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Inheritance of White Plumage and its Effects on Hatchability Traits in Japanese Quail (*Coturnix coturnix japonica*)

Fayeye, T. R. ; Ojo, V.; Sola-Ojo, F. E.; Dada, Y. O., and Ayorinde, K. L.

Department of Animal Production, Faculty of Agriculture, University of Ilorin, Nigeria.
**Corresonding Authors e-mails:fayetiro@yahoo.com, ojo victoria@yahoo.com*

Abstract

Thirty-eight (38) single-pair matings involving white (CS), Wild (CU) and CS x CU reciprocal mating were carried out to determine the inheritance of the white variant plumage colour and its phenotypic effect on hatchability in Japanese quail. The Chi Square Goodness of Fit showed that the observed progeny distribution in the CU x CS, CU x CU and CS x CS crosses were in consonance with Mendelian principle for monohybrid inheritance except in the CS x CU. The putative genotypes and the chi-square results indicated the dominance of the allele for wild plumage (Wb) over the white plumage (wb). Overall hatchability in this study was approximately 56%. Analysis of 210 unhatched eggs showed that infertile eggs, dead in embryo and dead in shell accounted for 32.38%, 17.14% and 50.48% of unhatched eggs, respectively. CS females (with putative genotype wb/wb and white plumage) produced a larger number of infertile eggs and had lower hatchability(%) than eggs produced by CU females. The lower proportion of white progenies among offspring of white sires crossed to wild-type females indicated that sperm carrying the wb mutation might have less capability in fertilizing the ovum. The lower hatchability of eggs from white quails suggested a negative association between the white allele(wb) and reproductive traits. It can be concluded that the white allele (wb) in the studied flock is a recessive gene with a lower viability relative to the wild-plumage gene (Wb). Selective breeding is therefore needed to preserve the population of white plumage quails.

Key words: White plumage, Wild plumage, Hatchability, Japanese quail.

Introduction

The Japanese quail belong to the order *galliformes,* genus *coturnix*, and species *japonica*. The scientific designation for Japanese quail is *Coturnix coturnix japonica*. Plumage colour mutations play important roles in breeding and production of quails and in research fields (Pang and Zhao, 2003). Alignment of the gene encoding the protein $SLC_{45}A_2$ (Solute Carrier family Forty-five, Member 2, Protein) is

responsible for pigmentation variation in several vertebrates including quails (Gunnarsson *et al.,* 2007). Breeding for customized feather colour phenotypes in Japanese quail using colour mutations has been found to be advantageous (Minvielle *et al.*, 2007; Mishra *et al.*, 2011). For instance, mutant plumage types may be used for commercial production as pure line or in crossbreeding programmes to produce auto-sexed lines (Minvielle *et al.*, 1999). It may also be exploited to increase quail bodyweight (Minvielle *et al.*, 2005), for tagging different lines (Minvielle, 1998) and for biomedical studies, such as the albino mutation with associated glaucoma (Mitsuru *et al.*, 2006). Several literature provide evidence that much of plumage-colour variation (both within and between species) has a strong genetic component (Merila and Sheldon, 2001; Price, 2002; Mundy, 2005). There is presently dearth of record on the investigation of the genetic basis and the effects of colour variants in the Japanese quail in Nigeria. The present study was designed to determine the inheritance of the white variant plumage colour and its phenotypic effect on hatchability trait in Japanese quail.

Materials and Methods

Thirty-eight (38) single-pair matings of adult Japanese quails of the same age involving white (CS), wild (CU) and CS x CU reciprocal crossing were carried out at the quail breeding unit of the Department of Animal production, University of Ilorin, Nigeria. The study area is located between the rainforest of the Southwest and Savannah grassland of the Northern Nigeria. It lies within 8° 30' 0" North, 4° 33' 0" East at an altitude of 305m, 1001' above sea level. Its annual rainfall is between 600-1200 mm per annum, with relative humidity of 75-80% in wet season and 65% in the dry season. The day temperature is mostly between 33-37^0 C. The White (CS) quail stock used in this study were a mixed population of Panda (overall white with spots of wild-type) and Dotted White (having small light wild spots on the head and/or back) as described by Tsudzuki *et al.* (1992, 1993) (Plate1). Female quails were randomly assigned to males in a completely randomised design to form a total of thirty-eight (38) single-pair matings groups (Table 1). The birds were given water and feed *ad libitum.* Eggs were collected for 3 weeks and incubated in three lots. Eggs from the four plumage mating groups were separated in the incubator (Reliable Vision model) to prevent intermingling. Temperature of 37.5^{0}C and humidity of 60% were maintained throughout the 17 days incubation period. Based on the knowledge of characteristic down colour visible in the parental quail varieties, chicks were classified and counted at hatch by their down colour into observable plumage-colour groups. Data were pooled to calculate the proportions of different plumage types from each cross. Based on the

expected Mendelian Phenotypic ratio in the F_1 for a monohybrid cross, four hypotheses were postulated for testing viz: $H_{O1:}$ The observed progeny distribution in the CS x CU cross was not significantly different from the theoretical distribution of a 1:0 ratio in favour of wild plumage. $Ho_{2:}$ The observed progeny distribution in the CU x CS cross was not significantly different from the theoretical distribution of a 1:0 ratio in favour of wild plumage. $Ho_{3:}$ The observed progeny distribution in the CU x CU cross was not significantly different from the theoretical distribution of a 1:0 ratio in favour of wild plumage and $H_{O4:}$ The observed progeny distribution in the CS x CS cross was not significantly different from the theoretical distribution of a 1:0 ratio in favour of white plumage. Chi Square Goodness of Fit (One Sample Test) at critical probability level of 0.05 was used to compare the categorical data and to know if the observed values differed significantly from expected Mendelian distribution. The calculated Chi Square (X^2) was done using the fomular below:

$$X^2 = \sum \frac{(obs - Exp)^2}{Exp}$$

Results and Discussion

The plumage colour phenotypes of parents and offspring with their putative genotypes are presented in Table 1. The observed and expected progeny phenotypes in different crosses are also presented in Table 1. The cross between white sires and wild plumage dams produced more wild-type chicks than white ones. The results of Chi Square Goodness of Fit test for null hypotheses $H_{O1,}$ $H_{O2,}$ H_{O3} and H_{O4} (Table 2) showed that the calculated x^2 statistics in each case was below the critical value for 0.05 probability level (3.841). The results therefore suggest that the observed progeny distribution in the CS x CU, CU x CS, CU x CU and CS x CS crosses were in consonance with Mendelian principle for Monohybrid inheritance. The pupative genotypes and the chi-square results indicated the dominance of the allele for wild plumage (*Wb*) over the white plumage (*wb*). Overall hatchability in this study was approximately 56% (Table3). The hatchability of eggs from CS x CU, CU x CS, CU x CU and CS x CS crosses are presented in Table 3. Eggs from CS x CS cross had the lowest hatchability in this study (Table 3). Eggs produced by CS females (with putative genotype *wb/wb* and white plumage) were lower in hatchability than eggs produced by CU females (Table 3). Analysis of 210 unhatched eggs showed that infertile eggs, dead in embryo and dead in shell accounted for 32.38%, 17.14% and 50.48% of unhatched eggs, respectively (Table 3). CS females (white plumage) produced a larger number of infertile eggs than CU females. The variation in the plumage colour of chicks produced by CS and CU dams is similar to the earlier result of Minvielle *et al.* (2007) who observed that the cross between yellow sires and

wild-type dams produced significantly more wild-type individuals than yellow ones while the other reciprocal crosses yielded equal numbers of wild-type and yellow progeny. The lower proportion of white progenies among offspring of white sires crossed to wild-type females indicated that sperm carrying the *wb* mutation might have less success in fertilizing the ovum. The lower hatchability of the quails that are homozygous for the recessive white allele in this study agrees with the observation of Petek *et al.* (2004) who reported lower hatchability for the homozygous white alleles in quail hatched from breeders of different ages.

Conclusion

The present study showed that the white alleles in the studied flock is a recessive gene and its inheritance was in consonance with Mendelian principle for monohybrid cross. The study further revealed that CS (white plumage) quail has a lower viability relative to CU (wild-plumage) quail. Selective breeding is therefore needed to preserve the population of white plumage quails.

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Plate 1.

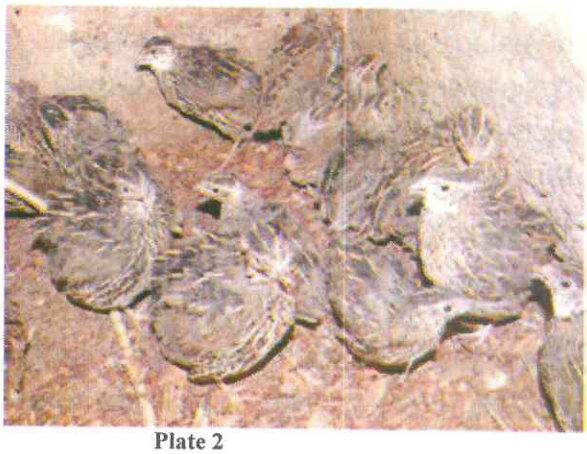

Plate 2

Plates *1 and 2* = *Plumage colour of white (Panda + Dotted white) and Wild parents quails, respectively.*

Table 1: Plumage colours and putative genotypes of parents and offspring with observed and expected progeny phenotypes in different quail crosses

Cross (B&x @&)	No. of Pairs	Plumage colour[1] and putative genotypes of parents	No. of progeny	Plumage phenotype and putative genotypes of offspring		Observed Phenotypic ratio	
				Genotype	Phenotypic ratio	PH	W
CS x CU	3	W x PH *wb/wb x Wb/Wb, Wb/wb*	32	B&&@& *Wb/wb , wb/wb*	PH:W(1:0)	0.75	0.25
CU x CS	2	PH x W *Wb/Wb,Wb/wb x wb/wb*	20	B&&@& *Wb/wb,wb/wb*	PH:W(1:0)	1.00	0.00
CU x CU	31	PH x PH *Wb/Wb, Wb/wb x Wb/Wb,Wb/wb*	222	B&&@& *Wb/Wb, wb/wb*	PH:W(1:0)	0.97	0.03
CS x CS	2	W x W *wb/wb x wb/wb*	12	B&&@& *wb/wb*	W:PH(1:0)	0.00	1.00

[1]Plumage colour: Wild(PH), Panda +Dotted white(W). *Wb and wb* represents the alleles for wild and white plumage, respectively

Table 2: Chi Square Goodness of Fit table for null hypotheses H_{01}, H_{02}, H_{03} and H_{04}

		Obs.	Exp.	(O- E)	$(O-E)^2$	$(O-E)^2/ E$
CSxCU	*Wb*-type	24	32	-8	64	2
	wb-type	8	0	8	64	0
	Total	32	32	0	128	2
CUxCS	*Wb* -type	20	20	0	0	0
	wb -type	0	0	0	0	0
	Total	20	20	0	0	0
CUxCU	*Wb* -type	215	222	-7	49	0.22
	wb -type	7	0	7	49	0
	Total	222	222	0	0	0.22
CSxCS	*Wb* -type	0	0	0	0	0
	wb -type	12	12	0	0	0
	Total	12	12	0	0	0

CSxCU, CUxCS, CUxCU and CSxCS represent the crosses

Table 3: Hatchability (%) and Hatched-out analysis in four mating groups of Japanese quails

CROSS	NMP	EC	ES	EH	Hatchability (%)	NUE	NIE(%)	DIE(%)	DIS(%)
CSxCU	3	48	43	23	53.49	14	7.14	28.57	64.29
CUxCS	2	29	29	11	37.93	16	12.50	31.25	56.25
CUxCU	31	404	235	142	60.43	167	33.54	16.16	50.30
CSxCS	2	26	24	9	37.50	13	69.33	0	30.77

NMP: Number of mating pairs, ,EC: total for Egg collected, ES: Egg Set, and EH: Egg Hatched. NUE: Number of Unhatched eggs, NIE: Number of infertile eggs, DIE: Dead in embryo and DIS: Dead in shell. CSxCU, CUxCS, CUxCU and CSxCS represent the crosses.