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Risk status of semi-arid Zimbabwean indigenous cattle populations under conservation programs

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Abstract: Indigenous cattle breeds play a crucial role in most agricultural systems, providing sustainable livelihoods, cultural value, and genetic diversity, well-suited to semi-arid environments. The study aimed to assess the population structure and risk status of three indigenous beef cattle breeds, Tuli, Mashona, and Nkone, focusing on effective population size (Ne), number of females (L), and additional risk factors. Pedigree records for 37,081 Tuli, 12,935 Mashona, and 9,489 Nkone cattle were analyzed using the online POPREP software. Pedigree completeness over six generations varied, with the lowest completeness observed in the Nkone (23.2%), and the highest in the Mashona (25.9%). Average generation intervals ranged between 6.4 and 11.0 years, with inbreeding rates per generation of 0.26% for Mashona, 0.32% for Tuli, and 0.18% for Nkone. Effective population sizes were estimated at 266 for Tuli, 182 for Mashona, and 135 for Nkone, classifying Mashona and Nkone populations as endangered and in need of conservation, while Tuli requires ongoing monitoring. Additional risk factors, including geographic concentration and cultural value, further confirm the endangered status of these breeds. These findings highlight the critical need to strengthen conservation efforts to preserve the genetic diversity of Zimbabwe's indigenous cattle populations.

Keywords: Anthropogenic factors; Pedigree completeness; Generation interval; Inbreeding; Effective population size

INTRODUCTION

Genetic diversity in indigenous cattle populations is essential for resilience, productivity, and adaptability, especially in the face of environmental changes and emerging diseases (Naskar et al., 2012; Nyamushamba et al., 2017; Woldeyohannes et al., 2024). These breeds often possess unique traits like drought tolerance and disease resistance, which are vital for sustaining productivity in harsh climates. However, indigenous cattle breeds face significant threats from genetic introgression, limited market incentives, and crossbreeding with exotic breeds, which can reduce genetic diversity and resilience over time (FAO, 2007; Nyamushamba et al., 2017).

Beyond enhancing resilience to environmental stressors, genetic diversity in indigenous cattle populations plays a crucial role in ensuring long-term food security and sustainable livestock production systems. As climate change continues to impact global agricultural systems, the ability of indigenous breeds to thrive in marginal environments becomes increasingly important. These breeds offer a reservoir of adaptive traits that could be vital in the development of more climate-resilient livestock systems (Tawonezvi et al., 2021). Moreover, preserving genetic diversity is integral to improving the overall sustainability of livestock farming, ensuring that farmers can adapt to changing environmental conditions and market demands without compromising the long-term viability of their herds (FAO, 2011). By safeguarding indigenous cattle breeds, nations in semi-arid and arid zones can enhance its agricultural biodiversity, reduce dependency on exotic breeds, and promote a more sustainable and equitable approach to food production in rural areas (Nyamushamba et al., 2017).

In Zimbabwe, approximately 90% of the national cattle herd comprises indigenous breeds, with the majority managed by smallholder farmers, who rely on these animals for livelihood and food security (Tavirimirwa et al., 2013). These breeds play a socio-economic role, particularly in rural areas, where they contribute to household income, social status, and cultural heritage (Tawonezvi et al., 2021). Conservation efforts by research institutes, agricultural colleges, and commercial organizations underscore the importance of safeguarding these populations, yet crossbreeding programs continue to threaten their genetic integrity (Francis and Sibanda, 2001; Nyamushamba et al., 2017).

Current conservation measures in Zimbabwe are aimed at preserving these genetic resources to maintain breed adaptability and potential for future breeding programs. This study seeks to assess the population structure, inbreeding levels, and risk status of the Tuli, Mashona, and Nkone cattle populations, contributing essential data to support conservation and breeding strategies for these valuable indigenous resources.

MATERIALS AND METHODS

The study assessed population structure and risk status in three indigenous Zimbabwean beef cattle breeds, Mashona, Tuli, and Nkone. No ethical clearance was sought since data used was from secondary sources however, consent for use was sought from data providers. The main data source used was pedigree data. The data, provided by the Zimbabwe Herd Book (ZHB) with the breeders' consent, comprised records of 59,477 animals born between 1970 and 2021. The pedigree data included sire, dam, birth date, and sex for each animal. This dataset was formatted to meet the requirements of the POPREP software, which analysed each population's pedigree completeness, generation intervals, inbreeding rates, and effective population sizes (Ne).

In addition, secondary data from previous livestock studies, national agricultural reports, and breed conservation records were utilized to enrich the analysis. These sources provided supplementary information on population trends, breed distribution, and conservation efforts over the past four decades. Reports from the Department of Livestock Production and Development, as well as data from the Zimbabwe Livestock Information and Traceability System, were reviewed to assess historical and regional trends for the Mashona, Tuli, and Nkone breeds. The data also included records of government-supported breeding programs, NGO conservation initiatives, and previous surveys conducted by breed societies. Information on herd sizes, breed-specific challenges, and conservation policies was cross-referenced with pedigree data to ensure consistency and accuracy. Table 1 presents the number of animals with available pedigree records and the year each breed society was established, which provides historical context for each breed and its documented population size.

Table 1. Breed Society Establishment and Available Pedigree Data

Breed	Establishment Year	Number of Animals with Pedigree Data
Mashona	1950	12,935
Tuli	1961	37,081
Nkone	1966	9,461

The study calculated the risk status of each population using a composite measure, based on the total number of females (L), effective population size (Ne), and six additional factors (D), that account for geographical concentration, demographic trends, cultural significance, parentage control, ex-situ conservation, and anthropogenic factors. The final risk status (X) was calculated as follows:

$$X = (L + Ne + 0.5D)/3 \qquad (1)$$

where:

X is the risk status, L is the total number of females, Ne is the effective population size,

D is the sum of six factors. A modified method by Verrier et al., (2015) for converting the number of females (L) into the score scale was used and the number of females for each population was converted into a point scale as illustrated in Table 2.

The effective population size, a crucial measure of genetic diversity, was calculated using Wright's formula to assess genetic viability:

$$N_e = 4N_M M_F / (N_M + N_F) \qquad (2)$$

where:

N_M is the number of breeding males,

N_F is the number of breeding females.

Effective population sizes were categorized according to thresholds set by Polak et al. (2021). Populations with an Ne below 50 were classified as critically endangered, those with $50 < Ne \leq 200$ as endangered and in need of conservation, and those with $200 < Ne \leq 1{,}000$ as endangered but requiring only monitoring. Table 3 summarizes the average generation interval, rate of inbreeding, and effective population size for each population.

Additional Factors (D)

The six additional factors (D) were included to provide a comprehensive risk assessment, capturing both genetic and socio-cultural aspects that impact breed viability. Geographic Concentration factor accounted for each population's distribution across Zimbabwe's 390,752 km² area, which encompasses diverse environmental conditions. Based on Alderson's (2010) methodology, if 75% or more of the population was found in a specific region, it scored 1. Populations with intermediate concentration (25% to 75%) scored 0.5, while those with <25% concentration scored 0. This measure helps gauge the breed's regional adaptation and isolation risks. Based on the population's five-year trend, a score of 1 was assigned for an upward trend, 0.5 for a stable trend, and 0 for a downward trend. The demographic trend reflects population sustainability over time, with declining trends indicating potential threats. Assessed through breeder surveys, cultural consideration evaluated the role of each breed in local cultural practices

Table 2. Scores for factor L

Score	0	1	2	3
Number of female Cattle	≤ 150	> 150 ≤ 1000	> 1000 ≤ 7500	> 7500 ≤ 25000

Table 3. Generation Interval, Inbreeding Rate, and Effective Population Size

Population	Avg. Generation Interval (Years)	Inbreeding Rate (%)	Effective Population Size (Ne)
Tuli	6.4	0.32	266
Mashona	11.0	0.26	182
Nkone	6.4	0.18	135

Data Analysis

The study employed quantitative methods to assess the population structure and risk status of indigenous Zimbabwean beef cattle breeds (Mashona, Tuli, and Nkone). Quantitative analysis of pedigree data, using POPREP software, focused on evaluating pedigree completeness, generation intervals, inbreeding rates, and effective population sizes (Ne). Effective population size was calculated using Wright's formula, and populations were categorized into risk levels based on thresholds by Polak et al. (2021). Descriptive statistics were used to summarize average generation intervals, inbreeding rates, and Ne values. A composite risk status (X) was derived by integrating the total number of females (L), Ne, and additional socio-cultural and demographic factors (D), with scores assigned following methodologies from Verrier et al. (2015) and Alderson (2010). Qualitative data from breeder surveys were analysed to assess cultural significance, geographic concentration, and population trends, triangulating insights from multiple data sources for a holistic understanding of breed risk status.

RESULTS AND DISCUSSION

The study analysed the population structure, inbreeding rates, and risk status of three indigenous Zimbabwean beef cattle populations, Tuli, Mashona, and Nkone. The findings reveal distinct genetic and demographic characteristics for each breed, summarized in Tables 4 and 5.

Pedigree Completeness

Pedigree completeness varied across the populations (Table 4), with the Tuli and Mashona cattle showing more complete pedigree records over six generations compared to Nkone cattle. The Tuli population achieved 70.8% pedigree completeness in the first generation, reducing to 27.0% by the sixth generation. Mashona cattle showed 62.8% completeness in the first generation, dropping to 25.9% at six generations, while the Nkone cattle had 49.8% completeness in the first generation, declining to 23.2% over six generations. The variation in pedigree completeness indicates the level of available historical data for each breed, impacting the precision of inbreeding rate and effective population size calculations.

Generation Interval, Inbreeding Rate, and Effective Population Size

The generation intervals and inbreeding rates calculated for each population, along with effective population sizes provide insights into genetic diversity. The Tuli and Nkone breeds had the shortest average generation interval of 6.4 years, while the Mashona had the longest at 11.0 years. The rate of inbreeding per generation was 0.32% for Tuli, 0.26% for Mashona, and 0.18% for Nkone. Effective population sizes were estimated at 266 for Tuli, 182 for Mashona, and 135 for Nkone. Based on these values, the Tuli population meets the threshold for a breed in need of monitoring, while Mashona and Nkone populations fall below the threshold and are classified as endangered, requiring conservation efforts.

Risk Status Evaluation

The risk status scores derived from the number of females, effective population size, and six additional factors (D) demonstrate the varying levels of risk across these populations. The risk

Table 4. Average pedigree completeness (%) for six generations for all animals in the pedigree of three indigenous Zimbabwean beef populations

Population	Gen 1	Gen 2	Gen 3	Gen 4	Gen 5	Gen 6
Tuli	70.80	56.10	45.20	37.70	31.70	27.00
Mashona	62.80	52.00	43.15	35.90	31.60	25.90
Nkone	49.80	45.30	41.20	38.50	28.70	23.20

scores for Mashona and Nkone populations, 1.7 and 1.6, respectively, classify them as endangered and in need of active conservation. The Tuli population, with a risk score of 2.1, is considered endangered but only requires monitoring at this stage. The summary of risk status evaluations is presented in Table 5, where each population's risk classification reflects a need for genetic resource conservation efforts to maintain diversity and mitigate further risk of genetic erosion.

The accuracy of the rate of inbreeding and relatedness depends on the extent of pedigree completeness (Groeneveld et al., 2009) and the computational method (Leroy et al., 2020). According to Boichard et al. (1997), pedigree completeness is the total proportion of known ancestors over all traced generations. Studies conducted to investigate the pedigree completeness of beef cattle have revealed variable degrees of pedigree completeness in different breeds. In South African cattle breeds, Tuli and Afrikaner had the best pedigree completeness of 68% and 56% at six generations, respectively (Abin et al., 2016). For Irish beef breeds, Simmentals and Sahiwal cattle had the lowest pedigree completeness compared to other study cattle, with only 43% and 46% at four generations deep (Mc Parland et al., 2007; Kamiti et al., 2016; Jarnecka et al., 2021). Based on the results of the current study's pedigree completeness, it is noted that the quality of pedigree information for the Zimbabwean indigenous cattle populations under study has negatively changed over the last 30 years in all three populations. However, efforts can be made to improve the animal recording system, which in turn would enhance pedigree quality. All three breed societies in this study are affiliated with the Breed Plan, which, in the future, is expected to improve performance records for Zimbabwean indigenous cattle (ZiMunda Farming, 2022).

The estimated generation intervals in this study are within the ranges reported by studies conducted on indigenous beef cattle breeds in South Africa (Pienaar et al., 2015; Abin et al., 2016). According to Kamiti et al. (2016), the overall weighted generation intervals for the Tuli and Nkone populations (6 years) are consistent with the reported generation intervals of other indigenous cattle populations in the literature (Pienaar et al., 2015). Similar results were reported for South African Tuli (6.2 years), Boran (6.3 years), Drakensberger (6.0 years), Nguni (6.0 years), and Afrikaner (6.4 years) cattle breeds, which are kept both in situ and ex situ (Abin et al., 2016). The estimates of generation intervals for Zimbabwean Tuli and Nkone populations are slightly longer compared to the reported generation intervals of 5.6 and 5.2 years for the Bonsmara, a local composite breed in South Africa (Groeneveld et al., 2009). Generation interval remains an important factor to consider in response to selection and efforts to shorten the generation interval to below six years in all three breeds would have added benefits for genetic improvement. The generation intervals for the Tuli and Nkone populations can be considered intermediate (Pienaar et al., 2015),

Table 5. Estimation of the risk status of the Zimbabwean Indigenous cattle populations based on L, $N_{e,}$ and D factors, converted into scores

Population	No. of Females (L)	Score (L)	N_e	Score (Ne)	D1	D2	D3	D4	D5	D6	Score D Total	Risk Status Score	Estimated Risk Status
Mashona	3845	2	182	1.0	1.0	0.5	0	1.0	0.5	1.0	4.0	1.7	EC
Tuli	12636	2	266	2.0	1.0	1.0	0	1.0	0.5	1.0	4.5	2.1	EM
Nkone	3640	2	135	1.0	1.0	0.5	0	1.0	0.0	1.0	3.5	1.6	EC

Notes: Ne: size of the population, D1: geographical concentration, D2: last five years' demographic trend, D3 population's cultural significance: D4: parentage control, D5: ex-situ conservation, D6: anthropogenic factors, EC: endangered, requiring conservation and EM: endangered, requiring monitoring.

although they may still compromise the rate of genetic change. The generation interval for the Mashona population was high compared to the other two cattle populations in this study. Longer generation intervals (>8 years) have been reported in Gir, Nelore, and Guzerat indigenous cattle breeds in Brazil (Faria et al., 2009; Reis Fihlo et al., 2010; Gwatirisa et al., 2022). The relatively long generation interval reported could be due to the time taken in progeny testing bulls and the longevity of animals in the Mashona population, where cows can be retained for up to 16 years of age.

Effective population size measures genetic variation within livestock populations and is a useful metric due to its direct relationship with the rate of inbreeding and loss of genetic diversity over time (Groeneveld et al., 2009; Leroy et al., 2020). A reduction in effective population size may increase selection response through selection intensity but conversely may lead to inbreeding depression and loss of genetic variance, which limits selection response from new mutations in the long term (Toro & Lopez-Fanjul, 1998; Mirzaee Ilaly et al., 2019). An effective population size between 50 and 100 increases the inbreeding coefficient rate by 0.5% to 1% per generation, which is sufficient to maintain genetic diversity within a population (Bijima, 2020; AU-IBAR, 2019). A drop in the effective population size below this limit would result in a decline in population fitness (Leroy et al., 2020).

The effective population size for all three populations in the present study varied in magnitude. The lowest value, 135, was found in the Nkone populations, which is above the minimum effective population size defined by FAO (1998b) and Bijima (2020). The effective population sizes of the three populations were all well above the minimum level for concerns of loss of diversity (Jarnecka et al., 2021). The range of $50<N_e\leq200$ for Mashona and Nkone populations indicates that the population is endangered and in need of conservation, while the Tuli's effective population size of $200<N_e\leq1000$ shows that the population is endangered and in need of monitoring. The estimated effective population sizes of the populations in this study are comparable to South African beef cattle populations: 89 for Tuli, 107 for Afrikaner, 121 for Drakensberger, 191 for Nguni, and 364 for the Boran breed (Abin et al., 2016). From these results, it can be concluded that genetic variability is sufficiently preserved in the three cattle populations under study. The estimated average rate of inbreeding per generation for all three populations (Table 3) is less than 1%, within the acceptable limit recommended by FAO (1998b) and Bijima (2020), which is 0.5–1.0% per generation to maintain fitness in a breed. Our results are in agreement with studies on two local Brazilian cattle breeds (Reis Filho et al., 2010) and five local South African breeds (Abin et al., 2016).

Most indigenous livestock breeds (such as Mashona, Tuli, and Nguni cattle, Sabi sheep, and Mashona goats), are at risk of disappearing due to introgression, dilution, and replacement by exotic genotypes (Gororo, 2018). In Zimbabwe, the current initiative for the conservation of genetic resources includes 58 populations, which is low compared to 156 in South Africa (FAO, 2011; AU-IBAR, 2019), 176 in France (Verrier, 2015), 161 in Spain, and 277 in Italy (Polak et al., 2021). Techniques used by other authors to estimate the risk status of livestock, such as assessing the degree of endangerment of populations by demographic and genetic aspects, or the time needed to reach a critical population size (Gandini et al., 2004), and by primary indicators (numerical, geographical, concentration in a country, genetic, and introgression; Alderson, 2010), are inadequate for Zimbabwe. This is because these risk categories are not specific to the country's geographic conditions. Additionally, the selection of additional factors in the current study differs from these models, as most native breeds are concentrated in historic regions of their origin. In Zimbabwe, indigenous breeds are widely dispersed throughout the nation (Tavirimirwa et al., 2013; Gororo et al., 2018), reflecting both the implementation of current conservation programs and past measures undertaken to save indigenous breeds from extinction.

CONCLUSIONS

The low inbreeding rates indicate that the three cattle populations are not currently at significant risk of losing genetic diversity. However, the final risk status estimation score revealed that the Mashona and Nkone cattle populations are endangered and in need of conservation, while the Tuli cattle population is endangered and requires monitoring. Although these populations are not immediately threatened with extinction, their future potential to contribute to agriculture and rural development remains uncertain. Continuous monitoring of these populations is crucial, as genetic erosion can reduce fitness, thereby increasing the risk of extinction.

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Data Availability

Data is available upon reasonable request from the first author.

Conflict of Interest

The authors declare that there are no conflicts of interests.

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