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Inheritance of plumage colour in the F_1 and test cross progeny of Japanese quail

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Abstract

Recessive genes produced its phenotypic effect only when its allele is identical while the dominant ones produced its effect either with identical or dissimilar alleles. This study was conducted to determine the mode of inheritance of plumage colour in Japanese quail flock in Nigeria, using the Manchurian Gold (MG), Pharaoh (PH) and Panda White (PW) plumage types. All possible crosses were made among the three colour variants making a total of nine mating groups. A total number of 2,348 F_1 chicks and 1,563 test cross progeny obtained from the incubated eggs were classified and counted by their down colour into observable plumage colour groups. The expected phenotypic ratios of the F_1 and test cross progeny were computed based on the assumption that parents that were homozygous for a particular plumage colour breed true. The results revealed that the Pharaoh plumage quails carry the wild-type allele (Wb) in homozygous form or in heterozygous with the Panda White (wb) allele. The Manchurian gold plumage quails carry the Manchurian Gold-type allele (Wb^+) in heterozygous with either Wb or wb. All the Panda White chicks were homozygous for the wb allele, which was recessive to both Wb^+ and Wb alleles. The Chi-square results confirm the heterozygousity of the dominant phenotype in the test crosses. It can be concluded that inheritance of plumage colour is controlled by autosomal genes with dominant hierarchy of MG> PH> PW (Wb^+>Wb>wb).

Keywords: Inheritance, plumage colour, test cross, progeny, Japanese quail

Introduction

Breeding for customized feather colour phenotypes using colour mutations is becoming increasingly important in Japanese quail (Minvielle *et al*., 2007; Mishra *et al*., 2011). This increased interest is from both biological and production standpoints (Pang and Zhao, 2003; Minvielle *et al.,* 2005). Genes encoding for a number of proteins have been implicated in the determination of plumage colour in quails. For instance, Gunnarsson *et al.* (2007) reported that plumage colour is controlled by the alignment of the genes encoding the protein $SLC_{45}A_2$ (solute carrier family forty-five, member 2, protein). The success of breeding programme for customised feather colour types would depend on the ability of the researchers to establish the zygosity of the dominant phenotype in the F_1. Test cross is the technique of crossing an individual of unknown genotype to a homozygous recessive individual. According to Gai and He (2013), test crossing is used to determine if the dominant phenotype is homozygous dominant or heterozygous. Test crossing as a technique is hinged on the premise that genes coding for traits in any individual are always in alternative form called alleles. Recessive genes produced its phenotypic effect only when its allele is identical while the dominant ones produced its effect either with identical or dissimilar alleles. The objective of this study is to identify the pattern of inheritance of plumage colour in the F_1 and test cross progeny of Japanese quail.

Materials and methods

Experimental site

The study was carried out in Apa-Lara farm, Tanke, Ilorin South Local Government area of Kwara State. Ilorin is located in northern

Guinea savannah of Nigeria. It has coordinates of latitude 08.98^0 N and Longitude 04.56^0E with annual rainfall range of 800 to 1,500mm and daily temperature of 22 to 33^0 C (Gannicott, 2008).

Experimental birds

Japanese quail used for this study consist of three plumage colour variants; Manchurian Gold (Plate 1), Pharaoh (wild type, Plate 2) and Panda White (Plate 3).

Plate 1

Plate 2

Plate 3

A total of 324 four weeks old Japanese quail (108 males and 216 females) which included 36 males and 72 females of each colour were used as base population. These birds were purchased from National Veterinary Research Institute, Vom (Ikire outstation). The birds used for the test crossing comprised of F_1 progeny and the recessive parents. Birds in the base population were fed with pre-lay formulated diet containing 22% crude protein and 2,900kcalME/kg from four weeks old to point of lay. At point of lay the feed was changed to layer's diet containing 16.5% crude protein and 2,500kcalME/kg. Feed and clean water were served *ad-libitum* throughout the experimental period. Male and female birds were housed separately until they were six weeks old. At six weeks of age, all possible crosses were made (Table 1) among the three breeds making a total of nine mating groups (nine genetic groups). Twelve female quails were randomly assigned to six males in a completely randomized design to form a breeding replicate. There were two replicates for each of the nine genetic groups in a mating ratio of one male to two females (Table 1) as proposed by Shanaway (1994), Ali *et al*. (2013), Dogan *et al*. (2013) and Karousa *et al*. (2015). Birds were mated at six weeks of age, but eggs for incubation were collected when the birds were nine weeks old (Daikwo *et al*., 2011). When the F_1 progeny reached 42 days old, they were assigned to the recessive parents in a completely randomized design to form a total of six crosses (Table 1). Also, in mating ratio of one male to two females, in two replicates of six males to twelve females per replicate. Six test crosses were carried out using a total number of 216 birds that were reared in battery cages.

Four hundred fertile eggs were collected from each of the nine genetic groups making a total of 3,600 eggs. The eggs were collected daily and kept separately according to their genetic group. The daily eggs collections were stored in a well-ventilated room, at normal room temperature and were accumulated for seven days (Romao *et al*., 2008). At every 7^{th} day, the eggs collected were selected to eliminate cracks and those with shape defects. They were cleaned, weighed individually and set in different sections of 1,500 capacity electric incubator. The different sections of the setter were marked

Table 1: Breeding plan showing the nine crosses and six test cross mating groups

Type of Cross	Sire x Dam	Number of Sire	Number of Dam
Straight and Reciprocal	MG x MG	12	24
	PH x PH	12	24
	PW x PW	12	24
	PH x PW	12	24
	PW x PH	12	24
	MG x PH	12	24
	PH x MG	12	24
	MG x PW	12	24
	PW x MG	12	24
Test Crosses	PHPW x PW	12	24
	PW x PWPH	12	24
	MGPH x PH	12	24
	PH x PHMG	12	24
	MGPW x PW	12	24
	PW x PWMG	12	24

Plumage Colour: Manchurian Gold (MG), Pharaoh (PH), Panda White (PW).

according to the genotype. Temperature of 37.3 °C to 37.7 °C and relative humidity of between 60% and 70% were maintained in the incubator. The eggs were turned manually thrice in a day for 14 days' incubation period after which the eggs were transferred into the hatcher. The four hundred eggs from each genetic group were incubated and hatched in three replicates.

Data collection

At hatch, chicks were classified and counted by their down colour into observable plumage colour groups using the knowledge of down colour visible in the parental quail varieties.

Statistical analyses

The expected phenotypic ratios of the F_1 progeny from the nine parental crosses and the six test crosses were computed based on the assumption that parents that are homozygous for a particular plumage colour breed true and that the inheritance of plumage colour follows the expected Mendelian phenotypic ratio in the F_1 for a monohybrid cross. Nine null hypotheses (H_0) were postulated for testing the straight crosses. The null hypotheses were that, the observed plumage colour distribution of the progeny in each of the crosses was not significantly different from the theoretical distribution of 1:0 ratios in favour of the dominant allele. In the test crossing, six null hypotheses (H_0) were tested. The null hypotheses were that, the observed plumage colour distribution of the progeny in each of the test crosses was not significantly different from the theoretical ratio of 50:50 between the dominant and the recessive phenotypes. The Chi-square goodness of fit (one sample test) at a significant level of 0.05 was used to compare the categorical data and to determine if the observed values differed significantly from expected Mendelian distribution. The calculated Chi-square (X^2) was obtained using the formula:

$$X^2 = \frac{\Sigma(\text{Observed} - \text{Expected})^2}{\text{Expected}}$$

Penetrance - was calculated as follows: $(x/n) * 100$

Where x = the proportion of individuals with dominant allele that expressed it phenotypically

n = observed total number of F_1 chicks

Results

Inheritance of plumage colour in F_1 progeny of Japanese quail

The plumage colours and putative genotypes of parents and the F_1 progeny as well as the observed and expected phenotypic ratios in different crosses are presented in Table 2. Table 3 shows the Chi-square analyses results. In mating between Manchurian Gold male and female parents (MG x MG) a total of 292 F_1 progeny were produced, with Manchurian Gold (MG) and Pharaoh (PH) phenotype appeared in a ratio of 90.41: 9.59. All the 268 chicks produced in the mating between Pharaoh male and female parents (PH x PH) appeared with Pharaoh plumage. Similarly, the 253 progeny which were produced from the mating involving Panda White male and female parents (PW x PW) appeared with Panda White plumage. The results of Chi-square goodness of fit tests (Table 3) shows that the calculated X^2 values of 2.68, 0.00 and 0.00, respectively for the crosses between MG x MG, PH x PH and PW x PW were below the critical value for 0.05 significant level (3.841). Therefore, the null hypotheses (the observed plumage colour distributions among the progeny of those crosses were not significantly different from the expected values) were accepted. The cross between Pharaoh male and Panda White birds (PH x PW) produced a total of 231 Pharaoh (PH) plumage and 17 Panda White (PW) plumage phenotype. Similar result was obtained in the reciprocal cross (PW x PH), with 241 Pharaoh plumage and 29 Panda White plumage. These proportions were in ratios 93.14: 6.86 and 89.26: 10.74, Pharaoh to White, respectively. The penetrance of *Wb* allele in the cross between Pharaoh and Panda White was only 89.26 and 93.14%, for the reciprocal crosses between PH and PW. The results of Chi-square goodness of fit tests for PH x PW and PW x PH crossbreds showed that the calculated X^2 statistics (1.17 and 3.11, respectively) were below the critical value for 0.05 significant levels (3.841). Therefore, the null hypothesis for this reciprocal cross which state that the observed plumage colour distributions among the progeny were not significantly different from the expected values was accepted. The results of putative genotypes further showed that the male and female Pharaoh parents used were either homozygous for wild plumage allele (*Wb*) or heterozygous with the recessive white colour allele (*wb*)

In the mating between Manchurian Gold male and Pharaoh female parents (MG x PH), a total of 278 F_1 progeny were obtained. In the reciprocal cross (PH x MG), 247 progenies were produced, these were in ratios 85.25: 14.75 and 71.26: 28.74, Manchurian Gold to Pharaoh, respectively. However, the penetrance of the Wb^+ was only between 71.26 and 85.25%. The results of Chi-square goodness of fit tests showed that the calculated X^2 values (6.05 and 20.41) for the crosses between MG x PH and PH x MG were higher than the critical value for 0.05 significant level (3.841). Therefore, the alternative to the null hypotheses which state that the observed plumage colour distributions showed significant difference from the expectation were accepted.

In the mating between Manchurian Gold male and Panda White female parents (MG x PW) and its reciprocal (PW x MG), three different individual phenotypes were observed in the F_1 progeny; Manchurian Gold, Pharaoh and White phenotypes (Table 2). The three plumage colour genotypes were produced in the ratio of 64.44: 30.00: 5.56 for MG, PH and PW respectively. The reciprocal cross (PW x MG) produced a total number of 222 chicks with Manchurian Gold, Pharaoh and White phenotypes and in ratio 58.11: 23.87: 18.02. The penetrance of the Wb^+ allele in these crosses was between 58.11 and 64.44%. The results of Chi-square goodness of fit tests (Table 3) shows that the calculated X^2 statistics in these two crosses (MG x PW and PW x MG) were higher (34.13 and 38.96) than the critical value for 0.05 significant level (3.841). This implies a

Table 2: Plumage colour and putative genotypes of parents and offspring with observed and expected phenotypic ratios in different crosses

Group	Crosses	Plumage Colour Phenotypes and Putative Genotypes of Parents		No. of Progeny	Putative Genotypes and Expected Plumage Phenotypic ratio of Offspring		Observed Phenotypic Ratio		
					Genotype	Phenotypic Ratio	MG	PH	PW
A	MGxMG	MGxMG	Wb^+/Wb, Wb^+/wbx Wb^+/Wb, Wb^+/wb	292	♂x♀ Wb^+/Wb, Wb^+/wb, Wb/wb, wb/wb	MG:PH:PW (1:0:0)	90.41	9.59	0.00
B	PHxPH	PHxPH	Wb/Wb, Wb/wbx Wb/Wb, Wb/wb	268	♂x♀ Wb/Wb, Wb/wb, wb/wb	MG:PH:PW (0:1:0)	0.00	100.00	0.00
C	PWxPW	PWxPW	wb/wbx wb/wb	253	♂x♀ wb/wb	MG:PH:PW (0:0:1)	0.00	0.00	100.00
D	PHxPW	PHxPW	Wb/Wb, Wb/wbx wb/wb	248	♂x♀ Wb/wb, wb/wb	MG:PH:PW (0:1:0)	0.00	93.14	6.86
E	PWxPH	PWxPH	wb/wbxWb/Wb, Wb/wb	270	♂x♀ Wb/wb , wb/wb	MG:PH:PW (0:1:0)	0.00	89.26	10.74
F	MGxPH	MGxPH	Wb^+/Wb, Wb^+/wbx Wb/Wb, Wb/wb	278	♂x♀ Wb^+/Wb, Wb^+/wb, Wb/Wb, Wb/wb, wb/wb	MG:PH:PW (1:0:0)	85.25	14.75	0.00
G	PHxMG	PHxMG	Wb/Wb, Wb/wbx Wb^+/Wb, Wb^+/wb	247	♂x♀ Wb^+/Wb, Wb^+/wb, Wb/Wb, Wb/wb, wb/wb	MG:PH:PW (1:0:0)	71.26	28.74	0.00
H	MGxPW	MGxPW	Wb^+/Wb, Wb^+/wbx wb/wb	270	♂x♀ Wb^+/wb, Wb/wb, wb/wb	MG:PH:PW (1:0:0)	64.44	30.00	5.56
I	PWxMG	PWxMG	wb/w b xWb^+/Wb,Wb^+/wb	222	♂x♀ Wb^+/wb, Wb/wb, wb/wb	MG:PH:PW (1:0:0)	58.11	23.87	18.02

Plumage Colour: Manchurian Gold (MG), Pharaoh (PH), Panda White (PW). Wb^+, Wb, wb represents alleles for Manchurian Gold, Pharaoh and Panda White, respectively.

Plate 4

Plate 5

Table 3: Chi-square goodness of fit test for observed and expected plumage colour distribution in the F_1 progeny

Crosses	Allele	Obs.	Exp.	(O-E)	$(O-E)^2$	$(O-E)^2/E$
MGxMG	Wb^+-type	264	292	-28	784	2.68
	Wb-type	28	0	28	784	0
	wb-type	0	0	0	0	0
	Total	292	292	0	1,568	2.68
PHxPH	Wb^+-type	0	0	0	0	0
	Wb-type	268	268	0	0	0
	wb-type	0	0	0	0	0
	Total	268	268	0	0	0.00
PWxPW	Wb^+-type	0	0	0	0	0
	Wb-type	0	0	0	0	0
	wb-type	253	253	0	0	0
	Total	253	253	0	0	0.00
PHxPW	Wb^+-type	0	0	0	0	0
	Wb-type	231	248	-17	289	1.17
	wb-type	17	0	17	289	0
	Total	248	248	0	578	1.17
PWxPH	Wb^+-type	0	0	0	0	0
	Wb-type	241	270	-29	11,236	3.11
	wb-type	29	0	29	11,236	0
	Total	270	270	0	22,472	3.11
MGxPH	Wb^+-type	237	278	-41	1,681	6.05
	Wb-type	41	0	41	1,681	0
	wb-type	0	0	0	0	0
	Total	278	278	0	3,362	6.05
PHxMG	Wb^+-type	176	247	-71	5,041	20.41
	Wb-type	71	0	71	5,041	0
	wb-type	0	0	0	0	0
	Total	247	247	0	10,082	20.41
MGxPW	Wb^+-type	174	270	96	9,216	34.13
	Wb-type	81	0	81	6,561	0
	wb-type	15	0	15	225	0
	Total	270	270	0	16,002	34.13
PWxMG	Wb^+-type	129	222	-93	8,649	38.96
	Wb-type	53	0	53	2,809	0
	wb-type	40	0	40	1,600	0
	Total	222	222	0	12,978	38.96

MG, PH, PW represents Manchurian Gold, Pharaoh and Panda White respectively. Wb^+, *Wb, wb* represent alleles for Manchurian Gold, Pharaoh and Panda White, respectively.

significant difference between the observed and expected plumage colour distributions in the F_1 progeny.

The F_1 white quails obtained from MG x PW reciprocal crosses were phenotypically different from their Panda White parents. They possessed either spots or large golden patches on the head, back, tail and wing. The golden patches resemble the plumage colour of their Manchurian Gold parents (Plate 4) different from the wild-type patches carried by their Panda White parents (Plate 5).

Inheritance of plumage colour in test cross progeny of Japanese quail

The proportions of observed plumage colour phenotypes of progeny resulting from the test crosses are shown in Table 4, while Table 5 presents the results of Chi-square analyses. The cross, involving Pharaoh male progeny and the recessive Panda White female parent (PHPW x PW) produced a total number of 240 chicks in ratios 52.92PH: 47.08PW while 250 progenies produced from the reciprocal of this cross (PW x PWPH) were in a ratio 52.40PH: 47.60PW. The results of Chi-square (Table 5) showed that the calculated values were lower (0.82 and 0.58) than the critical value at 0.05 significant level (3.841) for test crosses T_1 and T_2 (PHPW x PW and PW x PWPH). This indicates that the observed proportion of phenotypic distribution among the progeny did not differ significantly from the expected ratio. Two hundred and nintey three progenies obtained in the cross involving Manchurian Gold male progeny and the recessive Pharaoh parent (MGPH x PH) gave a ratio of 50.51MG: 47.44PH: 2.05PW. The reciprocal cross (PH x PHMG) produced 251 progenies in ratio 44.22MG: 55.78PH: 0.00PW. The Chi-square analyses (Table 5) showed that the calculated values (0.40 and 3.36 for the reciprocal crosses, respectively) were lower than the critical value at 0.05 significant level (3.841) for test crosses T_3 and T_4 (MGPH x PH and PH x PHMG). This implies that the expected and observed progeny phenotypic distributions were not significantly different.

The cross between Manchurian Gold male progeny and Panda White recessive parent (MGPW x PW) produced a total of 256 progeny which gave MG, PH and PW phenotypes, in ratio 23.44: 35.16: 41.40. The reciprocal of this cross (PW x PWMG) gave 273 progeny which were Manchurian Gold, Pharaoh and Panda White phenotypes in ratio 25.64: 34.80: 39.56. The Chi-square results (Table 5) showed the calculated values to be higher (39.91 and 38.35 for the reciprocal crosses, respectively) than the critical value for 0.05 significant level (3.841). This means that the expected and observed proportions of phenotypic distributions among the progeny in test crosses T_5 and T_6 differ significantly ($p<0.05$). The results of the X^2 used for testing the six null hypotheses presented in Table 5 shows that the number of progenies obtained in the test crosses T_1 and T_2 did not differ significantly from expectation ($p_{0.05}$ = 3.84) with the assumption of dominance of *Wb* allele over *wb*. Similarly, the number of progenies obtained in T_3 and T_4 were not significantly different from the expected phenotypic ratio among the test cross progeny. However, the X^2 values of 39.91 and 38.35 obtained for test crosses T_5 and T_6, respectively differ significantly ($p<0.05$) from the expected ratio for monohybrid inheritance.

Table 4: Plumage colour and putative genotypes of parents and offspring with observed and expected phenotypic ratios in the test crosses

Group	Test cross	Plumage Colour Phenotypes and Putative Genotypes of Parents	No. of Progeny	Putative Genotypes and Expected Plumage Phenotypic ratio of Offspring		Observed Phenotypic Ratio		
				Genotype	Phenotypic Ratio	MG	PH	PW
T_1	PHPWxPW	PHxPW *Wb/Wb,Wb/wb*x wb/*wb*	240	♂x♀ *Wb/wb,wb/wb* (0.00:50.00:50.00)	MG:PH:PW	0.00 47.08	52.92	
T_2	PWxPWPH	PWxPH *wb/wb*x *Wb/Wb, Wb/wb*	250	♂x♀ *Wb/wb, wb/wb* (0.00:50.00:50.00)	MG:PH:PW	0.00 47.60	52.40	
T_3	MGPHxPH	MGxPH *Wb⁺/Wb, Wb⁺/wb*x *Wb/Wb, Wb/wb*	293	♂x♀ *Wb⁺/Wb, Wb⁺/wb,* (50.00:50.00:0.00) *Wb/Wb, Wb/wb, wb/wb*	MG:PH:PW	50.51	47.44	2.05
T_4	PHxPHMG	PHxMG *Wb/Wb, Wb/wb*x *Wb⁺/Wb, Wb⁺/wb*	251	♂x♀ *Wb⁺/Wb, Wb⁺/wb,* (50.00:50.00:0.00) *Wb/Wb, Wb/wb, wb/wb*	MG:PH:PW	44.22	55.78	0.00
T_5	MGPWxPW	MGxPW *Wb⁺/Wb, Wb⁺/wb*x *wb/wb*	256	♂x♀ *Wb⁺/wb, Wb/wb* , 50.00) *wb/wb*	MG:PH:PW (50.00:0.00:	23.44 41.40	35.16	
T_6	PWxPWMG	PWxMG *wb/wb*x *Wb⁺/Wb, Wb⁺/wb*	273	♂x♀ *Wb⁺/wb, Wb/wb,* (50.00:0.00:50.00) *wb/wb*	MG:PH:PW	25.64 39.56	34.80	

Plumage Colour: Manchurian Gold (MG), Pharaoh (PH), Panda White (PW).Wb^+, *Wb,* wb represents alleles for Manchurian Gold, Pharaoh and Panda White respectively.

Table 5: Chi-square goodness of fit test for observed and expected plumage colour distribution in the test cross progeny

Crosses	Allele	Obs.	Exp.	(O- E)	$(O-E)^2$	$(O-E)^2/E$
PHPW x PW	Wb^+-type	0	0	0	0	0
	Wb-type	127	120	7	49	0.41
	Wb-type	113	120	-7	49	0.41
	Total	240	240	0	98	0.82
PW x PWPH	Wb^+-type	0	0	0	0	0
	Wb-type	131	125	6	36	0.29
	wb-type	119	125	-6	36	0.29
	Total	250	250	0	72	0.58
MGPH x PH	Wb^+-type	148	146.5	1.5	2.25	0.02
	Wb-type	139	146.5	-7.5	56.25	0.38
	wb-type	6	0	6	36	0
	Total	293	293	0	94.50	0.40
PH x PHMG	Wb^+-type	111	125.5	-14.5	210.25	1.68
	Wb-type	140	125.5	14.5	210.25	1.68
	wb-type	0	0	0	0	0
	Total	251	251	0	420.50	3.36
MGPW x PW	Wb^+-type	60	128	-68	4624	36.13
	Wb-type	90	0	90	8100	0
	wb-type	106	128	-22	484	3.78
	Total	256	256	0	13208	39.91
PW x PWMG	Wb^+-type	70	136.5	-66.5	4422.25	32.40
	Wb-type	95	0	95	9025	0
	wb-type	108	136.5	28.5	812.25	5.95
	Total	273	273	0	14259.5	38.35

MG, PH, PW represent Manchurian Gold, Pharaoh and Panda White respectively. Wb^+, *Wb, wb* represent alleles for Manchurian Gold, Pharaoh and Panda White, respectively.

Discussions

The results of this study showed that all the Pharaoh plumage quails carry the wild-type allele (*Wb*) in homozygous form or in heterozygous with the *wb* allele. The Pharaoh plumage of the heterozygous (*Wb/wb*) in the reciprocal crosses between Pharaoh and Panda White suggests that the wild-type allele (*Wb*) is dominant over the Panda White allele (*wb*). Tsudzuki *et al.* (1992, 1993) described the Panda White allele as an autosomal recessive mutation which has been marked to chromosome 4 (Miwa *et al.*, 2005 and 2006).

The results showed that Manchurian Gold plumage quails carry the Manchurian Gold-type allele (Wb^+) in heterozygous with the *Wb* or *wb* type allele. The appearance of Pharaoh plumage type in the F_1 progeny from the cross of Manchurian Gold male and female parents suggest that Manchurian Gold parents possess Pharaoh or wild-type allele (*Wb*) which was masked by Wb^+ in the heterozygous state. It is then probable that the *Wb* allele from male and female Manchurian Gold parents then combine at random to produce the observed chicks with pharaoh plumage. Previous report (Somes, 1979) showed that Manchurian Gold variety possess an autosomal dominant allele which is embryological lethal when found in the homozygous state (*i.e.* Wb^+Wb^+). The crossbred chicks produced from Manchurian Gold and Pharaoh parental lines suggest that the Manchurian Gold allele (Wb^+) was dominant over the wild-type allele (*Wb*). All the Panda White chicks were homozygous for the *wb* allele, which was recessive to both Wb^+ and *Wb* alleles. We can therefore establish that dominance hierarchy in the order of $Wb^+>Wb>wb$ exist among the alleles for plumage types in Japanese quail. The phenotypic ratio of the F_1 progenies that were obtained from the cross between Manchurian Gold male and Panda White female parents suggests that Manchurian Gold allele (Wb^+) was dominant over the wild allele (*Wb*), which in turn was dominant over the allele for Panda White (*wb*). The appearance of a proportion of Pharaoh plumage chicks among the progenies of the mating involving Manchurian Gold and Panda White (MG x PW) reciprocal crosses further confirm the result obtained in cross group A, which shows the presence of *Wb* allele in the Manchurian Gold parents. The *Wb* allele in Manchurian Gold parent may recombine with *wb* from Panda White to form heterozygous (*Wbwb*) with Pharaoh plumage in the offspring generation. Mishra *et al*. (2011) obtained a similar result in the cross between White Breasted and White quails. They explained that the Pharaoh Plumage quails among the progenies were due to the presence of a small proportion of heterozygous White Breasted individuals among White Breasted female and male parents. The new variant (Plate 4 Left) produced from MG x PW reciprocal crosses formed 5.56 to 18.02 percent of the offspring population and was characterized by Manchurian Gold stripes on the white plumage. The golden striped progeny may have obtained the allele for golden stripe from the Manchurian Gold parent. The number of progenies obtained in the cross between Pharaoh and Panda White did not differ from expectation with the assumption of dominance of *Wb* allele over *wb*. However, the four crosses involving Manchurian Gold with Panda White and Manchurian Gold with Pharaoh showed significant deviation from expectation. This agrees with Somes (1979) who reported that Manchurian Gold variety possess the yellow colour mutant Y, which is an autosomal dominant allele and embryological lethal when found in the homozygous state. According to Thear (2007), the crossing of two Manchurian Gold varieties results into mortality of 25% while the crossing of Manchurian Gold variety with a brown result mainly in Manchurian Gold and some brown in the ratio of 2:1. The white plumage on Panda White may be due to a deficiency in the biosynthesis of melatonin. Li *et al*. (2012) observed that a lack of Tyr and Tyrp1 expression led to a deficiency in the biosynthesis of melanin in white feather bulbs in ducks and concluded that the genes that inhibit Tyr expression could be responsible for plumage colour in their studied population. The golden patched white phenotype which was obtained from the cross between Manchurian Gold and Panda White warrant further study. The observed phenotypic ratios in the test cross chicks of PHPW x PW was very close to the expected ratio of 0.00MG: 50.00PH: 50.00PW. Result obtained from the reciprocal cross, PW x PWPH was also in the same direction. Earlier report by Fayeye *et al*. (2013) showed that Panda White is an autosomal recessive mutation. The slightly lower proportion of Panda White quails in T_1 and T_2 may be due to higher pre-hatch mortality associated with Panda White chicks. Fayeye *et al*. (2013) observed lower hatchability of the quails that are homozygous for the recessive Panda White allele. An earlier work by Petek *et al*. (2004) showed a lower hatchability for the homozygous white alleles in quail hatched from breeders of different ages. The value for phenotypic ratio in the test cross, MGPH x PH was close to the expected test cross ratio of 50.00MG: 50.00PH: 0.00PW. Result from the reciprocal cross, PH x PHMG was also in the same direction, except that the reciprocal cross had higher proportion of Pharaoh-type chicks. Panda White plumage was not also observed among chicks produced in T_4. The small fraction (2.05%) of Panda White chicks in T_3 probably came from F_1 (MGPH) males which carry *wb* allele in their autosomes. The appearance of Panda White colour among chicks produced in the test cross may be due to the presence of Panda White allele (*wb*) in the heterozygous form in the Manchurian Gold quails which combined at random with *wb* present in the heterozygous Pharaoh Dam. Similar observation was made by Mishra *et al.* (2011) in their work involving the mating of White Breasted with White quails. The reciprocal crossing between MGPW x PW and PW x PWMG test crosses resulted in a mixture of chicks with Manchurian Gold, Pharaoh and White plumage colours. The observed phenotypic ratio deviated from the expected ratio of 50.00MG: 0.00PH: 50.00PW in both T_5 and T_6. The Pharaoh plumage in T_5 and T_6 may have come from Manchurian Gold male and female quails which carry the *Wb* alleles in their autosomes. The preponderance of individuals with the *Wb* allele among the progeny is expected because of the lethality associated with the Wb^+ when present in the homozygous form (Somes, 1979). The results of the present study suggest that the inheritance of plumage colour in the test crosses between MGPW x PW and PW x PWMG did not conform to the expected Mendelian ratio. This departure may be due to the presence of *Wb* allele in heterozygous with the Manchurian Gold allele (Wb^+), which combines at random to produce Pharaoh plumage in the test cross progeny.

Conclusion

The study showed that the inheritance of plumage colour variation is controlled by autosomal plumage genes with dominant hierarchy of MG> PH> PW (i.e $Wb^+ > Wb > wb$). The Chi-square results confirm the heterozygousity of the dominant phenotype in the six test crosses. The inheritance of plumage colour among the test cross progeny conform to expected Mendelian test cross ratio of 50:50 (dominant: recessive alleles), except for test crosses involving Manchurian Gold male progeny with Panda White recessive parent (MGPW x PW) and the reciprocal (PW x PWMG).

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