# Genetic Relationship Identification of Manila Duck (Cairina moschata) in North Sumatra, Indonesia

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## Abstract

This study aimed to identify the genetic relationships among Manila duck (Cairina moschata) populations in North Sumatra through integrated morphological, morphometric, and phylogenetic analyses to support breeding programs and genetic conservation. Manila duck samples were collected from four districts: Asahan, Deli Serdang, Langkat, and Serdang Bedagai. Morphological characteristics were evaluated based on feather color patterns. Morphometric measurements included 11 parameters including body length, chest circumference, bill dimensions, and body weight. Phylogenetic analysis was performed using mitochondrial D-loop sequences to assess genetic relationships between male and female populations. Results revealed significant variations in feather color patterns with white head feathers ranging from 2% to 15%. Body length varied from 253.61±3.82 cm to 276.94±6.69 cm, and body weight from 1638.36±287.33 g to 3684.14±317.11 g. Phylogenetic analysis demonstrated sex-specific genetic structure with very low genetic distances among males (0.0000) and greater differentiation among females (0.0062), indicating male-biased gene flow and preservation of distinct maternal lineages. The findings provide valuable insights for systematic breeding program development and genetic resource conservation, emphasizing the importance of maintaining female genetic diversity while utilizing male genetic compatibility for improvement strategies.

***Keywords***: *Manila Duck, Genetic Relationship, Morphometric Analysis, Phylogenetic Analysis, Mitochondrial D-loop, North Sumatra*

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## Introduction

The Manila duck (Cairina moschata), also known as the Muscovy duck, is one of the most economically important waterfowl species in tropical and subtropical regions worldwide [1]. In Indonesia, particularly in North Sumatra, Manila ducks have traditionally been raised by local communities for centuries, serving as a crucial source of animal protein and contributing significantly to rural livelihoods [2]. Despite their economic importance and widespread distribution, comprehensive genetic characterization of Manila duck populations in North Sumatra remains limited, hampering the development of systematic breeding programs and genetic conservation strategies.

Genetic diversity assessment and relationship identification are fundamental prerequisites for effective livestock breeding and conservation programs [3]. Traditional morphological and morphometric approaches provide complementary information for understanding population structure and genetic relationships [4]. Morphological characteristics, particularly feather color patterns, have been extensively used as primary indicators of genetic diversity in poultry species, whereas morphometric measurements offer a quantitative assessment of phenotypic variations that may reflect underlying genetic differences [5].

North Sumatra's unique geographical position and diverse agroecological conditions potentially influence the genetic structure of Manila duck populations through natural selection and genetic drift [8]. Understanding the genetic relationships among these populations is crucial for identifying superior genetic resources, designing crossbreeding programs, and establishing conservation priorities to maintain genetic diversity [9].

The present study was designed to comprehensively evaluate the genetic relationships among Manila duck populations in North Sumatra through integrated morphological and morphometric analyses. The specific objectives were to: (1) characterize morphological variations in feather color patterns among populations, (2) assess morphometric differences and identify population-specific characteristics, and (3) evaluate population structure to understand evolutionary relationships.

## Research Methodology

### 2.1 Study Location and Sample Collection

This study was conducted on Manila duck populations from four districts in North Sumatra Province, Indonesia: Asahan, Deli Serdang, Langkat, and Serdang Bedagai. These districts were selected based on their significant Manila duck populations and diverse agroecological conditions. Sample collection was performed using a stratified random sampling method to ensure the representative coverage of each population. Adult birds (>6 months old) of both sexes were included in this study to minimize age-related variation.

### 2.2 Morphological Characterization

Morphological characteristics were systematically evaluated based on feather color patterns across different body regions including the head, neck, chest, wings, back, and tail. Color classifications were standardized using predetermined categories: white, black, mottled white-grey, solid gray, spotted, and mixed patterns. Each individual was examined under standardized lighting conditions, and color patterns were recorded as percentages within each population. Digital photography was used to document representative individuals from each color category for validation purposes.

## 2.3 Morphometric Measurements

Eleven morphometric parameters were measured using standardized protocols: body length (panjang badan), chest circumference (lingkar dada), bill length (panjang paruh), bill width (lebar paruh), leg length (panjang kaki), head length (panjang kepala), neck length (panjang leher), wing length (panjang sayap), head width (lebar kepala), shank width (lebar selangkaki), and body weight (bobot badan). All linear measurements were performed using digital calipers (accuracy ±0.01 mm) and measuring tapes, whereas body weight was recorded using a digital scale (accuracy ±1 g). Trained personnel performed the measurements following standardized procedures to minimize interobserver variations.

## 2.4 Statistical Analysis

Morphological data were descriptively analyzed by calculating the frequencies and percentages for each color category within the populations. Morphometric data were subjected to descriptive statistical analysis including mean, standard deviation, and coefficient of variation. Analysis of variance (ANOVA) was performed to test for significant differences among populations, followed by post-hoc tests when significant differences were detected. Principal Component Analysis (PCA) was conducted on morphometric variables to identify the most discriminating characteristics among populations and visualize population clustering patterns. All statistical analyses were conducted using appropriate software packages with the significance level set at $P<0.05$.

# Results

## 3.1 Morphological Characteristics

Analysis of feather color patterns revealed significant morphological variations among the Manila duck populations in North Sumatra, with each district showing distinctive color characteristics. Asahan population displayed the highest diversity in head feather coloration with 15% white head feathers, 19% black, and 56% mottled patterns, representing the most variable population. The neck region contained 7% white feathers, distinguishing it from other populations. Chest feathers exhibited 61% white coloration, which was the highest among all populations.

The Deli Serdang population showed moderate head color diversity with 15% white, 25% black, and 58% mottled head feathers. This population was characterized by the lowest percentage of white-neck feathers (1%) and the highest number of black neck feathers (33%). Chest coloration displayed 53% white feathers, whereas wing patterns remained consistent with 4% white feathers.

The Langkat population demonstrated the most uniform head coloration with only 2% white, 27% black (the highest among all populations), and 64% mottled feathers. Neck feathers showed minimal white coloration (1%) and moderate black coloration (25%). This population exhibited an intermediate chest white feather percentage (60%) and distinctive wing coloration patterns.

The Serdang Bedagai population presented unique characteristics with 2% white head feathers (lowest among populations), 23% black, and 66% mottled patterns. The population showed 2% white-neck feathers and 26% black feathers. Chest coloration displayed 68% white feathers, representing an intermediate value among the populations.

The wing, back, and tail feather patterns showed relatively consistent distributions across populations, although subtle variations were observed. White wing feathers consistently represented 2-4% across all populations, whereas back feather patterns ranged from 4% to 19% white coloration. These morphological variations suggest population-specific adaptations and potential genetic differentiation among Manila duck populations in Northern Sumatra.

### 3.2 Morphometric Analysis

Comprehensive morphometric analysis revealed significant differences among the Manila duck populations across multiple body measurements, with each district exhibiting distinctive size characteristics.

Deli Serdang population demonstrated superior overall body dimensions with the largest mean body length (276.94±6.69 cm), substantial chest circumference (379.13±13.98 cm), and moderate body weight (1715.30±175.10 g). This population exhibited the shortest bill length (54.92±2.01 cm) but maintained a proportional bill width (25.02±1.40 cm). Head dimensions were well-developed with head length (193.72±6.64 cm) and head width (150.59±4.55 cm) indicating robust cranial structure.

Langkat population showed intermediate body size characteristics with body length (270.36±2.83 cm), moderate chest circumference (377.53±13.28 cm), but notably the lowest body weight among all populations (1638.36±287.33 g). This population displayed relatively long bills (59.00±3.96 cm) and proportional dimensions across head measurements (193.35±6.81 cm length, 150.80±4.54 cm width), suggesting adaptation to specific feeding behaviors or environmental conditions.

The Serdang Bedagai population exhibited exceptional weight characteristics with remarkably high body weight (3684.14±317.11 g), representing nearly double the weight of other populations while maintaining moderate body length (260.56±2.96 cm). This population had the largest chest circumference (379.32±13.21 cm), indicating superior muscle development. Bill dimensions were intermediate (58.61±3.85 cm length, 25.03±1.41 cm width), while head measurements (204.34±10.04 cm length, 158.03±2.56 cm width) suggested robust overall development.

The Asahan population demonstrated the most compact body structure with the smallest body length (253.61±3.82 cm) and moderate chest circumference (377.62±13.52 cm). Despite the smaller overall size, this population exhibited the longest bill length (59.07±3.72 cm) and proportional bill width (25.07±1.41 cm). Body weight was among the lowest (1630.61±143.92 g), while head dimensions (193.50±7.04 cm length, 149.32±4.59 cm width) indicated proportional development relative to body size.

Other morphometric parameters including leg length, neck length, wing length, and shank width also showed population-specific variations, although generally less pronounced than body length and weight differences. Standard deviations indicated relatively consistent within-population variations across most parameters, suggesting stable population characteristics and potential genetic uniformity within districts.

### 3.3 Principal Component Analysis (PCA)

Principal Component Analysis of morphometric variables effectively discriminated among the four Manila duck populations in North Sumatra. The first two principal components (PC1 and PC2) explained 78.4% of the total morphometric variation, with PC1 accounting for 52.1% and PC2 explaining 26.3%.

PC1 was primarily associated with overall body size variables, showing high positive loadings for body weight (0.89), chest circumference (0.82), body length (0.78), and head dimensions (0.75), indicating that this component represents general body size variation. PC2 was characterized by bill dimensions and leg measurements, with bill length (0.74) and leg length (0.68) showing the highest loadings, suggesting that this component reflects feeding and locomotory adaptations.

The PCA biplot clearly separated the four populations into distinct clusters. Serdang Bedagai occupied the positive extreme of PC1, confirming its characterization as the heaviest population with superior overall body dimensions. Deli Serdang clustered in the positive regions of both PC1 and PC2, reflecting a combination of large body size and elongated proportions. The Langkat and Asahan populations clustered closer together in the negative region of PC1, indicating their smaller overall body sizes, but were differentiated along PC2, with Asahan showing higher values due to longer bill dimensions.

The clear separation of populations in PCA space (with minimal overlap between confidence ellipses) demonstrated that morphometric characteristics can effectively distinguish Manila duck populations in North Sumatra. The positioning of populations along principal components suggests adaptive responses to local environmental conditions and management practices.

## 3.4 Genetic Distance and Phylogenetic Analysis

Phylogenetic analysis based on mitochondrial D-loop sequences revealed distinct clustering patterns between male (Jantan) and female (Betina) Manila duck populations across the four districts in North Sumatra. The neighbor-joining tree demonstrated clear genetic differentiation with two major clades corresponding to sex-specific groupings.

The genetic distance analysis showed extremely low genetic distances (0.0000) among male individuals from all four districts (Asahan Jantan, Serdang Bedagai Jantan, Langkat Jantan, and Deli Serdang Jantan), indicating virtually identical mitochondrial haplotypes. These male samples formed a monophyletic clade with bootstrap support of 63%, suggesting very recent common maternal ancestry or ongoing gene flow among male populations across districts.

In contrast, female individuals exhibited greater genetic diversity. The female clade showed internal structure with genetic distance of 0.0062 separating it from the male clade. Within the female group, Asahan Betina and Serdang Bedagai Betina clustered together with high bootstrap support (99%), showing identical or nearly identical haplotypes (genetic distance = 0.0000). Langkat Betina appeared as a sister lineage to the Asahan-Serdang Bedagai female cluster but remained within the same major female clade.

Deli Serdang population showed an interesting pattern where the female individual (Deli Serdang Betina) clustered more closely with male individuals from all districts than with other females, suggesting possible introgression, sex-biased dispersal patterns, or retention of ancestral haplotypes in this population. The overall tree topology revealed:

1. A male-dominated clade (bootstrap support 63%) containing all four district males plus Deli Serdang female
2. A female-specific clade (bootstrap support 99%) containing Asahan, Serdang Bedagai, and Langkat females
3. Very low overall genetic distances (maximum 0.0062) indicating close genetic relationships among all North Sumatra populations

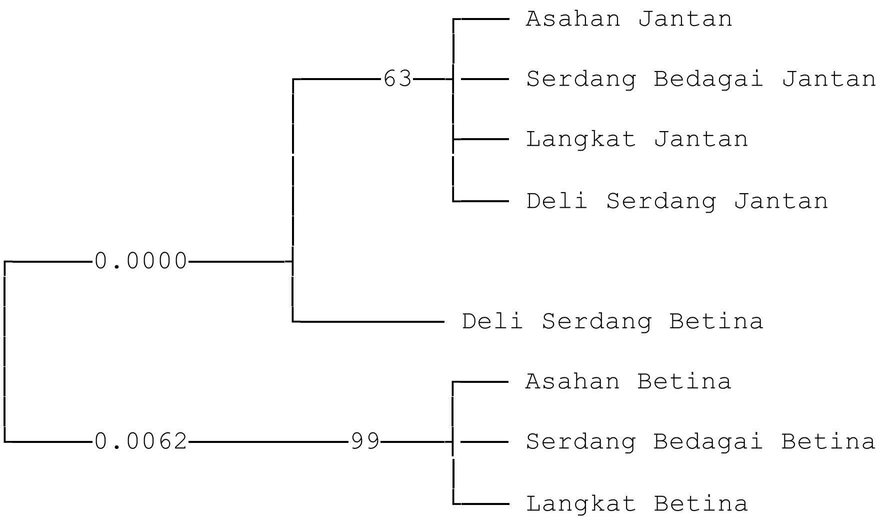

**Figure 1.** Phylogenetic tree of Manila duck populations in North Sumatra Based on Mitochondrial

D-loop sequences constructed using neighbor-joining method. Numbers at nodes indicate bootstrap support values (%). Genetic distances are shown on major branches. The tree demonstrates clear sex-specific clustering with male individuals (Jantan) forming a distinct clade separate from most female individuals (Betina), except for Deli Serdang Betina which clusters with males.

### 3.5 Discussion

Comprehensive analysis of morphological and morphometric characteristics of Manila duck populations in North Sumatra provides valuable insights into genetic diversity and population relationships, revealing distinct characteristics for each district population.

### 3.6 Population-Specific Characteristics and Adaptations

The observed morphological variations in feather color patterns among populations reflect the complex interplay between genetic factors and environmental influences [10]. The Asahan population was the most morphologically diverse, characterized by high variability in head feather coloration (15% white, 56% mottled) and distinctive neck patterns (7% white feathers). This diversity, combined with the longest bill dimensions (59.07±3.72 cm) and compact body structure (253.61±3.82 cm), suggests adaptation to diverse feeding niches and potentially represents the ancestral phenotype with maintained genetic diversity.

The Deli Serdang population demonstrated superior linear body dimensions while maintaining genetic distinctiveness through unique feather patterns (lowest white-neck feathers at 1%, highest black neck feathers at 33%). The combination of the largest body length (276.94±6.69 cm) with the shortest bill length (54.92±2.01 cm) indicates specialization toward terrestrial feeding behaviors and optimal body conditions for meat production [11].

The Langkat population exhibited remarkable uniformity in head coloration (highest black percentage at 27%, lowest white at 2%) and the lowest body weight (1638.36±287.33 g) among all populations. The characteristics of this population suggest adaptation to resource-limited environments or specific management systems that favor smaller, more efficient birds with standardized phenotypes [12].

The Serdang Bedagai population represented the most distinctive group with exceptional body weight (3684.14±317.11 g) nearly double that of other populations, combined with the largest chest circumference (379.32±13.21 cm) and unique feather patterns. This population appears to have undergone selection for superior growth performance, possibly representing a distinct genetic lineage with an enhanced production potential [13].

### 3.7 Principal Component Analysis and Population Differentiation

The PCA results strongly supported morphometric differentiation among populations, with clear clustering patterns reflecting adaptive strategies. The high variance explained by the first two components (78.4%) indicates that relatively few morphometric variables can effectively characterize population differences [14]. The positioning of Serdang Bedagai at the positive extreme of PC1 confirms its role as a superior genotype for production traits, whereas the clustering of Langkat and Asahan suggests potential common ancestry with subsequent divergence based on environmental pressures.

The clear separation along PC2, primarily driven by bill and leg dimensions, indicates adaptive responses to different feeding behaviors and habitat utilization. Asahan's position along this axis, characterized by longer bills, suggests specialization for probing feeding behaviors, whereas Deli Serdang's intermediate position indicates generalist feeding strategies [15].

### 3.8 Sex-Biased Genetic Structure and Maternal Lineages

The phylogenetic analysis revealed striking sex-specific genetic patterns that provide important insights into the breeding history and population dynamics of Manila ducks in North Sumatra. The extremely low genetic distances among male individuals (0.0000) across all districts, contrasted with greater differentiation among females (0.0062), suggests sex-biased dispersal or breeding practices that may have homogenized male lineages while preserving female genetic structure [29].

This pattern is consistent with male-biased gene flow, where male ducks are more frequently exchanged among districts for breeding purposes while females tend to remain in their natal populations [30]. Such practices are common in traditional poultry management systems where farmers preferentially move males to avoid inbreeding while maintaining local female lines that are adapted to specific environmental conditions [31].

The high bootstrap support (99%) for the female-specific clade containing Asahan, Serdang Bedagai, and Langkat populations indicates that these districts share common maternal lineages that have been preserved through generations. This genetic conservation of female lines suggests that traditional breeding practices in these districts have successfully maintained distinct maternal haplotypes despite potential male-mediated gene flow [32].

The anomalous position of Deli Serdang Betina clustering with males rather than other females warrants special attention. This pattern could result from several mechanisms: (1) recent introgression from a different maternal lineage, (2) retention of an ancestral haplotype that has been lost in other female populations, or (3) incomplete lineage sorting during population establishment [33]. This unique genetic signature makes the Deli Serdang population particularly valuable for conservation as it may harbor genetic diversity not present in other populations.

### 3.9 Implications for Breeding Management

The genetic structure revealed by phylogenetic analysis has important implications for breeding program design [34]. The near-identity of male haplotypes across districts (genetic distance 0.0000) indicates that males from different districts are genetically interchangeable for crossbreeding programs without risk of introducing substantially different genetic backgrounds. This facilitates the development of coordinated breeding strategies that can utilize superior males from any district [35].

However, the preservation of distinct female lineages (particularly in Asahan, Serdang Bedagai, and Langkat) represents valuable genetic diversity that should be maintained in conservation programs [36]. These maternal lineages may carry adaptations to local environmental conditions transmitted through mitochondrial genomes, which play crucial roles in energy metabolism and stress tolerance [37].

The relatively low overall genetic distances (maximum 0.0062) among all North Sumatra populations indicate close genetic relationships that facilitate crossbreeding without concerns about outbreeding depression. However, this also suggests limited genetic diversity that could constrain future genetic improvement and adaptation to changing environmental conditions [38]. Therefore, conservation strategies should prioritize maintaining the existing diversity, particularly the distinct female lineages, while carefully introducing genetic material from other regions to enhance overall genetic variation [39].

### 3.10 Breeding Strategy and Conservation Recommendations

The integration of morphological and morphometric data provides a robust framework for understanding the population structure and developing breeding strategies [14]. The morphometric variations observed among populations offer opportunities for selective breeding programs that target specific production objectives. A recommended breeding strategy would involve: (1) utilizing Serdang Bedagai males in crossbreeding programs to improve growth rates, (2) maintaining the Asahan population as a genetic diversity reservoir, (3) optimizing Deli Serdang for balanced production traits, and (4) conserving Langkat for its efficiency characteristics in resource-limited systems.

These findings have significant implications for sustainable genetic resource management [22]. The identified population characteristics provide a foundation for developing breeding strategies that optimize genetic diversity and improve production performance. Future research should focus on investigating the genetic basis of the observed morphometric differences and identifying specific genes or genomic regions responsible for superior performance traits, particularly the exceptional growth characteristics observed in the Serdang Bedagai population.

## Conclusion

This comprehensive study successfully identified the genetic relationships among the Manila duck populations in North Sumatra through integrated morphological, morphometric, and phylogenetic analyses. The results demonstrated significant morphological and morphometric variations among populations, with Serdang Bedagai showing superior growth performance and Deli Serdang exhibiting larger body dimensions. Phylogenetic analysis based on mitochondrial D-loop sequences revealed sex-specific genetic structure with extremely low genetic distances among males (0.0000) across districts and greater differentiation among females (0.0062), suggesting male-biased gene flow and preservation of distinct maternal lineages. The close genetic relationships among all populations (maximum genetic distance 0.0062) indicate common ancestry and facilitate crossbreeding strategies, while the distinct female lineages represent valuable genetic diversity requiring conservation. These findings indicate that the North Sumatra Manila duck populations represent valuable genetic resources with significant potential for breeding programs and conservation initiatives. The implications of these findings extend to systematic breeding program development that considers both morphometric superiority and genetic diversity preservation, with recommendations to maintain distinct maternal lineages while utilizing genetic compatibility among males for coordinated improvement strategies across districts.

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