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308 Lasani Town, Sargodha Road, Faisalabad - Pakistan
Mob: +92 300 3008585, Fax: +92 41 8815544
E-mail: editorijps@gmail.com

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Research Article
The Positive Effect of Crossing Speckled Hungarian Breed with Commercial Lines in Term of Meat Production and Meat Quality

[1,2]Á. Drobnyák, [1,5]T.N. Lan Phuong, [3]M. Heincinger, [3]K. Kustos, [4]A. Almási, [1,5]I.T. Szalay, [1,5]L. Bódi, [2]R.T. Szabó and [2]M. Weber

[1]Research Centre for Farm Animal Gene Conservation (HáGK), Gödöllő, Hungary
[2]Szent István University, Faculty of Agricultural and Environmental Sciences, Institute of Animal Husbandry, Gödöllő, Hungary
[3]Lab-nyúl Kft. Gödöllő, Hungary
[4]Bábolna TETRA Kft. Bábolna, Hungary
[5]Association for Hungarian Farm Animal Gene Conservation Gödöllő, Hungary

Abstract

Background and Objectives: The study aimed to investigate the meat production (live weight, carcass weight, breast fillet weight, leg weight) and quality (pH, colour, tenderness) of Speckled Hungarian chicken and grandparents' line of TETRA-H, TETRA HARCO and their crossbreeds. **Materials and Methods:** A total of 1120 birds (7 genotypes, 4 pens/genotype, 40 birds/pen) were reared under the same conditions (5 birds/m^2, ad libitum feeding, deep straw bedding) until the age of 84 days. Daily light was 16 h and dark cycle was 8 h. The temperature was maintained at 32°C at the start of the experimental period and gradually decreased to 20°C by the fourth week of age. **Results:** The live weight and carcass percentages of crossbreeds (2244 g, 73.0% for TETRA-H x Speckled Hungarian chickens and 2135 g, 72.3% for Speckled Hungarian chickens x TETRA-H) were significantly higher than Speckled Hungarian chickens (1339 g, 69.9 %). Although, carcass percentages of these genotypes were similar. The breast meat tenderness of TETRA-H × Speckled Hungarian chicken (1.92 kg) was significantly lower than that of Speckled Hungarian chickens (2.70 kg) and the other crossbreeds (3.10 kg for Speckled Hungarian chickens × TETRA-H, 2.81 kg for HARCO × Speckled Hungarian chickens and 2.96 kg for Speckled Hungarian chickens × HARCO). **Conclusion:** The results revealed that the reciprocal crossbred genotypes of TETRA-H and Speckled Hungarian have higher meat production and their meat quality remained the same as that of purebred Speckled Hungarian chickens.

Key words: Breast colour, breast pH, breast weight, carcass percentages, genotype, leg weight, meat quality, reciprocal cross, speckled Hungarian, tenderness

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Corresponding Author: Á. Drobnyák, Research Centre for Farm Animal Gene Conservation (HáGK), H-2100 Gödöllő, Hungary

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

The intensive keeping with immense selection process has led to poultry genetic variability and biodiversity decline[1]. More and more concerns about quality, environment and animal welfare of industrial chickens have emerged, which resulted in an increased demand of high-quality poultry products from non-intensive system[2,3]. The indigenous chickens are preferred in such systems since they are well known for good meat quality[4], high resistance to many diseases and low keeping cost[5].

All indigenous Hungarian poultry species and breeds involved in national protection programme can be found in the gene bank of the Research Centre for Farm Animal Gene Conservation[6]. To preserve the breeds uniformly and effectively, the exact description of their phenotype and performance is needed. However, only a few studies on Hungarian indigenous chickens can be found[7-10].

Crossing breeds and varieties could improve hatchability, growth rate and egg production[11]. Burke and Henry[12] compared the crossbred genotypes of the Black Wyandotte Bantam and the Arbor Acres breeds. The breast weight of crossbred [Black Wyandotte Bantam sire×Arbor Acres dam (10.91 g), Arbor Acres sire×Black Wyandotte Bantam dam (10.24 g)] genotypes was heavier than pure bred bantam group (3.37 g). In other investigation, the breast of commercial broilers was heavier than that of the crossed genotypes[13]. The breast weight of 84-day-old Jingxing 100 crossbred chickens (147 g) was significantly lower compare to the value of Arbor Acres broiler (421 g) but the shear force value showed different trend (35.73 Newton vs. 38.47 Newton).

In terms of meat quality, Promket *et al.*[14] found that the crossbred groups [(Broilers+Layers, dam)×Chee sire], [(Shanghai+Layer, dam)×Chee, sire], [Shanghai Road Bar+Layers, dam)×Chee, sire] did not differ from other groups in case of breast and thigh pH 0 h. However, after 24 h (Shanghai Road Bar+Layers, dam)×Chee, sire group had the lowest pH (5.186) compare to (Broilers+Layers, dam)×Chee sire (6.043) and (Shanghai+Layer, dam)×Chee, sire (6.046) groups in thigh meat.

According to Fletcher[15], appearance and texture are the most important qualities of meat. Meat colour attributes to consumer's decision making. The pale tan to pink raw meat was preferred by customers[15]. Additionally, significant relationship was demonstrated between raw meat colour and raw meat pH[16,17]. The high and the low pH levels cause defects (PSE, DFD) in meat quality and influence meat colour[18]. The pH value also relates to other meat quality traits including tenderness[15]. In the recent years, several authors have also reported the effect of slaughtering weight on the meat quality traits[19-22].

The study aimed to investigate the meat production and meat quality of Speckled Hungarian chicken and grandparents' line of TETRA-H, TETRA HARCO and their crossbreeds.

MATERIALS AND METHODS

Animals: The experiment was approved by the Directorate of Food Safety and Animal Health of Governmental Office of Pest County (Licence number XIV-I-001/1880-5/2012).

The study involved reciprocal crossing of Speckled Hungarian (SH) chickens and grandparent lines of TETRA-H (TT) and TETRA HARCO (HT). The SH chicken belongs to the medium size, dual-purpose Hungarian breeds. Final weight of hens is 2.0- 2.3 kg, cocks 2.5-3.0 kg. The TT is a dual-purpose hybrid. Live weight of day-old male birds is 1.5-1.7 kg, female bird is 2 kg at 20 weeks of age. HT is a black feathered, brown egg layer, which is internationally popular.

All birds received wing tags and were raised under similar conditions in the same building in 28 separated pens (7 genotypes, 4 pens/genotype, 40 birds/pen, 5 birds/m^2). The water and the feed were available *ad libitum*. Feed content varied with age and it showed in Table 1. The floor was covered with straw shaving. All birds were given an initial 23 h photoperiod, then a 16-hour light: 8 h dark lighting schedule from 8 days of age was provided. At the beginning, the temperature was maintained at 32°C and gradually decreased to 20°C in 4 weeks. No health problems were observed during the experiment.

Experimental groups: Chickens were investigated in seven groups: Four groups came from the reciprocal crossings and 3 groups were offspring of purebred SH, TT and HT. The labels of studied groups are showed in Table 2.

Table 1: Feed composition applied in the experiment

	Age		
Ingredients	0-3 weeks	4-6 weeks	7-12 weeks
Crude protein (%)	23.3	20.0	17.5
ME (MJ kg^{-1})	12.1	11.9	12.6
Crude fiber (%)	3.7	3.9	3.4
Crude ash (%)	5.8	5.8	5.7
Methionine (%)	0.6	0.4	0.4
Lysine (%)	1.2	1.1	0.9
Calcium (%)	0.9	1.0	1.0
Phosphorus, available	0.2	0.2	0.2

Table 2: Labels of studied genotypes

Parental genotypes		
Sire	Dam	Label of offspring
Speckled Hungarian (SH)	TETRA-H (TT)	SH×TT
TETRA-H (TT)	Speckled Hungarian (SH)	TT×SH
TETRA HARCO (HT)	Speckled Hungarian (SH)	HT×SH
Speckled Hungarian (SH)	TETRA HARCO (HT)	SH×HT
Speckled Hungarian (SH)	Speckled Hungarian (SH)	SH×SH
TETRA-H (TT)	TETRA-H (TT)	TT×TT
TETRA HARCO (HT)	TETRA HARCO (HT)	HT×HT

The purebred SH was compared to those crossbreeds in which the SH was participate d. Same method was used in case of TT and HT as given below:

- SH×SH to SH×HT, HT×SH, SH×TT, TT×SH
- HT×HT to HT×SH, SH×HT
- TT×TT to TT×SH, SH×TT
- The crossed group with each other

Sampling and measurements: Birds were slaughtered at the age of 84 days. Feed was withdrawn 8 h before the transporting to slaughterhouse. Live weight (LW) was measured immediately before slaughtering. After slaughtering, defeathered and eviscerated carcasses were chilled by cold water for 2 h. A total of 10 samples from breast and leg per pen per genotype were taken. All samples were stored separately in plastic bag at 4°C and transported to laboratory for quality analyses. Carcass weight (CW) was recorded after chilling. Carcass percentage (C%) was calculated as followings:

$$C\% = \frac{CW}{LW} \times 100$$

Breast filet (BFW) and leg including thigh and drumstick (LeW) were separated from the carcass and weighed. The valuable meat parts percent (VMP%) were calculated as follows:

$$VMP\ (\%) = \frac{BFW+LeW}{CW} \times 100$$

The pH and colour of the breast meat were monitored twice: after the chilling to 4°C (pH1) and 24 h after the slaughtering (pH2). Breasts were stored at 4°C. pH-STAR Matthäus® (Matthäus GmbH and Co., Eckelsheim, Germany) instrument was used to measure pH. Calibration was carried out before every measurement with reference solution of pH 4.01 and pH 7.Breast meat colour was measured by Minolta® CR 410 Chromameter (Konica Minolta INC., Tokyo, Japan) on the fresh surface and expressed by CIE colour system. In this system, L* shows the lightness (0 is black; 99 is white), a* shows the redness (+60 is red; -60 is green) and b* shows the yellowness (+60 is yellow; -60 is blue) of the meat.

To measure the tenderness, breast samples were stored in a freezer (-20°C) for one month then thawed overnight at room temperature. Samples were cooked with contact grill (Philips Cucina HD 2430, Hamburg, Germany) up to 72°C core temperature (predefined with TESTO 926 equipment, Lenzkirch, Germany). The cooked samples were cooled down for 1.5 h to room temperature. 1×1 cm samples were taken from the samples, with the cutting line parallel to muscle fibres. 5 independent measurements were performed on every samples in *cranial-caudal* direction. Tenderness was measured by TA. XT PLUS®Texture Analyser (Stable Micro Systems, Godalming, United Kingdome) Texture Analyser equipment with 1.2 mm Warner-Bratzler blade (60°, 250 mm sec^{-1}). The highest shear force values were selected by the Texture Exponent 32 (Stable Micro Systems, Godalming, United Kingdome) program which can display the force/time (kg sec^{-1}) graphs.

Statistical analysis: Results were analysed by the R 3.1.2 statistical software. All variables were checked for normality (Shapiro-Wilk test). Values are presented as Means±S.D. Data were analysed by one-way analysis of variance (ANOVA) followed by Tukey's post hoc test for comparison between control and treatment groups. Differences were considered significant at $p<0.05$.

RESULTS

Slaughtering results are shown in Table 3. Significant differences were found in live weight(LW) when compared SH×SH with TT×SH ($p\leq0.001$), SH×TT ($p\leq0.001$) and HT×SH ($p\leq0.001$). All crossbred genotypes [TT×SH ($p\leq0.001$), SH×TT ($p\leq0.001$), HT×SH ($p = 0.020$), SH×HT ($p = 0.049$)] had significantly higher carcass weight than SH×SH. Although, SH×HT had smaller LW but its carcass percentage (C) %) was significantly higher ($p = 0.010$) than HT×SH. TT×SH had the highest breast filet weight (BFW), followed by SH×TT.

The BFW of TTxSH was significantly higher than that of HT×SH ($p\leq0.001$), SH×HT ($p\leq0.001$) and SH×SH ($p\leq0.001$), The BFW of SH×TT was significantly higher than that of HT×SH ($p=0.002$), SH×HT ($p=0.007$) and SH×SH ($p\leq0.001$). The TT×SH ($p\leq0.001$) and SH×TT ($p\leq0.001$) had significantly lower BFW than that of TT×TT. The TT×TT had significantly higher LeW than TT×SH ($p\leq0.001$) and SH×TT, ($p\leq0.001$). On the other hand, SH×SH had lower LeW than

Table 3: Meat production and slaughtering yield of studied genotypes

Genotypes										
Sire	Dam		LW[1] (g)	CW[2] (g)	C%[3] (%)	BFW[4] (g)	LeW[5] (g)	BFW[6] (%)	LeW%[7] (%)	VMP%[8] (%)
TT	SH	Mean	2 244.0^{be}	1638.0^{be}	73.000^{be}	271.0^{be}	572.0^{be}	16.500^{e}	34.900	51.500^{e}
		SD	182.0	139.0	0.957	35.2	47.4	1.120	1.150	0.950
SH	TT	Mean	2 135.0^{be}	1555.0^{be}	72.900^{be}	253.0^{be}	540.0^{be}	16.300^{e}	34.800	51.100^{e}
		SD	185.0	127.0	1.080	25.3	42.9	1.070	1.380	1.360
HT	SH	Mean	1 678.0^{c}	1180.0^{c}	70.300^{a}	182.0^{a}	418.0^{c}	15.400	35.500	50.900
		SD	90.2	68.6	1.390	23.7	23.0	1.460	0.893	1.450
SH	HT	Mean	1 599.0^{ac}	1158.0^{c}	72.500^{b}	188.0^{a}	399.0^{ac}	16.200^{g}	34.400	50.600
		SD	90.9	64.9	1.270	12.9	20.6	0.895	0.805	0.835
SH	SH	Mean	1 369.0^{a}	958.0^{a}	69.900^{a}	151.0^{a}	338.0^{a}	15.800	35.300	51.100
		SD	142.0	106.0	1.360	25.0	42.2	1.590	1.120	1.590
TT	TT	Mean	3 109.0^{d}	2 332.0^{d}	75.000^{d}	430.0^{d}	814.0^{d}	18.40^{d}	34.900	53.300^{d}
		SD	386.0	305.0	2.060	85.8	99.0	1.670	1.310	1.380
HT	HT	Mean	1 618.0	1 164.0	72.000	167.0	410.0	14.400^{f}	35.200	49.500
		SD	89.9	59.5	0.875	18.4	20.2	1.300	0.787	0.879

[1]Live weight, [2]Carcass weight, [3]Carcass weight/Live weight*100; [4]Breast filet weight, [5]Leg (Thigh+Drumstick) weight, [6]Breast filet weight/Carcass weight*100, [7]Leg (Thigh+Drumstick) weight/Carcass weight*100, [8]Breast filet weight+Leg (Thigh+Drumstick) weight/Carcass weight*100. $^{a-c}$different superscript letters show significant differences ($p \leq 0.05$) between SH×SH and SH×HT, HT×SH, SH×TT, TT×SH in a column detected by Tukey-test. ^{d,e}different superscript letters show significant differences ($p \leq 0.05$) between TT×TT and TT×SH, SH×TT genotypes in a column detected by Tukey-test. ^{f,g}different superscript letters show significant differences ($p \leq 0.05$) between HT×HT and HT×SH, SH×HT genotypes in a column detected by Tukey-test. $^{a-f}$different superscript letters show significant differences ($p \leq 0.05$) between genotypes SH×HT, HT×SH, SH×TT, TT×SH with each other in a column detected by Tukey-test

Table 4: Meat quality traits (pH value, breast meat colour and tenderness) of studied genotypes

Genotypes					Breast colour						
					After the chilling to 4° C			24 h after slaughtering			
Sire	Dam		pH1 (after the chilling to 4°C)	pH2 (24 h after slaughtering)	L*[1]	a*[2]	b*[3]	L*[1]	a*[2]	b*[3]	Tenderness (kg)
TT	SH	Mean	5.760	5.840	48.20	2.69	8.81^{d}	43.10	1.600	7.800	1.920^{bd}
		SD	0.092	0.178	5.04	1.65	1.38	3.62	1.280	0.248	0.535
SH	TT	Mean	5.700^{b}	5.690	50.30	2.23	7.85	58.00	0.767	8.080	3.100^{a}
		SD	0.282	0.355	2.66	1.29	1.96	9.79	1.190	2.620	0.529
HT	SH	Mean	5.700^{b}	5.810	51.60	2.49	9.59	56.70	0.657	13.400	2.810^{a}
		SD	0.104	0.042	2.67	1.31	1.63	3.55	1.490	1.910	0.679
SH	HT	Mean	5.760	5.770	50.20	2.42	8.59	52.50	1.490	9.920	2.960^{a}
		SD	0.065	0.128	3.55	1.32	1.19	5.29	2.590	2.680	0.357
SH	SH	Mean	5.910^{a}	5.800	47.80	4.11	7.53	55.80	3.020	9.690	2.700^{a}
		SD	0.107	0.038	5.07	1.66	1.43	1.08	0.420	1.180	0.389
TT	TT	Mean	5.730	5.810	49.10	0.98	6.16^{c}	59.20	2.320	11.700	2.930^{c}
		SD	0.146	0.189	3.28	1.94	1.20	7.95	1.160	5.150	0.593
HT	HT	Mean	5.660	5.620	52.40	0.85	8.07	54.20	0.543	11.300	3.480
		SD	0.094	0.067	2.95	1.46	1.71	2.85	0.840	2.630	0.536

[1]Lightness (0 is black; 99 is white), [2]Redness (+60 is red; -60 is green), [3]Yellowness (+60 is yellow; -60 is blue). $^{a-c}$Different superscript letters show significant differences ($p \leq 0.05$) between SH×SH and SH×HT, HT×SH, SH×TT, TT×SH in a column detected by Tukey-test. ^{d,e}Different superscript letters show significant differences ($p \leq 0.05$) between TT×TT and TT×SH, SH×TT genotypes in a column detected by Tukey-test. ^{f,g}Different superscript letters show significant differences ($p \leq 0.05$) between HT×HT and HT×SH, SH×HT genotypes in a column detected by Tukey-test. $^{a-f}$Different superscript letters show significant differences ($p \leq 0.05$) between genotypes SH×HT, HT×SH, SH×TT, TT×SH with each other in a column detected by Tukey-test

TT×SH ($p \leq 0.001$), SH×TT ($p \leq 0.001$) and HT×SH ($p = 0.011$). The TT×SH ($p \leq 0.001$) and SH×TT ($p \leq 0.001$) had higher LeW than HT×SH and SH×HT. The BFW% were higher in SH×HT ($p = 0.041$) than that of HT×HT. No significant differences were found in case of the LeW% between genotypes. TT×TT had higher VMP% than that of TT×SH ($p = 0.022$) and SH×TT ($p = 0.002$). The current study showed that apart from LeW%, all other meat production traits of TT×SH and SH×TT were significantly lower than that of TT×TT.

The meat quality results are shown in Table 4. The pH1 value of SH×SH was significantly higher than that of SH×TT ($p = 0.028$) and HT×SH ($p = 0.022$). However, no difference could be detected between genotypes in case of pH2. The highest L* after the slaughtering was obtained in HT×SH and did not significantly differ from other genotypes. The b* of TT×SH meat was higher than that of TT×TT. No significant difference in breast colour measured 24 h after slaughtering could be seen. TT×SH had the lowest tenderness and it

significantly differed from the HT×SH ($p = 0.006$), SH×HT ($p = 0.001$), SH×TT ($p \leq 0.001$) SH×SH ($p = 0.025$) and TT×TT ($p \leq 0.001$).

DISCUSSION

In our study, meat production and quality of 84-day-old crossbreeds of Speckled Hungarian chicken, TETRA-H and TETRA HARCO genotypes were investigated. The genotype, the housing and the feeding have the biggest effect on the body growth and production parameters[23]. In the present study, crossbreeds (TT×SH, SH×TT) reached the 2 kg live weight on the 84th day. Consistent results were reported by Yamak *et al.*[24].

Sofalvy and Vidacs[9] investigated the effect of crossing of SH and two medium growing genotypes (New Hampshire, White Plymouth Rock). In their studies the SH weight was the smallest compared to its crossbred, this is similar with results of the current study about SH×SH genotype. Their performance was also not comparable to that of commercial lines. The obtained results are consistent with the results from Sofalvy and Vidacs[9]. However, the LW of SH in this study is higher than that reported by Sofalvy and Vidacs[9]. Their BFW% and LeW% are also higher than that of crossbreeds in the cross with New Hampsire obtained by Sofalvy[10], although their C% is lower.

The difference amongst the studied genotypes was more obvious in terms of meat production traits than in term of meat quality. Although, the pH values of SH×SH breast meat significantly differed from SH×TT and HT×SH breast meat, all values were within normal range (5.6-5.8) defined by Miller *et al.*[25]. The L* of crossbred breast meat (SH×TT 50.3, HT×SH 51.6, SH×HT 50.2) in this study was higher than the reported values of Fletcher[15] (48.8). However, the redness (a*) of all crossbred genotypes was also higher (TT×SH: 2.69, SH×TT: 2.23, HT×SH: 2.49, SH×HT: 2.42) than that of Fletcher[15] (1.7).

The tenderness of SH crossbred genotypes was lower than 3 kg and can be considered as tender meat type[4,26]. The tenderness of SH crossbred meat can be due to slow growing. Since the muscle fibres grow with age only and slow growing chicken such as SH or SH crossbreeds can generate smaller fibre diameter. Smaller the muscle fibre diameter, the more tender meat will be.

The result showed that crossbred genotypes (TT×SH, SH×TT) produced more meat than SH but less than TT. TT×SH and SHxTT were significant higher than HT×SH and SH×HT in live weight, carcass weight, carcass percentages and valuable meat parts percentages. In general, this study agrees with several previous studies which reported that the crossbred genotypes produced more meat[9,12-14,24].

CONCLUSION

The current study showed the crossbred genotypes of SH and TT have favourable meat production and their meat quality remained at the same level of the purebred SH. The present study investigated the genotypes in closed keeping system but SH were usually kept in alternative keeping systems. Therefore, there is a potential that these crossbred genotypes could realise marketable performance in alternative keeping systems. For this reason, further investigations are needed.

SIGNIFICANCE STATEMENT

This study discovered that crossing affected the meat production positively but the meat quality was not changed compare to purebred SH, that can be beneficial for the protection of native or indigenous breeds. This study will help the researchers to uncover the critical areas of sustainable gene conservation that many researchers were not able to explore. Thus, a new theory on meat production and quality of crossbreeds of SH may be arrived at.

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