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Inheritance of qualitative traits in two populations of Nigerian local chicken ecotypes.

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Abstract

The study was conducted at akpehe poultry farm, Makurdi. Nigeria. A total of seven hundred day old chicks obtained from the mattings of one hundred dams mated to twenty sires were used for the study. The study was designed to provide information on the inheritance of qualitative traits in two populations of the local chicken ecotypes of Nigeria. White shank and beak, white and black skin, black and brown earlobes, white, yellow and brown eye colors fitted closely to the expected mendelian ratios of 3:1 as their alleles shows independent assortment and were thus heritable. Other qualitative traits did not fit into the expected mendelian ratios, indicating that multiple alleles may be involves in their expressions. Plumage color variations all deviated from their expected ratios. This may be due to multiple alleles or polygenic influence, involving gene interactions, gene complexes as well as genetically controlled events, and as such would not be heritable. Artificial selection must be applied to large variation in plumage colors to ensure there availability for adaptation for future use.

Keywords: Gene-complexes, Local-chicken-ecotype, Inheritance, Polygenic, Qualitative-trait.

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Introduction

Phenotypic and genotypic characterization of indigenous chicken populations provides essential information to make rational decisions for improvement and development of effective breeding programmes. The report of Daguma [1] indicated that for African countries to improve indigenous poultry resources to meet their human needs, depends on their ability to identify the within and between variation existing among their chicken ecotypes. In Nigeria, work has been carried out on indigenous chicken [2-9]. There is however no report on the genetic inheritance of qualitative traits between ecotypes of indigenous chickens of Nigeria, a vital information required for the appropriate characterization, selection and identification of morphological variations. Thus, characterization of qualitative traits for both local adaptation with emphasis on morphological selection of traits that enhance adaptation are yet to be feasible with the Nigerian indigenous chicken. The potential of information on morphological variation within and between ecotypes that could identify capacities for adaptation for future use are not attainable. It is expected that natural and direct selection, and mutation may lead to non-random or directional changes in the allelic distribution and frequencies regulating qualitative traits. Thus, within and between ecotypes variation should occur, defining unique set of genes for special utility to environmental challenges [1]. Where diverse agro climates, enormous migration, natural and or man-made challenges existed, these are adequate reason for the substantial variation of various qualitative traits in the ecotypes of the indigenous chicken populations. The degree of genetic uniqueness and adaptive capacities of indigenous chicken can be assessed through phenotypic characterization.

The genetics of qualitative traits has been reported to be complex by Hutt [10]. According to the author, all the comb types, pea, walnut, rose, single and duplex are controlled by four pairs of genes; (RR, PP, rr, pp) the rose comb type (RrpP or RRPP), pea comb type (rrPp) [10]. The author also reported that single comb type (rrpp) is a simple homozygous recessive to rose and pea comb types. Walnut comb types (RrPp, RRPP) and duplex comb type (dd) are recessive. Hutt [10] reported that walnut comb type is controlled by gene complementarity or gene modifiers. Daguma [1] reported that skin coloration in birds is due to presence or absence of carotenoids. The authors observed that carotenoid are taken up from the circulation in both genotypes but are degraded by Beta-carotene deoxygenase 2 in the skin from birds carrying the white skin alleles (W*W)' thereby producing a white skin. The authors also observed that yellow skin is caused by recessive allele (W*Y) that allow deposition of carotenoids in the skin. Daguma [1] also reported that aside the activities of the recessive gene, yellow skin is facilitated by one or more cis acting and tissue specific regulatory mutation(s) that inhibit the expression of beta–carotene deoxygenase 2 (BCDO2) in the skin. Shank colour is controlled by genes that affect the skin at varying depths. The visible color was due to the combined effect of the different colours of the dermis and the epidermis. So shank colour is a combination of upper skin and deeper skin pigmentation. Other genes can modify shank colour.

Schwanyana et al. and Oluyemi and Roberts [11,12] also reported red and white earlobe colours with red been the most common. The relative abundance of the red earlobe determining gene (I) differed significantly ($P<0.05$) from that of the white earlobe determining gene (i), and it apparently had a higher transmission potential. Thus the dominant gene is usually transmitted to the next generation more frequently while the recessive allele are

transmitted less frequently and also due to mutations. The white earlobe could be due to the purine pigment which is controlled by a number of genes. The red earlobe colour could be due to the absence of the genes that invoke the purine pigmentation. The brown and black earlobe colours may be due to tinge on the white earlobe. Social preference and natural selection did favor the red earlobe colour hence its preponderance. Eye colours had been reported to be due to carotenoid pigments and blood supply of the iris. Brown eye colour was due to Er (birchen) and fibro melanotic gene (extended black, E) characterized by heavy eumelanin deposits throughout the eye in the absence of other melanin inhibitors. The white eye colour was due to the inhibitor of shank dermal melanin, Id, which also inhibits eye pigmentation [13].

Variations in melanin pigmentation of the skin and its epidermal integuments have long been reported [13]. Studies have also been carried out on the inheritance of melanization especially of the feathers, although the genetic bases for a number of phenotypes have not been determined [13]. Smith [13] also noted that genetics of melanization is complex, and also involves genetic interactions. These complexities are demonstrated between individual plumage colour genes, and certain gene complexes that are yet to be worked out. Smith [13] also observed that a number of different genetic routes produces identical or nearly identical phenotypes. Smith [13] also observed that physiological systems that are relatively unaffected by environmental components, controlled by a number of identifiable qualitative inherited genes, polygenic modifying complexes and the various interactions between these produces the final plumage coloration observed. The author also considered plumage colour as a polygenic trait and a simplified genetic model for other quantitatively inherited traits. While qualitative traits do not affect economic traits of farm animals directly, they played significant roles that enhances the adaptation and fitness of farm animals to their environment. The inheritance and distribution of qualitative traits becomes very critical in the subsequent generations of farm animals especially under the impact of climate change as they affect adaptation. There are reports of associations between qualitative and quantitative traits of farm animals. Gene interactions, modifiers and complexes controlling qualitative traits especially plumage colours and body pigmentation have associations with performance traits. The objective of this study was to provide information on the inheritance of qualitative traits of the local chicken ecotypes of Nigeria.

Materials and Methods

The study was conducted at akpehe poultry farm, Makurdi. Nigeria. A total of seven hundred day old chicks obtained from the mattings of one hundred dams mated to twenty sires were used for the study. The birds were given routine medication, water and feeds were provided adlibitum.

Data collection and analysis

Qualitative traits were measured as the ratio of the frequency of each trait in the offspring population to the number of observations of the trait in the parental population. Chi-square was used to evaluate the deviation of the occurrence of qualitative traits in the offspring population from their expectations in the same population.

Results

Inheritance of beak color

The Chi Square (χ^2) test applied to the three classes of beak color in the Tiv and the Fulani ecotypes expected in the mendelian radio of 3:1 were highly significant (P>0.05) different from the expected (Table 1).

Inheritance of skin and comb color

There were also significant (P>0.05) differences in the expected Mendelian ratio of 3:1 (Tables 2 and 3) in the Chi Square test on one class of the skin and comb colour of the Tiv and the Fulani ecotypes.

Table 1. *χ^2 on the three classes of beak colour with expected ratio of 3:1.*

Trait Ecotype	Phenotypes	Obs. (0)	Expeted No. (e)	Deviation (0-e)	$(0-e)^2$	$\frac{(0-e)2}{E}$	χ^2
Beak Tiv Colour	White	54	65	-11	121	1.86	Ns
	Black	91	65	26	676	10.4	*
	Brown	115	195	-80	6400	32.82	*
	Total	**260**	**325**	**-65**	**7197**	**45.08**	
Beak Colour Fulani	White	51	65	-14	196	3.02	Ns
	Black	95	65	30	900	13.85	*
	Brown	114	195	81	6561	33.65	*
	Total	**260**	**325**	**-65**	**7657**	**5052**	

*Significant at (P<0.05).
χ^2 =Chi square.
Ns=not significant.

Table 2. *χ^2 on one class of skin colour with expected ratio of 3.1.*

Trait/ Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	$\frac{(0-e)2}{E}$		χ^2
Skin Colour Fulani	White	260	195	65	4225	21.67	*
	Total	**260**	**195**	**65**	**4225**		
Skin Colour Tiv	White	260	195	65	4225	21.67	*
	Totals	**260**	**195**	**65**	**4225**	21.67	

*Significant at (P<0.05)
χ^2 =Chi square.

Inheritance of shank color

The χ^2 test on the three classes of shank colours observed did not agree with the ratio of 3:1 and was significant (P>0.05) (Table 4). In the Fulani ecotype, the χ^2 test applied to the two classes of shank color observed in the Mendelian ratio of 3:1 was not significantly (P>0.05) different from the expected.

Inheritance of eye color

The χ^2 test on the three classes of eye colors mendelian ratio of 1:2:1 were not significantly (P>0.05) different from the expected in the Tiv and Fulani ecotype (Table 5).

Inheritance of earlobe color

The χ^2 test on the three classes of earlobe colours observed showed that they were significantly (P>0.05) different from the expected ratio of 3:1 (Table 6) in the two ecotypes.

Inheritance of comb type

The χ^2 test on the three classes of comb types were significantly (P>0.05) different from the expected 3:1 ratio (Table 7).

Inheritance of plumage color

The χ^2 test on the nine classes of plumage colors observed in the Tiv ecotype showed significant (P>0.05) difference from the expected 3:1 ratio (Table 8). In the same vein, ^{2} test on the ten classes of plumage colors in the Fulani ecotype showed significant (P>0.05) difference from the expected 3:1 ratio (Table 9).

Discussion

Segregation of genes for bird's qualitative traits

The observed numbers in the different classes that fitted closely to the expected implied that such traits are monohybrid and their alleles showed independent assortment; hence the various descriptors of such characteristics are true to type in occurrence. Those observed numbers that did not fit into the expected indicated that, either the genetic model postulated to explain the result was wrong or multiple alleles were involved at a locus, between loci, or there were some form of relationship between the alleles determining the traits. Some of those identified, showed simple dominance, co-dominance, complementary effect or incomplete dominance. This could be possible reason why the observed ratios could not fit the expected values. For such traits, the best estimate of the true ratios of genotype groups is the observed ratios of the totals obtained from heterogeneous populations [14].

Skin colors

One skin color, white was observed in this study. Saidu [15] also

Table 3. *χ^2 on one class of comb colour with expected ratio of 3.1.*

Trait/ Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	$\frac{(0-e)2}{E}$		χ^2
Comb Colour Fulani	Red	260	195	65	4225	21.67	*
	Total	**260**	**195**	**65**	**4225**		
Comb Colour Tiv	Red	260	195	65	4225	21.67	*
	Totals	260	195	65	4225	21.67	

*Significant at (P<0.05)
χ^2 =Chi square.

Table 4. *χ^2 on two classes of shank colour with expected ratio of 3.1.*

Trait/Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	$(0-e)^2$	$\frac{(0-e)2}{E}$	χ^2
Shank colour Fulani	White	182	195	-13	169	0.87	Ns
	Black	78	65	+13	169	2.6	Ns
Total		**260**	**260**	**0.0**	**338**	**2.93**	
Shank colour	White	94	65	29	84.1	12.94	*
Tiv	Green	33	65	-32	1024	1573	*
	Black	133	195	-62	3844	19.71	*
Total		260	325	65	5707	48.38	

*Significant at (P<0.05)
Ns=not significant.
χ^2Chi square

Table 5. *χ^2 on three classes of eye colour with expected ratio of 3:1.*

Triat/Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	(0-e)2	$\frac{(0-e)^2}{e}$	χ^2
Eye colour Tiv	Yellow	132	195	-63	3969	20.35	*
	White	52	65	-13		2.6	Ns
	Brown	76	65	11	169	1.86	Ns
	Total	**260**	**325**	**-65**	**1242591**	**24.81**	
Eye colour Fulani	Yellow	200	195	05	25	0.13	Ns
	Brown	60	65	-05	25	0.39	Ns
	Total	260	260	0.0	50	0.52	

*Significant at (P<0.05)
Ns=not significant.
χ^2=Chi square.

Table 6. *χ^2on three classes of earlobe colour with expected ratio of 1:2:1.*

Triat/Ecotype	Phenotypes	Obs. No. (0)	Expected No.(e)	Deviation (0-e)	(0-e)	$\frac{(0-e)^2}{e}$	χ^2
Earlobe colour Fulani	Black	58	65	-7	49	0.75	ns
	White	117	65	-13	169	2.6	*
	Brown	85	65	+20	400	6.15	*
Total		**260**	**325**	**- 65**	**6533**	**38.1**	
Earlobe colour Tiv	Black	79	65	14	196	3.0154	ns
	White	30	65	-35	1225	18.8462	*
	Brown	103	65	-05	25	0.39	*
	Red	48	65	-17	289	4.4462	Ns
Total		**260**	**390**	**-130**	**10174**	**69.7178**	

*Significant at (P<0.05)
Ns=not significant
χ^2=Chi square.

Table 7. *χ^2 on three classes of Comb types with expected ratio of 3.1.*

Trait/ Ecotype	Phenotypes	Obs. No (0)	Expected No. (e)	Deviation (o-e)	$(o-e)^2$	$(0-e)^2/e$	χ^2
Comb type Fulani	Single	258	195	63	3986	20.3539	*
	Walnut	01	65	-64	4096	63.0154	*
	Rose	01	65	-64	4096	63.0154	*
Total		**260**	**325**	**12161**	**146.3847**		
Comb type Tiv	Single	259	65	194	37636	579.01	*
	Walnut	33	65	-32	1024	15.73	*
Total							

*Significant at (P<0.01)
χ^2 =Chi Square.

Table 8. *Chi Square (χ^2) test on nine classes of plumage colours with expected ratio of 3:1.*

Trait/ Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	$(0-e)^2$	$\frac{(0-e)^2}{e}$	χ^2
Plumage Colour							
Tiv	Silver-brown	15	65	-50	2500	38.46	*
	Mottle brown	50	195	-145	21025	107.82	*
	Blackish- brown	60	195	-135	18225	93.46	*
	Mottled	05	65	-60	3600	53.38	*
	Solid brown	30	65	-35	**1225**	**18.85**	*
	Solid black	30	65	-35	1225	18.85	*
	Mixed grey	10	65	-55	3025	46.54	*
	Light brown	20	65	-45	2025	31.15	*
	White mottle	10	65	**-55**	**3025**	46.54	*
	Total	**260**	**845**	**620**	**55875**	**455.05**	*

*Significant at (P<0.05)
χ^2=Chi square.

Table 9. *Chi square (χ^2) test applied to nine classes of plumage colours with expected ratio of 3:1.*

Trait/Ecotype	Phenotypes	Obs. No. (0)	Expected No. (e)	Deviation (0-e)	$(0-e)^2$	$\frac{(0-e)^2}{E}$	χ^2
Plumage Colour							
Fulani	White mottle	25	65	- 40	1600	24.62	*
	Blackish- brown	45	195	-150	22500	115.39	*
	Solid black	15	65	-50	2500	38.41	*
	Mottle brown	35	195	-160	25600	131.28	*
	Light brown	15	65	-50	2500	38.46	*
	Dull brown	07	65	-58	3364	51.75	*
	Solid white	08	65	-57	3249	49.99	*
	Solid brown	45	195	-150	22500	115.39	*
	Light black	35	195	-60	25600	131.28	*
	Black mottle	30	65	-35	1225	18.85	*
	Total	**260**	**1170**	**-910**	**110638**	**715.47**	

*Significant at (P<0.05)
χ^2=Chi square.

observed that white skinned birds dominated the local chicken population in Bauchi State, Nigeria. The frequency of the white skin determining gene (W) did not differ significantly from the frequency of the gene controlling yellow skin. Mancha [8] also reported non significant difference between the abundance of the white skin determining gene (W) and the yellow skin determining gene (w) in Plateau state, Nigeria. He reported that skin coloration in birds is due to presence or absence of carotenoids. The authors observed that carotenoid are taken up from circulation in both genotypes (white and yellow skin colored) but are degraded by Beta-carotene deoxygenase 2 in the skin from birds carrying the white skin allele (W*W)' thereby producing a white skin. The authors also observed that yellow skin is caused by a recessive allele (w*Y) that allows deposition of carotenoids in the skin. He also reported that aside the activities of the recessive gene, yellow skin is facilitated by one or more cis-acting and tissue specific regulatory mutation(s) that inhibit the expression of beta–carotene deoxygense 2 (BCDO2) in the skin. The wide preponderance of the white skin colour indicated that the white skin allele (W*W) had higher transmission potentials compared to the yellow skin allele (w*Y), natural selection and social preference (adaptation) seemed to have favored the white skin genotype, hence its wide preponderance.

Eye colors

Three eye colors, yellow, white and brown were observed in this study. At the W locus, two eye colors, yellow (w) and white (W) while at the E locus, the brown eye color (E) was observed. Meyer; Saidu; Mancha [8,15,16] reported similar observations. The high frequency of the yellow eye color determining gene again agreed with the highest yellow eye colour phenotype observed within the ecotypes. This was also true for the brown eye gene and its phenotype within the ecotypes. Again social preference and natural selection seemed to have favored the yellow eye color genotype. The yellow eye color was due to carotenoid pigments and blood supply of the iris. Brown eye color was due to Er (birchen) and fibro melanotic gene (extended black, E) characterized by heavy eumelanin deposits throughout the eye in the absence of other melanin inhibitors. The white eye colour was due to the inhibitor of shank dermal melanin, Id, which also inhibits eye pigmentation.

Comb colors

One comb color, red was noted in this study. Schwanyana et al. and Mancha [8,11] also reported red comb color to be the most commonest at Apae and kumi district in Uganda, and Jos in Plateau state, in Nigeria respectively. The frequency of the gene determining red comb color (R) was high, it transmitting potentials was equally high. These related positively to the high phenotypic frequency of red comb color in each population of the ecotypes.

Shank colors comb type

The estimated gene frequencies obtained in this study for comb types have been reported by Ikeobi et al. [17] who reported estimates of r=0.99, p=0.98, R=0.01 and P=0.02 in local chickens of South Western Nigeria. The lower frequencies of the dominant allele (P and R) obtained in this study indicated that the recessive alleles have higher transmission potential as noted in this study within and between the Fulani and Tiv local chicken ecotypes of the derived guinea savannah zone of Nigeria. The low frequency of R (0.03) and P (0.03) between the ecotypes observed in this study with a seemingly lower transmission potential of (0.007 and 0.01) and (0.003 and 0.00) for the P and R genes, in the Fulani and the Tiv ecotypes respectively. The insignificant occurrence of the Rose and Walnut comb type was justified. Social preference, natural selection and adaptation would favor single comb type since single large comb would be important in ensuring the survival and production performance of birds. At the R locus, one Wattle color, red, was observed in this study.

There were four shank colors observed in this study. At the W locus, two shank colors, White (W) and yellow (w) were noticed. While at the E locus, black shank color E was observed, and the interaction between W and E loci produced the green shank color (WE) Mbap and Zakar [4] Oluyemi and Roberts; Smith [18,19] also reported four shank colors (white, yellow, black and grey) in populations of local chicken in Yobe State, Nigeria and in warm wet climate respectively. The high frequency of the white shank determining gene (W) in the Fulani ecotype related positively to the high frequency of the white shank phenotype. This was also true for the occurrence of the black shank phonotype among the Tiv ecotype. Yellow and green shanks due to their low frequency of occurrence, was low in the population. In all, the white shank color appeared to be favored by social preference and natural selection. The preponderance of the black shank phenotype in the Tiv ecotype was due to their interaction with their environment. Shank colour is controlled by genes that affect the skin at varying depths. The visible color was due to the combined effect of the different colors of the dermis and the epidermis. So shank color is a combination of upper skin and deeper skin pigmentation. Other genes can modify shank colors. Yellow shanks are due to presence of lipochrome pigments when melanin is absent. They also noted that the intensity of the yellow color depends on the amount of exathophyll in the ration. These authors also noted that black shank is due to the presence of melanin pigment in the dermis, and when the melanin occurs in the epidermis, the shank color is greenish in appearance. When both melanin and lipochrome pigment are absent the shank is white

Earlobe color

At the 1 locus, two earlobe color, red and white, were observed in this study. The red earlobe color birds were more common. Schwanyana et al. and Oluyemi and Roberts [11,12] also reported red and white earlobe colors with red been the most common. The relative abundance of the red earlobe determining gene (I) differed significantly ($P<0.05$) from that of the white earlobe determining gene (i), and it apparently had a higher transmission potential. Thus the dominant gene is usually transmitted to the next generation more frequently while the recessive allele are transmitted less frequently and also due to mutations. The white earlobe could be due to the purine pigment which is controlled by a number of genes. The red earlobe color could be due to the absence of the genes that invoke the purine pigmentation. The brown and black earlobe colors may be due to tinge on the white

earlobe. Social preference and natural selection did favor the red earlobe color hence its preponderance. Two earlobe color, red and white, were observed in this study. The red earlobe color birds were more common. Schwanyana et al. and Oluyemi and Roberts [11,12] also reported red and white earlobe colors with red been the most common. The relative abundance of the red earlobe determining gene (I) differed significantly ($P<0.05$) from that of the white earlobe determining gene (i), and it apparently had a higher transmission potential. Thus the dominant gene is usually transmitted to the next generation more frequently while the recessive allele are transmitted less frequently and also due to mutations. The white earlobe could be due to the purine pigment which is controlled by a number of genes. The red earlobe color could be due to the absence of the genes that invoke the purine pigmentation. The brown and black earlobe colors may be due to tinge on the white earlobe. Social preference and natural selection did favour the red earlobe color hence its preponderance.

Beak colors

The chicken unlike mammals has no teeth. The mouth is in the form of a beak, which is thick and pointed. Obioha [20] noted that the beak is used for obtaining food, building nest, turning eggs, caring for chicks and preening feathers. He reported that on the dorsal surface of the tail of most birds is a small oil gland (uropygixal gland or oil preen gland) which supplies oil for keeping the feathers glossy and waterproof and prevent the beak from becoming brittle. Lucas and Stettenheim [21] reported that the yellow color of the beak is due to the presence of xanthophyll's. He reported that three types of beak colors were observed in Southern Plateaus Local Government Areas of Nigeria. This author observed that the brown beak chickens accounted for 43.09 percent were the most common followed by the black beaked (30.7%) while the yellow beaked (26.21%), which were the least common.

Plumage color variations

The significant deviations of the observed from the expected ratios of the various plumage colors was related to the various genetic mechanisms regulating plumage colors in chickens. The genetics of plumage color through melanization is complex, and also involves genetic interactions. These complexities are demonstrated between individual plumage color genes, and certain gene complexes that are yet to be worked out. Smith [13] also observed that a number of different genetic routes produces identical or nearly identical plumage phenotypes. Smith [13] also observed that physiological systems that are relatively unaffected by environmental components, controlled by a number of identifiable qualitative inherited genes, polygenic modifying complexes and the various interactions between these produces the final plumage colouration observed. He reported that although both melanin and carotenoid pigments contribute to feather color of certain avian species, it is the melanins that determines plumage color and patterns. The presence and distribution of the melanins result in differences in the feather forms within age and sex, as well as structural variations between and within other feather traits. Solid colors of black dominant, recessive white, albinism, depigmentation, silver, multiple colors of different grades and gold. These colors were not pale and do to not give the appearance of the diluting effect of genes. There were also diluted colors, though uniform, appear pale, suggestive of weakened action of genes responsible for their expression. The color extension and restriction where, even though color was present, it was not uniformly distributed to all parts. Instead of causing the distribution of color throughout the entire plumage or among regions, color distribution occurred within feathers resulting in patterns. This could only be possible if each plumage color was controlled by series of genes, genetic complexes or genetically controlled events. Oluyenu and Roberts [12,18] also reported that each plumage color and pattern is the result of a series of genetically determined events. The regulation of plumage colors and patterns through interaction effects of genes, gene-complexes and genetically controlled events, indicated that although plumage color is a qualitative traits, it is control by polygenic effects. The segregation of the alleles, their distribution and inheritance cannot fit into the expected Mendelian ratio of 3:1. The transfer of parental plumage colors to their offspring's in local chicken populations would be low due to the polygenic nature of the genetic mechanisms controlling plumage colours [22-24].

Plumage color however plays important role in body heat regulation and eventual adaptation of local chicken ecotypes to their environment. Selection of suitable plumage color for unique environmental needs is desirable for continued adaptation to environmental challenges from generation to generation especially in the phase of climate change impacts. The capacities of natural, unconscious and counter selections are inadequate to preserve potential plumage colors to enhance future adaptation to unique environmental needs of the future. Artificial selection can be applied to large variations in plumage colors for each geographical location to accumulate geographical zone-specific local chicken ecotypes.

Conclusion and Recommendation

Conclusion

White shank and beak, white and black skin, black and brown earlobes, white, yellow and brown eye colors fitted closely to the expected mendelian ratio of 3:1 indicating that these traits are monohybrid and heritable. Their alleles showed independent assortment. The other qualitative traits that differs significantly from the expected indicated that multiple alleles were involved. The deviation of plumage color traits from the expected was due the influence of polygenic influence of genes on the trait. Plumage color traits were controlled by series of genes, genetic interactions and gene-complexes as well as genetically controlled events and as such would not be heritable. The capacities of natural, unconscious and counter selections are inadequate to preserve potential qualitative traits to enhance future adaptation to unique environmental needs of the future.

Recommendation

Selection of suitable plumage color and other qualitative traits for unique environmental needs is desirable for continued adaptation to environmental challenges from generation to

generation. Artificial selection can be applied to large variations in plumage colors for each geographical location to develop geographical zone-specific local chicken ecotypes.

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