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Table of content – Volume 10, Issue 2 (2025)

Research articles

Announcements

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Pedigree based analysis of population structure in Hungarian sheep (Racka sheep)

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Abstract

The Hungarian sheep (also known as Racka sheep) is the best known and most characteristic native sheep breed of Hungary, which has been bred in the Carpathian Basin for centuries. Regular pedigree data collection has been ongoing since 1994. The black and white colour variants are bred separately and registered in closed studbooks, and although they are similar in appearance, they are genetically distinct. Thanks to subsidies, the breed is currently flourishing, but the processing of studbook data and population genetic analysis are essential for its long-term, secure maintenance. The white Racka herd numbers 4,314 living animals currently, while the black Racka herd numbers 3,905 animals. The white Racka variant is kept by 48 breeders and the black one by 43 breeders, with an average number of 90 and 91 individuals per farm, respectively, with a very large variation. There are few large flocks (with more than 200 ewes), six for each colour. Therefore, it can be said that the stock is fragmented, which is favourable for preserving the genetic diversity of the breed, as more rams are used than in the case of modern breeds at large operations. The sex ratio is advantageous, 1:24 for white and 1:21 for black variant. The current breeding situation therefore appears favourable. However, we have found that despite the seemingly favourable data, genetic narrowing is occurring in both colours. In the white colour, this process is particularly noticeable in the male sex. Here, the number of lines has decreased from 103 to 42 in 30 years. In the black colour, this process is visible in both sexes. The number of lines has decreased from

88 to 41, and the number of families from 3,163 to 1,128. These data show that the long-term sustainability of the breed is at risk. The effective population size exceeds 2,200 individuals for both colour variants, but this seemingly favourable data alone is not sufficient for a correct assessment of the situation. Taking into account external factors (the high selection pressure applied to rams, the strong dependence of breeders on subsidies, the fragmentation of breeding farms, and the low willingness of breeders to cooperate), it can be said that new methods need to be developed to ensure the sustainability of the breed. Our main goal is to preserve the original characteristics of the Hungarian sheep, a breed that has defined Hungarian shepherding for centuries, and to maintain its original genetic diversity. To this end, we have processed the pedigree data of 110,000 individuals recorded over the past 30 years. As part of this, the ram lines and maternal families have been identified and coded. Going forward, we aim to use this knowledge to propose a breed maintenance program based on the within-family selection.

Keywords: Hungarian Racka sheep, within-family selection, maternal lineages

Introduction

In the case of breeds registered as native to Hungary, it is more accurate to speak of old historical breeds, since they arrived in the Carpathian Basin in the last two or three centuries and adapted to the natural-geographical, housing, and feeding conditions here. There is only one exception, the breed known today as the Hortobágyi Racka, which is unique to the Hungarians, developed in the Carpathian Basin, was shaped by the Hungarian soil and Hungarian breeding, and does not occur anywhere else in the world – so we can rightly call it the most Hungarian sheep breed. The name of the breed is also interesting, for centuries the Hungarians called only the Racka “juh” (sheep in Hungarian), all other breeds were called “birka” (a somewhat derogatory name for sheep brought from abroad). Thus, the name of the breed is actually Hungarian sheep, the name Hortobágyi Racka is more a product of the 20th century, when the place where the remnants of the herd were found stuck to the breed.

The origin of the breed is uncertain according to most authors (FÖLDI et al., 2016), but several significant figures in agricultural history consider it to be a breed that arrived with our ancestors migrating from its Uralic homeland (HANKÓ, 1937). The earliest finds of Racka-like horn bones in archaeological findings date back to the Middle Ages (16th century), but they became really common in the early modern period (17th-18th centuries) (VÖRÖS, 2003). The population at that time was by no means uniform, GÁSPÁRDY (2011) describes several Racka variants from these centuries that have since died out or disappeared. Until the middle of the 18th century, the Hungarian sheep was the dominant breed until Maria Theresa ordered

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the crossing with fine wool breeds. HANKÓ (1941) already mourned the Hungarian sheep, as he put it, “ungrateful selfishness condemned it to death” – referring to the economic purpose of crossing. He was partly right, as between the two world wars the domestic sheep population numbered 1.1 million individuals, but only 1% of this was Hungarian sheep. HANKÓ also puts the number its white colour variant in 1941 at 2-3 thousand individuals, and the black one at 300 individuals. In 1975, at the beginning of the most recent registration of the breed, the registered population was 1370, and in 1985 it was 2100. In 1983, the *Rackajuh-tenyésztő Egyesület* (Racka Sheep Breeders Association) was founded with the participation of László Veress and Béla Dunka and the cooperation of farmers around Debrecen. Their goal was to register and maintain the individuals of the breed that were in private hands, and they did this with wise foresight, since by the 1990s the cooperative farms of the breed had been liquidated.

In 2008, at the initiative of breeders, breeders, representatives of the breeders' organization and experts from the specialized authority in Mátranovák reviewed the breeding guidelines for Hungarian sheep, updated and expanded the breed description - a document that is still in force today as part of the Breeding Program of the Hungarian Sheep and Goat Breeders' Association. From 2010, a new opportunity opened up for breeders of the breed, the “the support of native breed”, which brought breeders enthusiasm and brought a new golden age for the breed. According to our survey, in 2025 the registered mother stock of the White Hungarian sheep approached 4,500 individuals (4,485), that of the Black Hungarian sheep was 4,000 (3,979). Although centrally supported programs may have drawbacks, FÖLDI et al. (2016) state that no native breed can exist without state maintenance, where decisions are not dictated solely by the market.

The breed is known in two colours, SCHANDL, in 1953, mentions these two colour variants of the breed, however, considering that the shepherds grazed the black and white flocks separately and did not crossbreed, more and more opinions have come to light that they are separate breeds. ZSOLNAI et al. put an end to the debate in 2020, when they performed a genome analysis of 126 black and 128 white Racka sheep. The performance of the multidimensional scaling diagram showed that white and black Rackas represent well-separated groups among other sheep breeds and are also distinct from each other. It is suggested that the colour variants of Rackas be considered genetically distinct breeds. The fact that black and white Rackas are registered under the same name today is only a technical matter, the recording of data for the flock book is carried out separately. This also allows for data processing by colour.

KOMLÓSI (2012) mentions that in the case of small herds, herd structure studies are necessary to assess the vulnerability of the given breed and the vulnerability of their diversity. In the case of the Tsigai, Cikta and Gyimesi Racka sheep breeds, publications are already available that have explored the herd structure of the given

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breed in detail and assessed the mtDNA diversity (ANNUS et al., 2015; KOVÁCS, 2018; KÁRPÁTI et al., 2023).

There has been no publication describing the population structure of the Racka sheep in full. KUSZA et al. (2008) found that there was a potential risk of inbreeding in most of the populations they examined within the Racka breed group. Genetic distance estimates and cluster analysis showed that the main factor in genetic differences between populations is geographical distribution, namely that populations in given areas often show close genetic relationships. SÁFÁR (2017) performed calculations examining the inbreeding of native sheep breeds in Hungary. In his work, he found that the inbreeding coefficient was 0.029 and 0.036 in the White Hungarian sheep and in the Black Hungarian sheep, respectively.

According to the 2020 data of ZSOLNAI et al., the situation in this area has worsened, with the inbreeding coefficients (method-of-moments relatedness F coefficient) of black and white Rackas being 0.147 and 0.133, respectively. Genomic studies have only been carried out tangentially, examining the allele pairs determining scrapie resistance. According to our own studies, the proportion of individuals with R1 (ARR/ARR genotype) has increased from 5 to 18.5% over the past twenty years. BÁCSI et al. (2025) put the proportion of individuals with the same genotype at 17.62% but supplemented this data by stating that the ARR allele frequency increased by 42% across all genotypes. They note that despite the improvement, the potential impact of this change on other important traits remains uncertain.

Today, the Hungarian sheep follows the Hungarian Merino in second place in the list detailing the number of domestic sheep by breed. The EU and national support policy certainly plays a major role in the growth of the breed's population, which provides resources to breeders under several legal titles - expecting in return the additional work associated with maintaining native breeds. However, with a possible change in the support policy, an unpredictable situation may develop in terms of breed maintenance. In fact, the breed is not ideal for meat production, at least in terms of carcass characteristics of mutton type lambs. The muscle and body conformation is not as substantial in the Hungarian breed compared to a continental breed of sheep e.g. Charollais that has been selectively bred for a large, muscled carcass for slaughter. It would be a positive change if the breed could find its place in market conditions. Several authors highlight its role in landscape conservation, but this seems insufficient for sheep farms wishing to remain competitive in the market.

MUJITABA et al. (2024) found that in vitro techniques can play an important role in the genetic conservation of indigenous sheep breeds. To support this, sperm samples from indigenous sheep breeds were successfully collected, stored and used. They suggest the establishment of an indigenous in vitro gene bank. There are 3,378 frozen samples of the White Hungarian sheep, which were collected in 1990, but due to the low number of individuals, this would be worth expanding.

DOI: https://doi.org/10.59913/dagr.2025.20854

Material and methods

For the pedigree processing, we worked with Excel files provided by the Hungarian Sheep and Goat Breeders' Association, which contained data of White and Black Hungarian sheep from 1991 to 2024. In our processing, we assessed the size of the pedigree, the number of founding and living paternal lines and maternal lineages, the total and average number of offspring per lines and lineages, as well as per parents, respectively, furthermore the number of generations per founding ancestors. We calculated the effective herd size and, according to our own idea, we expanded this with the effective line and family number indicators. The statistical processing was performed with Pedigree Viewer (Kinghorn and Kinghorn, 2010), and the evaluations were performed with the Endog (Gutiérrez et al, 2005) and Poprep (Groneveld et al, 2009) programs.

Results and discussion

The number of White Hungarian sheep under herd book control is 4,485 individuals, of which 2,392 individuals are in the main herd book section. The same data are as follows for Black Hungarian sheep, the number of herds under herd book control is 3,979 individuals, of which 2,173 individuals are in the main herd book section. White Hungarian sheep are bred and registered in 48 farms, while Black Hungarian sheep are registered in 43 farms. The average herd size is 90 and 91 for White- and Black Hungarian sheep, respectively. The ratio of male and female breeding animals is 1:24 for White-, and 1:21 for Black Hungarian sheep. The herd structure data themselves paint a reassuring picture of both colour variants/breeds, and there is no significant difference in the comparison of them.

The processing of herd book data for individuals of White- and Black Hungarian sheep is detailed in Table 1.

DOI: https://doi.org/10.59913/dagr.2025.20854

Table 1: Flock book data of the White- and Black Hungarian sheep population

Indicator	**White Hungarian sheep**	**Black Hungarian sheep**
Total flock book stock (individual)	63,304	46,530
number of males	28,197	21,166
proportion of males	44.5%	45.5%
number of females	35,107	25,364
proportion of females	55.5%	54.5%
Number of individuals with a known date of birth	61,840	45,301
Number of individuals with an unknown date of birth	1464	1229
Number of founding sires (lines)	103	88
Number of descendants per line	506	451
Number of living lines	42	41
Total number of sires	591	498
Total number of sires' progeny	52,134	39,654
Average number of offspring per sire	88	80
Number of paternal generations	1 – 12	1 – 9
Number of founding dams (lineages)	3,175	3,163
Number of descendants per lineages	19	20
Number of living lineages	3,011	1,128
Total number of dams	14,859	11,395
Total number of dams' progeny	59,012	43,761
Average number of offspring per dam	4	4
Number of maternal generations	1 – 11	– 11

Processing of the White Hungarian sheep flock book data

The data in Table 1 show that unfavourable processes can be observed behind the seemingly reassuring herd structure data. It is striking that in the case of the White Hungarian sheep, the number of lines found has decreased from 103 to 42 (by 60%) in 23 years. The relatively large number of living sires (591) partially masks this change, but the above trend predicts the danger of genetic narrowing. The average number of offspring per sire (88) would provide ample opportunity to maintain an adequate number of rams representing the line, but due to the characteristics of the herd structure (low flock numbers, large harems, long-term use of rams), it is

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difficult to imagine that the number of lines will not decrease further without effective intervention. The high number of paternal generations provides an opportunity to conduct molecular genetic studies that may enable effective selection. In the case of the White Hungarian White sheep, the number of families seems reassuring, with a 5.5% decrease in the number of living families compared to the founding families during the period under study. The average number of offspring per mother (4) may seem low from a management perspective, but it is sufficient from a gene conservation perspective. In the case of families, molecular genetic studies may also be of great help, based on which not only the maintenance of families could be ensured, but also the targeted development of mating plans could be improved annually. The effective population size, calculated according to the number of sires and dams, is 2,274, which is above the value estimated by the literature as sustainable populations without the risk of a decrease in genetic diversity and an increase in inbreeding. The effective population size calculated according to the number of lines and families is 399, which, compared to the number of living lines and families, also does not indicate a short-term threat to the sustainability of genetic diversity.

Processing of the Black Hungarian sheep flock book data

In the case of the Black Hungarian sheep, the number of lines found decreased from 88 to 41 (by 55%) during 23 years. The number of living sires is also relatively high here (451), but the trends are similar to those of the White Hungarian sheep. The average number of offspring per sire (80) is also relatively high here. Unfortunately, however, the number of families in the Black Hungarian sheep has drastically decreased from 3,163 to 1,128 (by 65%), i.e. almost two-thirds of the families have disappeared in just over two decades. Given that the average number of offspring here is also 4, the genetic mapping of families and their relationships is an urgent task. The effective herd size calculated according to the number of sires and dams is 2,273, and that is 344, calculated according to the number of living lines and families.

There are factors that are difficult to quantify in relation to the maintenance of the White- and Black Hungarian sheep, which may endanger the medium-term future of the breeds. These should definitely be taken into account when making strategic decisions:

- The Hungarian sheep are less suitable for producing broiler lamb in purebred form, buyers do not seek them out, and their alternative sales opportunities are also limited. Their maintenance under market conditions is currently unthinkable.
- Landscape conservation, agrotourism, and other alternative options do not offer sufficient space for the long-term maintenance of breeding stock.

DOI: https://doi.org/10.59913/dagr.2025.20854

- Due to the above, breed maintenance is almost unthinkable without (EU and domestic) subsidies, and the current, relatively favourable situation could be fundamentally shaken by a possible change in the subsidy system.
- The herds are fragmented, there are only 4 farms where the herd size exceeds 200 mothers – and for this, they keep enough rams to keep the inbreeding level at around 0.05.
- Breeders keep a small number of large harems, and in addition, rams are used for a long time, even a decade. The majority of breeders have little tendency to cooperate, and the exchange of rams between themselves (which successfully stopped the decline in the Gyimesi Racka breed) is only conceivable to a limited extent.

For all these reasons, herd structure and pedigree data only serve to characterize the current situation and can be the basis for strategic planning for breed maintenance.

Conclusion and recommendation

The population structure of the White- and Black Hungarian sheep meets the requirements of breed maintenance, and the two breeds are very similar in their main characteristics. However, during the processing of the pedigree data, it was shown that the number of families and lines is changing in an unfavourable direction. The White Hungarian sheep is endangered on the paternal side, and the Back Hungarian sheep is endangered on both the paternal and maternal sides. It is important to provide a basis for effective breed maintenance using molecular biological methods (assessment of mtDNA and Y-chromosome diversity).

Based on the above, we consider it justified to continue our research. We planned to achieve the goal in the following steps: analysis of pedigree data, mtDNA sequence analysis in females, and Y-chromosome sequence analysis in males.

Currently, the first results of the analysis of the pedigree data are available. Sampling for the mtDNA analysis has been completed, and laboratory sequencing is currently underway. We plan to complete the tasks required for Y-chromosome testing by 2026.

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The Water Buffalo (Bubalus bubalis) as an Autochthonous Genetic and Dairy Resource in Republic of Serbia

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Abstract

Autochthonous breeds are considered as valuable reservoirs of genetic diversity owing to their capacity to adapt under specific ecological and economic conditions. Among these, the water buffalo (*Bubalus bubalis*) holds particular importance in European agriculture, especially in Italy, Romania, Bulgaria, and parts of the Balkans. In Serbia, buffalo populations have traditionally been concentrated along major river basins. Most herds are found in central and southern Serbia, restricted to areas where traditional buffalo husbandry has been maintained due to geographic factors and cultural practices. However, according to FAO data, their numbers have markedly declined over the past decades, with some local populations approaching extinction. Over the past five years, the Serbian water buffalo population has ranged between approximately 1,100 and 1,600 head, having a peak in 2022. According to the most recent records, the population now numbers just under 1,500 animals. In general, water buffalo are classified into Swamp and River subspecies, each with unique production traits and geographic distribution. Swamp buffalo are primarily kept in South and Southeast Asia, where they serve as draught animals and produce modest quantities of milk and meat. In contrast, River buffalo, which predominate in Europe, have been selectively bred for high milk yields and are the foundation of traditional dairy industries that produce specialty cheeses highly valued by consumers. Buffalo milk is characterized by its rich composition, containing 6–8% fat, elevated protein levels, and a high proportion of total solids, making it particularly suitable for processing into mozzarella and various traditional cheeses.

In addition to their valuable milk traits, buffaloes are recognized for their ability to thrive under suboptimal conditions, their effective feed utilization, and their resilience to various infectious diseases. Conservation of this genetic resource is fundamental for maintaining adaptive capacity and supporting the socio-economic sustainability of rural production systems. It is essential to implement selection and conservation programs and promote the valorization of buffalo-derived products in order to preserve this culturally valuable species in Europe.

Keywords: Water buffalo, milk fat, genetic resource, conservation

Introduction

Autochthonous livestock breeds constitute valuable reservoirs of genetic diversity and cultural heritage, especially in areas where traditional agricultural practices are still prevalent. The water buffalo (*Bubalus bubalis*) is an animal with a great potential for the future of agriculture in Serbia. First of all, they produce milk with a rich and unique composition (ZICARELLI et al., 2020). Buffaloes exhibit strong resilience and adaptability to specific ecological and economic conditions (VIANA et al., 2025). A characteristic external morphological feature of the buffalo cow includes black, long, and sparse hair, curved horns, notched ears, shiny eyes, and a well-developed mammary gland. Body weight in adult female water buffaloes is largely influenced by the rearing system and environmental conditions. Under extensive or semi-intensive management, mature buffalo cows typically weigh between 450 and 600 kg, although individuals reaching up to 700 kg have been recorded, primarily due to enhanced nutritional input and improved feeding regimes (BORGHESE, 2013). Among such breeds, the **water buffalo** holds a prominent role due to its adaptability to diverse agroecological conditions. This animal connects tradition with modern needs, because it offers opportunities for innovation in food production, especially in dairy industry(NAPOLITANO et al., 2021).Globally, the distribution of buffalos is predominantly concentrated in Asia, where approximately 98% of the total buffalo population is primarily located within South and Southeast Asian countries (BORGHESE et al., 2022).In Europe, the River buffalo has historically been present across Italy, Romania, Bulgaria, and eastern parts of the Balkan peninsula. In these areas, buffaloes have traditionally contributed to local economies through their capacity for milk and meat production. River buffaloes have been selectively bred for high milk yield, rich in fat, protein, and total solids, making them ideal for making dairy products such as mozzarella and other specialty cheeses (STEPIC et al., 2024). In Serbia, the presence of buffalo has a longstanding historical significance, particularly in lowland regions near river basins, where extensive and semi-extensive systems of husbandry were traditionally practiced. Historically, water buffalo were present in substantial numbers throughout the Balkans, including

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Serbia. In Serbia, this species is primarily found in the Raška and Zlatibor districts, specifically in the municipalities of Novi Pazar, Tutin, and Sjenica (Pešter–Sjenica plateau area), as well as in the region of Kosovo and Metohija and on the Stara Planina mountain (GRITTNER et al., 2021). Nevertheless, the shift toward intensive and mechanized agricultural systems has contributed significantly to their population decline.

In the context of global initiatives aimed at preserving agrobiodiversity and promoting sustainable, climate-resilient livestock systems, the conservation of the Serbian water buffalo holds considerable strategic importance. As a locally adapted and underutilized genetic resource, this species exhibits several favorable traits including resilience to endemic diseases, efficient feed utilization, and adaptability to low-input production environments which are critical for sustainable animal husbandry (CHIARIOTTI et al., 2025). Nevertheless, the persistent decline in population size, along with limited commercialization and the lack of organized breeding and conservation programs, presents a substantial threat to its long-term preservation and productive potential. The conservation of these breeds is crucial not only for preserving unique genetic traits but also for maintaining the resilience of rural communities.

The aim of this study was to assess the current status and conservation relevance of the water buffalo with particular emphasis on population trends, production potential, and genetic resource value. To achieve this, we conducted a retrospective analysis of population trends, production traits, and factors affecting the species' conservation status.

Material and methods

This study is based on a comprehensive review and synthesis of available data related to the population dynamics, geographical distribution, and production characteristics of **water buffalo (***Bubalus bubalis***)** in Serbia. Data were gathered from the following sources: Official national statistics published by the Statistical Office of the Republic of Serbia (SORS), Ministry of Agriculture, Forestry and Water Management, FAOSTAT and other publicly available databases maintained by the Food and Agriculture Organization (FAO). Also, we collected data from peer-reviewed scientific literature.

Results

Population trends in Serbia

An analysis of data presented by UROŠEVIĆ et al. (2023) indicates that the population of water buffalo in Serbia remains relatively small and geographically

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constrained. Over the past four years (2019–2023), the total number of registered animals has fluctuated between 1,100 and 1,600 animals, with a peak recorded in 2022 at approximately 1,600 animals. According to the most recent data from 2024, the current population numbers just under 1,500 head (Figure 1).

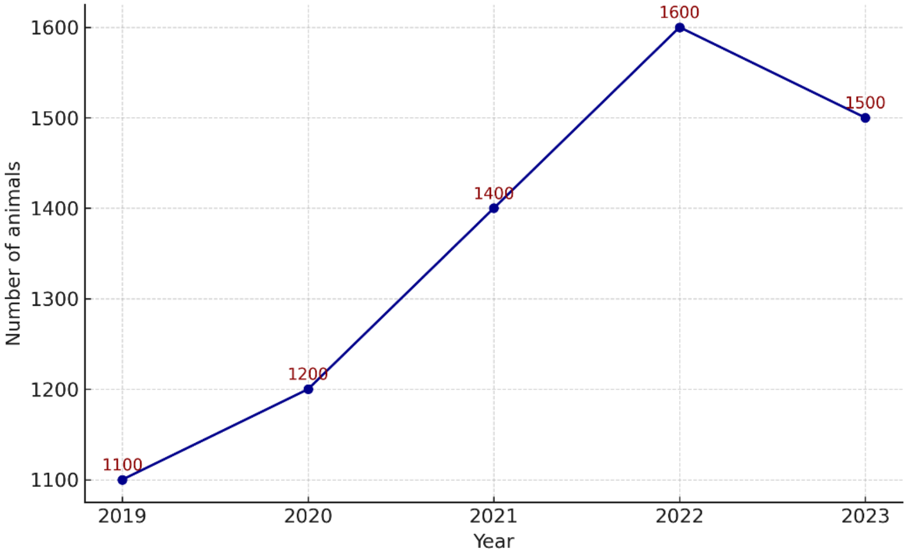

Figure 1: Water buffalo population in Serbia (2019-2023)
Urošević et al., 2023

Geographic distribution

According to available literature, buffalo husbandry in Serbia has historically been concentrated in lowland and riverine regions, especially along major river basins such as the Danube or Morava. Over time, populations have become confined to localized and fragmented areas, with evidence suggesting limited commercial expansion and only minimal structured breeding initiatives. Despite this tradition, the species is now found only in highly localized and fragmented areas, with some micro-populations being critically endangered. There is currently no evidence of significant commercial expansion, and breeding programs are extremely limited.

Production characteristics

Buffaloes raised in Serbia belong to the River buffalo type, which is globally recognized for its dairy productivity. However, due to the lack of structured selection and improvement programs, average milk yields remain modest compared to commercial herds in countries such as Italy or India. Milk yield in Serbian conditions is estimated between 1,000 and 1,500 liters per lactation, depending on management practices (PERISIC et al., 2015). Milk composition is characterized by: fat content:

DOI: https://doi.org/10.59913/dagr.2025.20664

6–8%, protein: 4.0–4.8%, total solids: over 16% (Becskei et al. 2020). This rich composition makes buffalo milk particularly suitable for cheese production, especially traditional dairy products such as mozzarella and local traditional cheeses. However, due to limited demand and lack of organized milk collection systems, no major dairies in Serbia currently collect buffalo milk.

Conservation significance

Although no comprehensive genetic studies have been conducted on Serbian buffalo populations in recent years, historical isolation and the small effective population size suggest the existence of a distinct genetic pool. There is no documented evidence of genetic introgression from foreign breeds, and the populations have remained reproductively isolated for decades.

Discussion

The findings of this study highlight the vulnerable status of the Serbian water buffalo, both in terms of population size and genetic conservation. Despite belonging to the River buffalo type, known for superior milk composition and adaptability to low-input systems (BORGHESE, 2013), buffaloes in Serbia remain severely underrepresented in the national livestock sector. Similar challenges have been reported in other European countries with marginal buffalo populations, where lack of institutional support, economic incentives, and genetic programs has led to stagnation or decline in herd numbers (EL DEBAKY et al., 2019). Genetic monitoring and molecular characterization have not been systematically conducted in Serbia. This absence limits the ability to identify potential private alleles or unique haplotypes that could confirm the autochthonous status of the population. In contrast, studies from Bulgaria, Romania, and Hungary have reported regional genetic structuring and variability within River buffalo populations (BODNAR et al., 2017), supporting the need for national-level initiatives in Serbia to document and preserve its buffalo gene pool. The population has remained relatively stable over the past five years, but at critically low numbers that suggest stagnation rather than recovery. This pattern reflects the absence of structured breeding programs, inadequate conservation strategies, and limited economic motivation for buffalo farming. While buffalo milk possesses a rich composition, characterized by high levels of fat, protein, and total solids (6–8%, 4–4.8%, and >16%, respectively). However, its potential remains underutilized due to the absence of organized milk collection systems, low consumer awareness, and lack of brand development for buffalo-based dairy products (BECSKEI et al. 2020). Geographically, buffaloes are still found in traditional lowland areas along the Danube, Sava, and Morava river basins. These regions provide optimal conditions for extensive and semi-extensive management systems. However, the continuing depopulation of rural areas, coupled with the abandonment of livestock farming by younger generations, leads to the progressive

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loss of traditional knowledge, breeding practices, and cultural associations linked to buffalo husbandry (FAO, 2022). Although commercial interest in buffalo production is minimal, the species holds significant potential for sustainable rural development. Its ability to thrive in marginal environments, combined with its nutritional and cultural value, makes the water buffalo a promising candidate for inclusion in resilient food production systems (BORGHESE, 2023). Lessons from countries like Italy and India demonstrate that strategic support such as targeted breeding, niche product development, and farmer education can successfully revitalize buffalo production (CAPPELLI et al., 2021; SHARMA et al., 2023).Over the past decade, the Serbian government has introduced targeted subsidy schemes to encourage buffalo breeding, with support levels determined by age category: €100 for calves up to six months, €150 for young stock aged six to twenty-four months, and €250 for adult cows and bulls. While this represents a positive policy intervention, its impact is limited without parallel infrastructure and market integration. In Italy, a mandatory tracing system implemented via ministerial decree has been used to regulate and monitor buffalo milk production across the supply chain (CAPPELLI et al., 2021).

Therefore, to ensure the survival and potential revitalization of buffalo farming in Serbia, it is necessary to adopt integrated approaches that include genetic monitoring, development of selective breeding programs tailored to extensive systems, and structured market channels. To confirm the existence of a distinct genetic pool and to assess the level of genetic diversity within the Serbian water buffalo population, it is essential to implement comprehensive molecular characterization studies using microsatellite markers and other genomic tools, as demonstrated in previous research conducted on water buffalo populations in North India (VOHRA et al., 2021).

Conclusion and recommendation

Water buffaloes in Serbia represent a genetically and culturally valuable livestock resource, yet remain confined to small, fragmented populations with limited support. While milk composition and ecological adaptability offer clear production advantages, the lack of structured conservation and breeding strategies continues to hinder population recovery and sustainable use. To ensure the preservation of this genetic resource, it is essential to develop and implement nationally coordinated programs that include comprehensive genetic characterization and long-term monitoring. These efforts should also incorporate selection and conservation strategies adapted to local environmental and production conditions, while simultaneously enhancing the economic viability of buffalo-derived products through targeted education, appropriate financial support mechanisms, and better access to sustainable markets. Without such interventions, the future of water buffaloes in Serbia will remain uncertain, risking the irreversible loss of a

DOI: https://doi.org/10.59913/dagr.2025.20664

multifunctional species with strong ties to both rural livelihoods and national agrobiodiversity.

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Morphometric Analysis and Sex Dimorphism of the Autochthonous Lipe Sheep

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Abstract

Lipe sheep is an autochthonous and endangered sheep endemic to a limited area in Serbia, representing an important element of national livestock biodiversity. As a locally adapted genetic resource, belonging to the Pramenka group of sheep, it holds ecological, cultural, and production-related value. However, population decline and exclusion from intensive breeding programs have made the population vulnerable to genetic erosion. This study evaluated sex dimorphism of the Lipe sheep through body measurements, craniometric, and pelvimetric morphometry. A total of 19 adults (10 ewes and 9 rams, aged 2.5 to 3.5 years) were analyzed. Results showed highly significant differences between sexes for body traits ($p < 0.001$), with rams consistently exhibiting greater values. Significant dimorphism was observed in cranial traits, with rams displaying more pronounced characteristics. Rams also had yellowish to dark, large, triangularly shaped, and spirally twisted horns, a key feature

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of sexual dimorphism. In contrast, no significant differences were found for pelvic traits, suggesting well-developed pelvis in ewes, ensuring easy lambing and uniform pelvic conformation. These findings indicate that the Lipe sheep exhibits stronger sex dimorphism in body and cranial morphology while maintaining functional uniformity in pelvic structure. The study contributes to a broader characterization of the Lipe sheep and provides a foundation for targeted conservation and breeding strategies. Preserving this sheep helps maintain agrobiodiversity and strengthens its role as a valuable genetic resource.

Keywords: autochthonous breed, genetic resource, Lipe sheep, morphometric analysis, sexual dimorphism

Introduction

Autochthonous breeds of sheep, such as the Pramenka, represent long-established populations whose genetic diversity has been shaped by specific agroecological conditions and traditional breeding practices in Serbia (ĐEDOVIĆ et al., 2024). One of the most significant types of Pramenka is the Lipe sheep, which originated and is traditionally bred in the village of Lipe near Smederevo. Known locally as Gara or Garulja, the Lipe sheep is a late-maturing, triple-purpose breed, highly valued not only for meat, milk, and wool, but also for its strong adaptability and resilience to the diverse environmental conditions of its native region (BECSKEI et al., 2018; CEKIĆ et al., 2019). Owing to its valuable genetic traits and reduced population size, the Lipe sheep has been designated a potentially endangered variety of the Pramenka breed in accordance with the Rulebook on the Preservation and Classification of Genetic Resources of Domestic Animals (RUŽIĆ-MUSLIĆ et al., 2022). In many animal species, males and females exhibit consistent differences in body size and shape (ANDERSSON, 1994), which can be of practical importance in breeding programs. Identifying and quantifying these phenotypic differences between males and females allows for informed selection strategies aimed at improving growth rates, reproductive efficiency, and maternal traits, thereby enhancing both productivity and genetic management of the breed (GUDEX et al., 2009). These patterns of sexual differentiation emerge as a consequence of distinct selective pressures acting on males and females, and understanding them provides a framework for designing breeding strategies that maintain the breed’s structural stability and phenotypic variability (BLANCKENHORN, 2005). The present study evaluates the Lipe sheep as a valuable genetic resource by analyzing its morphometric traits with particular attention to differences between rams and ewes. By examining these sex-specific characteristics, the study offers a comprehensive characterization of the breed, enhancing the understanding of its historical and adaptive traits and supporting the preservation of agrobiodiversity and sustainable

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management of this locally important sheep population. This approach contributes to the development of targeted breeding programs that safeguard genetic integrity while optimizing performance traits, ultimately promoting the long-term viability and conservation of the Lipe sheep as a genetically valuable autochthonous breed.

Material and methods

To collect phenotype-related parameters, identify the existing production systems, and assess the population status of the Lipe sheep, onsite visits were conducted, including detailed measurements of phenotypic traits, consultation of the breed registry, and interviews with local breeders, providing comprehensive information about the management and characteristics of the breed. The study specifically evaluated sexual dimorphism in the Lipe sheep through body, cranial, and pelvic morphometry, analyzing a total of 19 adult individuals, consisting of 10 ewes and 9 rams aged between 2.5 and 3.5 years. Body measurements focused on traits relevant for assessing growth and structural differences, including height at the withers, measured as the distance from the ground to the top of the withers; body length, determined from the cranial point of the shoulder to the caudal margin of the pin bone; chest circumference, recorded immediately behind the withers and shoulders; cannon circumference, measured at the midshaft of the cannon bone; and body weight, obtained using a calibrated scale. Cranial measurements comprised head length, measured from the tip of the nose to the top of the occipital crest; front length, from the occipital crest to the medial corner of the eye; face length, from the tip of the nose to the medial corner of the eye; head width, as the distance between the zygomatic arches; height of the ear base, from the incisura vasorum mandibulae to the ventral base of the ear; ear length, from the base to the tip along the lateral aspect; and horn length, measured from the base to the tip of the horn along its lateral aspect. Pelvic morphometry included rump length, defined as the distance between the cranial part of the hip and the most posterior point of the pin bone; hip width, measured between the coxal tubercles; coxo-femoral diameter, as the distance between the coxo-femoral joints; and rump width, measured between the two most posterior points of the pin bones. All statistical analyses were performed using GraphPad Prism version 6 (GraphPad, San Diego, CA, USA), with descriptive statistics including arithmetic mean, standard deviation (SD), coefficient of variation (CV), and variation index (VI), and differences between groups assessed using appropriate statistical tests, with significance set at $P < 0.05$.

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Results and discussion

The results of this study provide a detailed insight into sexual dimorphism in the Lipe sheep, revealing that rams consistently exhibit larger values for most body and craniometric traits compared with ewes, while pelvic measurements remain relatively uniform between sexes. These patterns are consistent with previous observations in domestic sheep, where males generally show greater body dimensions even under relaxed sexual selection pressures (PARÉS-CASANOVA, 2015). Such findings highlight both the breed's phenotypic variability and structural stability, reflecting its adaptation to traditional management and local environmental conditions. Understanding these sex-specific differences is crucial for informing targeted breeding and conservation strategies, as they provide guidance for maintaining genetic diversity, functional integrity, and the long-term viability of this autochthonous breed. The main body measurements of the Lipe sheep, presented in Table 1, provide a detailed overview of the morphometric characteristics of the population and enable an objective evaluation of sex-related differences across key growth and structural traits, which is consistent with previous approaches using quantitative measurements for breed characterization (PEÑA BLANCO et al., 1990; MARTIN et al., 1993).

Table 1: Main body measurements of the Lipe sheep

Trait	Sex F(n=10) M(n=9)	X̄ ± SD (cm)	VI	CV (%)	P
Height at withers	F	68.65 ± 0.58	0.005	0.84	***
	M	76.25 ± 2.44	0.078	3.20	
Body length	F	78.25 ± 3.99	0.204	5.11	***
	M	92.50 ± 4.24	0.194	4.58	
Chest circumference	F	89.95 ± 2.59	0.074	2.88	***
	M	97.87 ± 4.55	0.212	4.65	
Cannon circumference	F	7.85 ± 0.75	0.071	9.52	***
	M	9.31 ± 0.66	0.047	7.07	
Body weight	F	54.65 ± 5.11	0.478	9.35	***
	M	74.88 ± 6.55	0.572	8.74	

F – female; M – male; X̄ – mean; SD – standard deviation; VI – variation index; CV – coefficient of variation; P – significance level (ANOVA)

p-values: * – $p < 0.05$ (significant); ** – $p < 0.01$ (very significant); * – $p < 0.001$ (extremely significant); ns – $p > 0.05$ (not significant)*

The results presented in Table 1., indicate statistically highly significant differences between sexes for all analyzed morphometric traits, confirming the presence of pronounced sexual dimorphism within the population. Males consistently exhibited

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higher values than females in withers height, body length, chest circumference, cannon circumference, and body weight. This pattern is consistent with previous observations, where adult males also showed larger body measurements compared with females (RIVA, 2004). The most evident differences were observed in body length and live weight, indicating a clear sex-based differentiation in body conformation. The presence of such dimorphism is an indicator of retained genetic diversity and adaptive capacity, which are essential components for the resilience and long-term viability of local livestock breeds. Therefore, the morphometric distinctions identified in Table 1. serve not only as evidence of population structure, but also as a useful tool for conservation planning. Incorporating sex-specific traits into breeding and conservation strategies can enhance the effectiveness of programs aimed at preserving the biological identity and functional integrity of the Lipe sheep. As a part of traditional agroecosystems, this breed plays a valuable role in maintaining agrobiodiversity, and its conservation contributes to broader efforts in safeguarding genetic resources adapted to specific environmental and cultural contexts.The cranial dimensions of the Lipe sheep, detailed in Table 2, reveal notable sex-related variation and offer key information for understanding the structural differentiation and morphological characteristics within the breed.

Table 2: Main cranial measurements of the Lipe sheep

Trait	**Sex F(n=10) M(n=9)**	**X̄ ± SD (cm)**	**VI**	**CV (%)**	**P**
Head length	F	24.56 ± 1.45	0.085	5.89	***
	M	28.44 ± 1.16	0.047	4.07	
Front length	F	8.80 ± 0.82	0.077	9.36	**
	M	10.06 ± 0.98	0.096	9.76	
Face length	F	15.75 ± 1.40	0.124	8.89	***
	M	18.50 ± 1.06	0.061	5.73	
Head width	F	12.40 ± 1.81	0.263	14.58	**
	M	14.75 ± 1.22	0.102	8.30	
Height of ear base	F	9.25 ± 0.82	0.074	8.92	***
	M	12.13 ± 1.05	0.091	8.69	
Ear length	F	12.90 ± 1.23	0.117	9.56	**
	M	14.13 ± 0.95	0.064	6.72	
Horn lenght	F	-	-	-	-
	M	62.31 ± 4.29	0.068	6.88	***

F – female; M – male; X̄ – mean; SD – standard deviation; VI – variation index; CV – coefficient of variation; p – significance level (ANOVA)
*P-values: * – P < 0.05 (significant); ** – P < 0.01 (very significant); *** – P < 0.001 (extremely significant); ns – P > 0.05 (not significant)

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Table 2. demonstrates that all analyzed cranial traits show statistically significant differences between sexes, confirming the presence of sex dimorphism in the Lipe sheep population. Males exhibited greater values in all traits compared to females. Differences were extremely significant (p < 0.001) for head length, face length, and height of the ear base, and very significant (p < 0.01) for front length, head width, and ear length. Additionally, sexual dimorphism was evident in horn development, as males possessed well-developed horns while females were polled, further highlighting the pronounced differences between the sexes. This pattern aligns with previous studies showing that horn size and form, in addition to body size, may be under differential selective pressures, with horn traits often developing independently from overall body growth (CÔTÉ, FESTA-BIANCHET&SMITH, 1998; CARO et al., 2003). The most pronounced dimorphism was observed in head and face length, suggesting a more developed cranial structure in males, likely influenced by natural selection and reproductive roles. These results indicate that the Lipe sheep retains genetically and functionally meaningful variation, supporting its value as an autochthonous genetic resource. Recognizing sex-related cranial and horn differences contributes to more effective conservation and breeding strategies, aimed at preserving the breed's biological identity and long-term viability. The results of the comparison of pelvimetric traits between male and female Lipe sheep will be presented in Table 3, showing relative uniformity across sexes and indicating that pelvic morphology remains largely consistent within the population.

Table 3: Comparison of pelvimetric traits between sexes in Lipe sheep

Trait	Sex	X̄ ± SD (cm)	VI	CV (%)	P
Rump length	F	24.40 ± 1.68	0.116	6.89	ns
	M	25.56 ± 1.04	0.043	4.08	
Hip width	F	21.50 ± 2.13	0.212	9.93	ns
	M	22.69 ± 1.34	0.080	5.93	
Coxo-femoral diameter	F	24.15 ± 2.46	0.251	10.19	ns
	M	25.21 ± 1.72	0.118	6.83	
Rump width	F	13.55 ± 1.78	0.233	13.13	ns
	M	14.55 ± 1.20	0.099	8.26	

F – female; M – male;X̄ – mean; SD – standard deviation; VI – variation index; CV – coefficient of variation; p – significance level (ANOVA)
*P-values: * – P < 0.05 (significant); ** – P < 0.01 (very significant); *** – P < 0.001 (extremely significant); ns – p > 0.05 (not significant)

As presented in Table 3., no statistically significant differences (ns) were observed between females and males for any of the measured pelvic traits. Although male values were slightly higher on average, the variation was not sufficient to indicate a clear pattern of sexual dimorphism in pelvic morphology. The relative uniformity of

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pelvic traits between sexes may reflect the stability of body structure in the Lipe sheep population and suggest that these measurements are conserved and functionally balanced. Accurate measurement of pelvic dimensions is crucial for reducing dystocia, as evaluating the pelvic area allows identification of ewes with smaller pelvises, which are at higher risk during lambing (VAN ROOYEN, 2012). Such anatomical consistency is characteristic of autochthonous breeds that have developed under traditional management and environmental conditions, where natural selection favored adaptability and structural efficiency. These results reinforce the importance of preserving not only genetic, but also morphological integrity of the Lipe sheep. Documenting pelvic characteristics supports the phenotypic characterization of the strain and contributes to the development of conservation strategies aimed at maintaining its identity, functionality, and role in sustainable livestock production systems.

Conclusion and recommendation

In conclusion, the Lipe sheep exhibits pronounced sexual dimorphism in body and cranial traits, while maintaining a relatively uniform pelvic structure. These results indicate that the breed retains valuable genetic diversity and functional adaptation, making it an important local and well-adapted genetic resource. The findings provide essential data to support conservation and breeding strategies aimed at preserving the biological identity, adaptive potential, and long-term viability of the Lipe sheep. Moreover, studying sex-related differences in this breed contributes to a broader understanding of domestication, adaptation, and the conservation of animal genetic resources, highlighting the crucial role of local breeds in maintaining biodiversity.

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Financial support measures for endangered local (autochthonous) livestock breeds in Slovenia

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Abstract

In Slovenia, 14 local, 14 traditional and 27 foreign breeds are monitored, with particular emphasis placed on the preservation of local (autochthonous) Slovenian breeds. Local (autochthonous) breeds are breeds that originated in the territory of the Republic of Slovenia, whereas traditional breeds are those that have adapted to the climatic and other conditions of a specific geographical area and have been subject to continuous breeding for at least 30 years, or at least 50 years in the case of horses and cattle. All other breeds are referred to as foreign breeds.

Around the turn of the millennium, several populations of local (autochthonous) breeds in Slovenia faced the threat of extinction. Through targeted professional measures and financial support from the national government, not only has genetic heritage been preserved, but many breeds have shown substantial recovery in population size.

Breeders who raise endangered local (autochthonous) breeds receive financial support under the EU Common Agricultural Policy and the national long-term programme for the conservation of livestock diversity. The support is based on data regarding the number of purebred female and male breeding animals and the overall population size, which serves as the basis for assessing each breed’s risk status. This article presents an overview on the scope and amount of financial support allocated to breeders for the conservation of endangered local (autochthonous) Slovenian breeds in the period 2007–2024.

Keywords: animal genetic resources, biodiversity, endangered breeds, financial support measures

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Introduction

Conservation of animal genetic resources for food and agriculture encompasses the diversity of genes, breeds, and populations of animal species that contribute to food production and sustainable agricultural systems. This dimension of biodiversity constitutes a fundamental basis for agricultural development and represents a key element in global efforts to ensure food security and combat hunger (BOETTCHER et al., 2010; CBD, 2011; FAO, 2007).

Local (autochthonous) breeds are livestock populations that have developed through long-term adaptation to specific agro-ecological conditions, traditional farming systems, and cultural environments. They originate from defined geographical regions, exhibit traits shaped by local environmental pressures, and are predominantly utilised within these areas (FAO, 2013). However, in recent decades, the survival of local (autochthonous) breeds has been increasingly threatened by the expansion of intensive livestock production, genetic homogenisation, and broader processes of economic globalisation. According to FAO (2021), almost 30% of the world's local (autochthonous) breeds are currently classified as at risk of extinction.

In Slovenia, the conservation of animal genetic resources (AnGR) is embedded in sectoral strategies, national plans, and long-term programmes. The Long-Term Programme for the Conservation of Biodiversity of AnGR serves as a central strategic document, identifying priority measures for the preservation of genetic resources, with a particular focus on Slovenian local (autochthonous) breeds (MKGP, 2023a). National legislation officially recognises 14 breeds and one subspecies as local (autochthonous): five sheep breeds, four horse breeds, one cattle breed, one pig breed, one goat breed, one chicken breed, and the Carniolan honeybee (*Apis mellifera carnica*).

At the beginning of the 2000s, several Slovenian local (autochthonous) breeds were considered critically endangered. Through the implementation of targeted conservation measures and financial support provided by the national government, population recovery has been substantial. Not only has the genetic heritage been safeguarded, but population sizes have also markedly increased. The most notable recovery has been observed in the Cika cattle, whose population grew 5.4-fold during the monitoring period. Significant growth was also recorded in the populations of the Krškopolje pig, Drežnica goat, and Posavje horse, each more than doubling in size.

Under the framework of the EU Common Agricultural Policy (CAP) and Slovenia's long-term programme for the conservation of livestock genetic resources, farmers engaged in breeding endangered local (autochthonous) breeds are eligible for targeted financial incentives. Support allocation is based on demographic indicators such as the number of registered purebred breeding females and males and the effective population size, which together inform risk status assessments of each breed.

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This paper aims to provide a comprehensive analysis of the scope and scale of financial measures implemented to support breeders in conserving endangered Slovenian local (autochthonous) breeds during the period 2007–2024.

Status of animal genetic resources in Slovenia

For decades, the FAO has encouraged member states to prioritise the conservation of animal genetic resources (AnGR) that are essential for agriculture and food security (HOFFMANN, 2011). A comprehensive understanding of the biodiversity, distribution, phenotypic characteristics, and productive performance of AnGR is indispensable for their effective and sustainable utilisation, improvement, and long-term conservation. One of the most important instruments to achieve these objectives is the systematic monitoring and analysis of population status and demographic trends at global, regional, and national levels (FAO, 2007).

Slovenia has established a policy framework for the monitoring of livestock biodiversity through the Livestock Breeding Act (Ur. list RS, 2002) and the Biodiversity Regulation (UR. LIST RS, 2004a). The national Breed Register with zootechnical assessment **(**REGISTER, 2024) currently recognises 14 local (autochthonous) breeds, 14 traditional breeds, 27 foreign breeds, and one additional breed that does not fall into any of these categories. The highest number of recognised breeds is recorded in cattle and horses (12 each), while goats account for four breeds and chickens for five breeds. Local (autochthonous) breeds represent only 17.6% of all purebred animals in Slovenia, whereas traditional breeds account for 40.1% and foreign breeds for 41.3%. Notably, most of these breeds have been incorporated into structured breeding programmes and systematic selection schemes for over two decades.

Among the local (autochthonous) breeds, the largest populations are represented by the Jezersko-Solčava sheep (Figure 1), the Improved Jezersko-Solčava sheep, the Cika cattle, and the Bovec sheep. Collectively, these four breeds constitute 73.5% of all breeding animals within the category of local (autochthonous) breeds. By contrast, the smallest populations are observed in the Bosnian Mountain Horse, followed by the Lipizzaner horse and the Drežnica goat. Within the group of traditional breeds, Simmental cattle is the most numerous, followed by Brown cattle**.** Excluding these two dominant breeds, the remaining traditional breeds account for only 5.8% of the total population. The group of foreign breeds is overwhelmingly dominated by Black-and-White cattle, which represent 90.5% of all purebred animals in this category.

Population dynamics between 2003 and 2024 reveal divergent trends. Most local breeds have shown population growth, while the majority of traditional breeds have declined. The strongest increase was observed in Cika cattle: in 2006, only 567

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purebred females and males were registered, but by 2024 the number had risen 5.4-fold, reaching 3,371 animals recorded in the herd book. Other breeds with notable population recovery include the Krškopolje pig (Figure 1), the Drežnica goat, and the Posavje horse, all of which have increased by at least 2.8-fold during the same observation period.

Figure 1: left: Jezersko-Solčava sheep, right: Krškopolje pig

Financial support for conservation of animal genetic resources in Slovenia

In Slovenia, the conservation of animal genetic resources (AnGR) relevant for agriculture and food production is primarily regulated by the Livestock Breeding Act (UR. LIST RS, 2002) and by measures implemented within the framework of the Common Agricultural Policy (CAP). The Livestock Breeding Act explicitly recognises the protection of local (autochthonous) livestock breeds and establishes the principal conservation methods (*ex situ* and *in situ*), along with the objectives and guidelines of the National Programme for the Protection of Biodiversity in Livestock Breeding.

Building on this legislative basis, the Rules on Biodiversity (UR. LIST RS, 2004a) further specify the practical conservation approaches, define the structure and content of the biodiversity conservation programme, regulate the operation of the national gene bank, and establish the criteria for determining the endangered status of breeds.

On this foundation, the Ministry of Agriculture has adopted a series of long-term programmes for the conservation and sustainable use of AnGR:

- **2001–2008** – the first comprehensive national programme,
- **2010–2016** – continuation with emphasis on monitoring,
- **2017–2023** – updated alignment with EU policy,
- **2024–2030** – the current programme with a stronger focus on sustainability and international commitments.

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These strategic documents were developed in accordance with international and European policy frameworks, most notably: the Convention on Biological Diversity (UN, 1992), the Global Plan of Action for Animal Genetic Resources (FAO, 2007), and the EU Biodiversity Strategy to 2030 (CBD, 2020). The financial framework for the implementation of conservation activities and programme tasks during the period 2007–2024 is presented in Figure 2.

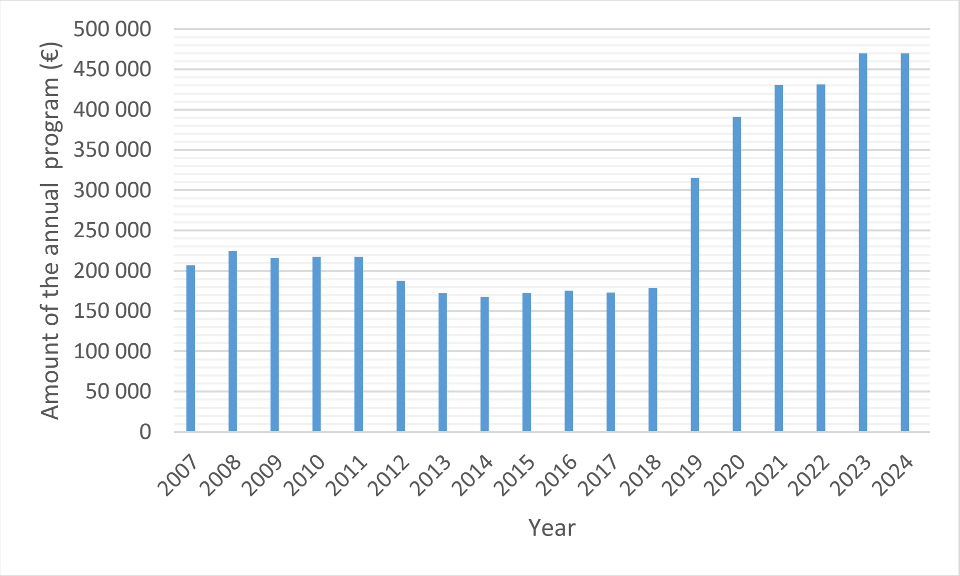

Figure 2: Financial framework for the implementation of the Biodiversity Conservation Program in Slovenian livestock 2007-2024

Support for breeders of local (autochthonous) and traditional breeds within Agri-Environmental Schemes

Since Slovenia's accession to the European Union in 2004, the breeding of local (autochthonous) livestock breeds at risk of extinction has been financially supported through agri-environmental programmes (Ur. list RS, 2004b). Beginning in 2023, this support has been incorporated into the "Local Breeds" intervention within the framework of the national CAP Strategic Plan.

The payment levels per individual animal or per livestock unit have varied substantially across different programming periods. In the initial years of programme implementation, the total funds disbursed for conservation activities remained relatively stagnant. However, from 2014 onwards, a consistent annual increase has been recorded. This positive trend can be attributed to several interrelated factors:

- gradual increases in the payment rate per animal,

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- a rising number of participating breeders, and
- an expansion in the number of animals registered under the *“Breeding of local breeds”* measure.

The aggregate funds allocated for the conservation of Slovenian local (autochthonous) and traditional breeds under agri-environmental and CAP measures during the period 2007–2024 are presented in Figure 3.

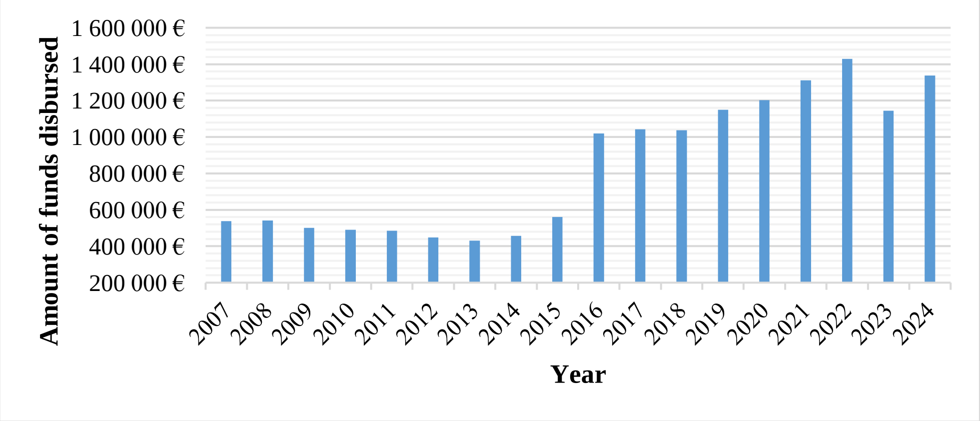

Figure 3: The total amount of funds disbursed under the strategic plan for local (autochthonous) and traditional breeds

In Slovenia, *in situ* conservation is implemented through CAP measures, the funding of collective breeding programmes, and activities carried out under the national conservation programme. The conservation of local (autochthonous) and traditional farm animal breeds encompasses a range of strategies aimed at maintaining genetic diversity, promoting sustainable utilisation, and ensuring long-term survival (FAO, 2009).

In situ conservation refers to the maintenance of local (autochthonous) breeds within the production systems in which they have developed their specific traits and where they traditionally occur (FAO, 2013). In Slovenia, the payment levels per individual animal for the measure *"Breeding of local breeds"*, which targets breeds threatened with extinction, are presented in Table 1.

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Table 1: Payment amounts per individual animal of local (autochthonous) breeds (Ur. list RS. 2004b; MKGP, 2023b).

Year of implementation	**2004-2006**	**2007-2010**	**2007-2014**	**2015**	**2016-2022**		**2024**	
					indigenous	traditional	indigenous	traditional
Payment	€/LU*	€/LU*	€/LU*	€/LU*	€/LU*	€/LU*	€/LU*	€/LU*
Cattle/horses	120	72	89.38	116.17	193.62	116.17	168.79	112.52
Sheep/Goats	120	10.8	89.38	116.17	193.62	116.17	168.79	112.52
Pigs	120	28	89.38	116.17	193.62	116.17	168.79	112.52
Poultry	120	1.008	89.38	116.17	193.62	116.17	168.79	112.52

*LU=livestock unit

In 2024, financial support under the CAP was provided for 19,825 animals belonging to Slovenian local (autochthonous) breeds. Within this group, the Jezersko-Solčava sheep, the improved Jezersko-Solčava sheep, and the Cika cattle accounted for the highest share of payments. Among the horse breeds, the Slovenian Cold-blooded horse received the largest amount of support, followed by the Posavje horse, the Lipizzaner, and the Bosnian Mountain horse (Table 2).

Table 2: Number of animals of individual local (autochthonous) breeds for which breeders have received agri-environmental payments under the measure *"Breeding of local breeds"*

Breed/Year	**2004**	**2008**	**2012**	**2016**	**2020**	**2024**
Lipizzan horse	504	587	517	539	513	614
Posavje horse	368	567	492	617	813	1130
Slovenian cold-blooded horse	1520	2053	1282	992	1130	1336
Bosnian mountain horse	/	/	/	/	/	36
Cika cattle	434	829	905	1451	2168	2952
Krškopolje pig	292	566	471	983	1327	1074
Jezersko-Solčava sheep	3828	4810	3855	3275	3444	4227
Improved Jezersko-Solčava sheep	/	/	/	/	/	3928
Istrian pramenka	661	752	542	662	670	735
Bela Krajina Pramenka	439	588	406	503	552	487
Bovec sheep	1353	1543	1608	1635	1848	1951
Drežnica goat	210	288	255	372	450	712
Styrian hen	410	360	/	601	628	643

The distribution of payments reflects both the demographic structure and the conservation status of Slovenian local (autochthonous) breeds. The Jezersko-Solčava sheep, the improved Jezersko-Solčava sheep, the Cika cattle, and the Bovec sheep received the largest share of support, which is consistent with their relatively large population sizes and their central role in traditional farming systems. These breeds represent the backbone of local production and, despite their recovery in recent decades, remain classified as endangered, thereby justifying targeted financial incentives.

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Among horses, the predominance of payments for the Slovenian Cold-blooded horse and the Posavje horse corresponds to their economic importance and wider distribution, while the Lipizzaner and the Bosnian Mountain horse received smaller shares, reflecting their lower population sizes and narrower breeding bases. The structure of financial support therefore mirrors the dual objectives of conservation policy: to prevent further decline of numerically small populations and to sustain breeds with a stronger role in agricultural practice.

The common breeding programmes are financed by the Ministry of Agriculture, Forestry and Food in accordance with Regulation (EU) 2016/1012, which obliges Member States to support sustainable breeding schemes aimed at both the improvement and conservation of breeds. Particular emphasis is placed on endangered local (autochthonous) breeds, while maintaining genetic diversity within and between populations. In Slovenia, the total funding allocated for all breeding programmes amounts to approximately 8.8 million euros. In comparison, payments provided through the CAP for the conservation of local (autochthonous) and traditional breeds account for about 1.4 million euros. The number of breeders receiving CAP payments for the breeding of local (autochthonous) breeds is presented in Table 3.

Table 3: Number of breeders receiving payments for the breeding of autochthonous breeds

Breed/Year	**2004**	**2008**	**2012**	**2016**	**2020**	**2024**
Lipizzan horse	87	83	47	47	44	62
Posavje horse	123	161	89	89	112	164
Slovenian cold-blooded horse	589	616	287	189	186	232
Bosnian mountain horse						12
Cika cattle	189	226	178	259	319	437
Krškopolje pig	30	48	35	50	50	41
Jezersko-Solčava sheep	122	136	102	93	90	101
Improved Jezersko-Solčava sheep						67
Istrian pamenka sheep	5	4	3	3	4	8
Bela-Krajina sheep	17	18	13	17	17	18
Bovec sheep	23	25	18	16	18	17
Drežnica goat	16	17	14	17	22	45
Styrian hen	9	2	/	7	9	8

The data in Table 3 illustrate the number of breeders participating in CAP measures for the conservation of local (autochthonous) breeds. The trends are heterogeneous: while participation has increased substantially for some breeds, such as Cika cattle, Posavje horse, and Drežnica goat, other breeds, including the Slovenian Cold-blooded horse, Lipizzaner, and Jezersko-Solčava sheep, have experienced a decline in breeder numbers over the observation period. These fluctuations are closely linked

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to changes in payment rates per animal, administrative requirements, and the demographic dynamics of breeding populations. For newly included breeds, such as the Improved Jezersko-Solčava sheep and the Bosnian Mountain horse, participation in 2024 reflects their more recent recognition within conservation programmes.
The number of breeders is therefore not only a direct indicator of financial support but also a proxy for the long-term viability of conservation efforts. A stable or increasing breeder base is essential to ensure the continuity of breeding activities, maintain effective population sizes, and safeguard genetic diversity for the future.

The Rural Development Programme also introduced several measures with an indirect but significant impact on the conservation and breeding of local (autochthonous) livestock breeds. Among these are the agri-environmental measures *“Alpine pasture farming”* and *“Breeding of livestock in areas where large carnivores occur.”* The beneficiaries of these measures were frequently breeders of local (autochthonous) Slovenian sheep and cattle breeds in alpine and karst regions, where adaptation to challenging environments is an essential trait. Another relevant measure is *Organic farming*, which is closely linked to the robustness and resilience of local (autochthonous) breeds. Their adaptive traits can contribute substantially to the long-term sustainability and productivity of organic systems (BIEBER et al., 2019). Payments for farming in areas with natural or other specific constraints also play an important role, as they provide additional income support in regions particularly well suited to the maintenance of local breeds. These measures have been retained and further developed within the Common Agricultural Policy Strategic Plan 2023–2027 (MKGP, 2023b), demonstrating continuity in policy support and recognition of the broader multifunctional role of local (autochthonous) breeds in sustainable farming systems.

De minimis support for endangered Slovenian local (autochthonous) breeds

According to the Long-Term Conservation Programme (MKGP, 2023a), breeders of endangered and critically endangered Slovenian local (autochthonous) breeds are eligible for financial support under the *de minimis* aid system. This form of support is financed from the budget of the Republic of Slovenia and operates within the framework of EU state aid rules, which allow limited financial assistance to be granted without prior notification to the European Commission. The main advantage of *de minimis* aid is its administrative simplicity and targeted nature, which enables timely support for small-scale breeders who play a crucial role in conserving local (autochthonous) genetic resources. In practice, such aid can provide a significant contribution to the viability of farms located in remote or mountainous areas, where production conditions are demanding and alternative income sources limited. However, the system also has certain limitations. The maximum amount of aid that can be granted to a single beneficiary is capped under EU legislation, which may

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restrict the overall impact on larger breeding populations or on breeders with higher conservation costs. In addition, *de minimis* aid is typically granted on a short-term basis, which can limit its effectiveness as a long-term incentive for sustainable breeding of endangered populations. Despite these limitations, *de minimis* aid represents an important complementary tool alongside CAP measures and national breeding programmes. It contributes to the overarching goals of maintaining genetic diversity, preventing inbreeding, and sustaining traditional livestock breeding in regions where such activities are of both cultural and ecological importance.

Conclusion and recommendation

Animal genetic resources play a vital role in ensuring food security, maintaining genetic diversity, and enabling adaptation to climate change. The erosion or loss of livestock breeds entails the disappearance of unique traits characteristic of local (autochthonous) populations, such as disease resistance and environmental adaptability, as well as the irreversible loss of specific genes underlying these adaptive features (REIST-MARTI & SIMIANER, 2006). Breed loss is also associated with the decline of traditional breeding practices and the erosion of related knowledge and skills, including techniques for processing animal products into traditional agricultural and food products.

In Slovenia, the conservation of local (autochthonous) and traditional breeds threatened with extinction has been supported by agri-environmental payments since 2004. In parallel, the state provides funding for professional breeding organizations, the implementation of breeding programmes, and complementary biodiversity conservation measures. These interventions have contributed to changes in population dynamics, with most local (autochthonous) breeds showing significant growth since 2003.

Looking ahead, it is crucial to ensure the continuity of conservation efforts for endangered Slovenian breeds. Sustained support should be provided primarily through financial incentives, but additional mechanisms are required to buffer breeders against risks associated with sudden disease outbreaks or force majeure events that can decimate livestock populations. Strengthening resilience in this way is essential not only for the preservation of genetic resources, but also for the protection of cultural heritage and the long-term sustainability of Slovenian livestock farming.

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Initiative for genebanking of European endangered animal breeds

The European Regional Focal Point for Animal Genetic Resources (ERFP) and the European Union Reference Centre for Endangered Animal Breeds (EURC-EAB) have developed “Guidelines for the development of national health regulations for material intended for Gene Banks, with particular reference to the long-term conservation of endangered livestock breeds.” They invite professionals to review the guidelines and consider adopting national regulations that recognize the specific role and objectives of gene banks.

The guidelines for the development of national animal health regulations for material intended to be kept in gene banks can be summarized as it follows.

Chapter 1 is dedicated to contextualizing the rest of the content of the guide, it is describing what gene banks are, their main functions and the type of material that can be stored in them. When analysing this context, it is essential to highlight the need for the constitution of gene banks within the breeding programmes of livestock breeds, both for their conservation and for their improvement. Finally, the link between gene banks and health regulations is established, which is determined by the fact that stored products are susceptible to disseminate animal diseases and, therefore, must meet a series of requirements that minimise this risk. However, some of these requirements, designed for the commercial breeds, represent real bottlenecks that hinder the conservation of animal genetic resources, as consequence the existence of specific regulations for gene banks is desirable, as it is explained at the end of the chapter.

Chapter 2 is intended for the objectives of the guide, which for its simplicity is reproduced verbatim:
- To draw further attention to the importance of gene banks and gene bank collections in the context of breed specific conservation and breeding programmes and for the long-term conservation of farm animal genetic diversity, in particular among the competent national authorities and breed societies.
- To promote awareness and capacity building to gene banks regarding the necessary protocols for collection, processing, storage, documentation and use of germinal products to guarantee health status and safety.

To inform National Competent Authorities, responsible for the implementation of Animal Breeding, about the importance of gene banks, and available options to allow the use of germinal products from gene banks in approved breeding programs.

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•To inform National Competent Authorities, responsible for the implementation of Animal Health Law, about the importance of gene banks and the need to set national health frameworks and protocols for gene banks, when appropriate.
•To Contribute to the official recognition of gene banks at national level in the context of Animal Breeding and Animal Health regulations.
•To highlight the possibilities of Commission Delegated Regulation (EU) 2020/686 on the implementation of derogations for the movement of germinal products stored in gene banks between Member States under EU animal health legislation.
•To advise the European Commission, the Standing Committee on Zootechnics, and the Standing Committee on Plants, Animals, Food and Feed on the further development of EU animal breeding and EU animal health legislation that will facilitate the conservation and sustainable use of valuable animal genetic resource at both national and EU level.

In Chapter 3 a look at the regulations are taken that would be applicable at international, European and national level within two different areas, Animal Health and Animal Breeding.
This chapter describes how animal health regulations on germinal products derive from the WOAH Terrestrial Animal Code, applying similar EU requirements for intra-EU. However, the EU's own regulations already provide exceptions for the movement of germinal products between gene banks between different member states. In this section of the guide, it is also recalled that each EU member state (or third party) is competent to regulate germinal products in its territory and therefore the one that has the capacity to adopt specific regulations for gene banks. Likewise, the European regulations on animal breeding and their references to ex situ conservation are mentioned. The last section of Chapter 3 details the difficulties faced by gene banks due to the current regulatory requirements for germinal products, which were designed for commercial breeds. This section details how certain EU countries have already established adapted regulations to facilitate the work of gene banks.

Chapter 4, although not very long, is key, since the first step in establishing adapted regulations for gene banks is to identify and officially recognize these facilities. In this chapter a series of recommendations for officially recognising gene banks are given, based on zootechnical and health regulations.

Chapter 5 is the most relevant of the entire guide, as it establishes the recommendations for developing animal health regulations adapted to gene banks. It should be noted that a series of measures are included that are complementary to each other and that each competent authority can choose according to its needs or starting situation. In this sense, the guide should be understood as a toolbox, from the simplest to the most complex possible, from which to choose. Within the text of

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the chapter, only general aspects are included, while the technical detail is developed in several of the annexes of the guide.

A common point when applying this regulation is that it should only cover animals registered in a herd book according to the EU (or national) regulations on animal breeding, so that the activities are carried out under the umbrella of a breeding programme.

When developing animal health regulations adapted for genebanks, the recommendations have been divided according to the type of material. Thus, those intended for the constitution of semen collections are located in Annex I, part A. In turn, two different locations have been contemplated to carry out the constitution of these collections: specialized sperm collection centres or collection on farm where the donor is located, a situation in which the availability of donors is facilitated. Annex I, Part B contains the provisions for the collection of embryos and oocytes. In addition to these generic regulations for the routine constitution of genebank collections, it is necessary to take into account specific situations in which it may be necessary to collect or store reproductive products to conserve animal genetic resources. These specific situations are the application of stamping-out measures in the face of the appearance of communicable diseases or the storage of old material whose health status is unknown. To deal with these situations, it is recommended to establish specific authorisations as the material is considered relevant for the conservation of livestock biodiversity. The recommendations for authorising collections in the event of stamping-out are set out in Annex 1. Part C and for the preservation of old samples in Annex 1. Part D. In this chapter 5 the importance of an adequate system of documentation of the material and its collection and storage conditions are also highlighted. The recommendations for establishing such a documentation system are set out in detail in Annex II. In support of all the previous sections, Annex III contains a list of pathogens that can be detected directly in semen. The last section of Chapter 5 is dedicated to summarizing the health requirements applicable to collections of genomic material, which are derived from the animal by products regulations.

The last chapter of the guide, Chapter 6, contains a series of recommendations when applying the exception contemplated in Articles 45, 46 and 47 of Commission Delegated Regulation (EU) 2020/686, to allow the movement of reproductive products between gene banks located in different member states. This has been a huge milestone in the regulations, as it demonstrates that a regulation adapted to the needs of the conservation of animal genetic resources in gene banks is possible. Annex IV contains the advanced notification form to carry out this movement.

András Gáspárdy

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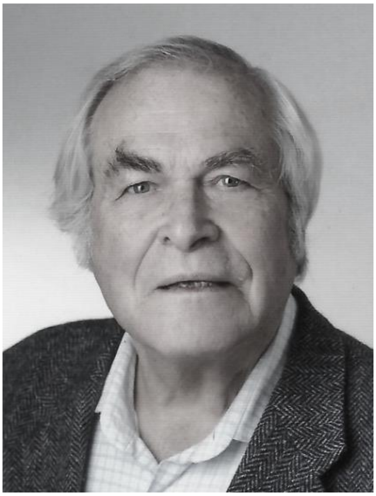
In Erinnerung an Prof. Dr. Dr. Hans Hinrich (Hinnerk) Sambraus (1935 – 2025)



Geboren am 31. August 1935 in Bargteheide in Holstein (Norddeutschland). Er besuchte den mathematisch-naturwissenschaftlichen Zweig des Stormarn Gymnasiums in Ahrensburg, wo er sein Abitur 1957 ablegte.

Er studierte von 1957 bis 1965 Tiermedizin, Zoologie und Anthropologie in München, Berlin und Bern (Schweiz). Promotion in der Tiermedizin zum Dr. med. vet. 1965. Promotion in der Zoologie zum Dr. rer. nat. 1968 und war Schüler des Nobelpreisträgers Konrad Lorenz. Zudem habilitierte er im Fach „Verhaltenskunde" an der Tierärztlichen Fakultät der Ludwig-Maximilians-Universität München. Die Ernennung zum Fachtierarzt für Verhaltenskunde erfolgte 1973. Ernennung zum Professor, im Jahre 1976. Gastprofessor in den U.S.A. war er 1979/80, dann 1982-2001 Leiter des Lehrgebiets für Tierhaltung, Verhaltenskunde und Tierschutz an der Technischen Universität München.

Von 1988 bis 2000 Leiter der Tierschutzkommission beim Deutschen Bundesministerium für Ernährung, Land- und Forstwirtschaft. Er war Berater von Helmut Kohl bei der Entwicklung des deutschen Tierschutzgesetzes.

Darüber hinaus engagierte er sich stets für Veränderungen in der Massentierhaltung und war Mitglied des Herausgeberstab der international renommierten Zeitschrift „Applied Animal Behaviour Science".

Autor bzw. Mit-Herausgeber von zehn Fachbüchern über Tierverhalten, Tierhaltung, Tierschutz und Nutztierrassen. Über 250 Publikationen in wissenschaftlichen Zeitschriften.

Die folgenden Bücher gelten als grundlegende Werke zum Thema gefährdete Arten und Rassen: Atlas der Nutztierrassen, 1986 und 2016; Gefährdete Nutztierrassen: ihre Zuchtgeschichte, Nutzung und Bewahrung, 1994 und 2010; Farbatlas seltene Nutztiere, 2010 und Exotische Rinder: Wasserbüffel, Bison, Wisent, Zwergzebu, Yak, 2006.

1981 gehört er zu den Mitgründern und ist später langjähriger Vorsitzender der „Gesellschaft zur Erhaltung alter und gefährdeter Haustierrassen"(GEH). Er hielt bereitwillig und regelmäßig Ornithologie Kurse für Grundschulkinder ab und pfiff dabei gewissenhaft die Rufe einzelner Garten- und Waldvogelarten.

2008 wurde ihm vom Deutschen Bundespräsidenten das Bundesverdienstkreuz am Bande verliehen. 2013 wurde er mit der Verfassungsmedaille in Silber des Freistaats

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Bayern ausgezeichnet. Im Jahre 2000 wurde er Ehrenmitglied der GEH und Ehrenbürger der Stadt Jánoshalma (Ungarn).
Ein Beispiel für seine Verbindung zu Ungarn ist sein Gastvortrag an der Veterinärmedizinischen Universität im Jahre 2015, wo er den Studierenden des deutschsprachigen Studiengangs im Rahmen des Wahlfachs „Besondere Wiederkäuer“ die exotischen Rinderarten vorstellte. Am darauffolgenden Tag nahm er an der Busreise der Studierenden teil, bei der sie einen Milchviehbetrieb und einen Naturpark mit ungarischen Graurindern und Wasserbüffeln besuchten und im Garten von Schloss Brunszvik in Martonvásár einen Kranz an der Beethoven-Statue niederlegten.
Er pflegte immer einen engen Kontakt zur DAGENE-Vereinigung. Am 23. April 2016 hielt er den Eröffnungsvortrag auf der 27. Jahrestagung der DAGENE-Vereinigung mit dem Titel „Was ist eine alte und gefährdete Rasse?“. Die Tagung fand in Hilgertshausen-Tandern, Bayern, im Unternehmen von Professor Gottfried Brem, der Agrobiogen GmbH, statt.
Hans Hinrich Sambraus ist am 9. Oktober 2025 in München verstorben. Ein langes, erfülltes Leben ist zu Ende gegangen. Seine Beisetzung fand am 20. Oktober im Neuen Südfriedhof in München statt.

Dr. András Gáspárdy
President of DAGENE

Zusammengestellt aus den folgenden Quellen:

Boehncke, E.: Professor Dr. Dr. Hans Hinrich Sambraus 65 Jahre, Arch. Anim. Breed., 43, 313–314, https://doi.org/10.5194/aab-43-313-2000, 2000.
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