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Discriminant analysis of growth traits in indigenous, crossbred and exotic turkeys in Nigeria: A review

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Abstract

In rural areas where measuring scales are expensive and unavailable, linear body measurements can be used as predictors of body weight. Breast girth (BG), body length (BL), wing span (WS), wing length (WL), and thigh length (TL) of Nigerian local turkeys are the best discriminating variables in differentiating the birds, according to recent studies. There are also significant physical differences between the sexes, as well as differences in trait associations within each sex. Genetic differences may account for the majority of morphological differences in turkeys. In developing and underdeveloped countries, discriminant analysis provides a practical analytical framework for characterizing and managing turkey's genetic resources. To fully understand the genetic variation among indigenous, crossbred, and exotic turkeys, this study should be followed up with molecular approaches. The ability to distinguish the growth traits of indigenous or native, exotic and crossbred turkeys in Nigeria using multivariate discriminant analysis could aid in the implementation of a conservation and improvement strategy for indigenous turkeys, ensuring the long-term development of animals using their genetic merits.

Keywords: discriminant analysis, turkey, growth traits, Nigeria

Analyse discriminante des traits de croissance chez les dindes indigènes, croisées et exotiques au Nigeria : une critique

Résumé

Dans les zones rurales où les échelles de mesure sont chères et indisponibles, les mesures corporelles linéaires peuvent être utilisées comme prédicteurs du poids corporel. La circonférence de la poitrine (CP), la longueur du corps (LC), l'envergure des ailes (EA), la longueur des ailes (LA) et la longueur des cuisses (LC) des dindes locales nigérianes sont les meilleures variables discriminantes pour différencier les oiseaux, selon des études récentes. Il existe également des différences physiques significatives entre les sexes, ainsi que des différences dans les associations de traits au sein de chaque sexe. Les différences génétiques peuvent expliquer la majorité des différences morphologiques chez les dindes. Dans les pays en développement et sous-développés, l'analyse discriminante fournit un cadre analytique pratique pour caractériser et gérer les ressources génétiques de la dinde. Pour bien comprendre la variation génétique parmi les dindes indigènes, croisées et exotiques, cette étude devrait être suivie d'approches moléculaires. La capacité de distinguer les traits de croissance des dindes indigènes ou indigènes, exotiques et croisées au Nigeria à l'aide d'une analyse discriminante multivariée pourrait aider à la mise en œuvre d'une stratégie de conservation et d'amélioration des dindes indigènes, assurant le développement à long terme des animaux en utilisant leurs mérites génétiques.

Mots-clés : analyse discriminante, dinde, traits de croissance, Nigeria

Introduction

A comparative analysis of animal body conformation (such as shape and size) is of great interest to animal breeders. This research contributes to the development of a holistic approach to determining the genetic performance of an Animal Genetic Resource (AnGR) within a population, as well as a delineating scale for distinguishing between different AnGR and evaluating available variations (Sponenberg *et al*., 2000). It includes all identification methods, qualitative and quantitative descriptions, livestock population records (such as breeds, strains, and ecotypes), management systems, and natural habitats to which they are adapted (or acclimatized) or not (Gizaw *et al*., 2011). To move Nigeria and Africa towards a food secure future, it is critical to characterize and analyze growth traits in order to create a solid representation of the variability and genetic diversity among farm animal breeds. The most common poultry species in West Africa are native chicken, Guinea fowl, duck, and turkey. Global meat production and consumption will range from 233 million to 300 million tonnes in the coming years, according to the Food and Agriculture Organization (FAO), while milk production and consumption will range from 568 to 700 million tonnes. In addition, egg production will increase by 30%. These forecasts show a massive increase in animal protein demand, which will be necessary to meet the growing human population and rising wealth of emerging economies (FAO, 2002). According to Isiugo-Abanihe (2020), Nigeria's population will be around 263 million in 2030 and 401 million in 2050, making it the world's fourth most populous country. As a result, to meet demand, an increase in animal protein source production is required. Turkey farming is profitable and vital, with rising global demand for its products (Emmah, 2006). When compared to other poultry species such as chickens, guinea fowl, and ducks, which total around 160 million, 8.3 million, and 1.7 million, respectively, local turkey number around 1.05 million, making them the smallest poultry species in Nigeria (FAOSTAT, 2011). The mechanisms involved in the control of morphology in birds are too complicated to be (statistically) explained using a single dependent variable analysis of variance when characterising morphological traits because all connected qualities have similarities due to pleiotropy or genetic linkage (ANOVA). As a result, a single dependent analysis of variance fails to account for all of the distinctions' relationships. Growth metrics (Rosario *et al*., 2008; Al-Aliyat, 2009), morphological factors, and multivariate discriminant analysis are currently being used to determine genotype (Rosario *et al*., 2008). (Food and Agriculture Organization of the United Nations, 2009; Yakubu and Ibrahim, 2011). Although multivariate characterization of morphological and heat-tolerant traits has been attempted for studying diversity in Nigerian turkeys (Yakubu *et al*., 2009; Yakubu *et al*., 2010), there is a scarcity of information on multivariate morphological characterisation for studying genetic diversity in Nigerian turkeys. As a result, using multivariate discriminant analyses to distinguish between native, cross-bred, and exotic turkeys will aid in the establishment of long-term breeding programs in Nigeria to preserve indigenous turkeys' AnGR.

Turkey production in Nigeria

Meleagris gallopavo is the scientific name for the turkey, which belongs to the Meleagrididae family of birds. The young birds are called poults, while the males are called turkey cocks or toms, and the females are called turkey hens (Ogundipe and Dafwang, 1980). The majority of turkeys are raised for meat or as breeders to produce hatching eggs. Even though the eggs are edible, they are rarely kept to produce table eggs. Nigeria's turkey industry has grown to 1.5-2 million tons per year. This rapid rise in the industry was enabled by increased production and the creation of giant breeds with standard weights ranging from 15-17 kg for males and 8-10kg for females; some of these come from homesteads (Ogundipe and Dafwang, 1986; Ojewola, 1993). Due to a variety of factors ranging from management issues to a lack of government incentives, turkey production in Nigeria has largely remained at the smallholder level (Udokainyang, 2001). In Nigeria, there is a distinct lack of information on specific requirements for turkey production, which may be due to the country's low level of research (Ojewola *et al*., 2001). Furthermore, government policy, which liberalized turkey importation beginning in 1977, was a major factor in the lack of interest in turkey production. According to Thear and Fraser (1986), imported turkey accounts for about 60% of total turkey in the Nigerian market, with the rest coming from other sources like troops. Despite its enormous potential in the provision of high-quality animal protein and rapid rate of investment turnover, Nigerians consume approximately 8.6 grams of animal protein per day, with turkey accounting for approximately 1.5 grams (Emmah, 2006). The lack of interest in turkey farming was due in large part to government policy, which began liberalizing turkey importation in 1977. (Udokainyang, 2001).

Genetic diversity of turkey populations in Nigeria

Given the significant foreign exchange implications of the importation of improved exotic stock, as well as the genotype by environment interaction that has resulted in significant loss of fitness of the exotic stock, Nigeria is endowed with an impressive array of indigenous livestock, the potential of which cannot be overlooked (Ibe, 1990). Indigenous animals have genetic material that can be used to improve them, making them valuable both functionally and genetically. Understanding their genetic diversity is important because it is the foundation for developing breeding programs and making rational decisions about the sustainable use of animal genetic resources, selection, and development of new breeds with improved resistance to environmental challenges (Mwacharo *et al*., 2005). The loss of genetic diversity among indigenous livestock populations has prompted efforts to study genetic diversity in livestock species in order to lay the groundwork for conserving these potentially beneficial germplasms. Genetic variation within and between breeds is important, not only from a cultural and conservation standpoint but also from a utility standpoint, because lost genes may be of future economic value (FAO, 2011). Within-breed genetic variety loss is significant, reducing the chances of breed survival due to poor fitness caused by inbreeding depression. The FAO's global plan for farm animal genetic resource management includes the genetic characterisation of domestic animals. The use of molecular technologies to aid in the conservation of endangered breeds and to determine breed genetic status is emphasized in this strategy. These include everything from electrophoretic detection of gene product polymorphism at structural loci to DNA analysis. Although DNA-based technologies are now the preferred tool for genetic characterisation of livestock (Arora *et al*., 2011), microsatellite loci and single nucleotide polymorphisms (SNPS) are still used in most diversity and phylogeny studies (Erhardt and Weimann, 2007). *Meleagris gallopavo* is kept in semi-intensive systems because of its improved tolerance to the harsh climatic conditions of the tropical habitat and its ability to survive with low management inputs. Despite their importance, information on blood protein and or enzyme types in Nigerian Indigenous Turkey is limited; however, these have been extensively reported in other poultry species, such as chicken (Ismoyowati, 2008; Johari *et al*., 2008; Guney *et al*., 2003; Das and Deb, 2008; Al-Samarrae *et al*., 2010; Ige *et al*., 2013; Yakubu and Aya, 2012; Ajayi *et al*., 2013), ducks (Azmi *et al*., 2006; Johari *et al*., 2012; Zhang *et al*., 2002; Ismoyowati, 2008; Okabayashi *et al*., 1999), and chukars and pheasants (Ugur *et al*., 2006).

Local turkeys have been found to thrive in arid environments, have a higher heat tolerance, range further, and have higher meat quality (Yakubu *et al*., 2013). Local turkeys are one of Nigeria's least studied poultry species, with little effort made to characterize them using biometrical characteristics. Over the last few years, the traditional method of morphological characterization of species has gained popularity (de Vincente *et al*., 2005). Various studies using traditional morphometric methods have been conducted on genetic variations in indigenous poultry birds (Egahi *et al*., 2010; Apuno *et al*., 2011; Daikwo *et al*., 2011; Adekoya *et al*., 2013). According to Mulyono *et al*. (2009), the capacity for additive genes affecting the body measurements of each bird's genotype to the nature of growth, development, and osteogenesis distinguishes phenotypic responses of different breeds. Each breed has its morpho-structure, which is a manifestation of its quantitative morpho-structure in response to the environment in which it was adapted or reared. Unlike their exotic cousins, which have undergone directional selection for a high growth rate, the native turkeys were a diverse and unimproved population. Native turkeys demonstrated greater adaptability in terms of heat tolerance than their exotic counterparts. Understanding the tolerance and adaptive potential of different genetic groups is critical as a technical foundation for turkey research, including the direction of cross-breeding programs. It has been discovered that the phenotypic expression of a genotype varies depending on the environment (Kolmodin *et al*., 2003).

Discriminant analysis in animal breeding and genetics

Discriminant analysis is a technique for analyzing data – in this case, morphological data – in which the parameter or dependent variable is categorical and the indicator or independent variable is interval. A discrimination model is developed step by step in a stepwise discriminant function analysis. All variables are checked and evaluated at each stage to see which one can have the greatest impact on group discrimination. For studying the genetic diversity of locally adapted Nigerian turkeys, there is a scarcity of information on the multivariate characterisation of growth traits. In discriminant analysis studies, the analysis of variance is used to test the fixed effect of genotype on turkey morphostructural traits. To determine how similar or dissimilar the turkey populations are, a multivariate analysis is used. To determine which variable contributed the most to the differentiation between the three groups - indigenous, crossbred, and exotic turkeys - the STEPDISC procedure (SAS Institute, 2010) was used to conduct a stepwise discriminant analysis of the respective traits. In addition, based on the traits of interest, Canonical discriminant analysis (CANDISC procedure) is used to calculate canonical variables, canonical coefficients, and Mahalanobis distances between the three populations. For discriminant analysis, the linear model shown below is commonly used.

$$Y_{ij} = \mu + G_i + \varepsilon_{ij} \text{ or } Y_{ij} = \mu + G_i + S_j + \varepsilon_{ij}$$

Where:

Y_{ij}: Observed value of the independent

variable;
μ: Population mean;
G_i: The i^{th} level of factor G with a fixed effect (the effect of the genotype; I is indigenous, crossbred, or exotic);
S_j is the effect of sex (j is male or female); and
ε_{ij}: The independent normally distributed random variable with random residual error, with $E(e_{ij})=0$ and $V(e_{ij}) = \sigma^2$

Discriminant analysis of growth traits (or morphometric traits) in turkey

According to Adenaike *et al*. (2020), the morphometric parameters body weight (BW), breast girth (BG), body length (BL), shank length (SL), wing span (WS), wing length (WL), keel length (KL), and thigh length (TL) were not significantly different (P > 0.05) in both male and female Lavender turkey genotypes. Both male and female White turkey genotypes had significantly different morphometric features (P 0.05). Male White turkeys outperformed their female counterparts across the board on all morphometric criteria. The bivariate correlation coefficients (r) between BW and linear body measurements were very positive and significant among the various body features based on the report of Adenaike *et al.* (2020). For Lavender turkey linear measurements with body weight, the coefficient of correlation ranged from 0.73 to 0.94. According to Adenaike *et al*. (2020), the correlation between linear measurements and BW ranged from 0.84 to 0.96 for White turkey, with the highest associations being body length (r = 0.80, P 0.05) and the trio of thigh length, keel length, and body length (r = 0.91, P 0.05) for the Lavender and White turkeys, respectively (2020). The same author reported that the first canonical variable, the second canonical variable, and the third canonical variable explained 52.13 percent, 37.48 percent, and 10.39 percent of the variation, respectively. Similarly, Yakubu *et al*. (2011) found two statistically significant (p < 0.01) canonical variables that explained 83.04 % and 16.96 % variation in their canonical analysis of morphological and heat-tolerant variables (BW, TL, and HI). The first canonical variable (CAN 1) was a linear set of characteristics that best distinguished the three genetic groups. With CAN 1, BW and HI had a strong relationship. The second canonical variable was the next best linear combination, which was orthogonal to the first (CAN 2). TL was found to be strongly associated with CAN 2. The three canonical variates retrieved explained 100% of the total variation.

When each original feature was weighed according to how much it contributed to each canonical variable, Adenaike *et al*. (2020) found that wing length and breast girth had higher positive loadings on the first canonical variate, while wing span, thigh length, and body length had higher negative loadings. On the second canonical variate, wing span, shank length, and body length had higher positive loadings, while body length, wing length, and thigh length had higher negative loadings. On the third canonical variate, the keel length had the highest loading. In the study by Adenaike *et al*. (2020), all pairwise distances were statistically significant (P 0.05). Male and female White major turkeys had the greatest distance (415.16), followed by male White major and female Lavender (303.58), and male and female Lavender had the shortest distance (303.58). Note that the populations used by Adenaike *et al*. (2020) were separated by a large distance. Yakubu *et al*. (2012) had done a similar analysis to Adenaike *et al*. (2020) but from a different perspective. The longest Mahalanobis distance (36.68) was found between indigenous and exotic turkeys, while the shortest distance was found between indigenous and cross-bred turkeys (7.97), according to Yakubu *et al*. (2012). Exotic turkeys and crossbreds had a distance of

29.14, which was in the middle of the pack. Yakubu *et al*. (2012) presented all pairwise distances as significant (p 0.001), indicating that population differences are significant. Local and crossbred turkeys, on the other hand, were more closely related than their exotic counterparts. Finally, according to Yakubu*et al*. (2012), using nearest-neighbor discriminant analysis, 100 percent of exotic, 98.73 percent of crossbreed, and 96.43 percent of indigenous turkeys were correctly classified to their genetic groups (an average of 98.37 percent for the three populations). Adenaike *et al*. (2020) stated that genetic differences and sexual dimorphism are the main causes of morphological differences. Differences in the White Major's main sexes may be linked to differences in growth rates, growth tactics, metabolic rates, and reproductive strategies. According to McCracken *et al*. (2000) and Baeza *et al*. (2000), sexual dimorphism is attributed to the regular between-sex differential hormonal action, which usually leads to differential development rates (2001). Similar findings were found by other researchers (Blondel *et al*., 2002; Yakubu, 2011; and Ajayi *et al*., 2012). However, Adenaike *et al*. (2020) reported a lower average body weight than Yakubu *et al*. (2012) for the Nigerian locally adapted turkey breed, which was 2.85 kg. Because BW and body measurement have a positive and significant relationship in both genotypes (of White Major and Lavender), BW can be determined from body measurements and vice versa. Because animal growth can be measured using the animal's constituent parts (Wolanski *et al*., 2006), an increase in body measurements will almost always result in an increase in the Nigerian turkey's BW, especially if the correlation is positive. As a result, thigh length, breast girth, wing length, wing span, and body length can all be used as indicators to determine population differences. Adenaike *et al*. (2020) found that discriminant analysis could be used to distinguish between genetic groups or ecotypes of birds, which was in line with previous research (Chen *et al*., 2004; Abdelqader *et al*., 2008; Rosario *et al*., 2008; Yakubu *et al*., 2011). Except for TL, which was significantly higher in cross-breeds than in their parent populations, all morphological features were similar between indigenous and cross-breeds, according to Yakubu *et al*. (2012). BW, BL, SL, TL, and KL were significantly higher in male turkeys (Toms) than females (p 0.05), indicating sexual dimorphism in morphological characteristics. According to Yakubu *et al*. (2011) in a stepwise discriminant analysis, the most discriminating variable was BW, which was followed by TL, BG, and SL in that order. Yakubu *et al*. (2011) concluded that using univariate and multivariate statistical methods, they were able to distinguish between native, exotic, and cross-bred turkeys using morphometric and heat-tolerant features.

Conclusion

In the industrialized world, livestock recording programs provide a continuous stream of data for monitoring industry developments, including a better understanding of breeds and production practices. In most developing countries, such systems do not exist. As a result, it's critical to develop objective methods for assessing the morphological and physiological characteristics of birds. In addition, geometric morphometry (shape analysis), molecular genetic investigations with diagnostic marker loci, and larger sample size would be ideal in future research because they could improve the classification's discriminant power and precision. The ability to design and implement genetic interventions for the improvement of the (entire) turkey population requires accurate and thorough morphological characterization of turkeys native to Nigeria. Discriminant analysis is useful in genetic association studies, which is important for understanding the genetic intricacies underlying complex phenotypes in livestock. It can be used to characterize poultry birds, specifically turkeys, for further genetic evaluation.

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