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Multivariate Analysis of Thermal Adaptive Profile of Three Genetic Groups of Duck

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ABSTRACT

Inherent thermal adaptation in livestock is an important economic trait that cannot be overlooked, most especially in animals reared in sub-optimal thermally stressful environments. The present study explored the possibility of using multifactorial discriminant analysis (DA) to separate two duck genera {Muscovy and Common (Mallard) ducks) and their hybrid (Mule ducks) to distinct genetic groups using physiological, haematological and biochemical parameters. Data were collected after exposure of ducks to solar radiation for 90 minutes (12.00 – 13.30 hours). The result of analysis of variance indicated that genotype significantly ($P < 0.05$) affected haemoglobin (Hb), basophil (Bas), total protein (TP), albumin (Alb), globulin (Glb), skin temperature (SKT), respiratory rate (RRT), panting rate (PTR) and rectal temperature (RTC). Stepwise DA revealed that PTR, RRT, Bas and TP in descending order were the most important parameters discriminating the three duck genotypes. The result of cross validation showed that 71.00%, 97.30% and 50.00% of Muscovy, Common and Mule ducks were correctly classified in their expected genetic group respectively. The Euclidean distance between the duck genotypes indicated that longest distance (86.507) was between Muscovy and Common (Mallard) ducks while shortest distance (12.415) was between Muscovy and Mule ducks. The results are applicable in breed adaptation studies, management, conservation and improvement programmes.

Keywords: Discriminant analysis, Duck genera, Euclidean distance, Mule duck, Panting rate, Thermal adaptation

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Introduction

Duck is one of the poultry classified as local birds in Nigeria and its husbandry has been since time immemorial in spite of the fact that the ancestors of the *genera* reared are alien to the country (Oguntunji, 2013). Muscovy duck (*Cairina moschata*), Mule duck (*Anas sterilis/hybrida*) and different breeds of Common duck (*Anas platyrhynchos*) such as Khaki Campbell, Pekin, Mallard e.t.c. are reared in Nigeria. However, studies on duck distribution indicated that Muscovy duck is the prevalent *genus* (Oguntunji and Ayorinde, 2015; Adeyemi *et al.*, 2008; Nwanta *et al.*, 2006). Muscovy ducks commonly referred to as local or indigenous ducks are widely distributed throughout the country, owned by small scale farmers and reared mostly under extensive management system (Oguntunji and Ayorinde, 2015). Conversely, Common duck breeds popularly known as exotic ducks are mostly found in Northern Nigeria and are the preferred *genus* in government farms, research institutes,

commercial farms and among elites. The sterile *intergeneric* hybrid of Muscovy and Common ducks known as Mule duck is also reared in the country. Nevertheless, this hybrid is not as popular as the parents, having low population while its consumption is restricted to northern Nigeria.

Heat stress occurs when the core body temperature of a species exceeds the range specified for its normal activity resulting from a total heat load (internal heat production and heat gained from the environment exceeding capacity for heat dissipation (Ganaie *et al.*, 2013). Oguntunji *et al.* (2008) submitted that increased environmental temperature poses a threat to the general well-being of fowls. The authors stated further that an increase in body temperature outside the thermo-neutral range without a prompt compensatory heat loss due to prolonged exposure to high environmental temperature, results in heat stress and its attendant effects.

High ambient temperatures in tropical and sub-tropical regions have been reported to

constitute a major constraint on animal productivity, and this effect is aggravated when heat stress is accompanied by high ambient humidity (Shelton, 2000; Daramola and Adelaye, 2009).

In addition to the widely reported poor performance of livestock under heat stress, this environmental stressor also elicited alterations in the bio-medical (haematological, biochemical, endocrinological, immunological, e.t.c.) and physiological systems of the animals through dysfunctioning of various organs and mechanisms connected with them. Therefore, genotypes/breeds having superior adaptability to thermal stress or that can tolerate and perform better under high environmental temperatures would be suitable for arid, tropical and sub-tropical environments characterized with high ambient temperatures.

The evaluation of available genotypes/breeds for adaptation to the prevailing adverse environmental conditions such as climatic, nutritional, pathological, managerial among others is central to livestock performance, profitable livestock enterprise, genotypes/breeds conservation and improvement. For instance, awareness on the significant impact of thermal stress on livestock productivity by livestock farmers and researchers has elicited series of adaptation tests of livestock to thermal stress using physical factors (McManus *et al.*, 2005; McManus *et al.*, 2011), molecular (Gupta *et al.*, 2013; Sharma *et al.*, 2013), physiological and biologically-controlled systems (Castanheira *et al.*, 2010; Ilori *et al.*, 2011; Fadare *et al.*, 2012; Gupta *et al.*, 2013; Oguntunji *et al.*, 2019) among others.

The ability to maintain homeostasis under heat stress is a valuable trait in sub-tropical and tropical regions which helps to maximize utilization of animal genetic resources (Foster *et al.*, 2009). Therefore, study involving application of multivariate analyses to data generated from different heat stress indicators (heat stress proteins, biochemical, physiological, molecular, endocrinological, haematological e.t.c.) would be of immense contribution to the understanding of thermal adaptation of farm animals. Results of such studies would be more robust and provide better insight to inherent heat tolerance ability of different species, population, breeds or genotypes in contrast to the use of one or two. Besides, it will also contribute significantly to the development of the appropriate management system capable of enhancing productivity of thermal-susceptible genotypes.

In view of the foregoing, the objectives of this study were to investigate thermal stress adaptation of Muscovy and Common ducks and their hybrid (Mule ducks). The objective also includes investigation of variables capable of discriminating the three genotypes into distinct genetic groups using physiological, haematological and biochemical parameters.

Materials and Methods

Study area

This study was conducted at the Duck Research Unit of Bowen University, Iwo, South-west, Nigeria. The coordinate of the study area is Lat. 7° 38' 6.97" N and Long. 4° 10' 53.62" E. The vegetation and climatic characteristics of the area has been well described by Oguntunji *et al.* (2015).

Experimental animals

Representative samples of two duck genera {genus *Cairina* represented by Muscovy duck (*Cairina moschata*) and genus *Anas* (represented by Mallard duck (*Anas platyrhynchos*)) and their hybrids (Mule duck *Anas sterilis/hybrida*) were used for this study: 92 adult ducks were sourced from northwest Nigeria and comprised thirty seven (37) Mallard ducks, twenty four (24) Mule ducks and thirty one (31) Muscovy ducks. Prior to data collection, they were reared in deep litter system for three weeks in order to acclimatize. The management and quarantine methods were as described by Oguntunji *et al.* (2019). Only animals that were clinically healthy were used for this study.

Data collection

Data on physiological parameters and blood samples for haematological and biochemical indices were taken in the afternoon after ducks have been exposed to solar radiation for 90 minutes (12.00 – 13.30 hours). During the exposure period, ducks were confined in local cross ventilated palm woven baskets and were denied access to water and feed.

Physiological parameters

The procedure for collection of physiological indices (panting rate-PTR, respiratory rate-RRT, skin temperature-SKT and rectal temperature- RTC) was as described by Oguntunji *et al.* (2019). Besides, RTC was also taken in the morning (7.00 -8.30h) to generate heat stress index value.

The index of capacity of tolerance to insolation (ICTI), a heat stress index was also used to access the heat tolerance of duck genotypes.

$ICTI = 10 - (RT_2 - RT_1)$ (Baccari, 1986).

Where

10 = maximum efficiency in maintaining body temperature;

RT₂ = mean body temperature at 12.00 h (RTC final);

RT₁ = mean body temperature at 6.50 h (RTC initial).

Value closer to 10 indicates better adapted animals (Baccari, 1986). However, this formula was modified in the present study. The initial RTC was taken between 7.00 and 8.30h while the final was taken between 12.00 and 13.30h.

Haematological and Biochemical parameters

6ml blood sample was collected from individual duck by puncturing the jugular veins. Three millimeter of the blood sample was collected in vacutainer containing heparin as anticoagulant for haematological parameters while the rest (3ml) was collected in plain test tubes and left to clot for serum biochemical analysis.

The heparinized blood sample was then analysed for the following haematological parameters: haemoglobin- Hb, red blood cell-RBC, white blood cell differential count-WBC, heterophil-lymphocyte ratio- H/L, basophil- Bas and platelet- Plat. In addition, serum concentrations of total protein (TP), glucose (Glu), albumin (Alb) and Urea (Urea) were determined using commercial kits (United Diagnostics Industry, Dammam, KSA). Globulin (Glb) concentration was determined as the difference between total protein and albumin concentrations while albumin-globulin ratio (A/G) was determined by dividing albumin by globulin.

Statistical analysis

Univariate analysis. Physiological, haematological and biochemical parameters were analysed with the generalized linear model as follows:

$$Y_{ij} = \mu + G_i + e_{ij}$$

Y_{ij} = Individual observation

μ = Fixed overall mean

G_i = Fixed effect of genotype (i = Muscovy, Mallard and Mule ducks)

e_{ij} = experimental error assumed to be independently, identically and normally distributed, with zero mean and constant variance i.e. $\text{ind}(0, \sigma^2)$.

Statistical differences between means were determined with the New Duncan Multiple Range test at 5% probability level.

Multivariate analysis. The data collected on heat tolerant indicators were further analysed with multivariate Discriminant analysis (DA). Stepwise DA was used to identify variable

combination capable of separating the three duck genotypes to distinct groups. The relative importance of discriminating variables was accessed through Wilk's Lambda, F-statistics (F-to-remove) and level of significance. The identified discriminating variables were further analysed to generate canonical functions. The ability of the generated canonical functions to assign individual duck to its genetic group was calculated as percentage of correct assignment. The degree of genetic diversity between the genetic groups was estimated through Euclidean distance and graphically presented in canonical scatter plot. All statistical analyses were performed with the SPSS (2001) version 16.

Result and Discussion

To the best knowledge of the authors, this report is the first on the application of DA to the heat tolerant traits of duck genotypes. Therefore, empirical reports to compare and validate the results herein reported are scarce.

Univariate analysis

The result of analysis of variance revealed that genotype significantly ($P < 0.05$) affected Hb, Bas, TP, Alb, Glb, SKT, RTC, PRT and RRT (Table 1). The Mallard ducks had the highest values in Hb, Bas, TP, Alb, Glb, SKT, RTC, PRT and RRT compare to Muscovy and Mule ducks.

Physiological, haematological and biochemical indices are good indicators of the health status of the animals. Their deviations from the established normal range are suggestive of the response of a species/genotype/breed to the internal and environmental stressors. Physiological parameters such as RTC, PTR and RRT are some of the most important determinants of the adaptation of poultry to the tropical environment (Ilori *et al.*, 2011). RTC is frequently used as an adaptability index in hot environments as its increase is indicative that the

Table 1. Descriptive statistics of heat tolerant traits in duck genotypes

Parameters	Genotype			
	Muscovy duck	Mallard duck	Mule duck	
Haematological	Hb (g/100mL)	12.432±1.634 ^a	13.797±2.362 ^b	11.839±1.650 ^a
	RBC (x10 ¹² /L)	3.419±0.343 ^a	3.444±0.39762 ^a	3.2631±0.224 ^a
	WBC (x10 ⁹ /L)	13208.065±1662.333 ^a	13346.154±1789.898 ^a	13523.077±1788.460 ^a
	Plat	156322.581±36722.733 ^a	155666.666±38736.854 ^a	155923.077±41509.967 ^a
	Bas (%)	0.161±0.374 ^a	1.821±1.931 ^b	0.3846±0.506 ^a
	H/L ratio	0.489±0.210 ^a	0.483±0.178 ^a	0.5369±0.172 ^a
Biochemical	TP (g/dl)	5.181±0.594 ^a	6.124±0.784 ^b	5.4231±0.920 ^a
	Alb (g/dl)	1.159±0.417 ^a	1.716±0.508 ^b	1.4462±0.740 ^a
	Glb (g/dl)	3.984±0.341 ^a	4.368±0.601 ^b	3.9231±0.564 ^a
	A/G (%)	0.288±0.145 ^a	0.349±0.126 ^a	0.331±0.210 ^a
	Urea (g/dl)	11.293±1.403 ^a	11.491±2.040 ^a	10.5769±396 ^a
	Glu (mg/dl)	348.031±52.464 ^a	343.784±53.975 ^a	333.2308±30.717 ^a
Physiological	RRT (Breath/min)	54.484±14.226 ^a	70.775±33.590 ^b	58.3846±18.150 ^a
	PTR (panting/min)	9.934±7.767 ^a	88.775±43.361 ^b	14.9231±7.285 ^a
	RTC (°C)	41.645±1.009 ^a	42.575±0.73824 ^b	42.0385±0.338 ^a
	SKT (°C)	40.293±1.114 ^a	40.785±1.624 ^a	37.5107±10.863 ^b
	ICTI	8.515±0.960 ^a	8.189±0.668 ^a	8.300±0.607 ^a

^{a,b} Means with different superscripts in the same row are significantly different at 5% probability level.

heat-dissipation mechanisms have become insufficient to maintain homothermia (Mota, 1997; Castanheira *et al.*, 2010). The significantly lower RTC of local Muscovy and crossbred Mule duck compared to Mallard duck indicated that they were more heat tolerant or their heat-regulating mechanisms were superior. This assertion is in tandem with the report of Yahav and Hurwitz (1996) that acclimatized animals present lower core temperature under thermal stress (which can be represented by cloaca temperature) in comparison with birds without acclimatization.

Poultry employ various strategies such as behavioural, hormonal, physiological, and biochemical adjustments to maintain homeostasis at high ambient temperatures (Oguntunji and Alabi, 2010). Among behavioural adjustments observed in hyperthermic birds are flapping of the wings and increased panting (Oguntunji and Alabi, 2010) and higher respiratory rate. Very high RRT are associated with severe heat stress, non-adaptation and a last ditch attempt to control body temperature (Finch, 1986). Explaining physiological mechanism behind higher RRT and PTR of heat-stressed animals, Oguntunji *et al.* (2019) asserted that as body temperature increases above the thermo-neutral range through increased metabolic activities and absorption of heat from environment via conduction and convection; the heat-dissipating mechanism of the animal is overwhelmed and is unable to dissipate the accumulated heat load through sensible heat loss mechanisms (conduction, convection and radiation). Therefore, non-sensible heat loss mechanisms such as evaporative heat loss through higher respiratory rate and panting take over. This submission corroborated the report of Calder and Schmidt-Neilsen (1966) that birds rely primarily on respiratory evaporative cooling to maintain thermal homeostasis when exposed to high ambient temperatures.

In view of the foregoing, the significantly lower PTR and RRT recorded for Muscovy and Mule ducks compared to Mallard ducks are suggestive of their superior thermo-regulatory ability or superior heat tolerance. It implies further that they were more physiologically stable at higher temperature. This is consistent with the report of Yousef (1985) that physiological parameters can quantify the extent of the physiological displacement from the normal state; the greater the physiological response, the nearer the animal is to collapse.

Plasma proteins consist of albumin, globulin and fibrinogen (Okonkwo *et al.*, 2011). They are the key component of plasma and they play crucial role in maintaining homeostasis (Melesse, 2011). The observed elevated serum concentration of plasma protein, globulin and albumin in Mallard ducks compared to local and crossbred ducks are indicative of biochemical adjustment to thermal stress. In a related study, Gupta *et al.* (2013) reported that prolonged exposure to solar radiation increased plasma TP, Alb and Glo (Gupta *et al.*, 2013). Ganaie *et al.*

(2013) reported that increased serum protein could be a physiological attempt to maintain extended plasma volume. Similarly, Erickson and Poole (2006) attributed the observed significant increase in serum concentration of total protein and albumin to dehydration as a result of increased respiratory rate; and possibly panting during heat stress.

Haematological constituents reflect the physiological responsiveness of the animal to its internal and external environments which include thermal stress. Haemoglobin has the physiological function of transporting oxygen to tissues of animals for oxidation of digested food so as to release energy for the other body functions and also transport carbon dioxide from the animals' body (Omiyale *et al.*, 2012; Soetan *et al.*, 2013). Physiologically, heat-stressed animals respond through increased breathing and panting in order to maintain homothermia; hence, increased need for circulating oxygen. Since RBC and HB are concerned with carrying and circulation of oxygen in the blood, this could be a pointer to the possible reason for higher blood concentration of Hb and RBC in the most susceptible duck genotype (Mallard ducks) to heat stress compared to the less thermally-stressed indigenous Muscovy and crossbred Mule ducks. In similar vein, the higher basophil content in Mallard duck is an indicator of thermal stress. Increased basophil counts has been suggested as a method of detecting stress in birds (Maxwell *et al.*, 1992).

Heat tolerance is an important heritable economic trait that is central to livestock performance and profitable investment by livestock farmers most especially in hot environments. Therefore, the ability to maintain homeostasis under heat stress is a valuable trait in Sub-tropical and Tropical regions which helps to maximize utilization of animal genetic resources (Foster *et al.*, 2009).

Though empirical reports on heat tolerance of duck genotypes are not existing or sparse; nevertheless, the trend of result in the present study whereby local Muscovy and crossbred Mule ducks had superior thermal tolerance than the exotic Common duck align with the report of related studies on turkey (Ilori *et al.*, 2011; Yakubu *et al.*, 2012) and chicken (Aengwanich, 2008) genotypes. Superior thermal stress adaptation of Muscovy ducks compared to Mallard duck is indicative that unselected indigenous livestock are more adaptive to harsh unfavorable biotic and abiotic environmental stressors than their exotic counterparts. This assertion is consistent with the report of Marai *et al.* (2007) that indigenous animals reared in tropical and arid regions are more adapted to hot climate, than those living under temperate environments.

It could be inferred that local Muscovy and inter-generic crossbred Mule ducks are more heat tolerant than Mallard ducks.

Wilk's lambda

The stepwise DA of the thermal adaptive profile of duck genotypes revealed that four of the investigated heat tolerant parameters (PTR, RRT and Bas and TP) were identified as the principal discriminating variables (Table 2). The result of stepwise DA revealed further that of the four discriminating variables, PTR chronologically followed by RRT, Bas and PT were the most important in classifying the three genotypes in respect of heat tolerant traits. This is clearly demonstrated in their Lambda, F-statistics and level of significance. The implication of result of Stepwise analysis is that in an attempt to separate the three genetic groups in respect of their thermo-tolerant traits, PTR was the most important variables, having the highest discriminating power.

Canonical discrimination

Two canonical functions (CANs 1 and 2) were generated from the canonical analysis of the four discriminating variables generated in stepwise DA (Table 3). The CAN 1 was the best/highest and accounted for 99.70% of the total variation while CAN 2 accounted for negligible proportion (0.30%) of the total variation. PTR was the only variable with significant loading that correlated with CAN 1 while RRT, PT and Bas were the identified correlated variables in CAN 2. Considering the highest total variation explained by CAN 1 and PTR as the only correlated variable, this indicates that CAN 1 is the most important and PTR is the best discriminant variable in separating the three duck genotypes to distinct genetic groups using thermal stress adaptation (physiological, haematological and biochemical) parameters. In addition, it is worth

emphasizing that the 2 canonical functions are orthogonal i.e. each canonical function is independent of each other and their variable loadings are not correlated.

Discriminant analysis

The result of DA (Table 4) revealed that highest correct classification of the studied genetic groups was 96.70%, 71.00% and 50.00% for Mallard, Muscovy and Mule ducks, respectively. Besides, the total correct classification success rate was 80.00%. The Muscovy and Common (Mallard) ducks were poles apart without any form of overlapping between them (Table 4 and Figure 1).

This implies that the two duck *genera* are not only genetically divergent in source but are also genetically different in respect of heat stress adaptation. The highest correct assignment reported for Mallard ducks agrees with the scatter plot of the three genotypes (Fig. 1). The cluster graph indicated that Mallard ducks clustered separately as a distinct genetic group from indigenous Muscovy and crossbred Mule ducks. This is clear evidence that Mallard ducks are genetically different from the other two genotypes in respect of thermal stress adaptation.

One possible reason for higher misclassification (50%) of Mule ducks as Muscovy ducks and high intermingling of Mule ducks with Muscovy ducks in scatter plot (Fig. 1) could be linked to the fact that the genetic identity of one of their parents is known (i.e. Muscovy duck) while not clear for the second parent. Since Mule ducks are products of *inter-generic* crossing of Muscovy and Common ducks; this implies that half of their genome was contributed by Muscovy ducks. The

Table 2: Stepwise discriminant analysis of heat tolerant traits of duck genotypes

Step	Variable entered	Wilk's lambda	F-value	P < F
1	PTR	0.340	125.409	0.000
2	RRT	0.156	97.876	0.000
3	BAS	0.136	72.261	0.000
4	PT	0.125	57.718	0.000

Table 3: Total canonical structure of three duck genotypes

Traits	CAN 1	CAN 2
Bas	0.354	0.436
PT	0.300	0.660
RRT	-1.574	1.115
PTR	2.004	-0.780
Canonical correlation	0.934	0.143
Eigen value	6.858	0.021
Variance accounted for (%)	99.70	0.300
Cumulative variance (%)	99.70	100.00

Table 4: Classification result of discriminant analysis of three duck genotypes

Cross-validated		Predicted genotype membership			Total (92)
		Muscovy duck (31)	Mallard duck (37)	Mule duck (24)	
Count	Muscovy	22	0	9	31
	Common	0	36	1	37
	Mule	12	0	12	24
(%)	Muscovy	71.00	0.00	29.00	100.00
	Mallard	0.00	97.30	2.70	100.00
	Mule	50.00	0.00	50.00	100.00

80.0% of cross-validated grouped cases correctly classified.

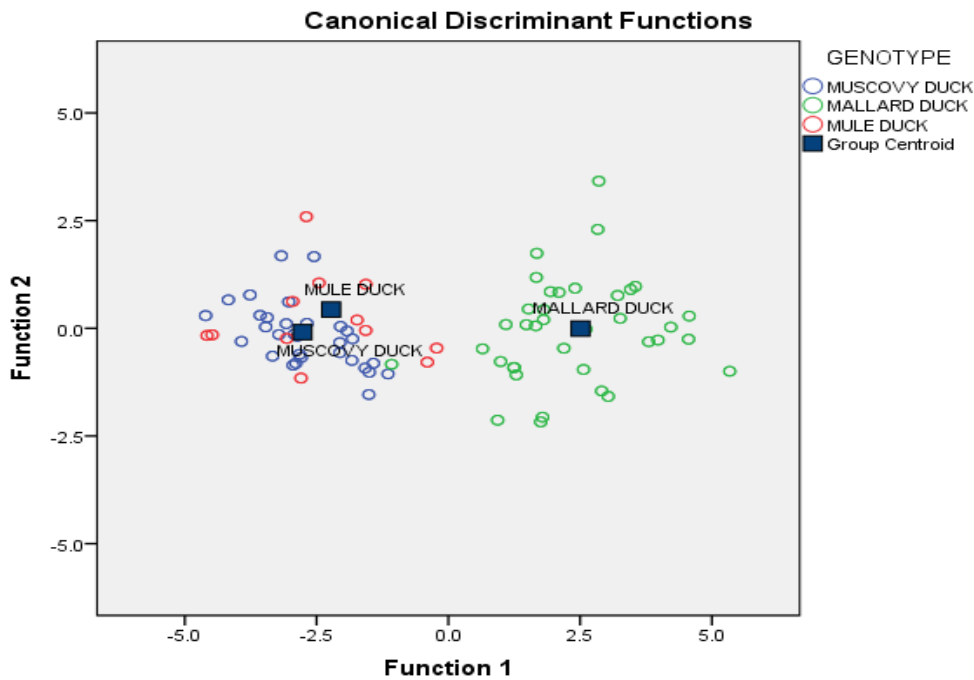


Figure 1. Canonical scatter plot of three duck genotypes.

remaining half was contributed by the Common duck breeds that are genetically heterogeneous; thus resulting in overlapping and classification of half of them as Muscovy ducks. Conversely, Yakubu *et al.* (2012) reported higher classification success rate for local (96.43%) and crossbred (98.73%) turkey genotypes and a very low overlapping between the two groups using morphological and heat stress index. The reported higher classification rate in crossbred turkey might not be unconnected with the fact that the turkey hybrids were produced in controlled environment from parental lines whose genetic identities were known and were also genetically homogenous. This is in contrast to the crossbred Mule ducks used in this experiment that were products of indiscriminate crossbreeding of Muscovy duck with various breeds of Common duck. Nevertheless, the overlapping clustering of Mule ducks with Muscovy ducks is suggestive that these genetic groups are genetically related or similar in respect of thermal stress adaptation.

Euclidean distance

The result of the Euclidean distance (Table 5) between the two duck *genera* {Muscovy and Common (represented by Mallard) ducks) was

farthest (86.507), intermediate between Mule and Mallard ducks (75.016) but shortest between Mule and Muscovy ducks (12.415).

The Euclidean distance between the genetic groups corroborated the results of the percentage correct assignment (Table 4) and canonical discriminant graph (Fig. 1). The farthest distance between Muscovy and Common (Mallard) ducks is not unexpected. The two genotypes belong to different *genera*; while Muscovy duck belongs to the *genus Cairini*, Mallard ducks belongs to the *genus Anas*. The reported distance reflects the wide genetic diversity existing between the two duck *genera* and also in their thermal tolerance.

The trend of Euclidean distance between the genetic groups is in agreement with a recent report on three turkey genotypes using morphometric and heat tolerant (physiological) traits (Yakubu *et al.*, 2012). These researchers reported longest distance between local and exotic turkeys, shortest distance between indigenous and crossbred genotypes and intermediate distance between crossbred and exotic genotypes. The shortest distance between Muscovy and Mule ducks implies that though Mule ducks are hybrid of Muscovy and Common ducks,

Table 5: Euclidean genetic distance between duck genotypes

	Muscovy duck	Mallard duck	Mule duck
Muscovy duck	0.000	86.507	12.415
Mallard duck	86.507	0.000	75.016
Mule duck	12.415	75.016	0.000

they appear to be closer to Muscovy ducks than the latter parent in respect of thermal stress adaptation.

Furthermore, the longest Euclidean distance between representatives of two duck *genera* portends hope for the possibility of exploiting heterosis in their genetic diversity for production of hybrids that are better adapted to hot environment than the most susceptible parent (Common duck). Wide genetic distance between parental groups is central to higher heterosis/hybrid vigour (Oguntunji and Ayorinde, 2014). These researchers stated further that since heterosis exploits wide genetic differences between parental groups; therefore, the wider the genetic bases the higher the heterosis and vice versa.

Conclusions

DA of heat tolerant traits revealed that PTR, RRT, BAS and TP were the most important variables in separating the three duck genotypes into distinct genetic groups. Local Muscovy and crossbred Mule ducks had better adaptation to thermal stress while Common (Mallard) ducks were more sensitive or less adapted. The superior heat stress adaptation of hybrid Mule ducks compared to the less adapted parent (Common duck) is suggestive that heat stress adaptation is heritable and this economic trait could be selected for and also be exploited for production of thermal-tolerant hybrids. Besides, the application of informative molecular indicators and or biomarkers could provide additional information that would enhance better understanding of thermal stress adaptation in duck genotypes. Considering the better heat tolerance of local Muscovy ducks; the result of the present study would be useful in planning breed management, conservation and improvement of the local genetic resources.

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