

Carcass Characteristics in Three Lines of Quail (*Coturnix coturnix spp*) and their Crosses. I- The Weights.

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Abstract

A total of 54 birds aged 42 days old from both sexes (equally) of different quail genotypes resulted from complete diallel cross design of three lines (White-W, Light brown-L and Dark brown-D) were used in the present study. The trial was conducted at Animal Production Dept., College of Agricultural Engineering Sciences, University of Duhok, Sumail, KR-Iraq, during 2016. The aim was to investigate the carcass characteristics of the quail genotypes. Live body weight and the following carcass characteristics; blood, feather, shank, head, gizzard, heart, liver, thigh, drumstick, breast, back, neck, wing and dressing carcass (with giblets) were weighed (gm.). The results showed that there were significant differences among studied genotypes and between both sexes, in addition to their interaction. In general, the best genotype for carcass characteristics was LL line; but for some main cuts, economic cuts and inedible out-parts, the DW reciprocal cross shared LL line the superiority; while for gizzard weight, the DL reciprocal cross recorded the superiority compared to the rest genotypes. However, the average carcass weights as affected by genotype were ranged from 118.5 – 144.5 gm. The females recorded higher values than males for all significant characters. The interaction between genotype and sex appeared that few genotypes interacted significantly with specific sex (female). As conclusion, the crosses didn't appear any superiority for carcass characteristics; while a specific line and specific reciprocal cross appeared superiority in specific characters.

Key words: Quail, Lines, Crosses, Carcass weights.

Introduction:

Commercial yield of quail nowadays seems to be alternative high quality meat and eggs, instead of chickens yield in different countries. Quail also accepted widely as a laboratory birds used for genetic investigations due to its small size of body, resistance to diseases, rapid growth, easily handling, and limited space needed (Minvielle *et al.*, 2007 and Tarhyel *et al.*, 2012a). The number of mutations due to color in quail are still very limited compared with the number reported in other poultry species (Somes, 1979 and Cheng and Kimura, 1990). Most of the feather color found in quail have been merely documented and described (Merat *et al.*, 1981; Minvielle *et al.*, 1999). White plumage quail has been reported by Roberts *et al.*, (1978). The quail farming has more benefits compared to chickens as food (Akram *et al.*, 2008). An investigation carried out by Jatoti *et al.*, (2015) who reported significant differences in body weight of four different strains of quail in Pakistan. As well as the study that conducted by Inci *et al.*, (2015) indicated the same differences for four different lines (White, Dark brown, Golden and Wild-type). Hussen *et al.*, (2016) indicated that the live body weight of quail is changed across generations and responded to selection, they added that the response to selection for growth rate

at 42 days (slaughter age) was 15.7 %. On the other hand, Hussien and Salih, (2018) stated that the heritability of live body weight at 42 days old in three quail lines was relatively weak and ranged from (0.19-0.23). In another study conducted by Hussien and Saleh, (2019) reported that the live body weight within each sex at 42 days old (slaughter age) of nine quail genotypes didn't differ significantly ($p>0.05$) and ranged from (156.8 – 171.2 gm.). Carcass characteristics were affected by plumage color (Marks, 1990; Minvielle *et al.*, 1999). Tarhyel *et al.*, (2012b) found that the white-colored birds had significantly higher breast weight and thigh weight (as averages) than the wild-type ones, but the differences between carcass weights of the studied groups were not significant. Unfortunately, the studies about carcass dissection of quail in diallel cross design are very rare.

The aim of this study is to illustrate carcass dissections of different quail genotypes resulted from complete diallel cross design.

Materials and Methods

The present research was carried out at Dept. of Animal Production, College of Agricultural Engineering Sciences, University of Duhok, Kurdistan Region-Iraq. The experiment was designed as CRD with complete diallel cross (Table 1). A total of 54 birds aged 42 days old from both sexes (equally) of all quail genotypes resulted from complete diallel cross design were used in this investigation. Three live birds of each sex within each genotype were weighed, then they slaughtered by cutting the head using sharp knife and let bleeding for 30 minutes; after bleeding they reweighed to calculate blood weight from the difference between live body weight and the weight after bleeding; in addition to weighting head and shank after cutting from the body. Then feathers plucked manually from all the body and the birds reweighed to calculate the weight of plumage (always from live body weight). The bird's abdomen was opened to remove intestine (digestive tract eviscerated), and then the giblets (liver, gizzard and heart) as edible parts were separated and weighed independently. However, the rest body was carcass and weighed with giblets as edible carcass weight. The carcass then dissected into breast (both sides), back, thigh (both sides), drumstick (both), wing (both) and neck. All mentioned dissections were weighed using sensitive digital balance (gm.) at the same day.

The studied genotypes were White (W), Light brown (L) and Dark brown (D) as pure quail lines; their crosses (WL), (WD) and (LD) and their reciprocal crosses (LW), (DW) and (DL). Where the first letter indicates to the sire and the second indicates to the dam in crossing system. These genotypes were resulted as F_2 generation from complete diallel cross experiment. During the trial, birds were reared in cages; water and feed provided *ad libitum* and the diet was submitted according to NRC, (1994). Light was provided as 15 hours/day for all trial period except first day which was 23 hours. The objective was to investigate the carcass characteristics of quail genotypes.

Statistical analysis

The collected data was analyzed using GLM procedure within SAS software (SAS, institute, 2016), 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.

μ = overall mean;

G_i = the effect of genotype;

S_j = the effect of sex;

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

e_{ijk} = experimental error.

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

Table 1. Experimental design as complete diallel crossing

Lines	W	L	D
W	WW	WL	WD
L	LW	LL	LD
D	DW	DL	DD

Where: The diameter represents the pure lines; above diameter represent crosses; and below diameter represent the reciprocal crosses.

Results and discussion:

Main cuts:

Table (2) shows live body weights (LBW) and main carcass cuts as affected by genotype, sex and their interaction. The results appeared that LL line surpassed significantly ($p<0.01$) all other genotypes in live body weight (216.25 gm.) at 42 days old, except the cross WD and its reciprocal cross DW. Also, the same trend was true for dressing carcass weight (LL=149.45 gm.) and breast weight (WD=54.05 gm.) except DW which differ significantly from LL and WD. On contrary, the reciprocal cross DW surpassed significantly all other studied genotypes in back weight (35.77 gm.), such result confirm that the cross is different than its reciprocal cross. In terms of the effect of genotype in Table (2) it could be conclude that any increase in the breast or in the back weight (each complete the other for body conformation as mass) will depend on either W line or D line when introduce to the cross design as sire or as dam and vice versa, respectively.

Table 2. Main cuts weights (gm.) of studied quail genotypes

Genotype	Sex	Live Body Weight		Carcass		Breast		Back	
		X ±SE	Genotype Overall Mean	X ±SE	Genotype Overall Mean	X ±SE	Genotype Overall Mean	X ±SE	Genotype Overall Mean
DD	M	163.00±0.58	181.50 ^{cd}	115.96±1.22	122.32 ^d	43.14±13.16	44.613 ^{bc}	21.92±0.68	24.69 ^{cd}
	F	200.00±1.15		128.60±0.75		46.09±2.88		27.46±3.19	
DL	M	172.00±0.30	186.50 ^{cd}	119.22±0.10	124.95 ^{cd}	38.95±1.11	40.343 ^{cd}	26.73±2.24	29.47 ^{bc}
	F	201.00±0.58		129.97±3.2		41.74±2.44		32.21±6.52	
DW	M	192.00±3.46	205.50 ^{ab}	135.17±1.12	140.93 ^b	63.83±0.96	45.150 ^{bc}	30.31±0.99	35.77 ^a
	F	219.00±2.89		146.69±2.67		46.76±1.59		41.24±1.55	
LD	M	165.00±9.81	183.00 ^{cd}	119.18±7.85	125.41 ^{cd}	44.16±4.72	44.305 ^{cb}	22.55±1.48	26.36 ^{bc}
	F	201.00±7.50		131.64±3.49		44.45±0.65		30.17±2.93	
LL	M	196.00±2.31	216.25 ^a	141.47±1.10	149.45 ^a	48.34±1.52	53.853 ^a	29.93±1.58	29.14 ^{bc}
	F	236.50±4.90		157.43±5.74		59.36±2.24		28.34±1.40	
LW	M	171.00±6.35	174.00 ^d	120.98±4.56	119.84 ^d	42.97±0.39	43.518 ^{bc}	22.12±1.48	21.19 ^d
	F	177.00±4.43		118.69±5.24		44.07±3.73		20.26±1.23	
WD	M	199.00±2.89	210.0 ^a	149.49±0.77	147.87 ^{ab}	55.60±0.13	54.05 ^a	29.12±0.87	30.15 ^b
	F	221.00±2.87		146.25±0.56		52.49±2.62		31.18±2.09	
WL	M	162.00±9.24	193.50 ^{bc}	119.08±7.59	132.81 ^c	43.70±3.16	47.290 ^b	24.58±1.72	26.09 ^{bc}
	F	225.00±7.50		146.54±3.55		50.88±0.60		27.59±0.14	
WW	M	164.00±2.31	174.00 ^d	114.42±3.58	118.52 ^d	34.61±2.80	37.682 ^d	26.81±0.14	26.38 ^{bc}
	F	184.00±3.47		122.62±0.67		40.75±0.66		26.07±0.63	
Sex Overall Mean	M	176.00 ^b		126.187 ^b		43.923 ^b		25.993 ^b	
	F	207.167 ^a		136.500 ^a		47.366 ^a		29.391 ^a	
P>F (Sig.)	G		<0.001		<0.001		<0.002		<0.002
	S	<0.001		<0.001		0.001		0.001	
	G *S	0.003		0.01		NS		NS	

Common letters within columns did not differ significantly at 0.05 level of probability.

The present results are in agreement with that obtained by Inci *et al.*, (2015) in respect to the effect of genotype on carcass weight, where they indicated that wild type birds surpassed significantly ($p<0.01$) other studied genotypes (white, dark brown and golden quail). Also Minvielle *et al.*, (1999 and Genchev *et al.*, (2008), were reported similar results.

In respect to sex effect, it could be observed from Table (2) that always females surpassed males significantly ($p<0.01$) for all studied traits. The present results are in agreement with the findings of Alkan *et al.*, (2010) and Pourtorabi *et al.*, (2017).

Regarding to the interaction between genotype and sex, just live body weight and carcass weight were significant. The interaction curves of carcass are illustrated below (Figure 1) where female birds tend to interact with specific genotype (LL) in order to be super in carcass weight.

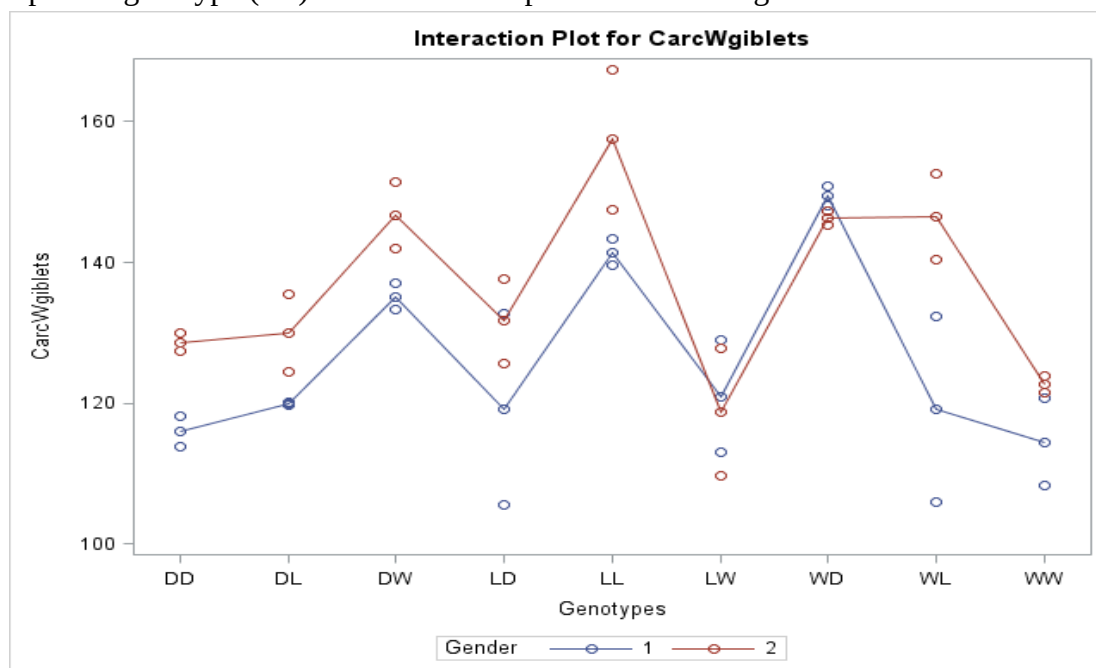


Figure 1. The interaction between genotype and sex for carcass weight of quail genotypes

Economic cuts:

The results of some quail economic cuts (that may sale separately in markets) are presented in Table (3). It could be notice from the previous table, that there were highly significant differences ($p<0.01$) among studied genotypes, where the pure line LL recorded significantly the highest weights for both thigh and wing (20.11 and 12.73 gm., respectively) compared to the other studied genotypes. While both drumstick and neck weights, recorded results in WD cross similar to LL line birds, and surpassed the other genotypes significantly. These results ensure that either pure line LL or the combination between W sire and D dam had benefits for economical cuts of quail. The present results are in agreement with the findings of Yalcin *et al.*, (1995) and Alkan *et al.*, (2010) for just thigh weight, where they found that the line LL surpassed others in such trait significantly; while these results were disagreed with the findings of the same authors in respect to other economic characteristics, where they didn't find any significant differences among their studied quail lines.

In respect to the effect of sex on the studied economic cuts of quail, the present results indicated that just drumstick and wing weights had differed significantly ($p<0.01$) between both sexes (Table 3), where females surpassed males. The present results were in agreement with the findings of Pourtorabi

et al., (2017). On the contrary to this study, the results of Bonos *et al.*, (2010) reported insignificant differences ($p>0.05$) between both sexes in some studied economic cuts of quail.

Table 3. Economic cuts weight (gm.) of studied quail genotypes

Genotype	Sex	Thigh		Drumstick		Wing		Neck	
		M $\pm$ SE	Genotype Overall Mean	M $\pm$ SE	Genotype Overall Mean	M $\pm$ SE	Genotype Overall Mean	M $\pm$ SE	Genotype Overall Mean
DD	M	16.81 $\pm$ 0.16	16.58 ^{cd}	10.24 $\pm$ 0.68	10.79 ^b	10.25 $\pm$ 0.21	10.69 ^e	6.36 $\pm$ 0.96	6.49 ^d
	F	16.36 $\pm$ 0.22		11.35 $\pm$ 0.07		11.12 $\pm$ 0.21		6.63 $\pm$ 0.67	
DL	M	16.13 $\pm$ 0.71	15.89 ^d	10.46 $\pm$ 0.22	10.85 ^b	9.73 $\pm$ 0.07	10.82 ^{de}	8.34 $\pm$ 0.28	7.79 ^{bcd}
	F	15.67 $\pm$ 0.96		11.24 $\pm$ 0.13		11.91 $\pm$ 0.19		7.25 $\pm$ 0.26	
DW	M	18.49 $\pm$ 1.09	17.08 ^{cd}	12.39 $\pm$ 0.09	12.28 ^a	11.66 $\pm$ 0.17	11.95 ^b	9.77 $\pm$ 0.67	8.81 ^{abc}
	F	15.66 $\pm$ 0.07		12.16 $\pm$ 0.17		12.24 $\pm$ 0.13		7.9 $\pm$ 0.38	
LD	M	16.34 $\pm$ 0.34	16.46 ^{cd}	10.57 $\pm$ 0.11	11.10 ^b	10.78 $\pm$ 0.77	10.95 ^{cde}	7.41 $\pm$ 0.39	7.40 ^{cd}
	F	16.57 $\pm$ 0.34		11.64 $\pm$ 0.01		11.11 $\pm$ 0.10		7.37 $\pm$ 0.45	
LL	M	18.45 $\pm$ 0.88	20.11 ^a	11.92 $\pm$ 0.07	12.53 ^a	12.53 $\pm$ 0.36	12.73 ^a	9.51 $\pm$ 1.19	10.16 ^a
	F	21.78 $\pm$ 1.37		13.13 $\pm$ 0.34		12.93 $\pm$ 0.48		10.81 $\pm$ 0.97	
LW	M	17.02 $\pm$ 0.63	17.24 ^{cd}	10.77 $\pm$ 0.08	10.59 ^b	11.49 $\pm$ 0.02	10.79 ^{de}	8.87 $\pm$ 1.81	8.64 ^{bc}
	F	17.46 $\pm$ 0.63		10.42 $\pm$ 0.66		10.11 $\pm$ 0.73		8.42 $\pm$ 0.09	
WD	M	20.57 $\pm$ 0.13	19.45 ^{ab}	12.49 $\pm$ 0.04	12.72 ^a	11.51 $\pm$ 0.29	11.72 ^{bc}	11.06 $\pm$ 0.66	10.29 ^a
	F	18.34 $\pm$ 0.61		12.96 $\pm$ 0.10		11.92 $\pm$ 0.02		9.53 $\pm$ 0.91	
WL	M	16.57 $\pm$ 1.09	18.1750 ^{bc}	10.16 $\pm$ 0.41	12.27 ^a	10.09 $\pm$ 0.83	11.62 ^{bcd}	6.54 $\pm$ 0.54	7.54 ^{bcd}
	F	19.78 $\pm$ 0.76		14.39 $\pm$ 0.16		13.15 $\pm$ 0.35		8.55 $\pm$ 0.45	
WW	M	16.47 $\pm$ 0.36	16.57 ^{cd}	10.17 $\pm$ 0.11	10.73 ^b	10.52 $\pm$ 0.10	10.60 ^e	9.49 $\pm$ 0.10	8.99 ^{ab}
	F	17.01 $\pm$ 1.43		11.27 $\pm$ 0.23		10.69 $\pm$ 0.14		8.49 $\pm$ 0.58	
Sex Overall Mean	M	17.39 ^a		11.02 ^b		10.95 ^b		8.59 ^a	
	F	17.63 ^a		12.07 ^a		11.69 ^a		8.33 ^a	
P>F (Sig.)	G		<0.001		<0.001		<0.001		<0.001
	S	0.52		<0.001		0.002		0.40	
	G*S	0.003		<0.001		0.002		0.10	

Common letters within columns did not differ significantly at 0.05 level of probability

Regarding to the interaction between genotype and sex, there were a highly significant interaction ($p<0.01$) for thigh, drumstick and wing (Table 3). Figure (2) shows an interaction between genotype and sex for thigh weight character. Where LL line seems to be interacted positively with females in order to maximize thigh weight. However, Bonos *et al.*, (2010) didn't find a significant interaction between studied groups and sex of quail.

Giblets cuts:

Table (4) represents the weights of giblets cuts including liver, gizzard and heart as affected by quail genotypes, sex and their interaction. It could be noticed from the table that the genotype effect is highly significant ($p<0.01$) for the three studied characters; where for liver weight, the line LL and reciprocal cross DL recorded the highest values (5.40 and 5.23 gm., respectively) compared to the other studied genotype, which mean that may such genotypes had effective metabolism. While for gizzard weight, the reciprocal cross DL had the highest value (3.83 gm.) compared to the other genotypes, which mean that such genotype had effective mechanism grinding compared to the other genotypes. But as high heart weight it may observed from the Table (4) that the line LL had significantly the biggest value (2.01 gm.); this may make the birds of LL line the activist ones. However, (Moran, 1977; and Alkan, 2010) were reported that different factors affecting carcass traits, involving line, sex, and environment. Regarding to the effect of sex on giblets cuts weights, it may observe from Table (4) that liver character differed significant ($p<0.01$) between both sexes, while the gizzard and heart weights didn't differ

significantly ($p>0.05$). In all cases females were recorded higher values than males' counterparts. These results were in agreement with the findings of Moran, (1977); and Bones, (2010).

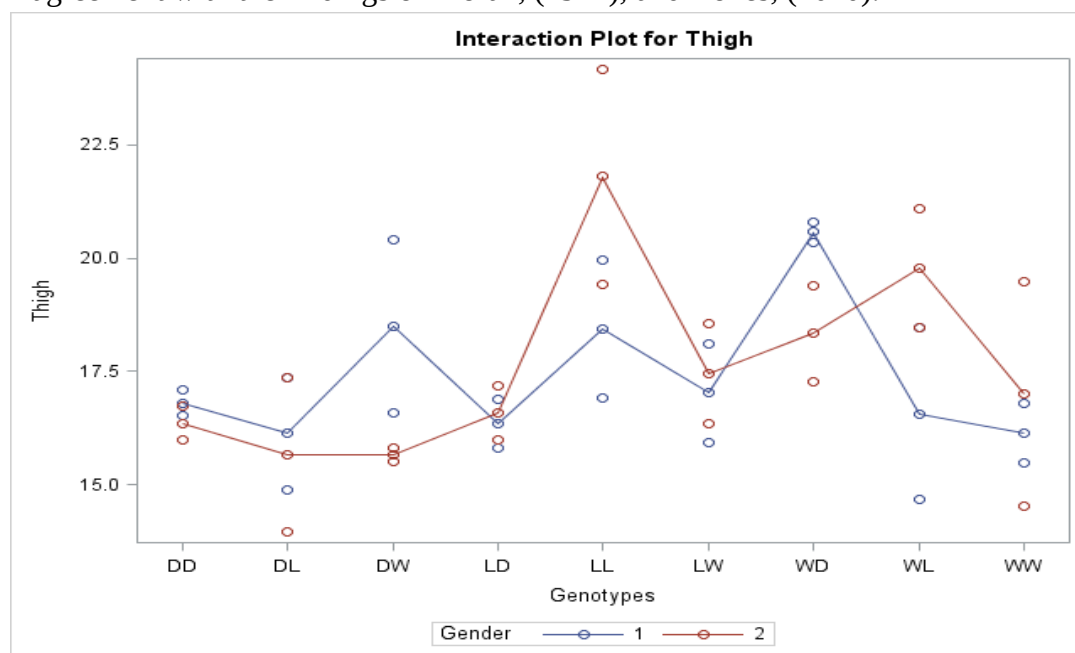


Figure 2. The interaction between genotype and sex for thigh weight

In respect to the interaction between genotype and sex, it could be seen from Table (4) that the genotype interacted significantly ($p<0.01$) with sex for liver weight character, while in gizzard there was no significant interaction; but in heart case the interaction was just significant ($p<0.05$). However, Figure (3) illustrates the interaction curve of all the three studied characters together called as giblet weights; which shows that the highest value of giblet was achieved by the females of WL cross. Such interaction may reflect the digestible effectiveness of females that resulted from the combination between White sire with Light brown dam.

Inedible out-parts:

Table (5) represents carcass inedible out-parts weights as affected by both genotype and sex, in addition to their interaction. It could be noticed from the table that the genotype, sex and their interaction are highly significant ($p<0.01$), except the effect of genotype on feather weight which was differed significantly ($p<0.05$).

The highest weights of both blood and feather were recorded for the reciprocal cross DW (16.75 and 26.09 gm., respectively), while the lowest ones were recorded by the cross LD (6.75 and 17.84 gm., respectively). In respect to head and shank weights, there were no obvious trend, but it could be observed that for head weight, the highest weight was achieved by LL pure line (11.16 gm.) and the lowest one was obtained by the cross WL (9.47 gm.); also, the LL pure line achieved the highest shank weight (3.74 gm.) while the DD pure line was obtained the lowest shank weight (2.9 gm.). It could conclude from these findings that reciprocal cross DW and the line LL surpassed their counterparts in inedible out-parts of carcass. Unfortunately, there were no available review on such inedible out-parts of quail as affected by genotype. Unfortunately, from the survey conducted by authors there were not any similar research deal the inedible out-parts in quail birds as affected by genotypes, sex and their interaction.

Table 4. Giblets cuts weights (gm.) of studied quail genotypes

Genotype	Sex	Liver		Gizzard		Heart	
		M ± SE	Genotype Overall Mean	M ± SE	Genotype Overall Mean	M ± SE	Genotype Overall Mean
DD	M	3.15±0.11	3.97 cd	2.71±0.06	2.99 bc	1.40±0.008	1.51 bc
	F	4.80±0.48		3.27±0.27		1.62±0.003	
DL	M	4.17±0.08	4.58 abcd	3.89±0.48	3.83 a	1.53±0.05	1.38 c
	F	4.99±0.22		3.76±0.54		1.23±0.06	
DW	M	4.28±0.30	5.23 a	2.85±0.09	3.02 bc	1.59±0.05	1.64 bc
	F	6.17±0.01		3.18±0.02		1.70±0.00	
LD	M	2.66±0.12	4.27 bcd	2.91±0.44	2.85 bc	1.81±0.28	1.73 b
	F	5.88±0.01		2.78±0.12		1.65±0.01	
LL	M	4.62±0.52	5.40 a	3.92±0.25	3.53 ab	2.25±0.31	2.005 a
	F	6.18±0.94		3.14±0.44		1.76±0.11	
LW	M	3.82±0.45	3.76 d	2.39±0.22	2.62 cd	1.53±0.10	1.48 bc
	F	3.70±0.33		2.84±0.14		1.42±0.14	
WD	M	4.17±0.12	4.80 abc	3.27±0.003	3.11 bc	1.71±0.05	1.58 bc
	F	5.43±0.22		2.94±0.06		1.46±0.02	
WL	M	3.00±0.32	4.95 ab	3.02±0.47	3.28 abc	1.43±0.13	1.60 bc
	F	6.89±0.46		3.55±0.51		1.77±0.10	
WW	M	3.25±0.02	4.05 cd	2.13±0.02	2.13 d	1.41±0.06	1.38 c
	F	4.85±0.63		2.13±0.08		1.35±0.11	
Sex Overall Mean	M	3.68 b		3.01 a		1.55 a	
	F	5.43 a		3.06 a		1.63 a	
Sig. (Pr > F)	G		0.0007		0.002		0.0003
	S	0.0001		0.68		0.19	
	G*S	0.0004		0.38		0.044	

Common letters within columns did not differ significantly at 0.05 level of probability

Regarding to the sex effect, it shown obviously the superiority for females on males for all inedible studied out-parts. This result reflects the true that quail female weight surpassing male one.

In respect to the interaction between genotype and sex, females try to interact with specific genotype in order to maximize specific character. Where males interacted positively with the reciprocal cross DW for blood and feather weights, while the same sex interacted positively with LL line for head and shank weights. However, such characters have not marketing importance.

Conclusion:

It could be concluded from the previous results that LL line had the best carcass characteristics. The crosses didn't appear any superiority for all carcass characteristics; while a specific reciprocal cross appeared superiority in specific characters, suggesting the use of DD line as sire and WW line as dam for the best carcass dissections in their progeny.

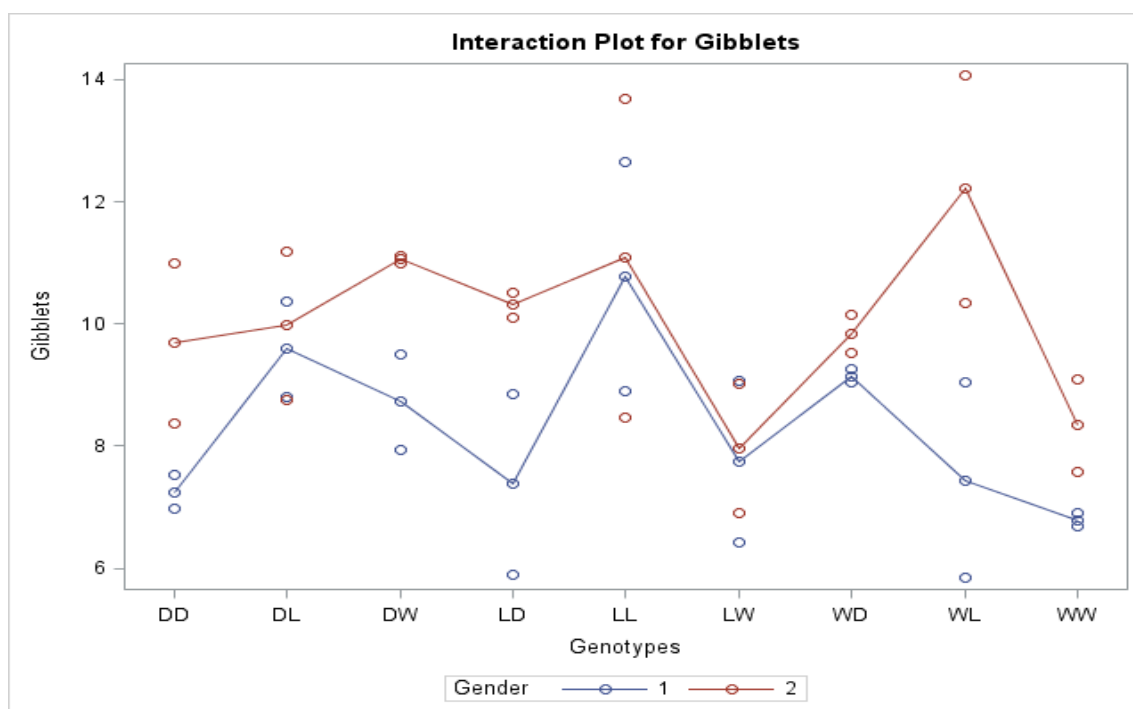


Figure 3. The interaction between genotype and sex for gibblets weight of quail genotypes

Table 5. Inedible out-parts weight (gm.) of different quail genotypes

Genotype	Sex	Blood		Feather		Head		Shank	
		M ± SE	Genotype Overall Mean	M ± SE	Genotype Overall Mean	M ± SE	Genotype Overall Mean	M ± SE	Genotype Overall Mean
DD	M	8.00±2.31	12.75 b	16.74±1.55	18.93 b	10.77±0.11	9.70 b	2.82±0.13	2.90 e
	F	17.50±2.60		21.13±2.32		8.63±0.14		2.99±0.14	
DL	M	7.00±2.31	9.00 cd	17.69±0.38	18.86 b	9.56±0.33	9.52 b	3.08±0.01	3.15 cde
	F	11.00±0.58		20.03±0.65		9.47±0.08		3.22±0.03	
DW	M	17.00±0.58	16.75 a	17.03±1.28	26.09 a	11.22±0.31	10.79 a	3.22±0.08	3.39 bc
	F	16.50±1.44		29.25±1.59		10.36±0.37		3.55±0.06	
LD	M	5.00±1.15	6.75 d	15.98±1.59	17.84 b	10.27±0.28	9.41 b	2.94±0.09	3.21 bcd
	F	8.50±0.29		19.70±0.70		8.55±0.30		3.48±0.17	
LL	M	11.00±2.31	8.75 cd	19.33±0.36	19.46 b	11.42±0.36	11.16 a	3.45±0.21	3.74 a
	F	6.50±0.87		19.60±0.18		10.90±0.47		3.94±0.27	
LW	M	8.50±0.87	11.5 bc	18.28±0.40	18.04 b	10.61±0.05	9.86 b	3.30±0.00	3.06 de
	F	14.50±4.33		17.81±1.63		9.10±0.24		2.83±0.15	
WD	M	7.00±1.15	9.00 cd	18.12±0.67	19.67 b	10.62±0.33	10.61 a	2.73±0.29	3.03 de
	F	11.00±0.00		21.22±1.00		10.59±0.27		3.33±0.03	
WL	M	7.00±0.58	7.25 d	17.29±1.04	18.4 b	9.22±0.40	9.47 b	3.06±0.11	3.48 ab
	F	7.50±0.29		19.53±0.39		9.72±0.25		3.89±0.08	
WW	M	6.50±0.87	7.75 d	16.11±0.16	17.57 b	9.40±0.008	9.59 b	2.89±0.05	2.97 e
	F	9.00±0.58		19.04±0.82		9.78±0.42		3.05±0.01	
Sex Overall Mean	M	8.56 b		17.40 b		9.68 b		3.06 b	
	F	11.33 a		21.47 a		10.34 a		3.36 a	
P>F (Sig.)	G		<.0001		0.02		<.0001		<.0001
	S	0.001		0.001		<.0001		<.0001	
	G*S	0.01		0.01		0.001		0.001	

Common letters within columns did not differ significantly at 0.05 level of probability.

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خصائص الذبيحة في ثلاثة خطوط من السمان وهجنها

1- الأوزان

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الملخص

استخدم في هذه الدراسة عدد 54 صوصاً بعمر يوم واحد من الجنسين وبالتساوي لتراكيب وراثية مختلفة نتجت من التهجين ثنائي الأليل لثلاثة خطوط من السمان الياباني (الأبيض، والبني الفاتح، والبني الغامق). وكان الهدف من البحث دراسة خصائص الذبائح والتي اشتملت على أوزان كل من الدم، والریش، والساق، والرأس والقانصة، والقلب، والكبد، والفخذ، والدبوس، والصدر، والظهر، والأجنحة، وتصافي الذبيحة (متضمنة الحوائج-الكبد، والقلب، والقانصة). أظهرت النتائج وجود فروقاً معنوية بين التراكيب المدروسة وكذلك بين الجنسين بالإضافة لتداخل التركيب مع الجنس. بشكل عام كان أفضل تركيب وراثي متمثلاً بالخط البني الفاتح، ولكن في بعض قطع الذبيحة الرئيسية وكذلك في بعض قطع الذبيحة الاقتصادية وأيضاً في بعض قطع الذبيحة غير الصالحة للأكل (غير المأكولة)، كما أظهر الهجين التبادلي DW (الناتج من الآباء البنية الغامقة والأمهات البيضاء) التفوق على باقي الطرز الوراثية المدروسة، كما سجل الهجين التبادلي DL (الناتج من الآباء السابقة انفسهم مع الأمهات البنية الفاتحة) تفوقاً معنوياً في صفة وزن القانصة. وتراوح معدل وزن الذبائح من 118.5 – 144.5 غ. كما سجلت الإناث أوزاناً أعلى من مثيلاتها الذكور ولكل الخصائص المدروسة. إن التداخل بين التركيب والجنس قد عكس تفاعلاً نوعياً بين تراكيب معينة مع الإناث. خلص البحث إلى أن الهجن لم تبد أي تفوق ملحوظ ولكل الخصائص المدروسة، بينما أظهر خط محدد وكذلك هجين تبادلي محدداً تفوقاً ملحوظاً ولصفات محددة.

الكلمات المفتاحية: السمان، الخطوط، الهجن، أوزان الذبيحة.