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Zoometric characterization of native "Copetonas" hens in indigenous communities

Guevara-Hernández, Francisco[1]; **La O-Arias, Manuel A.**[1]; **Pinto-Ruiz, René**[1]; **Ramírez-Díaz, Roselia**[1]; **Cadena-Iñiguez, Pedro**[2*]; **Gómez-Castro, Heriberto**[1(†)]

[1] Universidad Autónoma de Chiapas. Facultad de Ciencias Agronómicas, Carretera Ocozocoautla-Villaflores km. 84.5, Apdo. Postal 78, C.P. 30470 Villaflores, Chiapas, México.

[2] Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias. Campo Experimental Centro de Chiapas del INIFAP / Km. 3.0, Carretera Ocozocoautla - Cintalapa, Ocozocoautla de Espinosa, Chiapas

* Correspondence: cadena.pedro@inifap.gob.mx

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ABSTRACT

Objective. To perform a zoometric characterization of a population of "Copetona" native hens to assess their degree of racial uniformity and and detect evidence of crossbreeding with commercial breeds in the municipality of San Andrés Larráinzar, Chiapas.

Design/Methodology/Approach: Twenty-three zoometric traits were measured in 50 adult hens from 16 production units across three communities. The coefficient of variation (CV) was calculated for each variable, and principal component analysis (PCA) and hierarchical cluster analysis (Ward's method) were performed to identify morphological groupings. Five zoometric indices were computed and compared among groups using ANOVA followed by Tukey's test.

Results. The population exhibited high phenotypic heterogeneity. Seven traits showed low variability ($CV<10\%$), nine displayed moderate variability ($CV=10\text{-}20\%$), and six showed high variability ($CV>20\%$), particularly those related to fleshy appendages (comb and wattles). Cluster analysis revealed three distinct morphological groups: small hens lacking native features (GCH), small hens retaining "Copetona" traits (GCC), and medium-sized hens showing signs of exotic introgression (GCM). The cranial index differed significantly ($p \leq 0.05$) among groups, with the GCC group presenting the highest values.

Implications. The pronounced variability and the formation of distinct morphological groups indicate ongoing genetic erosion caused by introgression from commercial breeds. The absence of selection criteria and the introduction of exotic birds threaten the conservation of this local genetic resource.

Conclusions: The studied "Copetona" hen population shows a marked loss of breed uniformity, supporting the hypothesis of genetic dilution due to crossbreeding with commercial lines. Immediate conservation actions focusing on the selection of native phenotypes and the restriction of exotic genotypes are urgently needed.

Keywords: Zoometry, genetic erosion, phenotypic variability, zoogenetic resources, cluster analysis.

INTRODUCTION

The development of animal and plant breeds is a dynamic process of genetic change driven by environmental conditions and human selection. Humans, in turn, are shaped by culture and economic circumstances. The dynamic nature of ecosystems and the evolution

of human preferences have historically allowed the diversification of breeds and, until recently, a net increase in genetic diversity over time (FAO, 2010).

However, during the past century, biological diversity has declined sharply due to the extinction of breeds and varieties, particularly among indigenous domestic animals. This loss has accelerated as a result of several factors, including: (a) the rapid intensification of livestock production; (b) the lack of evaluation of local breeds; (c) the use of exotic germplasm; (d) changes in production systems or producers' preferences driven by socioeconomic factors; and (e) inappropriate replacement or crossbreeding of breeds facilitated by access to high-yielding lines and reproductive biotechnologies. These processes have led to genetic homogenization, as evidenced in Brazilian native chicken populations, where ISSR molecular markers revealed reduced diversity caused by the introgression of commercial genotypes (Silva Júnior *et al.*, 2021). This pattern has been corroborated by molecular studies demonstrating loss of genetic diversity in local poultry through microsatellite and mitochondrial DNA analyses, which enable the quantification of erosion and the design of conservation strategies (Vázquez Gil & Guevara Viera, 2021). The global intensification of poultry production has further accelerated the replacement of local breeds by commercial lines, contributing to genetic erosion (Gržinić *et al.*, 2023). Recent studies confirm that the genetic distance between domestic populations and their wild ancestors is a key predictor of genetic diversity, explaining up to 88.6% of its variation (Malomane *et al.*, 2021).

Backyard or smallholder poultry farming, also referred to as household, rural, native, or traditional poultry production, remains a common practice among rural families in Chiapas, Mexico. It involves rearing small groups of native chickens under traditional management, feeding them with household leftovers or resources found in the production unit, such as kitchen residues or scavenged materials. Regarding health management, some medications or homemade remedies are occasionally used, and birds are housed in simple rustic shelters (Guevara *et al.*, 2011).

Traditional poultry farming is of great importance in many rural regions of developing countries and is often managed predominantly by women. Its maintenance and protection are of unquestionable value in rural areas because it preserves local management practices, breeds, and biodiversity, as well as their relevance to traditional regional cuisines, regardless of ethnic background (Guelber Sales *et al.*, 2010). In addition to genetic challenges, native chickens also face sanitary risks from ectoparasites such as the hematophagous mite *Ornithonyssus bursa*, which negatively affects productivity and welfare. These parasites are common in traditional systems where extensive management favors their proliferation (Arce *et al.*, 2025). Effective control is essential to safeguard the health and productivity of local breeds, particularly in backyard contexts where veterinary resources are limited.

According to FAO (2015), many breed attributes are determined by zoometric characteristics developed through long-term local adaptation, transmitted across generations. Zaragoza Martínez (2012) emphasized that since ancient times, the relationship between animal traits and the environment or region in which they evolved has been recognized. Consequently, local environmental conditions and human selection cause animals within a region to become progressively more similar to each other than to those from neighboring regions, eventually giving rise to distinct breeds.

Currently, local or creole breeds are undergoing genetic erosion due to the introduction of "improved" exotic breeds, and in many cases, they are disappearing without proper documentation of their racial characteristics. In Mexico, Illescas-Cobos *et al.* (2022) established morphometric standards for creole chicken eggs, identifying three groups with distinct bioproductive parameters. This highlights the urgent need to systematically document the zoometric and genetic characteristics of these birds before they vanish. In this regard, morphometric evaluation of native chickens is essential to determine the homogeneity or heterogeneity of populations, identify racial zoometric traits, and link these with social, economic, and cultural aspects relevant to the conservation and valorization of backyard chickens.

The present study aimed to zoometrically characterize a sample of "Copetona" native hens to determine their degree of racial uniformity under backyard conditions in the municipality of San Andrés Larráinzar, Chiapas.

MATERIALS AND METHODS

Study area

Fieldwork was conducted in the communities of Valle Limón, Holahoj, and Mehono in the municipality of San Andrés Larráinzar (Region V, Altos Tsotsil-Tseltal), Chiapas, Mexico (16.88° N, 92.71° W (WGS84) at an elevation of 2,200 m a.s.l.).

Selection of Animals

Animal selection was conducted using a non-probabilistic sampling approach, considering the willingness and interest of the hens' owners. To identify the predominant type of native hen, field visits and visual inspections were carried out across the different communities. A total of 23 zoometric measurements were recorded from 50 adult hens. In addition, a photographic record was compiled to document the morphological characteristics of each bird included in the study.

Zoometric Characterization

Linear body measurements were obtained using a vernier caliper and a measuring tape, whereas live body weight was determined using a mechanical dial scale. This standardization procedure is critical in avian studies, as previously applied to establish reliable baseline values for intraocular pressure in several species (Karimi *et al.*, 2020). The set of zoometric variables evaluated in this study followed the methodology proposed by Francesch *et al.* (2011) and are presented in Table 1.

Cephalic Index (CI)

$$CI = \frac{Head\ width \times 100}{Head\ length}$$

Proportionality Index (PI)

$$PI = \frac{Body\ height \times 100}{Body\ lenght}$$

Wattle Index (WI)

$$WI = \frac{Wattle\ width \times 100}{Wattle\ length}$$

Comb Index (CoI)

$$CoI = \frac{Comb\ width \times 100}{Comb\ lenght}$$

Ear-Lobe Index (ELI)

$$ELI = \frac{Ear\text{-}lobe\ width \times 100}{Ear\text{-}lobe\ length}$$

Statistical Analysis

A database was constructed using the body measurement data from all sampled hens. For the 23 zoometric variables, descriptive statistics (mean, standard deviation, range, and coefficient of variation) and Pearson's linear correlation coefficients were computed. Prior to multivariate analyses, all variables were standardized (z-scores) to eliminate scale effects. Principal Component Analysis (PCA) was performed on the correlation matrix to identify the main sources of variation (Mishra *et al.*, 2017). Components with eigenvalues greater than 1 and inspection of the scree plot were used as criteria for selection. The principal component scores were subsequently subjected to hierarchical cluster analysis using Ward's minimum variance method and Euclidean distance as the similarity measure (Koh *et al.*, 2022). The number of clusters was determined from the agglomeration schedule and the visual structure of the dendrogram.

Table 1. Zoometric measurements used in the study.

Head and neck	Code	Body	Code	Limbs	Code
Comb length	CL	Body length	BL	Leg length	LL
Comb width	CW	Wingspan	WS	Tarsus length	TL
Skull length	SL	Chest length	ChL	Tarsus diameter	TD
Skull width	SW	Body height	BH	Central toe length	CTL
Beak length	BkL	Wing length	WiL	Distance between legs	ID
Ear-lobe length	ELL				
Ear-lobe width	ELW				
Wattle length	WaL				
Wattle width	WW				
Neck length	NL				
Neck width	NW				

A one-way analysis of variance (ANOVA) was applied to detect significant differences among groups for the zoometric variables and indices. The assumptions of normality (Shapiro-Wilk test) and homogeneity of variances (Levene's test) were verified, applying data transformations when necessary. Post-hoc multiple mean comparisons were performed using Tukey's test (Montgomery, 2020). The level of statistical significance was established at $\alpha=0.05$ (two-tailed). For data processing, SAS (Statistical Analysis System) was used.

RESULTS AND DISCUSSION

As shown by the coefficients of variation (CV) in Table 2, the variables exhibited different degrees of uniformity. Some traits were highly uniform (CV <10%), such as body length (BL), skull width (SW), neck length (NL), body height (BH), leg length (LL), Central toe length (CTL), and wingspan (WS). Other variables showed moderate variability (CV=10-20%), including live body weight (LBW), skull length (SL), beak length (BkL), ear-lobe length (ELL), chest length (ChL), wing length (WiL), tarsus length (TL), tarsus diameter (TD), and Interleg distance(ID). Finally, several traits exhibited high variability (CV >20%), such as comb length (CL), comb width (CW), ear-lobe width (ELW), wattle length (WaL), wattle width (WW), and neck width (NW).

Table 2. Coefficients of variation, skewness, and kurtosis of the zoometric variables.

Variable	Coefficient of Variation (%)	Skewness	Kurtosis
Live body weight (LBW)	17.12	1.31	3.01
Body length (BL)	3.73	0.74	1.06
Wingspan (WS)	6.01	0.35	2.01
Comb length (CL)	23.95	0.08	0.19
Comb width (CW)	30.48	−0.23	−0.31
Skull length (SL)	11.18	0.57	0.57
Skull width (SW)	5.47	−1.28	2.37
Beak length (BkL)	12.16	0.07	−0.32
Ear-lobe length (ELL)	19.5	0.15	1.87
Ear-lobe width (ELW)	24.7	0.88	0.2
Wattle length (WaL)	25.2	0.23	−0.27
Wattle width (WW)	35.62	0.71	0.1
Neck length (NL)	8.35	0.11	−0.23
Neck width (NW)	24.56	1.84	5.13
Chest length (ChL)	18.5	1.09	0.66
Body height (BH)	9.05	0.1	0.22
Leg length (LL)	9.6	0.11	0.06
Wing length (WiL)	11.25	−2.01	11.44
Tarsus length (TL)	13.01	1.24	4.66
Tarsus diameter (TD)	11.68	0.01	−0.85
Central toe length (CTL)	9.25	0.01	−1.22
Interleg distance(ID)	11.24	0.46	0.87

The measurements exhibiting the highest degree of variability were those related to the fleshy appendages of the hens (comb width and length, wattle width and length, and ear-lobe width). The high variability observed in these appendages agrees with the findings reported for creole chicken eggs, in which parameters such as shell color and shape index showed significant dispersion (Illescas-Cobos *et al.*, 2022). This pattern suggests that phenotypic heterogeneity is inherent to creole populations, possibly due to the genetic flexibility reported in genes associated with metabolic processes and protein transport (Malomane *et al.*, 2021).

This variability may also be linked to traumatic injuries occurring in the environments where these birds develop. In "Copetona" hens, the combination of artificial selection for exuberant craniofacial traits and extensive management conditions increases the risk of recurrent dermal lesions. These lesions induce tissue remodeling during healing, altering the original dimensions and amplifying metric dispersion. Studies on crested birds have confirmed that their cranial morphology, with deossified areas beneath the fleshy appendages, renders them particularly prone to deformation even after minimal trauma, a relevant factor in backyard systems where physical stress is high (Manuel Paredes *et al.*, 2019; Yoshimura *et al.*, 2012).

In contrast, body conformation traits such as body height (BH) and body length (BL) exhibited very low variability, suggesting a high degree of uniformity in these characteristics. As demonstrated by Hedman *et al.* (2020) in Iberian creole hens, such populations tend to converge toward optimal body phenotypes that balance survival and productivity under nutritional constraints.

Table 2 presents the skewness and kurtosis values of the distribution curves for each variable. For most traits, skewness was positive, indicating right-skewed distributions; however, for three variables (WGL, SW, and CW), skewness was negative, showing a left-skewed pattern. Regarding kurtosis, the degree of "peakedness" of the distribution, high values were observed for WGL, NW, and TL, suggesting leptokurtic distributions. These findings question the assumption of normality for these three variables. For the remaining traits, both skewness and kurtosis values were moderate, supporting the assumption of normal distribution. Dagnino (2014) stated that moderate values of both indices (skewness and kurtosis) are indicative of normality.

A moderate degree of morphological integration was observed among the measured traits. Out of the 231 possible correlations, only 28.5% were significant (Table 3), indicating a low structural coherence within the population. This pattern suggests recent gene flow with exotic breeds, consistent with the observations of Gržinić *et al.* (2023) in traditional systems under pressure from intensive production models. The weak association among body measurements also reveals that the structural model of the studied hens is poorly harmonic, which evidences the absence of defined selection criteria or the use of inappropriate standards (Tang *et al.*, 2023). In the studied communities, there is no clear definition of selection criteria; consequently, the introduction of commercial hens, frequently through "gifts" or government programs, may be disrupting the morphological harmony of native breeds.

Table 3. Simple correlations among zoometric variables of native hens studied in San Andrés Larráinzar, Chiapas.

Variable		**Variable**
LBW		LBW
BL		BL
WS		WS
CL		CL
CW		CW
SL		SL
SW		SW
BkL		BkL
ELL		ELL
ELW		ELW
WaL	**Correlation**	WaL
WW		WW
NL		NL
NW		NW
ChL		ChL
BH		BH
LL		LL
WiL		WiL
TL		TL
TD		TD
CTL		CTL
ID		ID

A consistent pattern of morphometric relationships emerged among the studied traits. The variables live body weight (LBW), wingspan (WS), and comb length (CL) exhibited the highest number of significant correlations (Table 4). This trend agrees with the observations of Scanes (2022), who reported that LBW and EN are associated with skeletal-muscular development, while Scanes and Dridi (2022) linked CL to sexual maturity and endocrine regulation.

This result can be explained by the fact that LBW is positively associated with BL, EN, BH, LL, WGL, TL, and ID, since these traits are physiologically related to the birds' body composition, age, feeding regime, and endocrine characteristics (Huo *et al.*, 2021; Nawaz *et al.*, 2021; Olson *et al.*, 2022; Sanz *et al.*, 2021; van Eck *et al.*, 2023). These relationships agree with findings in other species, where molecular markers such as piRNAs show significant correlations with physiological traits, suggesting shared genetic mechanisms that link gene expression and morphometric structure (Ablondi *et al.*, 2020).

Comb length was positively correlated with cranial and integumentary traits, including CW, SL, SW, WW, and WaL, as well as with NL and WGL. Conversely, negative correlations were observed between tarsus diameter (TD) and CL, CW, SL, and WaL. Martínez-López *et al.* (2024) confirmed positive correlations between LBW

Table 4. Variables showing the highest number of significant correlations.

Variable	Significant correlations (n)
Live body weight (LBW)	8
Wingspan (WS)	8
Comb length (CL)	6
Comb width (CW)	6
Skull length (SL)	4
Body length (BL)	4
Beak length (BkL)	3
Neck length (NL)	4
Chest length (ChL)	3
Wattle length (WaL)	2
Leg length (LL)	3
Wing length (WiL)	2
Body height (BH)	1
Tarsus length (TL)	1
Ear-lobe length (ELL)	1
Ear-lobe width (ELW)	1

and cranial traits (skull width and beak length) and fleshy appendages (wattle length and comb length), all statistically significant ($p<0.01$ and $p<0.05$). Additionally, they reported negative associations of wing length (WiL) and tarsus length (TL) with bone diameters in adult males, which coincides with the negative correlation between TD and CL observed in the present study. These relationships are explained by sexual selection mechanisms: hens with more developed combs (higher CL values) often exhibit greater energy allocation to cranial and integumentary structures at the expense of peripheral bone development.

A multivariate pattern of morphometric association emerged from the principal component analysis (PCA), revealing four independent axes of variation that describe the main morphological trends of the "Copetona" hens (Table 5). The first component (PC1) was directly proportional to the wing-related traits, mainly WGL and EN; the second component (PC2) showed an inverse relationship with CL and WW, but correlated positively with BkL and TD; the third component (PC3) displayed positive loadings for CLT, SL, and SW; and the fourth component (PC4) was associated with ELL, TL, CTL, and ID. These patterns contrast with the findings of Getachew *et al.* (2016), who grouped Balearic creole hens into only two principal components, the first linked to body weight traits, and the second to tarsus measurements. The difference observed may be attributed to the inclusion of three different Balearic hen biotypes in their study, whereas the present research focused on a single biotype.

A clear morphological structure emerged from the cluster analysis, revealing three well-defined groups of "Copetona" hens, composed of 18, 21, and 11 individuals in Groups

Table 5. Principal components, correlation with zoometric variables, and explained variance.

Variable	PC-I	PC-II	PC- III	PC- IV
Body length (BL)	0.22	0.16	0.24	0.01
Wingspan (WS)	0.33	0.26	0.07	0.05
Comb length (CL)	0.28	−0.35	0.10	−0.06
Comb width (CW)	0.24	−0.27	−0.16	−0.13
Skull length (SL)	0.22	0.02	0.42	−0.19
Skull width (SW)	0.14	−0.14	0.43	−0.24
Beak length (BkL)	−0.04	0.33	0.24	−0.21
Ear-lobe length (ELL)	0.16	−0.01	−0.16	0.31
Ear-lobe width (ELW)	0.14	−0.22	−0.27	−0.04
Wattle length (WaL)	0.11	−0.37	0.25	0.38
Wattle width (WW)	0.19	−0.23	−0.07	−0.09
Neck length (NL)	0.26	−0.08	−0.10	0.19
Neck width (NW)	0.10	0.23	0.00	0.07
Chest length (ChL)	0.26	0.19	−0.31	−0.05
Body height (BH)	0.21	0.16	0.06	0.17
Leg length (LL)	0.29	0.11	−0.24	−0.09
Wing length (WiL)	0.31	−0.03	−0.04	−0.13
Tarsus length (TL)	0.28	0.25	−0.12	0.32
Tarsus diameter (TD)	−0.11	0.33	−0.11	−0.09
Central toe length (CTL)	0.13	0.17	0.35	0.36
Interleg distance(ID)	0.25	0.08	−0.04	−0.51
Eigenvalue	**4.49**	**2.75**	**1.87**	**1.54**
Explained variance (%)	**21.42**	**13.12**	**8.91**	**7.34**
Cumulative variance (%)	**21.42**	**34.54**	**43.46**	**50.8**

I, II, and III, respectively (Figure 1). A detailed examination of the photographic records heCLTd identify the distinctive features of the creole hens from the region, particularly the crested plumage and feathering on the face and tarsi, traits that, according to Osio-Orihuela *et al.* (2022), enabled hens to adapt to environmental conditions after periods of semi-wild existence. Likewise, Zaragoza Martínez (2012) noted that female owners in this region tend to favor hens exhibiting such traits, as they are considered aesthetic attributes of beauty and distinction.

Based on the photographic documentation, Group I included small-sized hens with few "Copetona" creole traits (GCH), Group II also comprised small hens, but with more pronounced "Copetona" features (GCC), while Group III consisted of medium-sized hens showing limited "Copetona" characteristics (GCM).

The presence of hens lacking native traits (Groups I and III) suggests a process of genetic erosion due to crossbreeding with commercial breeds, a phenomenon previously documented in Brazil, where populations exposed to exotic introgression exhibited lower

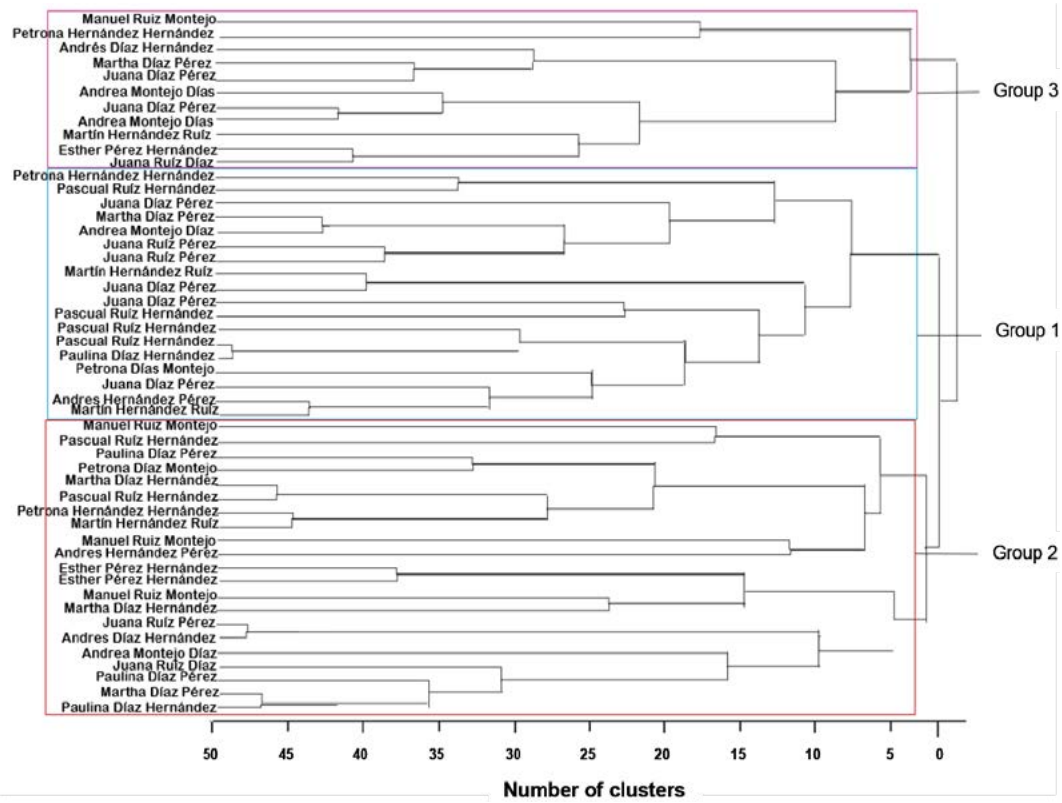

Figure 1. Morphometric grouping of Creole "Copetona" hens from the communities of San Andrés Larrainzar, Chiapas. Hierarchical clustering revealed three distinct morphometric groups (Group 1, Group 2, and Group 3). The X-axis represents the number of clusters according to Ward's method.

genetic diversity and fixation of non-adaptive alleles (Silva Júnior *et al.*, 2021). This finding also aligns with studies linking non-local genotypes to reduced physiological resilience (Machado *et al.*, 2020).

A clear distribution pattern among the three morphometric groups reflects the structural and genetic heterogeneity within the population. Group I included hens from all three studied communities, although the majority originated from Holahoj. The 18 hens in this group came from nine different production units. Despite their small size, characteristic of creole breeds, they lacked the crest and tarsal feathering typical of the "Copetona" phenotype.

Similarly, Group III, which comprised 11 hens from 10 production systems across the three communities, also lacked these native traits. As shown in Table 6, hens in this group exhibited significantly higher values for LBW, BL, EN, WGL, and NW. It is likely that, in both Groups I and III, the frequency of genes controlling native morphological traits has been substantially reduced, allowing commercial-breed alleles to become more prominent. Finally, Group II, the largest group with 21 hens from 15 production units, displayed the characteristic appearance of the "Copetona" creole hens, small-sized birds with crest, facial, and tarsal feathering (Osio-Orihuela *et al.*, 2022). As shown in Table 6, hens in Groups I and II had lower mean values for LBW, BL, EN, SL, and SW, differing significantly from those of Group III.

Table 6. Means and standard errors of the variables studied in the three groups of Creole hens from the communities of San Andrés Larrainzar, Chiapas.

Body measurements	Group I (GCH)	SE	Group II (GCC)	SE	Group III (GCM)	SE	P-value
LBW (kg)	1.49[b]	0.05	1.47[b]	0.05	1.73[a]	0.11	0.02
BL (cm)	41.97[b]	0.35	41.79[b]	0.25	43.82[a]	0.48	0
EN (cm)	44.36[b]	0.52	43.93[b]	0.53	47.44[a]	0.82	0
CL (cm)	4.40[a]	0.14	3.09[b]	0.13	3.55[b]	0.27	0
CW (cm)	2.04[a]	0.09	1.51[b]	0.1	1.52[b]	0.18	0
SL (cm)	7.67[a]	0.2	6.97[b]	0.13	8.14[a]	0.2	0
SW (cm)	3.12[a]	0.03	2.97[b]	0.04	3.14[a]	0.03	0
BkL (cm)	2.01[a]	0.04	2.20[b]	0.05	2.40[a]	0.07	0
ELL (cm)	1.96[a]	0.08	1.93[a]	0.1	2.02[a]	0.11	0.84
ELW (cm)	1.49[a]	0.08	1.37[a]	0.08	1.21[a]	0.07	0.1
WaL (cm)	2.69[a]	0.1	1.91[b]	0.11	2.28[b]	0.12	0
WW (cm)	1.89[a]	0.14	1.44[ab]	0.11	1.42[b]	0.16	0.02
NL (cm)	12.92[a]	0.24	12.07[a]	0.22	12.64[a]	0.28	0.03
NW (cm)	1.45[b]	0.04	1.55[ab]	0.1	1.85[a]	0.13	0.02
CLT (cm)	16.26[a]	0.5	17.16[a]	0.74	16.68[a]	1.22	0.67
BH (cm)	27.31[a]	0.58	26.98[a]	0.54	28.90[a]	0.67	0.1
LL (cm)	13.21[a]	0.25	13.40[a]	0.27	13.50[a]	0.51	0.82
WGL (cm)	20.22[ab]	0.25	18.76[b]	0.57	20.71[a]	0.67	0.03
TL (cm)	8.23[a]	0.22	8.36[a]	0.21	9.06[a]	0.44	0.12
TD (cm)	1.48[b]	0.04	1.66[a]	0.04	1.59[ab]	0.05	0.01
CTL (cm)	5.68[a]	0.08	5.50[b]	0.12	6.35[a]	0.06	0
ID (cm)	8.08[a]	0.14	8.12[a]	0.23	8.47[a]	0.32	0.51

Different letters in the same row indicate significant differences ($p \leq 0.05$) according to Tukey's multiplecomparison test (Montgomery, 2020). SE=Standard error of the mean; GCH=Small-sized hens with fewer creole traits; GCC=Small-sized hens with more creole traits; GCM=Medium-sized hens with scarce creole traits.

Similarly, it was observed that out of the 23 variables analyzed, 16 showed significant differences among groups, except for the following six variables: ELL, ELW, CLT, BH, LL, TL, and ID. However, although the remaining variables did exhibit significant differences, these were not sufficient to clearly distinguish distinct types of Creole hens. This finding aligns with that of Francesch *et al.* (2011), who, despite identifying several differences, also reported notable morphological similarities among the groups studied.

The distribution of the zoometric indices across the three groups is summarized in Table 7, which highlights a significant difference in the cranial index for Group II compared with Group III, although values were similar to those of Group I. Therefore, it can be inferred that all hens exhibited a slightly elongated head, a feature more pronounced in Group III. For the proportionality, wattle, comb, and earlobe indices, no significant differences ($p \leq 0.05$) were found, indicating that hens presented flattened wattles and earlobes, proportional combs, and a body shape higher than long. This contrasts with the findings of Méndez *et al.* (2011), who reported significant differences in wattle, comb, and earlobe indices, likely due to the different hen biotypes included in their study.

The difference observed in the cranial index may result from various crossbreeding practices carried out by producers using introduced breeds. However, such crossings did not appear to affect the other indices, possibly due to what Valdés Corrales *et al.* (2010) described: that the phenotypic traits of Creole hens' integuments are preserved even after crossing with other breeds, despite being controlled by recessive genes. This characteristic represents a form of adaptation to climatic conditions, as integumentary structures reflect the external expression of a genotype under specific environmental influences (Osio-Orihuela *et al.*, 2022).

In accordance with Valdés Corrales *et al.* (2010) and Zaragoza Martínez (2012), and based on the characteristics observed in hens from Groups I and III, it can be affirmed that these communities have already experienced a degree of introgression from exotic (commercial) breeds into the originally existing Creole hen population. This process reflects a gradual replacement of local poultry genotypes by other, more "specialized" ones that are nevertheless poorly adapted to the local environment.

Based on the results obtained in this study, it can be concluded that there is clear evidence of gene introgression from commercial breeds, largely resulting from government programs donating birds without considering the importance of genetic biodiversity or the benefits of conserving autochthonous or local breeds. These native genotypes possess traits that enable them to thrive under the specific backyard conditions of rural regions in Mexico.

As demonstrated by Machado *et al.* (2020) and Illescas-Cobos *et al.* (2022), the conservation of Creole hens requires policies that prioritize their adaptive and biodiversity value. Breeding programs should be developed based on local morphometric standards (*e.g.*, crest, tarsal feathering) and the avoidance of crossbreeding with commercial lines, which is essential to preserve these unique genetic resources.

Table 7. Mean and standard error of zoometric indices in the three groups of Creole hens from communities of San Andrés Larrainzar, Chiapas.

Index	Group I	SE	Group II	SE	Group III	SE	P
Cranial	41.18[ab]	1.08	42.87[a]	0.88	38.75[b]	0.85	0.03
Proportionality	65.10[a]	1.42	64.57[a]	1.25	66.01[a]	1.7	0.8
Wattle	70.93[a]	5.27	85.20[a]	9.92	65.04[a]	8.65	0.25
Comb	46.58[a]	1.93	51.26[a]	4.51	42.82[a]	4.84	0.36
Earlobe	77.13[a]	4.07	74.57[a]	6.26	62.12[a]	5.22	0.21

Letters within rows indicate significant differences ($p \leq 0.05$) according to Tukey's multiple mean comparison test (Montgomery, 2020). SE=Standard error of the mean.

CONCLUSIONS

This study determined that the population of "Copetona" Creole hens in San Andrés Larrainzar, Chiapas, exhibits significant phenotypic heterogeneity, particularly in traits associated with fleshy appendages (comb, wattle, and earlobe). These findings indicate an ongoing process of genetic erosion, attributable to the introgression of high-yield commercial breeds. The loss of racial uniformity was confirmed through the identification of three distinct morphological groups: small-sized hens lacking native traits (GCH), small hens retaining typical "Copetona" characteristics such as crest, facial, and tarsal feathering (GCC), and medium-sized hens showing evidence of exotic genetic influence (GCM).

The low correlation among morphometric variables (only 28.5% significant) reflects a disharmonic body model, likely resulting from the indiscriminate introduction of commercial birds through government programs and the absence of local selection criteria. Although the wattle, comb, and earlobe indices remained stable, possibly due to the recessive nature of their genes, the cranial index proved to be a sensitive marker of racial purity, exhibiting higher values in the GCC group.

These findings highlight the urgent need to implement conservation strategies that prioritize: 1) breeding programs based on local morphometric standards (*e.g.*, crest and tarsal feathering); 2) restriction of exotic breed introduction into backyard systems; and genetic and cultural documentation of these unique zoogenetic resources, thereby ensuring the preservation of their environmental adaptation, socioeconomic value, and 3) biocultural heritage for the indigenous communities of the region.

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