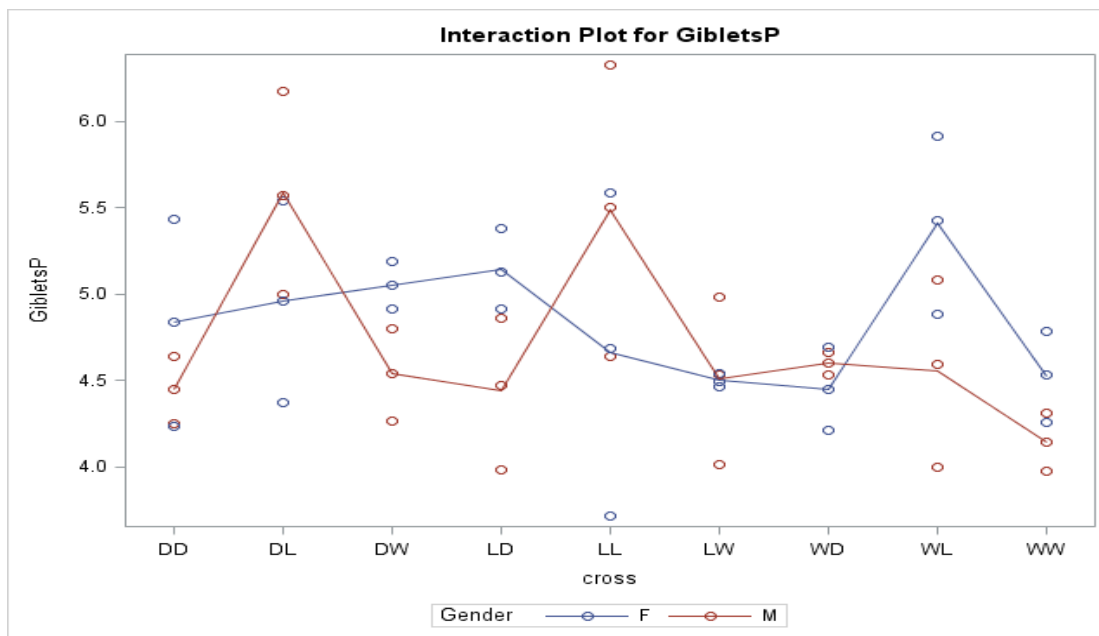


Figure 2. Interaction between genotype and sex for dressing carcass percentage of quail



**Figure 3. Interaction between genotype and sex for leg percentage of quail**

Carcass percent correlated significantly ( $p < 0.01$ ) with leg and body % (0.74 and 0.79, respectively), but not with giblets % ( $p > 0.05$ ); this finding indicate that if carcass % increased then both leg and body %, will be increased. Finally, leg % didn't correlated significantly with body % ( $p > 0.05$ ). The present results are in agreement partly with the findings of Alkan *et al.*, (2010) for the correlation between carcass and body %, who found negative correlation coefficient between body weight and breast and carcass percentages; but they didn't find significant correlation coefficient between body weight and thigh percent; also, Vali *et al.*, (2005) indicated that the correlation coefficient between both carcass and breast percentages was weak (-0.08), while the same coefficient between thigh % and carcass % was negative and relatively medium (-0.35).



**Figure 4. Interaction between genotype and sex for giblets percentage of quail**

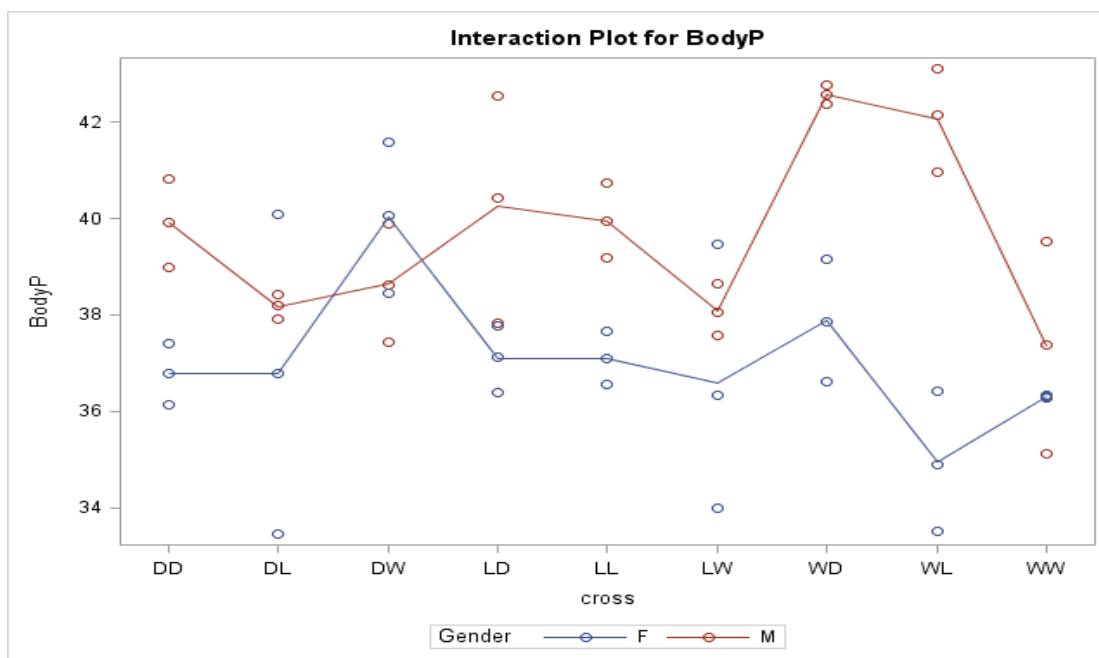


Figure 5. Interaction between genotype and sex for body percentage of quail

**Relationship between carcass percent and LBW**

The regression coefficients of depending carcass % on LBW are shown in Table (6). It could be noticed that both intercept and LBW affect carcass % significantly ( $p < 0.01$ ); and it could be predicted with the carcass % of quail via LBW (gm.) by using the following equation:

$$\text{Carcass\%} = 80.49 - 0.09 (\text{LBW})$$

Regarding to the regression analysis parameters (Table 7), it could be observed that coefficient of determination ( $R^2 = 0.34$ ), which mean that LBW has been covered 34 % of the prediction, but there are 66 % of prediction causes not yet covered. Also, the same Table illustrating that the overall mean of carcass % from all genotype is equal 64.04 %; and coefficient of variation (CV %) is just equal 4.6 %, which mean that there are homogeny among all studied genotypes for carcass %.

Table 5. Correlation coefficients between carcass dissection percent of studied traits

Pearson Correlation Coefficients, N = 54 Prob >  r  under H0: Rho=0					
	LBW	GibletsP	LegP	BodyP	CarcassP
LBW	1.00000	0.34135 0.0115	-0.62485 <.0001	-0.28204 0.0388	-0.58384 <.0001
GibletsP	0.34135 0.0115	1.00000	-0.24510 0.0741	-0.08853 0.5244	-0.24585 0.0731
LegP	-0.62485 <.0001	-0.24510 0.0741	1.00000	0.23365 0.0891	0.74146 <.0001
BodyP	-0.28204 0.0388	-0.08853 0.5244	0.23365 0.0891	1.00000	0.78947 <.0001
CarcassP	-0.58384 <.0001	-0.24585 0.0731	0.74146 <.0001	0.78947 <.0001	1.00000



**Table 6. Regression coefficients of dressing carcass % depending on live body weight**

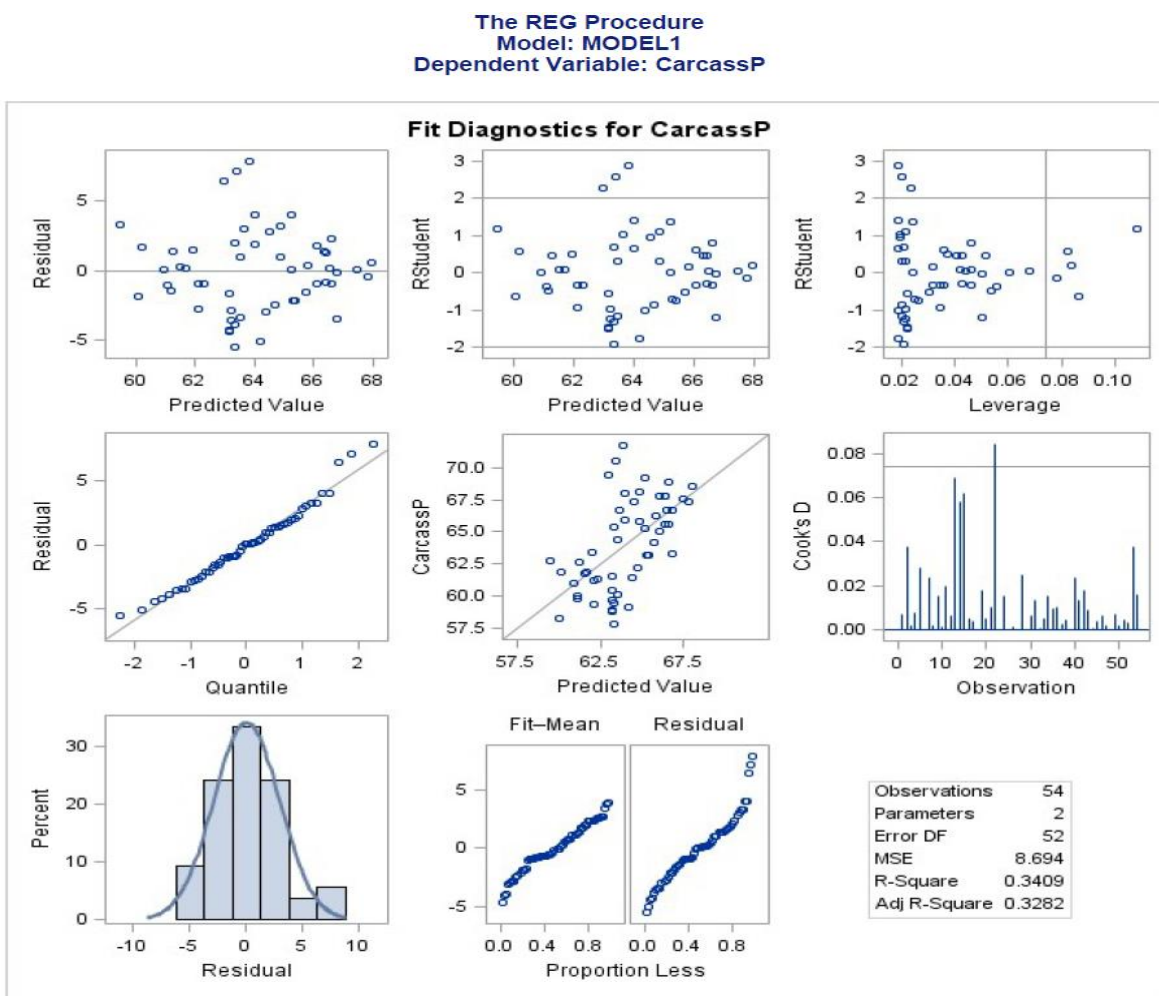
<b>Parameter Estimates</b>					
<b>Variable</b>	<b>DF</b>	<b>Parameter Estimate</b>	<b>Standard Error</b>	<b>t Value</b>	<b>Pr &gt;  t </b>
<b>Intercept</b>	1	80.48687	3.19615	25.18	<.0001
<b>LBW</b>	1	-0.08583	0.01655	-5.19	<.0001

In respect to the carcass % plots from regression analysis, are shown in Figure (6). The plots of predicted and residual values are shown to be normally distributed except few values which deviated than the optimum distribution.

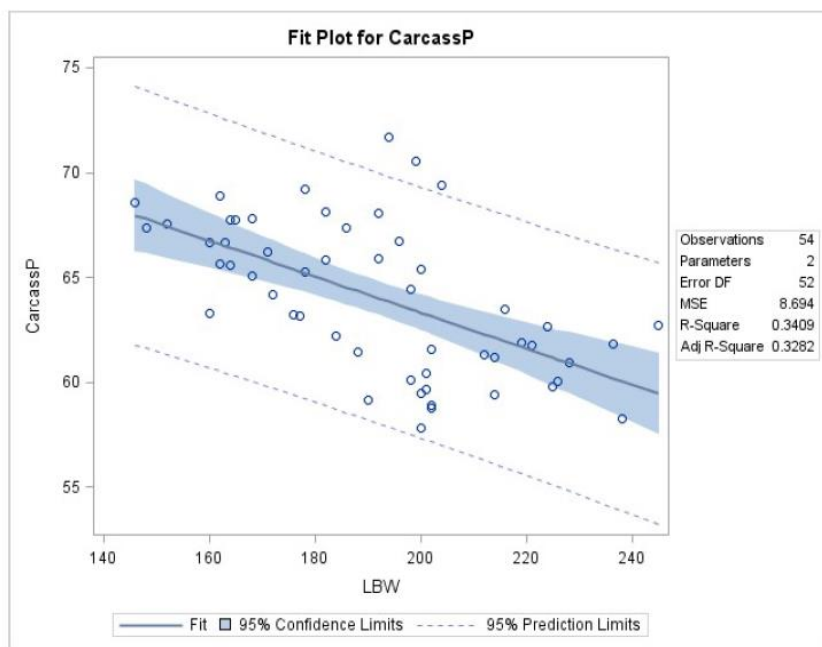
Finally, regarding to linear regression curve of carcass %, the Figure (7) is illustrate it obviously, and it appear as negative relationship, when body weight of live quail is increases, the carcass percent is decreases. This fit relationship give an idea about how overall dressing carcass % affected by LBW irrespective to genotype or sex influence.

**Table 7. Parameters of Regression Analysis for dressing carcass %**

<b>Root MSE</b>	2.94855	<b>R-Square</b>	0.3409
<b>Dependent Mean</b>	64.04372	<b>Adj R-Sq</b>	0.3282
<b>Coeff Var</b>	4.60397		



**Figure 6. Regression plots (observed, predicted and residual) for dressing carcass %**



**Figure 7. Linear regression curve for carcass % depending on LBW of quail**

## Conclusion

It could be concluded from this investigation that introducing D line as dam in mating system, will play an important role to improve both carcass and body percentages economically. Also the same line (D) introducing as dam may combine positively with any other lines to obtain male offspring with higher leg %.

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## خصائص الذبيحة في ثلاثة خطوط من السمان (*Coturnix coturnix spp*) وهجنها

### 2- النسب المئوية

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### الملخص

أُستخدم في هذا البحث عدد 54 صوصَ سَمان بعمر 42 يوماً من كلا الجنسين ضمن تسعة تركيب وراثية (WW, LL, DD, WL, WD, LD, LW, DW, DL) نتاج التهجين ثنائي الأليل لثلاثة خطوط (الأبيض والبني الفاتح والبني الغامق). أجريت التجربة في قسم الإنتاج الحيواني، كلية علوم الهندسة الزراعية بجامعة دهوك، كردستان- العراق، عام 2016. تم وزن الطيور الحية، ثم ذُبجت واستبعدت الأحشاء، وقُطعت إلى أربعة أجزاء رئيسية هي: الحوائج وتصافي الذبيحة، والأرجل والجسم (الذي تضمن عضلي الصدر والظهر). تم وزن الأجزاء المذكورة وحسبت كنسب مئوية من وزن الجسم الحي (%). أظهرت النتائج أن تأثير التركيب الوراثي، والجنس، وتداخلاتهما كانت معنوية في كل خصائص الذبيحة المدروسة، ما عدا تأثير الجنس في نسبة الحوائج. ولقد سجل الهجين (WD) أعلى نسبتي تصافي الذبيحة والجسم، بينما تميّز الطراز الوراثي (WW) بأعلى نسبة حوائج، وأما الهجين التبادلي (DL) فقد تفوق في نسبة الأرجل. كما تفوق الذكور على الإناث في نسب كل من تصافي الذبيحة والأرجل والجسم، بالرغم من تفوق الإناث في أوزان أجسامها على نظيراتها الذكور. إن الهجن الناتجة من الأم (D)، أبدت تداخلاً معنوياً مع الذكور لخصائص نسب تصافي الذبيحة والأرجل والجسم، بينما الهجن النظرية والتي نتجت من الخط نفسه كآباء والخط L كأمهات، فقد تداخلت معنوياً مع الهجن الذكور لخاصية نسبة الحوائج. ارتبطت تصافي الذبيحة معنوياً وسلبياً مع وزن الجسم الحي للطيور، كما أوضح تحليل الانحدار أهمية اعتماد نسبة تصافي الذبيحة على وزن الجسم الحي.

**الكلمات المفتاحية:** السمان، الهجن، نسب أجزاء الذبيحة المئوية.