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Exploring the situation of transboundary breeds in Europe for their effective management and conservation

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Abstract: Geographical distribution plays a crucial role in the effectiveness of breeding and conservation programmes, especially for livestock breeds with a small population size. Among these, transboundary breeds present unique challenges and opportunities for conservation efforts. This study specifically examines the case of transboundary breeds in Europe and the associated challenges. Population and descriptive data were sourced from the Domestic Animal Diversity Information System (DAD-IS) to assess their current state of monitoring and management. The analysis revealed that 42% of the 6,460 National Breed Populations reported in Europe are transboundary, with 25% occurring exclusively within the region (Europe). Alarmingly, 85% of European transboundary breeds are classified as 'at risk' or have an 'unknown' conservation status, a fact that further accentuates the urgent need for improved sustainable management. This paper identifies key data gaps, for instance related to common understanding of concepts used by managers, and proposes improvements to enhance the monitoring, conservation and management of transboundary breeds in Europe.

Keywords: Transboundary breeds, DAD-IS, conservation, animal genetic resources, livestock diversity

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Introduction

Livestock diversity in Europe has been shaped by the collective management and selection practices of farmers, evolving within the region's political, economic and social environment. In Europe, systematic performance recording, animal identification and pedigree recording have contributed to the development of numerous livestock breeds (FAO, 2015). However, changes in market demand, environmental factors and political instability continue to impact farmers' selection decisions, directly influencing farmers' preferences and have a direct impact on a breed's population size (Cao et al, 2021; Verrier et al, 2015). A variety of migration, introgression and isolation events over time have influenced the domestic diversity within and among countries (Leroy et al, 2015). While some breeds remain confined to specific geographical areas, others are distributed across multiple countries or even globally. It is estimated that, on a global scale, half of all breeds are transboundary, i.e. shared between at least two different countries (FAO, 2024a; see Box 1 for definitions). Transboundary breeds (TBs) may be native to their current locations or introduced as exotic breeds, recently or a long time ago, sufficient to be considered adapted to the local environment (Box 1).

The conservation of animal genetic resources (AnGR) for food and agriculture became a priority in the late 20th century, driven by concerns over the loss of genetic diversity. This was motivated by observant breeders in some countries, who realized the risk early on. The next steps were taken by scientists, providing solid scientific evidence and contributing to enhanced awareness concerning the threats to global biodiversity. The understanding that the disruption of

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Box 1. Definitions of breed and breed classification concepts

Breed (FAO, 2000): is a homogenous, subspecific group of individuals with definable and identifiable external characters that enable it to be separated by visual appraisal from other similarly defined groups within the same species. Alternatively, it is a homogeneous group where geographical separation from phenotypically similar groups has led to general acceptance of its separate identity.

National Breed Population (NBP) (FAO, 2021): The NBP refers to the animals belonging to one specific breed in one country. In case it is a local breed, occurring only in one country, it represents the breed. In case it is part of a transboundary breed, occurring in more than one country, it represents only a part of a breed.

Adaptedness classification (FAO, 2015): The DAD-IS adaptedness classification differentiates exotic breeds from native/indigenous breeds and from locally adapted breeds. The latter correspond, in the classification, to non-native breeds that have become adapted to the local environment and/or production system.

Locally adapted breeds have been initially defined as breeds of exotic origin imported into the national territory from another country that show limited genetic relationship with the original population. Later the definition has been broadened as breeds which have been in the country for a sufficient time to be genetically adapted to one or more of the traditional production systems or environments in the country.

Native Breed (FAO, 2001): (also termed Indigenous Breeds, autochthonous) originating from, adapted to and utilized in a particular geographical region, form a subset of the **Locally Adapted Breed** (broader definition). It refers to a breed in its country of origin (i.e. the country where the breed was created originally from genetic material that was available when the initial breed development commenced). It is important to note that a breed may be a native breed in more than one country depending on the history of the breed.

historical links between breeders and the breeds developed by their ancestors had led to a decline in those breeds' population was the driving force for taking actions to interrupt this trend. Threats such as indiscriminate crossbreeding, the introduction of exotic breeds, weak institutional policies and economic challenges continue to endanger genetic diversity (FAO, 2015). Conservation efforts encompass a wide range of activities, including awareness raising, strengthening governance, adding value to natural resources and implementing conservation schemes (Ligda et al, 2013; Sponenberg et al, 2019). Genetic diversity losses and conservation issues are not limited to local breeds, as international breeds can also be subject to genetic erosion phenomena (Ablondi et al, 2022). Relevant strategies for AnGR management also concern international breeds due to their importance in ensuring food security and public health globally. Sustainable management of both local and international breeds is essential for global food security and agricultural resilience (Lefevre et al, 2024). Europe initiated conservation efforts in the late 1970s; however, global consensus on preservation of livestock diversity only emerged after the publication of the first report on the *State of the World's Animal Genetic Resources for Food and Agriculture* (FAO, 2007a). This led to the development of the *Global Plan of Action for Animal Genetic Resources* (GPA) (FAO, 2007b).

This framework outlines four strategic priorities: (1) characterization, inventory and monitoring of the breeds, (2) sustainable use and development, (3) conservation, and (4) policies, institutions and capacity building. The Domestic Animal Diversity Information System (DAD-IS), developed by the Food and Agriculture Organization of the UN (FAO), serves as a comprehensive database supporting these conservation and management efforts worldwide. DAD-IS contains information on breed characteristics, uses, geographic distribution and demographics, and images and tools for generating reports. The recorded information, based on agreed definitions on terms and classification criteria and provided by nominated National Coordinators, enables the monitoring of breeds at global, regional and national levels (Polack et al, 2022). Moreover, DAD-IS is the data source for two UN Sustainable Development Goals (SDG) indicators (2.5.1b and 2.5.2), as approved by the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) (FAO, 2011; FAO, 2013). In particular, SDG indicator 2.5.2 takes into account the proportion of breeds considered at risk of extinction, on the basis of their population size estimation. Initially focusing on local breeds, the focus of the indicator is currently extended to transboundary ones (FAO, 2024b).

Efficient breeding and conservation programmes for breeds with small population sizes are particularly challenging due to several reasons (Biscarini et al, 2015). These breeds often face geographic constraints, policy limitations and economic disadvantages, creating a cycle that restricts their development. However, the presence of such breeds across multiple countries presents opportunities for collaborative management. Understanding breed distribution across Europe, along with different environments and breeding conditions, can improve resilience assessments and utilization of genetic resources. Advances in molecular genetics enable systematic genomic studies that can further support the classification and management of TBs.

Definitions of specific terms used in this article are given to help the reader understand the situation of TBs (Box 1).

This study aims to explore the current status of TBs in Europe using DAD-IS data. It provides information on the distribution of TBs around Europe, their Risk Status at local and regional level and adaptedness classifications. The outcomes reveal the complexity of factors that impact the decisions concerning the management of TBs and focusses on certain areas for further analysis, using a case study approach.

Material and methods

Data for this analysis were extracted from FAO's DAD-IS using the 'Data export' tool. The data used include the descriptive and population data files, as well as the transboundary list file. The study included all 31 registered species in the 45 countries classified as 'Europe and Caucasus' (FAO, 2007b). All data was provided by the National Coordinators (NCs) appointed by the countries. The analysis was based on the population and historical data available as of 8 August 2023.

The analysis was built on the **National Breed Populations (NBPs)**, as defined in Box 1. The descriptive data included information on the Risk Status, Geographic and Adaptedness classification provided by DAD-IS. The population data file contained the information on the population size of the breeds for all years with recorded data. Based on this information, an NBP was classified into the Risk Status categories. An NBP was reported as TB when this NBP was linked (by the NC) to a breed in the TB list provided in DAD-IS. This is done automatically by DAD-IS, without taking into consideration the number of NBPs linked to the transboundary name. DAD-IS classified NBPs as local (reported in only one country), regional transboundary (reported as TB, only by countries from a given region, e.g. Europe), or **international transboundary** (reported as TB by countries from multiple regions). Breeds were further classified by DAD-IS as **native, locally adapted, or exotic**, based on reported data (Box 1).

Statistical comparisons were made to assess patterns in breed distribution, risk status, and adaptedness. Associations between categorical variables were analyzed using the Chi-square test via the Crosstabs procedure in SPSS version 27.0 (IBM Corp., 2020). Statistical significance was set at $p < 0.001$. Data gaps and inconsistencies were analyzed to identify possible reporting issues and areas for improvement.

Results

Assessment of the current situation

Among the 6,460 NBPs analyzed, 3,761 (58.2%) are local breeds, while 2,699 (41.8%) are transboundary. Of the transboundary NBPs (Figure 1), 674 (25%) are European TBs (found only within Europe), and 2,025 (31.3%) are international TBs (present in at least one non-European region).

These findings highlight the importance of coordinated conservation strategies within Europe. The presence of TBs across multiple countries suggests opportunities for shared conservation programmes.

TBs are reported by all countries in Europe, as shown in Figure 2. The TB share among NBPs exhibits considerable variation, ranging from 11,6% (Spain) to 77,1% (Ireland). No significant correlation is found between the share of TBs among NBPs and the number of NBPs reported by the countries.

The number of countries that declare a specific TB linked to their NBP, may reflect the dynamics of cooperation among

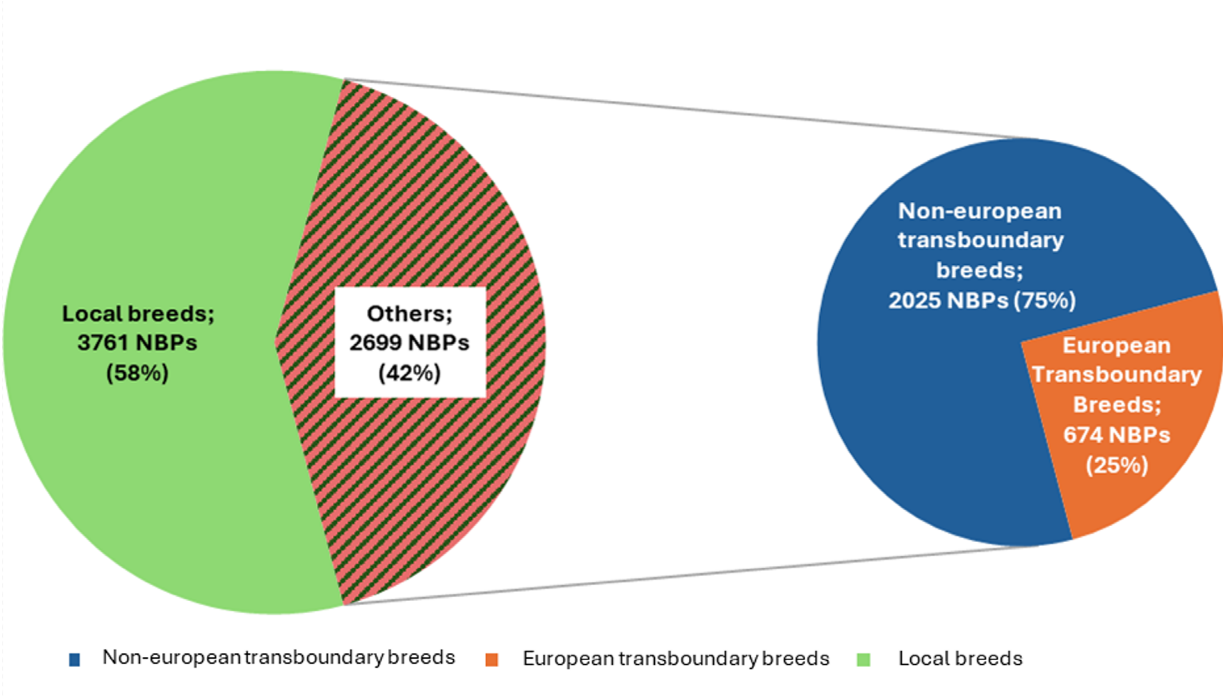


Figure 1. Repartition of the European National Breed Populations (NBPs) following their geographical classification, their corresponding number of NBPs (in brackets, the corresponding proportions). Data source DAD-IS.

the countries. However, further information on the historical evolution of the NBPs, the ongoing breeding or conservation programmes, organizational and social aspects is required.

Figures 3a and 3b provide information on the distribution of regional TBs between countries, in mammalian and avian species. In Figure 3a, the results are presented separately for the five mammalian species (cattle, goat, horse, pig and sheep), for which breed-related information is reported by almost all countries in the European region (cattle and sheep in 100% of countries, goats in 93%, and horses and pigs in 91%) (FAO, 2007a). Similarly, the results in Figure 3b concern avian species, for which breed-related information is reported by 50% or more European countries.

These figures present a general overview of the distribution of TBs at species level and do not infer a species impact on the number of countries linked to a TB.

Figure 3a (mammalian species) shows that a significant number of TBs is linked to only one NBP. This percentage varies between 25.9% (21 NBP) for sheep and 50% (7 NBP) for swine. In cattle, 13 (41.9%) of the 31 European TBPs are reported by only one country. Similar trends are observed in avian species (Figure 3b); however, this is referred to an overall smaller number of TBs and lower number of countries reporting breed data on these species. Those results underline a substantial gap between breeds classified as TBs according to DAD-IS rules and the fact that those breeds are actually reported by more than one country.

The fact that an NBP has not been linked to an existing TB name could be attributed to a different perception of the concept of TB; however, several other reasons may also exist. Therefore, a case study approach would be required to better understand the situation and propose a step forward.

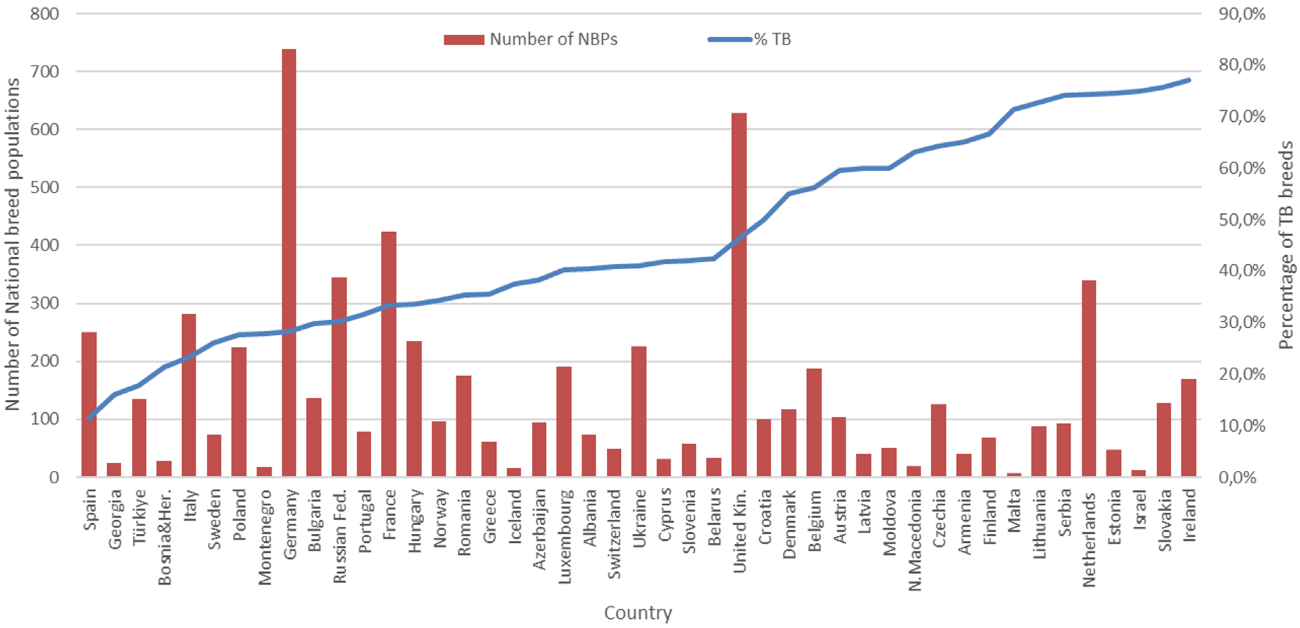


Figure 2. Number of National Breed Populations (NBPs) and percentage of Transboundary Breeds (TBs) declared per European country, ordered by increasing share of TBs.

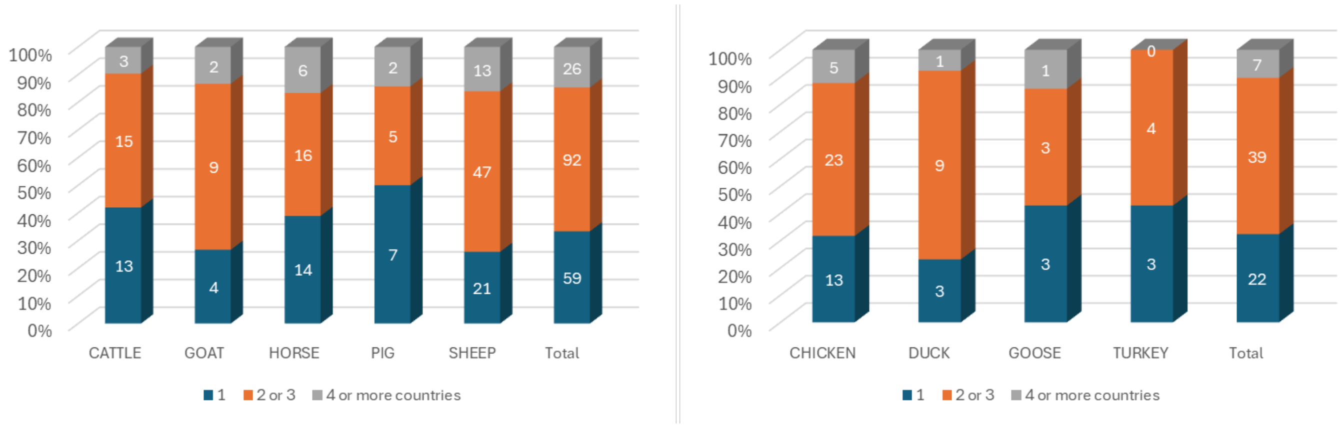


Figure 3. Regional transboundary breeds reported by one, two or three, and four or more countries across mammalian (a) and avian species (b).

Adaptedness classification

Considering the classification by adaptedness, from the total of 2,699 registered (regional and international) NBPs, 15% were classified as native, 10% as locally adapted and 36% as exotic (Table 1). The remaining 38% NBPs were not classified in any category, as no relevant data has been reported by any country. The substantial number of NBPs with no information on adaptedness classification in Europe (260 NBPs only reported in Europe) indicate that further progress is still needed in this domain. The high percentage of unclassified breeds suggests the need for clearer reporting standards across countries.

Nevertheless, compared to the corresponding figures at global level (45% of non-available classification, FAO 2023), the results of the European region are more complete. The high percentage of non-classified NBPs is attributed to several capacity or policy-related factors, reflecting the organization of AnGR management in each reporting country and the specific considerations on the definition of terms, at country level. Nevertheless, this gap may hinder the efficient management of AnGR, as the missing information could result in misleading reports and biased decisions. From the remaining, 26% (177 NBPs) are classified as exotic, thus they are considered as introduced from another country and have not been developed for sufficient time in the country.

Compared to international ones, European TBs display a larger proportion of locally adapted and native breeds ($P < 0{,}0001$), which could be partially explained by the fact that locally adapted and native breeds are more regionally distributed than the exotic ones, which have a wider global expansion.

The distribution of NBPs in adaptedness classes in European countries can be considered indicative of the current picture of breeds; however, an in-depth analysis of relevant case studies is needed. The data show that in 14 countries no information is available concerning the adaptedness classification of their recorded NBPs (linked to TB), while in 21 countries, more than 80% of their NBPs have recorded information on the adaptedness classification (Figure 4).

Table 1. Number and percentage of international and regional national breed populations linked to transboundary breeds in Europe in DAD-IS (classified as native/locally adapted/exotic)

	Breed classification (geographic)		
Breed classification (adaptedness)	**International**	**Regional (Europe)**	**Total**
	No (%)	**No (%)**	**No (%)**
Native	225 (11)	184 (27)	409 (15)
Locally adapted	218 (10)	53 (7)	271 (10)
Exotic	809 (39)	177 (26)	986 (36)
Non-available	773 (38)	260 (38)	1,033 (38)
Total	2,025 (100)	674 (100)	2,699 (100)

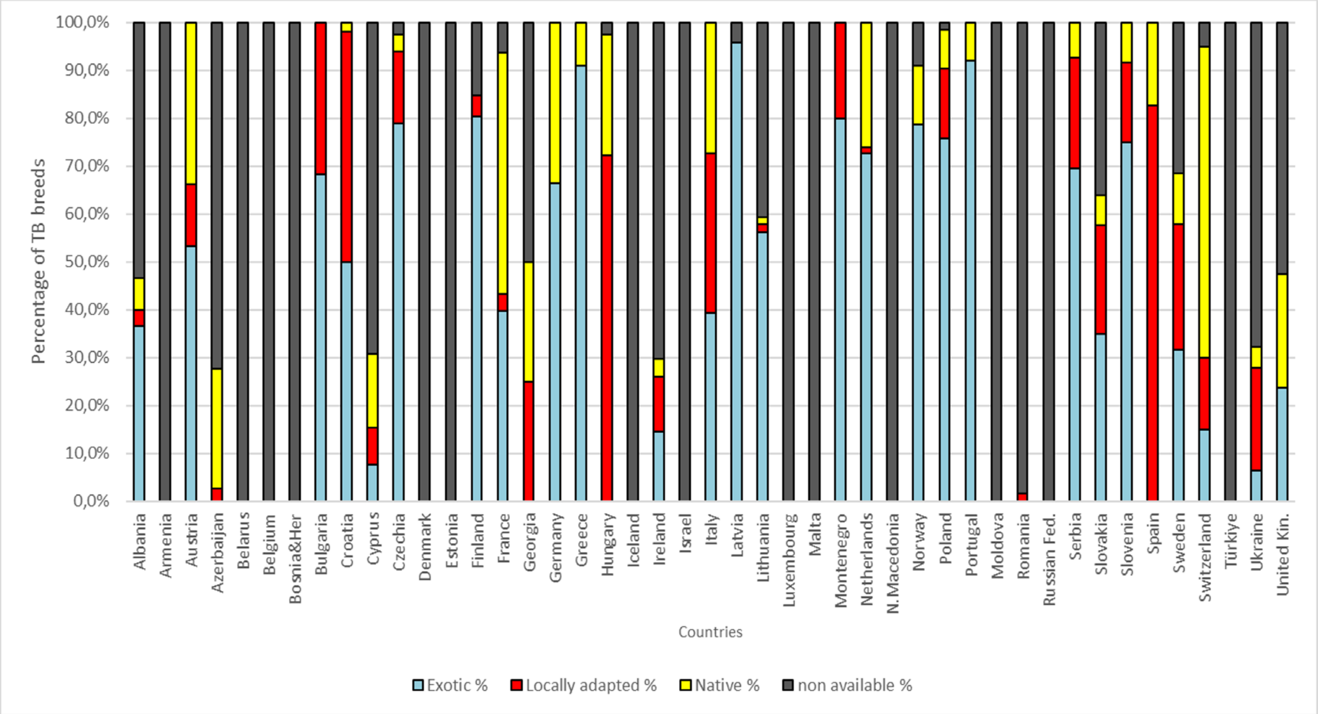


Figure 4. Adaptedness classification of national breed populations linked to transboundary breeds (TB) in Europe

Risk status

Specific thresholds differentiated by species are defined in various countries through national and international regulations that provide the framework for AnGR management. The current analysis is based on the local risk status, following FAO's classification system, which is recognized as the global reference according to CGRFA (FAO, 2013). In the case of TBs, in DAD-IS the risk status is estimated at local, regional and global levels, provided that the country has been reporting population data for the past ten years. The estimation of risk status at different levels, in the case of TBs, could support their efficient conservation management, as different approaches are needed when a TB is at risk in one country, but not at risk in other(s), or when the TB is at risk everywhere.

Among the 674 NBPs found in more than one European country, 44.2% were considered at risk in at least one country (Table 2). Moreover, considering that the existence of sufficient recorded data and knowledge of population trends is a key point for the efficient management of breeds, 45% of NBPs in the 'unknown' category, i.e. without population data provided over the last ten years, could be interpreted as a first sign of being at risk. Therefore, this could be considered an early indicator of the current or potential risk at national level of the nearly 90% of NBPs that are transboundary (reported only in Europe). However, a more in-depth analysis of these data is needed, as NBPs (from TBs) could be at risk in one country and not in others, as previously mentioned.

Therefore, further examining the data in Table 3, the NBP's risk status was calculated under different combinations for the five species considered in this study. In Table 3, it is shown that 42% of goat and 30% of sheep NBPs linked to a TB, were reported at risk in all countries. When the 'unknown' category is added, this percentage increased to 75% and 70%, respectively. The higher percentage of sheep and goat NBPs that were at risk in all countries could be explained, at least to some extent, by the different evolution of sheep and goat populations compared to cattle and pigs, for which intensification has been more widespread.

Table 2. Local risk status of all national breed populations related to TBs reported by at least two countries in Europe.

Breed classification (geographic)		At Risk	Cryoconserved only	Extinct	Not at Risk	Unknown	Total
International	Count	844	2	108	230	841	2,025
	Row N %	41.7	0.1	5.3	11.4	41.5	100.0
Regional	Count	298	1	33	39	303	674
	Row N %	44.2	0.1	4.9	5.8	45.0	100.0
Total	Count	1,142	3	141	269	1,144	2,699
	Row N %	42.3	0.1	5.2	10.0	42.4	100.0

Table 3. Local risk status of transboundary breeds present in more than one country, (%) by species

	Not at risk in at least one country (%)	At risk in all countries (%)	At risk or unknown or extinct in all countries (%)
Cattle	11.76	5.88	88.24
Goat	8.33	41.67	91.67
Horse	22.73	9.09	77.27
Pig	14.29	14.29	85.71
Sheep	26.67	30.00	73.33
Total	21.19	22.88	78.81

The diversity of cases is presented with selected examples in Table 4. The Hutsul horse reported as TB by eight countries, is at risk in six countries and unknown in the remaining two, due to lack of data. The Hutsul horse is categorized as native in Hungary, Austria and Poland, while it is defined as locally adapted in Slovakia and Czechia, and exotic in Germany. The field was not filled in the remaining two countries. The TB is at risk at regional level. The case of Precoce sheep, reported by France (native), Spain (locally adapted) and Portugal (exotic) is a similar case, as the breed is at risk at national and regional levels. However, the case of the Ouessant sheep – present in six countries, native in France and exotic in the Netherlands, Germany and Czechia (no classification in Belgium and Denmark) – differs as it is at risk in all countries, but the breed is not at risk at regional level. The Podolian cattle represents a case where the breed is developed in the country of origin (Italy), bred in high numbers, while a small population (at risk) is bred in another country (Serbia). In the DAD-IS data analyzed, there was no information on the links and exchanges between breeders' associations or on the genetic differences between NBPs.

Discussion

This study, based on the data reported in DAD-IS, provides a general overview of the status of TBs in Europe and reflects the quality of data and level of recorded information. In Europe, NBPs linked to TBs account for a large part (42%) of NBPs reported. This number could reach up to 80% of NBPs in some countries, with varied percentages across countries. The interpretation of this variation is not straightforward, as various factors contribute to this picture. AnGR have evolved under specific conditions (physical, technical, social, political and organizational) in each country, forming the current breeds and links among countries. Furthermore, AnGR management is under a country's sovereignty, and national decisions and measures are in accordance with global (FAO) and European guidelines.

Approaches to identify the link between NBPs and TBs may differ among countries according to national needs and perceptions of terms. Our results highlight that, depending on the species, a percentage between 20% and 50% of European TBs are reported by only a single country. This raises concerns about data accuracy and consistency. Although this issue appears less significant at the global level – where only 17% of TBs are reported by a single country – it remains noteworthy in the European context. In Europe, several such breeds are not linked to the TB list by their country of origin. Examples include the Turopolje pig from Croatia, the Asino Sardo donkey from Italy and the Olkusz sheep from Poland. In some cases, this cannot be considered a reporting gap, as it is a justified decision by the NC. Such decisions could be based on specific national policies and priorities. Certain countries could have chosen to classify their native breeds as local, given that global indicators mainly focus on local breeds.

Table 4. Transboundary breed cases examples

Species	Transboundary breed name	Local breed name	Country	SDG local risk status	Adaptedness	Regional risk status
Horse	Hutsul	Hucuł	Poland	At risk	Native	At risk
		Hutsul	Romania	Unknown	No info	
		Hucuł	Slovakia	At risk	Locally adapted	
		Hucuł	Hungary	At risk	Native	
		Huzule	Germany	At risk	Exotic	
		Gutsul	Ukraine	At risk	No info	
		Huzule	Austria	At risk	Native	
		Huculsky kun	Czechia	At risk	Locally adapted	
Cattle	Podolian	Podolica	Italy	Not at risk	Native	Not at risk
		Podolian	Serbia	At risk	Locally adapted	
Sheep	Precoce	Merino Precoz	Spain	At risk	Locally adapted	At risk
		Merina Precoce	Portugal	At risk	Exotic	
		Mérinos précoce	France	Unknown	Native	
Sheep	Ouessant	Ouessant	France	At risk	Native	Not at risk
		Ouessant	Belgium	At risk	No info	
		Ouessant	Netherlands	At risk	Exotic	
		Ouessant Schaf	Germany	At risk	Exotic	
		Kesantská ovce	Czechia	At risk	Exotic	
		Ouessant	Denmark	At risk	No info	

The global indicators employed to assess goal attainment may introduce biases in data entry into global databases. These biases can also arise from the implementation of national indicators or adherence to national legislation. An illustrative example of a national rules-based decision is the case of the Icelandic Horse, which is reported by several countries, even though Iceland itself does not link it to the TB list. This is due to national legislation prohibiting the re-importation of Icelandic horses, which results in the national population being considered genetically isolated (Campana et al, 2011). In addition to these cases, certain widely used industrial pig and poultry lines – such as the Topigs Lignée E (TN Tempo) pig line, currently reported only by the Netherlands – may appear underreported due to limited data exchange between private breeders and NCs. It cannot be excluded that in a number of cases, a breed in the TB list is actually present in only one country; however, it is likely that the greater part of this gap is caused by underreporting in countries. To address this issue, NCs could be encouraged to review the breeds listed in Supplemental Table 1 – particularly those listed in the first column (TB reported by only one country) – and assess whether NBPs from their own country should also be linked to this list. Complementarily, FAO, in collaboration with NCs and relevant stakeholders, should undertake efforts to clarify the definitions and utilization of breed classifications. This includes revisiting the criteria used to associate NBPs with TB names, to ensure greater consistency and completeness in reporting.

Several actions initiated within the framework of the European Regional Focal Points for Animal Genetic Resources (ERFP) aim to facilitate exchange among countries and promote agreement on common perspectives. At the same time, however, it is important to recognize that the existing variation among countries could also be beneficial, as it reflects diverse needs and priorities. Genomics could play a key role in the management of TBs and provide strong scientific evidence to justify further steps. The developments in genetics and the wide availability of genomic tools could reveal genetic diversity between NBPs that have evolved in different environments and have been bred under separate breeding programmes for certain time periods. Whole genome sequencing (WGS) could offer valuable information on the demographic history of populations to support decisions relevant to the management of TBs.

Thus, the management of TBs can be approached considering the existing definitions of breeds. According to the definition used by FAO (FAO, 1999), a breed is not a simple genetic concept, but it also has a social dimension. Breeds are developed by the farmers' breeding practices, which are not exclusively technically driven. Several exogenous factors have an impact on them. In certain cases, such factors could radically change the environment in which the farmers work. Generalized guidelines and rules cannot be easily applied in the case of TBs. A common understanding of the term 'transboundary breed', based on both genetic and social parameters, could help in developing appropriate approaches. However, one should be very sceptical in defining specific criteria that could be used in all cases, as the decision is not clearly technical, but also political, to a large extent.

Besides the aspect of demographic data quality, which results in an unknown risk status, the outcomes of our analysis highlight certain inconsistencies related to the approach followed in setting the TB groups, as shown by the number of TB groups, to which only one NBP is linked. Taking this into account, the results can be considered as a first step in choosing breed cases that could be further analyzed, incorporating additional information.

By examining TBs through case studies, either in neighbouring countries or across more widely spread breeds, useful conclusions could be drawn that may serve as guiding principles on a broader level. The knowledge of whether breeders cooperate already, i.e. through the exchange of breeding animals, is important for grouping TB cases and could be essential for making decisions in terms of *ex situ* conservation. Mainstream breeds that are exported to other countries and are raised under separate breeding programmes, or with continuous import of breeding animals or semen, fall into this category; however, further elements are needed to decide on implementing common breeding programmes. Which criteria could be used to consider these NBPs as the same breed? Furthermore, changes in European borders over the past 25 years, which have resulted in some TBs being native to multiple countries with different local risk status, present an interesting case study, linking genetics with economic, social and political changes.

The level (local, regional or global) at which the risk status is estimated is a crucial point for TB management. The relevance of risk status at regional level is questionable when two (or more) NBPs have been developed separately for years. Besides that, the risk status classification is one of the critical points leading to reluctance in linking a NBP to an existing transboundary name. This is demonstrated in the current analysis by the number of NBPs that are declared as transboundary by only one country (listed in Supplemental Table 1).

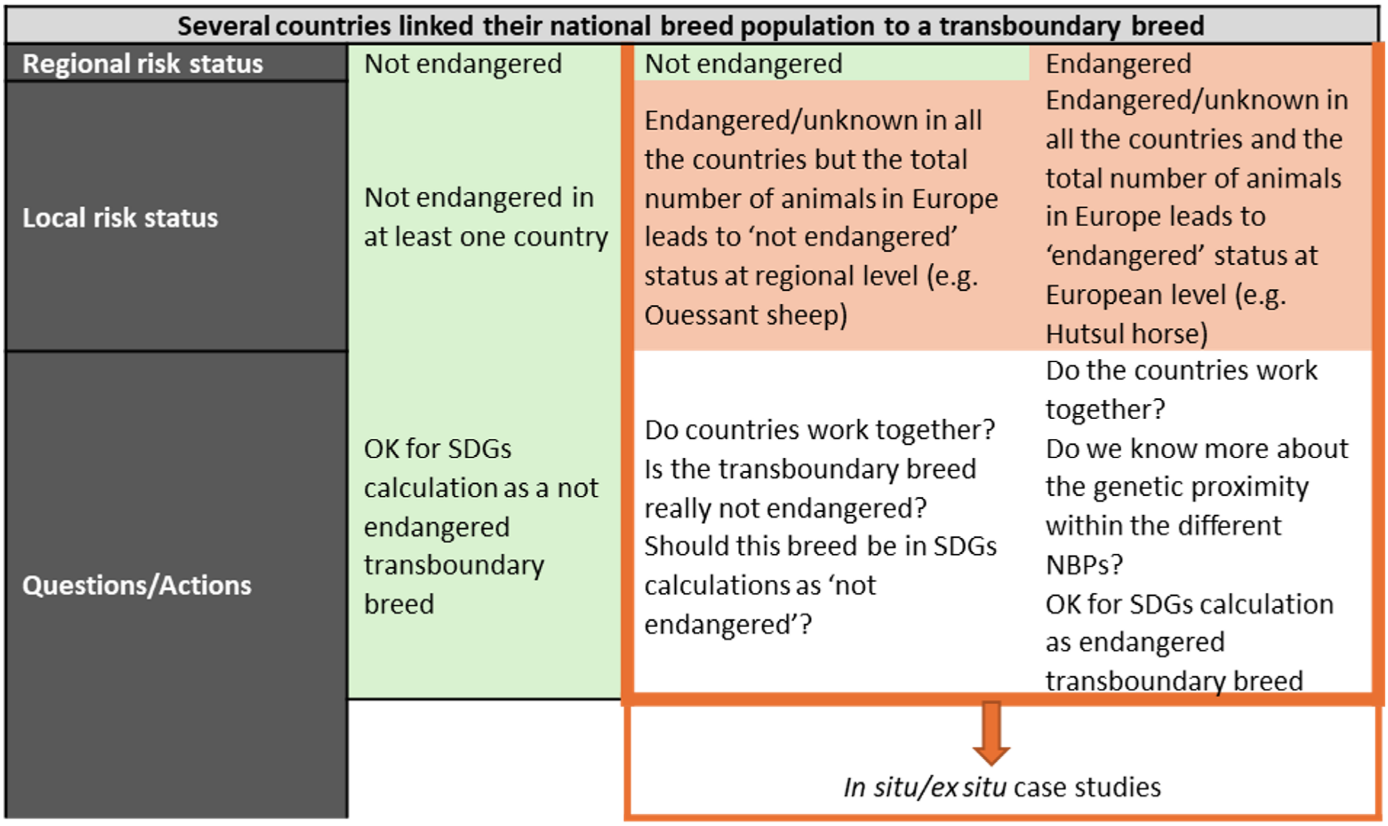
The various combinations of risk status at local and regional levels could be the starting point of the case study approach, following the general approach presented in Figure 5. Supplemental Table 1 provides the list of European TBs that could be examined following this general approach.

Conclusions

This article provides new evidence on the status of TBs in Europe, assessing the quality of data and the frequency of updates to population data and relevant fields, as reported in DAD-IS. These outcomes could be useful in improving data quality and population management by enhancing data exchange and communication among countries.

Data analysis revealed several inconsistencies, as is the case with TBs linked to only one NBP, which opens the discussion on the definitions of TBs and the criteria applied to link a NBP to a TB. Under which conditions would it be feasible to establish unified criteria, including historical data and genetic information? The lack of standardized definitions and consistent risk classifications across countries poses significant challenges for TB management. Collaborative breeding programmes, genetic studies and enhanced data sharing could improve conservation outcomes. Advances in genomics can further clarify genetic relationships among NBPs, supporting more effective conservation planning.

As discussed above, TBs cannot be examined exclusively through demographic data and genetic information, as several technical, social and political aspects shape future management opportunities. Thus, a case study approach is recommended for the analysis of breeds, either *in situ* or *ex situ*, when they



Several countries linked their national breed population to a transboundary breed			
Regional risk status	Not endangered	Not endangered	Endangered
Local risk status	Not endangered in at least one country	Endangered/unknown in all the countries but the total number of animals in Europe leads to 'not endangered' status at regional level (e.g. Ouessant sheep)	Endangered/unknown in all the countries and the total number of animals in Europe leads to 'endangered' status at European level (e.g. Hutsul horse)
Questions/Actions	OK for SDGs calculation as a not endangered transboundary breed	Do countries work together? Is the transboundary breed really not endangered? Should this breed be in SDGs calculations as 'not endangered'?	Do the countries work together? Do we know more about the genetic proximity within the different NBPs? OK for SDGs calculation as endangered transboundary breed
		In situ/ex situ case studies	

Figure 5. Questions and actions depending on transboundary breeds' risk status at different levels, depending on the national breed population's status (NBPs) and the impact on the calculation of the indicators for the Sustainable Development Goals (SDGs).

participate in common breeding programmes, frequently exchange breeding animals, or share a common history and/or environment.

This discussion is in accordance with the recommendations of the Animal Genetic Resources Strategy for Europe, that promotes *in situ* and *ex situ* strategies for TBs (ERFP, 2021). Specific actions are foreseen to improve the knowledge on TBs, support the exchange between actors involved in the conservation and breeding programmes of these breeds and promote cooperation in this field (ERFP, 2021). In this complex context, the advances in genomics and the progress of relevant research could further enrich existing knowledge on TBs and support their sustainable management.

Supplemental data

Supplemental Table 1. Distribution of European transboundary breeds (TBs) and their risk status

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Author contributions

All the authors have conceptualized the analyses and drafted the manuscript. Eleonore Charvolin and Dimitrios Tsiokos performed the data analyses. All the authors have substantially contributed to the interpretation, drafting, revision and final version of the manuscript.

Data availability

Data used in this study were extracted from FAO DAD-IS and are publicly available (https://www.fao.org/dad-is/data/en/).

Conflict of interest statement

The authors declare that they have no conflicts of interest.

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