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AI-supported statistical analysis of livestock biodiversity trends in Türkiye using ecological diversity indices (1991-2024)

Türkiye'de hayvancılık biyoçeşitliliği eğilimlerinin ekolojik çeşitlilik indeksleri kullanılarak yapay zekâ destekli istatistiksel analizi (1991-2024)

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ABSTRACT

Objective: This study investigates long-term trends (1991–2024) in the population dynamics of 13 major livestock species in Türkiye by examining changes in species abundance, breed composition and biodiversity structure, with emphasis on the impacts of intensive breeding practices on local genetic resources.

Materials and Methods: Annual livestock statistics from the Turkish Statistical Institute (TUIK) were used to analyse species and breed trends. Biodiversity was assessed using ecological indices including Shannon, Simpson, Pielou's Evenness, Berger–Parker and Margalef. Multivariate analyses (PCA and hierarchical clustering) and visualizations (heat maps, radar charts and dendrograms) were conducted in Python 3.11. Data were normalized to ensure comparability among species.

Results: Commercial cattle and broiler chicken populations increased markedly, whereas native sheep and goat breeds declined. Biodiversity indices showed reductions in species richness and evenness after 2000. Bray–Curtis analyses revealed significant differences in species composition across five-year periods (F = 8.06, p<0.001).

Conclusion: The decline of local breeds threatens genetic sustainability and highlights the need for balanced livestock policies.

Keywords: Artificial intelligence, Biodiversity indices, Pielou's evenness index, Shannon diversity index, Simpson diversity index

ÖZ

Amaç: Bu çalışma, Türkiye'deki 13 önemli çiftlik hayvanı türünün popülasyon dinamiklerindeki uzun dönemli eğilimleri (1991–2024) inceleyerek tür bolluğu, ırk kompozisyonu ve biyoçeşitlilik yapısındaki değişimleri değerlendirmektedir. Çalışmada özellikle yoğun yetiştirme uygulamalarının yerel genetik kaynaklar üzerindeki etkilerine odaklanılmıştır.

Materyal ve Yöntem: Tür ve ırk eğilimlerini analiz etmek amacıyla Türkiye İstatistik Kurumu'nun (TÜİK) yıllık hayvan varlığı istatistikleri kullanılmıştır. Biyoçeşitlilik; Shannon, Simpson, Pielou'nun eşitlik indeksi, Berger–Parker ve Margalef gibi ekolojik indeksler kullanılarak değerlendirilmiştir. Çok değişkenli analizler (PCA ve hiyerarşik kümeleme) ile görselleştirmeler (ısı haritaları, radar grafikleri ve dendrogramlar) Python 3.11 ortamında gerçekleştirilmiştir. Türler arasında karşılaştırılabilirliği sağlamak amacıyla veriler normalize edilmiştir.

Bulgular: Ticari sığır ve broyler tavuk popülasyonlarında belirgin artış gözlenirken, yerli koyun ve keçi ırklarında azalma tespit edilmiştir. Biyoçeşitlilik indeksleri özellikle 2000 yılı sonrasında tür zenginliği ve eşitliğinde azalma olduğunu göstermiştir. Bray–Curtis analizleri, beş yıllık dönemler arasında tür kompozisyonunda istatistiksel olarak anlamlı farklılıklar bulunduğunu ortaya koymuştur (F = 8.06, p<0.001).

Sonuç: Yerel ırkların azalması genetik sürdürülebilirliği tehdit etmekte olup verimlilik ile genetik kaynakların korunmasını dengeleyen hayvancılık politikalarına ihtiyaç olduğunu göstermektedir.

Anahtar sözcükler: Yapay zeka, Biyoçeşitlilik indeksleri, Pielou'nun eşitlik indeksi, Shannon çeşitlilik indeksi, Simpson çeşitlilik indeksi

INTRODUCTION

Biodiversity plays a key role in the stability, resilience and productivity of livestock systems. In such systems, species diversity enhances ecological balance and acts as a buffer against environmental changes and disease. Understanding long term trends in livestock diversity is vital for sustainable management, conservation and evidence based policy.

To evaluate biodiversity change over time, various indices are used, each reflecting a different ecological dimension. Classical indices like Shannon-Wiener capture both richness and evenness (Shannon, 1948), while the Simpson index measures dominance (Simpson, 1949). The Berger-Parker index highlights the most dominant species (Berger & Parker, 1970), and Hill numbers offer a unified, parametric diversity framework (Chao et al., 2014). Richness focused metrics, such as Margalef (1958) and Menhinick's (1964) indices, adjust richness by sample size. Pielou's evenness index (1966) addresses distribution equity. To assess temporal or spatial shifts, Bray-Curtis dissimilarity quantifies species turnover. Using these collectively, allows for a comprehensive biodiversity assessment critical to livestock policy.

Assessments often include breed specific indices reflecting genetic and phenotypic traits. Metrics like allelic richness and heterozygosity capture intra breed diversity and adaptability (Foulley & Ollivier, 2006). Effective breed number reveals conservation status and distinctiveness (Peter et al., 2007). Combining such indices enhances understanding of livestock genetic diversity.

Biodiversity indices capture different but complementary dimensions of biological structure. Indices such as Shannon and Simpson integrate both species richness and relative abundance, providing a general measure of diversity. Pielou's evenness index focuses specifically on how uniformly individuals are distributed among species, while dominance oriented metrics such as the Berger–Parker index highlight the extent to which one or a few species prevail. Richness based indices, including Margalef and Menhinick, emphasize the number of species while accounting for sample size. Hill numbers and Rényi diversity profiles offer a unified framework that translates these metrics into effective numbers of species and allows comparison across different sensitivity levels to rare or dominant taxa. When combined, these indices enable a multidimensional assessment of biodiversity, revealing structural changes that cannot be detected using a single metric alone.

In Türkiye, many studies rely on TURKSTAT data (Koşum et al., 2019). This study was analyzed 1991-2024 trends in 13 livestock and poultry species (TUIK, 2024) using Shannon diversity, Simpson diversity, Pielou's evenness, Berger-Parker dominance, Margalef richness, Hill numbers and Rényi diversity indices. In addition to the annual data, Principal Component Analysis (PCA), Non-metric Multidimensional Scaling (NMDS) and Correspondence Analysis (CA) were applied to visualise racial changes and identify clusters. Structural changes over time were revealed using Bray-Curtis matrices and hierarchical clustering. This study aims to provide integrated insights into livestock diversity trends in Türkiye by combining ecological indices and AI-based analytical frameworks.

MATERIALS and METHODS

Data

The livestock data used in this study were obtained from official records of the Turkish Statistical Institute (TUIK, 2024). Changes in livestock structure in Türkiye from 1991 to 2024 were analysed using census records covering 13 livestock species and 9 major breed categories. The species included cattle, sheep, goats, buffalo, horses, donkeys, mules, chickens, turkeys, ducks, geese, bees and silkworms. The nine major breed categories consisted of Native cattle, Crossbred cattle, Cultured cattle, Native sheep, Crossbred sheep, Native goats, Crossbred goats, Commercial broiler chickens and Commercial layer chickens. The dataset was compiled from national agricultural databases, ensuring broad coverage of both small and large scale livestock production systems across the country.

Artificial intelligence (AI) supported analysis

Artificial intelligence (AI) supported analytical framework Artificial intelligence was used solely as a computational support tool rather than as an autonomous decision making system. ChatGPT-4o Turbo assisted in code structuring, debugging and workflow optimisation within Python (v3.11). All statistical method selections and analytical interpretations were determined by the authors according to established statistical principles and dataset characteristics.

The choice of statistical tests followed a predefined evaluation framework. Distributional assumptions were assessed prior to inferential testing. Because biodiversity indices did not satisfy normality assumptions across the 1991–2024 time series, nonparametric procedures (Kruskal–Wallis and Wilcoxon tests) were selected in accordance with ecological statistical standards (Zeng et al., 2022). Multivariate analyses (PCA and Ward's hierarchical clustering) were applied based on their suitability for compositional ecological datasets (Bray & Curtis, 1957; Jolliffe, 2002).

AI outputs were critically compared against classical statistical criteria including distribution diagnostics, variance structure, interpretability and ecological relevance. Therefore, the analytical approach is described as "AI-supported," indicating computational assistance under full researcher supervision rather than automated model-driven inference.

To improve detection of temporal patterns, diversity and clustering, AI assisted scripting was applied. All analyses were run in Python (v3.11) on Windows 11 using open source libraries common in ecological and biodiversity research.

Numerical preprocessing steps including log (1+x) transformation to reduce right skewed distributions (Osborne, 2010), Min–Max scaling for cross species comparability (Kuhn & Johnson, 2019) and the conversion of raw census counts into proportional representations required for diversity metrics (Chao et al., 2014) were performed using NumPy (Harris et al., 2020) and Pandas (McKinney, 2010). Static and dynamic visualizations were produced with Matplotlib and Seaborn (Hunter, 2007; Waskom, 2021). Multivariate methods, including PCA, K-means and Ward's hierarchical clustering were implemented via Scikit-learn (Pedregosa et al., 2011). These visualization and multivariate procedures were used to reveal structural patterns that are not directly observable from raw census counts. Time series line plots highlighted long term trajectories in species abundance, while heatmaps enabled comparison of normalized population structures across years. Radar charts captured proportional growth differences among species and dendrograms illustrated hierarchical similarity clusters. Ward's hierarchical clustering, combined with Bray–Curtis dissimilarity was employed to classify years based on overall livestock composition and to visualize temporal continuity or structural shifts over the 34 year period. Together, these approaches provided a coherent analytical framework for identifying transitions and grouping periods with similar ecological characteristics. These procedures ensured comparability among species with highly unequal population sizes (e.g., chickens, camels, pigs) and provided normalized inputs suitable for multivariate and AI-supported modeling.

Biodiversity indices (e.g., Shannon, Simpson, Pielou, Berger-Parker, Hill numbers) and dissimilarity metrics (e.g., Bray-Curtis) were computed using Scikit-bio and SciPy libraries (Virtanen et al., 2020; Scikit-bio development team, 2023).

Analyses of indices

To quantify biodiversity and population dynamics, multiple complementary diversity indices were calculated, including the Shannon Index (Shannon, 1948), Simpson Index (Simpson, 1949), Pielou's Evenness (Pielou, 1966), Berger-Parker Dominance (Berger & Parker, 1970), Margalef Index (Margalef, 1958) and Hill Numbers (Hill, 1973; Chao et al., 2014). These indices collectively capture species richness, evenness, dominance and effective species numbers, providing a multifaceted view of genetic and phenotypic diversity over time. The mathematical definitions of the indices are as follows:

Shannon diversity index (H')

Measures both species richness and evenness:

$$H' = -\sum_{i=1}^{S} p_i \ln(p_i)$$

Where p_i is the proportion of the ith breed in the population and S is the total number of breeds. Higher values indicate greater diversity and evenness (Shannon, 1948).

Simpson diversity index (D)

Represents the probability that two randomly selected individuals belong to the same breed:

$$D = \sum_{i=1}^{S} p_i^2$$

Where p_i denotes the proportional abundance of the ith breed, computed as the number of individuals in that breed (n_i) divided by the total number of individuals across all breeds (N). Thus, $p_i = n_i / N$. Diversity is often expressed as 1 − D to represent the probability that two randomly selected individuals belong to different breeds (Simpson, 1949).

Pielou’s evenness index (J')

Standardizes Shannon index to a value between 0 and 1 to measure evenness:

$$J' = \frac{H'}{\ln(S)}$$

Where *S* is the number of breeds. Values close to 1 indicate an even distribution among breeds (Pielou, 1966).

Berger-Parker dominance index (d)

Reflects the dominance of the most abundant breed:

$$d = \frac{N_{\max}}{N}$$

N_{max} is the number of individuals in the most abundant breed and N is the total number of individuals. Higher values suggest lower diversity (Berger & Parker, 1970).

Margalef richness index (D_M)

Estimates species richness accounting for sample size:

$$D_M = \frac{S-1}{\ln(N)}$$

Where *S* is the number of breeds and *N* the total number of individuals (Margalef, 1958).

Hill numbers (Effective number of species)

Hill numbers translate diversity indices into “effective” species counts: (Hill, 1973; Chao et al., 2014).

For *q=1 (*exponential of Shannon index):

$${}^{1}D = \exp(H')$$

For q=*2* (reciprocal of Simpson index):

$${}^{2}D = \frac{1}{D}$$

Rényi diversity index

The Rényi diversity index is a generalized diversity measure that depends on a parameter α (order of diversity) and is defined as:

$$H_\alpha = \frac{1}{1-\alpha}\log\left(\sum_{i=1}^{S} p_i^{\alpha}\right)$$

Where:

S = total number of breeds
p_i = proportion of the ith breed in the population
α = order parameter (α ≥ 0, α ≠ 1)

The Rényi diversity index is a family of diversity measures parameterised by the order α, which determines the sensitivity of the index to rare versus dominant species and is selected a priori rather than estimated from the data. In this study, Rényi diversity was assessed using diversity profiles across a range of α values, from species richness (α = 0) to dominance driven structure (α → ∞), to capture structural differences among communities. As α → 1, the Rényi index converges to the Shannon index, while increasing α values progressively emphasise dominant species, thereby highlighting different aspects of biodiversity structure (Rényi, 1961).

Multivariate analyses were performed to reveal structural variation and breed groupings. PCA reduced dimensionality and identified the main variation axes (Jolliffe, 2002), while Hierarchical Clustering using Ward's method and Bray-Curtis dissimilarity classified breeds by temporal similarity (Bray & Curtis, 1957; Ward, 1963).

Visualization methods, including heatmaps, radar charts and time series plots, were used to present dynamic trends and interrelations. Analyses were run in Python with AI assisted scripting to improve pattern detection and clustering.

Limitations in data consistency and sampling over time were addressed by using multiple indices and robust normalization. Combining metrics reduces bias from any single index, allowing for more reliable biodiversity interpretation.

Statistical analyses

Analyses were conducted in Python (v3.11) using AI assisted scripting to enhance accuracy and reproducibility (Brodeur et al., 2025). Biodiversity indices (Shannon, Simpson, Berger-Parker, Pielou, Hill numbers) were computed via Scikit-bio and SciPy (Virtanen et al., 2020).

Nonparametric statistical tests were selected because diversity indices did not follow a normal distribution across the 1991–2024 time series. Temporal differences in Shannon, Simpson, Pielou and Hill numbers were evaluated using the Kruskal–Wallis test to determine whether overall diversity varied significantly among years. When group level differences were detected, Wilcoxon signed rank tests were used to assess pairwise year to year shifts in diversity, following established procedures for long term ecological datasets with unequal variance and non-Gaussian structure (Zeng et al., 2022). Correlation analyses (Spearman & Pearson) were performed to examine relationships among diversity metrics (Benesty et al., 2009).

Bray–Curtis dissimilarity was calculated to quantify compositional differences across years (Bray & Curtis, 1957). Multivariate analyses, including PCA and Ward's hierarchical clustering were incorporated through Scikit learn to visualize structural patterns in species composition and to identify periods exhibiting similar diversity profiles (Pedregosa et al., 2011). Although PCA results were not presented separately, the method supported exploratory assessment of dominant variation axes within the dataset.

RESULTS

To examine temporal dynamics in species composition, a set of standard diversity indices was calculated annually (1991-2024). The results indicated that overall diversity patterns, reflected by Shannon and Simpson indices, evenness (Pielou), richness (Margalef), dominance (Berger–Parker) and effective diversity based on Hill numbers ($q = 1$, $q = 2$), displayed pronounced annual trends and structural shifts over the study period (Figure 1).

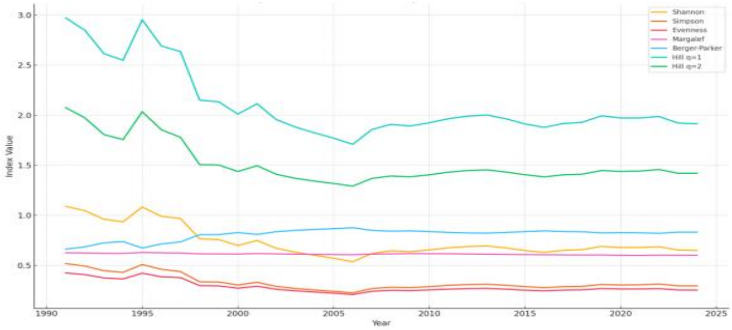

Figure 1. Diversity indices over time.

Şekil 1. *Zaman içinde çeşitlilik indeksleri.*

Trends in the diversity indices showed distinct temporal patterns rather than a uniform increase or decrease. Shannon and Simpson indices displayed gradual rises during the late 1990s and early 2000s followed by periods of stabilization indicating moderate increases in overall diversity rather than continuous richness expansion. Hill numbers at $q = 2$ showed moderate increases during the late 1990s and early 2000s indicating periods in which dominance by a limited number of species temporarily strengthened followed by more stable patterns in the subsequent decade. Pielou's evenness index showed noticeable dips during the mid 2000s and early 2010s, corresponding to years in which the proportional distribution of species became more uneven. Peaks observed in the Berger–Parker index aligned with these reductions in evenness and increases in dominance, confirming that certain years were characterized by heavier reliance on one or a few species. These shifts collectively suggest that diversity structure changed across decades, although the underlying mechanisms (e.g., production priorities, breed utilization patterns, or national policy changes) require further investigation beyond the scope of this dataset.

Hierarchical clustering based on Bray–Curtis dissimilarity and Ward's linkage was applied to annual livestock composition data across all species simultaneously, grouping years according to overall species structure and revealing clear temporal patterns, which were visualised as a dendrogram (Figure 2).

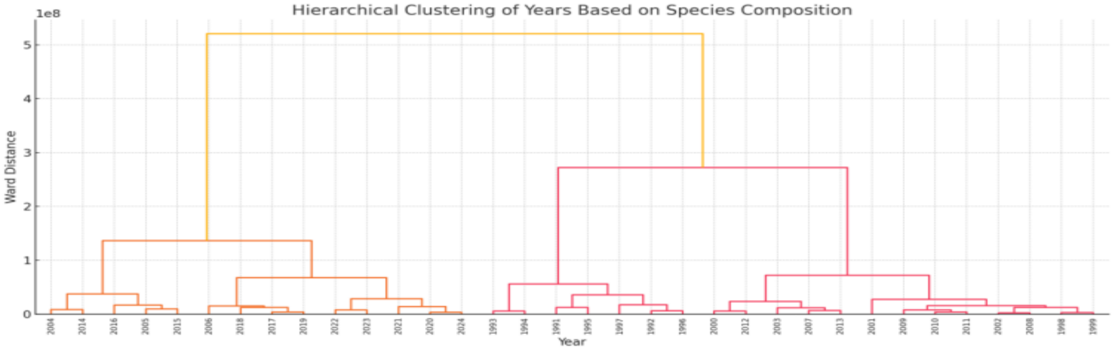

Figure 2. Hierarchical clustering (Ward's method) of years by species composition.

Şekil 2. *Tür kompozisyonuna dayalı yılların hiyerarşik kümelenmesi (Ward metodu).*

A dendrogram was generated using Ward’s hierarchical clustering and Bray–Curtis dissimilarity to identify groups of years with similar species composition. The resulting structure revealed two broad temporal clusters: an earlier group (approximately 1991–2005) characterized by greater variability and periodic dominance of specific species and a later group (2006–2024) in which species proportions became more stable and diversity patterns more consistent. These decade aligned groupings suggest long term continuity in management or breeding tendencies, whereas branch divergences likely correspond to historical disruptions in livestock composition. Such divergences may reflect changes in subsidy policies, shifts in breed utilization or improvement programs, or external shocks including disease events that altered species proportions. Through this dendrogram, a chronological perspective on stability and transition within Türkiye’s livestock sector is provided, offering an analytical foundation for interpreting broader policy, management and production trends across the study period.

To quantify compositional differences between years the Bray-Curtis dissimilarity index was calculated using annual species abundance data. Since both presence and abundance were taken into account this index was deemed appropriate for detecting subtle structural shifts. The resulting dissimilarity matrix was visualized through a heatmap by which continuity and disruption patterns were highlighted (Figure 3).

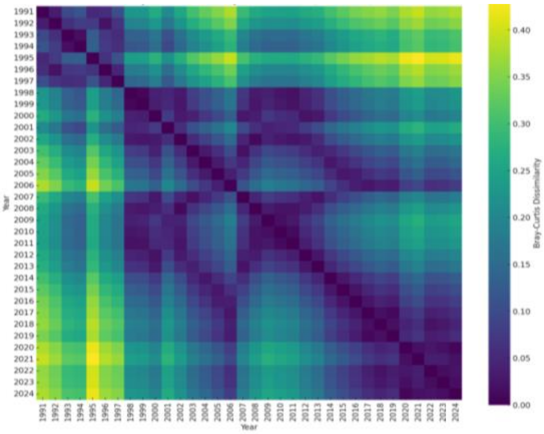

Figure 3. Bray-Curtis dissimilarity between years (1991-2024).

Şekil 3. *Yıllar arası Bray-Curtis farklılığı (1991-2024).*

The Bray-Curtis heatmap was used to reveal periods of high and low similarity. Darker cells denote temporally stable community structures, whereas lighter cells represent compositional divergence, suggesting periods of ecological restructuring. Notably, clusters of low dissimilarity were detected within individual decades, whereas comparisons across decades were found to exhibit greater variation likely influenced by changes in policy or management practices.

To characterize how diversity patterns differed across sensitivity levels, Rényi profiles were computed for each year from 1991 to 2024. Unlike fixed order indices, Rényi diversity evaluates each annual species composition across a continuum of q values, ranging from species richness ($q = 0$) to dominance weighted diversity ($q \geq 2$). This approach provides a multidimensional view of each year’s diversity structure, capturing the relative contributions of rare and dominant species without implying temporal trends (Figure 4).

Structural shifts in species composition across decades were illustrated by the Rényi curves. Flat curves were interpreted as indicative of balanced and stable communities, whereas steep declines were associated with dominance by a few species likely influenced by breeding strategies, economic pressures or species specific productivity trends. Rényi profiles revealed a temporal shift from relatively balanced livestock communities in the 1990s to increasingly specialized systems dominated by a few high yield breeds in the 2010s and beyond.

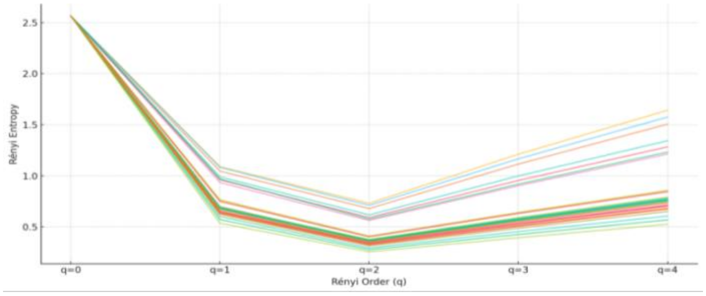

Figure 4. Rényi diversity profiles (1991-2024).

Şekil 4. *Renyi çeşitlilik profilleri (1991-2024).*

To evaluate temporal stability at the species level, the coefficient of variation (CV) was calculated using annual abundance data from 1991 to 2023. The CV, defined as the standard deviation divided by the mean, was used to express population fluctuation. Higher CV values were interpreted as indicators of greater variability, while lower values suggested population stability. CV values for all 13 species were presented in Figure 5.

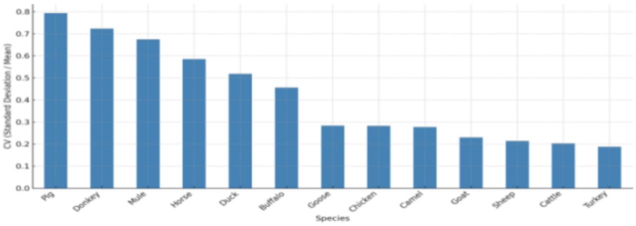

Figure 5. Coefficient of variation (CV) by species (1991-2024).

Şekil 5. *Türlere göre değişim katsayısı (CV) (1991-2024).*

Differences in species stability were revealed through CV analysis. Although fluctuations were observed for all species over time, CV values ranged moderately (0.12-0.79), indicating that no extreme instability was detected. It was inferred that the overall livestock structure remained within acceptable operational limits. Species such as duck, pig and mule were found to have higher CV values, suggesting more volatile population patterns that may be influenced by policy changes, disease outbreaks or market fluctuations. In contrast, cattle, chicken and sheep exhibited lower CV values, indicating more stable year to year population dynamics. These differences reflect how species with differing production roles and economic importance experience distinct levels of demographic variability within the livestock sector.

To improve resolution, Bray-Curtis beta dispersion was recalculated in 5-year intervals rather than by decade. This recalculation revealed short term variations in species composition. The average distance to centroid for each period was visualized using boxplots (Figure 6), by which internal community homogeneity or instability was indicated.

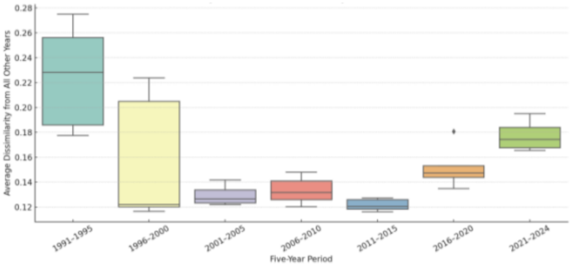

Figure 6. Bray-Curtis centroid distance by 5-year period.

Şekil 6. *5 yıllık döneme göre Bray-Curtis ağırlık merkezi uzaklığı.*

Five-year analysis showed significant variation in community dispersion (F = 8.06, p<0.001). Periods like 1991-1995 and 2006-2010 had low dispersion, reflecting stable structures. In contrast, 1996-2000 and 2021-2024 showed greater centroid distances, suggesting rising variability likely due to breeding changes, economic shifts or external shocks. The observed stepwise patterns suggest that compositional stability may follow cyclical or policy driven trends, warranting further study.

In the heatmap, a two step normalization was applied. First, log (1 + x) transformation reduced the effect of large values and skewed distributions (e.g., chickens versus camels), allowing less dominant species to remain visible. Then, Min-Max scaling adjusted all values to the [0, 1] range, enabling fair comparison across species. Min-Max scaling was chosen over Z-score to retain interspecies proportional differences, particularly in datasets with skewed livestock distributions (Figure 7).

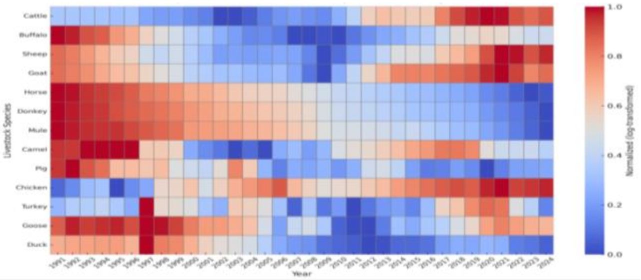

Figure 7. Heatmap of normalized livestock species numbers by year.

Şekil 7. *Yıla göre normalize edilmiş evcil hayvancılık türlerinin sayılarının ısı haritası.*

Consistent patterns of species dominance and rarity became evident in the normalized heatmap (Figure 7). Poultry driven primarily by chickens displayed persistently high relative abundance across nearly the entire 1991–2024 period, reflecting their long standing predominance within the livestock sector. In contrast, camels, pigs and mules remained at consistently low representation throughout all years, highlighting their marginal demographic contribution. Small ruminants such as sheep and goats showed moderate but stable abundance levels with limited year to year variation, whereas donkeys and horses demonstrated a gradual decline over the study period. These normalized patterns likely reflect broad structural dynamics in Türkiye's livestock sector, potentially shaped by shifts in production priorities, market demand and policy environments; however, the specific drivers of these trajectories require targeted investigation beyond the scope of the present dataset.

In the subsequent heatmap, normalized yearly breed composition for cattle, sheep, goats and chickens from 1991 to 2024 was presented. Each cell was used to represent a breed's proportion within its respective species for a given year. Visualization was conducted using a color vision deficiency (CVD) friendly magma scale (Figure 8).

Breed trends by species:

Cattle: Native breeds exhibited a marked decline beginning in the early 1990s, while crossbred and improved cattle increased substantially during the 1990–2000 period and then stabilized after the early 2000s (Figure 8). This pattern reflects a transition toward genetically improved cattle types, although no major proportional changes are evident in the last two decades. Sheep: The breed structure remained highly stable throughout the study period. Native sheep consistently dominated the population and Merino showed a slight but steady increase yet without altering the overall composition in a substantial way. Goat: Hair goats maintained dominant representation across all years, whereas Angora goats remained persistently low. The minimal year to year variation in both groups indicates a relatively static structural pattern within the goat sector. Chicken: After 2005, broilers displayed a clearer upward trajectory compared to layers, gradually shifting the poultry composition toward meat oriented production by the late 2010s. However, this shift occurred progressively rather than abruptly as shown in Figure 8.

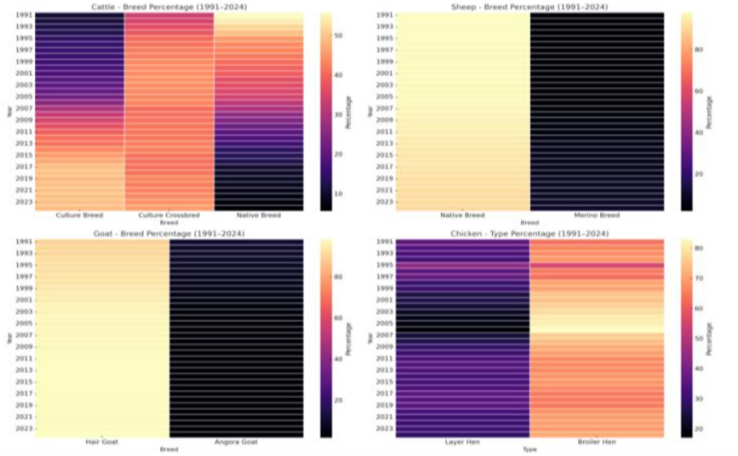

Figure 8. Breed percentages by year (1991-2023) *Color scale optimized for users with CVD.

Şekil 8. *Yıllara göre (1991-2023) ırk oranları * CVD'li kullanıcılar için optimize edilmiş renk skalası.*

To evaluate distributional balance among cattle breed groups, evenness metrics were examined at five year intervals from 1991 to 2024. Pielou’s Evenness Index together with complementary diversity measures presented in Figure 9 was used to assess how uniformly the cattle population was partitioned among Cultured, Crossbred and Native breeds. These indices allowed the identification of periods in which breed composition became more or less evenly structured. The figure has been redesigned with enlarged labels, enhanced contrast and a simplified legend to ensure clear readability and accurate interpretation.

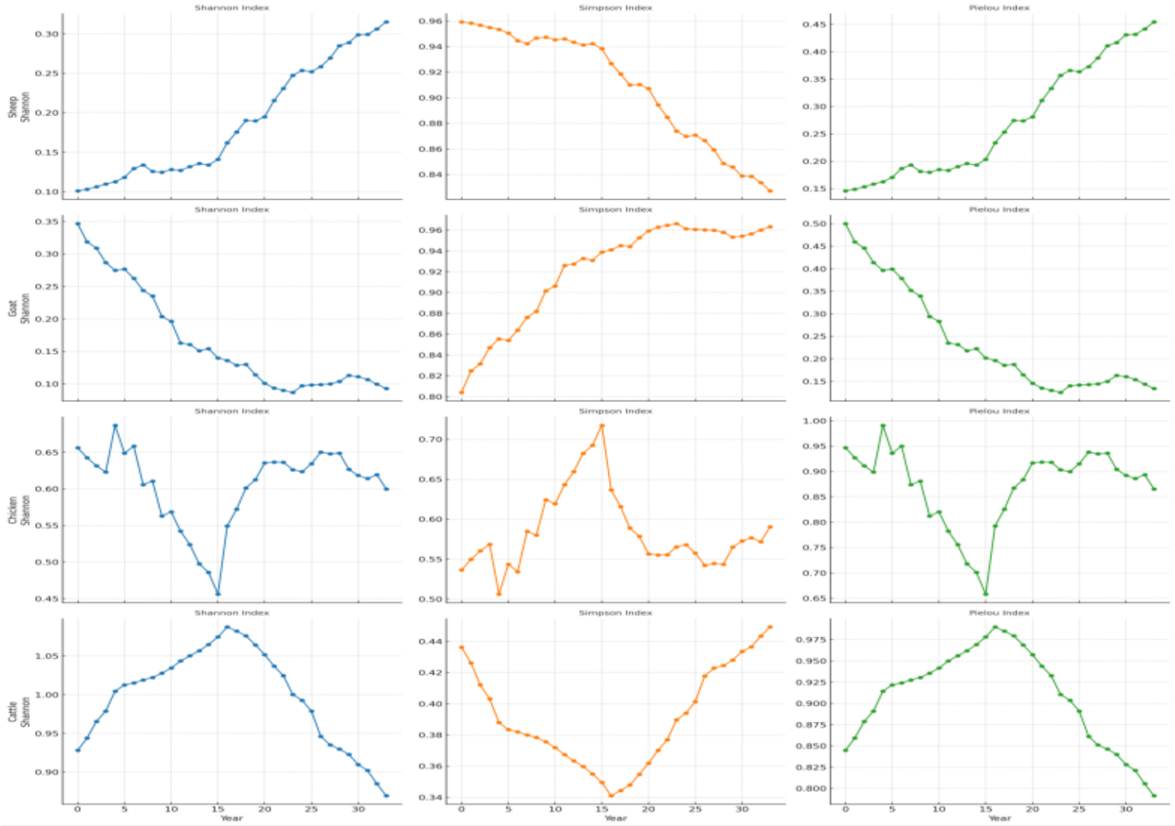

Figure 9. Diversity indices (Shannon, Simpson, Pielou) by year and species.

Şekil 9. *Yıllara ve türlere göre çeşitlilik indeksleri (Shannon, Simpson, Pielou).*

Pielou's Evenness Index for cattle remained consistently high across the study period, starting at approximately 0.85 in the early 1990s and increasing steadily to reach a pronounced peak 1.0 around 2007. After this maximum point, the index exhibited a mild decline followed by stabilization at high evenness levels, indicating that the proportional distribution among cattle breed groups remained relatively uniform despite temporal fluctuations (Figure 9).

This was interpreted as an indication that a well balanced distribution of cattle breeds was maintained in each time segment, even though the absolute proportions of individual breeds were shifted over time (Figure 10).

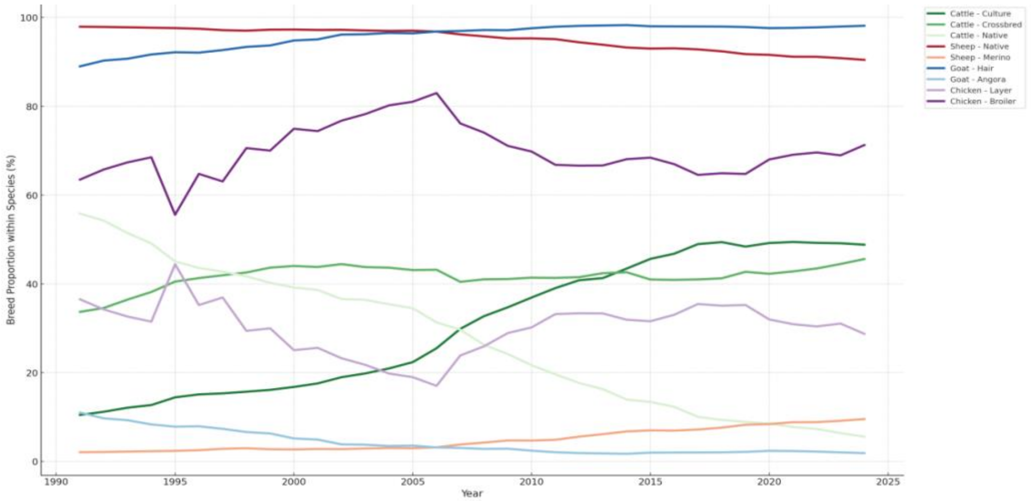

Figure 10. Distribution of species by breed by year.

Şekil 10. *Türlerin ırklara ve yıllara göre dağılımı.*

In the early 1990s, the proportional share of Native cattle was markedly high; however, beginning in the 2000s, this pattern reversed as the proportion of Cultured cattle showed a steady and nearly linear increase over time, gradually overtaking the Native component (Figure 10).

For sheep, the dominance of Native breeds remained evident throughout the entire period, although a gradual decline was visible in the Figure 10. Merino sheep showed only a slight upward trend, consistent with limited replacement of local breeds rather than rapid expansion.

In goats, Hair goats maintained a consistently high proportion, while Angora goats remained marginal with almost no measurable temporal change. The low contrast in the goat panel of Figure 10 indicates a relatively static composition, suggesting limited market driven or policy driven shifts in this species.

In the chicken category, Broiler and Layer proportions followed a relatively similar pattern during the 1990s; however, after the mid 2000s, a clearer divergence became visible (Figure 10). Broiler proportions showed a steady upward trend, while layer proportions remained more stable, resulting in a gradually widening difference between the two categories over time.

Overall, the breed level trends presented in Figure 10 provide clear evidence of strong temporal restructuring in Türkiye's livestock sector, driven by intensification, changing production priorities and evolving market dynamics.

In Figure 11, linear regression trends were presented for major breed groups belonging to four livestock species in Türkiye: cattle (three breeds—Native, Crossbred and Culture), sheep (two breeds—Native and Merino), goats (two breeds—Hair and Angora) and chickens (two production types—Broiler and Layer). For each breed category, annual proportions from 1991 to 2024 were modelled using species specific linear regression to depict the general direction and magnitude of long term changes in breed composition.

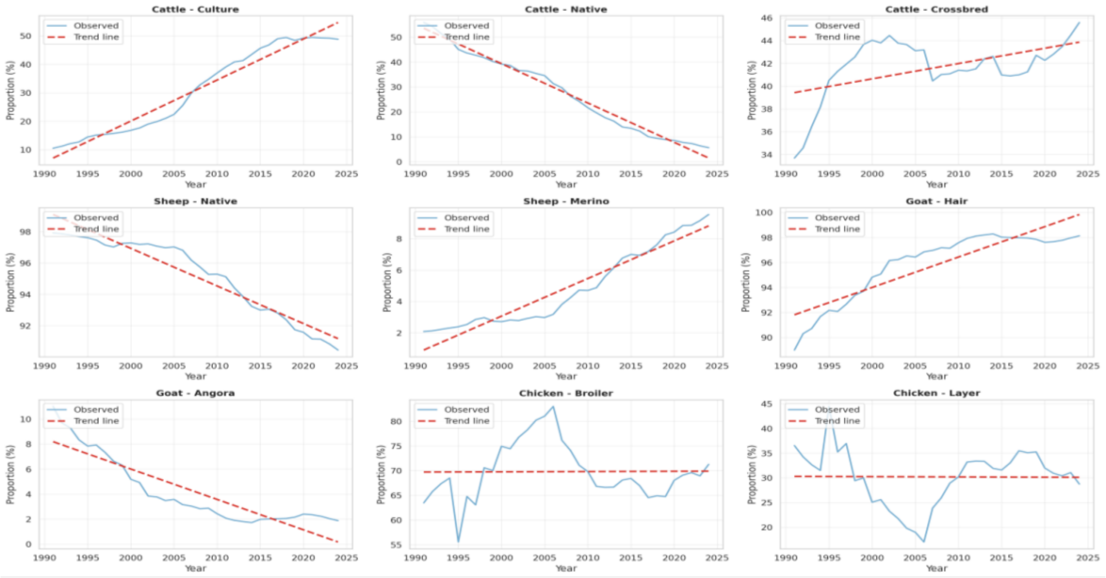

Figure 11. Simple linear regression trends in cattle, sheep, goat and chicken breeds (1991-2024).

Şekil 11. *Sığır, koyun, keçi ve tavuk ırklarının basit doğrusal regresyon eğilimleri (1991-2024).*

In Figure 11, simple linear regression curves were used to evaluate long term proportional changes among the 9 main breed groups of cattle, sheep, goats and chickens. Three distinct trend categories were identified. Continuous increases in proportional representation were observed for Cultivated cattle, Crossbred cattle, Merino sheep and Hair goats throughout the 1991–2024 period. In contrast, consistent declines were detected for Native cattle, Native sheep and Angora goats. For poultry, both Broilers and Laying hens displayed nearly flat regression lines, indicating that their proportional shares did not exhibit any significant long term upward or downward trends. Taken together, these grouped regression patterns were interpreted as evidence of a structural transition toward commercially preferred, high yield breeds, while traditional native genotypes were gradually reduced over time.

Figure 12 used radar charts in which the growth rates calculated for species (Figure 12a) and breed levels (Figure 12b) were summarised for the period 1991–2024. Through this visualisation format, the proportional magnitude and direction of long term population change were displayed simultaneously across multiple groups. By examining the radial positions of each category, an overview was provided regarding which species and breeds were expanded and which were reduced over time.

In Figure 12a, species level assessments were shown to yield near zero net growth for cattle, sheep and goats while chickens were recorded as the only species exhibiting a marked positive increase. These species level shifts were interpreted as reflections of evolving agricultural policies, cultural preferences and the broader modernization of livestock production systems. Overall, the radar chart was understood to highlight that numerical changes in livestock populations were accompanied by structural reconfiguration in species composition.

In Figure 12b, breed level evaluations were indicated to differ substantially, as the strongest increase was observed in Cultivated cattle, followed by Merino sheep, Broilers, Layers and Crossbred cattle. Native sheep and Hair goats were measured as showing approximately zero net change, whereas notable declines were detected in Native cattle and Angora goats. The patterns illustrated in Figures 12a and 12b were taken together as demonstrating that commercial, high yield genotypes were increasingly favoured, while traditional native breeds were progressively diminished over the study period. Collectively, these breed level outcomes were understood to reinforce the dominance of productivity focused genotypes within modern livestock systems.

Figure 12. Species growth rates (1991-2024) (%) (a); Breed growth rates (b).

Şekil 12. *Tür büyüme oranları (1991-2024) (%) (a); Irk büyüme oranları (b).*

DISCUSSION

The long term biodiversity trajectories uncovered in this study reveal a profound structural reconfiguration of Türkiye’s livestock sector, driven by shifting market incentives, state led genetic improvement programmes and changing production priorities. Annual diversity indices from 1991 to 2024 demonstrated highly nonlinear behaviour: oscillations in Shannon and Simpson indices signalled repeated transitions between diversification and homogenisation phases. Comparable temporal instability has been reported in European and Asian systems undergoing intensification, where rising species richness can coexist with declining evenness as commercial breeds replace local types (Peter et al., 2007; Taberlet et al., 2008). The intermittent depressions in Pielou’s evenness, particularly in the mid 2000s, coincide with documented periods in which Türkiye’s cattle breeding initiatives increasingly concentrated on a narrow portfolio of high yield genotypes, supported by expanding artificial insemination networks and subsidies that privileged cultured breeds (Koşum et al., 2019). These findings are consistent with global evidence showing that intensification often amplifies Simpson dominance and accelerates the erosion of effective diversity (Chao et al., 2014; FAO, 2021).

Unsupervised clustering and Bray–Curtis dissimilarity metrics further illuminated this temporal restructuring, resolving two distinct phases: a volatile early period (1991–2005) and a comparatively stabilised later period (2006–2024). The identification of compositional outliers in 2004, 2009 and 2022 is particularly noteworthy. Each of these inflection points corresponds to critical national developments early 2000s subsidy reforms, the expansion of Ministry led artificial insemination and improvement schemes and post pandemic reorientation toward Broiler dominated poultry systems. These findings mirror global research demonstrating that policy shocks, economic disruptions and disease pressures imprint detectable discontinuities on livestock community structure (Christin et al., 2019; Zeng et al., 2022). The marked sensitivity of Bray–Curtis distances to these transition years underscores the analytic advantage of integrating ecological indices with AI supported multivariate modelling.

The Rényi diversity profiles reinforced these observations by illustrating a gradual shift from the relatively balanced configurations of the 1990s to increasingly dominance heavy structures in the 2010s, a pattern widely associated with poultry intensive and high input cattle regimes (Hill, 1973; Zhao et al., 2024). Parallel interpretations emerged from the coefficient of variation analyses, which showed that low density species including pigs, camels and mules exhibited pronounced demographic volatility, consistent with their limited economic relevance and weaker market integration (Taberlet et al., 2008; Koşum et al., 2019). Meanwhile, cattle, sheep and chickens maintained comparatively stable CV values, reflecting their entrenched socio economic significance in Türkiye.

Species level heatmaps highlighted the persistent numerical dominance of chickens echoing the global transition toward poultry centred protein systems (Kamilaris & Prenafeta-Boldú, 2018) and revealed the near disappearance of camels, pigs and mules whose declines align with broader regional patterns of reduced utilisation (FAO, 2021). Breed level heatmaps further demonstrated accelerated internal restructuring: Native cattle declined sharply from the 1990s onward, whereas Cultured and Crossbred types expanded rapidly in response to policy driven genetic improvement, mirroring findings from multiple international livestock modernisation studies (Peter et al., 2007; Koşum et al., 2019). In contrast, sheep and goat breeds displayed more static long term trajectories, though a gradual loss of dominance was evident for native sheep in the last decade. The divergence between broilers and layers after the mid 2000s reflects the sector's industrial intensification and its shift toward meat oriented production (Kamilaris et al., 2017).

Despite pronounced shifts in genotype proportions, evenness metrics revealed that cattle maintained a relatively structured equilibrium among Native, Cultured and Crossbred types for much of the study period. However, consistent reductions in Native cattle raise early warning signals of diminishing allelic richness a well documented precursor to long term genetic vulnerability (Foulley & Ollivier, 2006; Taberlet et al., 2008). Regression models (Figure 11) corroborated these patterns, showing persistent upward trends in Cultured cattle, Crossbred cattle, Merino sheep and Hair goats, contrasted with declines in native breeds. The near flat regression lines of broilers and layers further demonstrated that proportional stability can mask substantial underlying expansion, a phenomenon previously noted in industrial poultry systems (Christin et al., 2019).

Figure 12 clarified that species level net growth masks substantial internal restructuring. While cattle, sheep and goats exhibited near zero net species growth, breed level analyses revealed strong positive expansion in Cultured cattle and Merino sheep and moderate increases in Broilers, Layers and Crossbreds. Conversely, Native cattle and Angora goats contracted sharply. Such divergence between species level and breed level trends exemplifies the limitations of abundance based interpretations and aligns with ecological genetics research highlighting hidden biodiversity erosion under stable total numbers (Chao et al., 2014).

AI-assisted analytical tools proved indispensable in resolving these multilayered dynamics. Their demonstrated capacity to detect subtle anomalies, isolate nonlinear trends and identify high sensitivity transition years complements and extends classical ecological tools, aligning with emerging evidence of the superior reproducibility and predictive value of AI-based biodiversity monitoring (Christin et al., 2019; Brodeur et al., 2025).

Taken together, these findings demonstrate that Türkiye's livestock biodiversity has undergone a gradual yet pronounced homogenisation, driven by policy pressures, market alignment and production intensification. Native breeds despite their ecological and cultural significance now face increasing marginalisation. International experience suggests that once genetic erosion accelerates, reversal is costly and often incomplete (FAO, 2021). The results therefore underscore the need for integrated conservation strategies, breed specific monitoring frameworks and institutionalised AI based surveillance platforms to secure long term resilience in Türkiye's livestock biodiversity.

CONCLUSION

This study offers a pioneering approach to assessing long term livestock biodiversity trends in Türkiye by integrating classical ecological indices with AI powered analytics. Combining metrics like Shannon, Simpson, Pielou, and Hill numbers with AI assisted clustering, dissimilarity modeling, and visual tools enabled the capture of complex temporal patterns and key shifts in species composition (1991-2024). Results highlight a clear move toward high yield commercial breeds, especially in cattle and poultry, alongside a decline in native and marginal species. While total livestock numbers remained stable or rose, internal diversity declined, reflecting a loss of genetic resources. This trend is evident in rising Berger-Parker dominance and Rényi profiles, indicating reduced evenness and increasing genetic uniformity. Crucially, the AI based framework allowed detection of subtle shifts, anomalies, and structural convergence not easily captured by conventional methods. These findings underscore the potential of machine learning in biodiversity monitoring and its applicability to scalable livestock assessments globally. Given these outcomes, there is an urgent need for integrated policies balancing productivity and genetic sustainability. Such frameworks should support dynamic monitoring, offer incentives for native breed conservation, and adopt AI driven forecasting tools. Preserving livestock biodiversity is vital not only for ecological health but also for sustainable food systems and rural livelihoods.

In summary, this AI enhanced study provides a modern blueprint for biodiversity monitoring. By fusing ecological indices with machine learning, this approach offers both methodological innovation and strategic insight. The findings affirm that productivity and conservation must be co-optimized through intelligent, adaptive livestock policies and informs evidence based planning for sustainable animal genetic resource management, particularly in adapting to climate variability and evolving production models.

Data Availability

Data will be made available upon reasonable request.

Author Contributions

Conception and design of the study: AÖD; sample collection: AÖD, SH; analysis and interpretation of data: AÖD, SH; statistical analysis: AÖD, SH; visualization: AÖD, SH; writing manuscript: AÖD.

Conflict of Interest

There is no conflict of interest between the authors in this study.

Ethical Statement

We declare that an ethics committee is not required for this study.

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