





Article

Genetic Diversity of Five Galician (Northwestern Spain) Local Primitive Bovine Breeds Using Pedigree Records

María Asunción García-Atance ¹, Carlos Carleos ², Sandra Andrino ³ , José Ramón Justo ⁴, Castor José Rivero ⁴, Miguel Fernández ⁵ , Javier Cañon ³  and Oscar Cortes ^{3,*} 

¹ Facultad de Veterinaria, Universidad Alfonso X El Sabio, Avda. Universidad, 1., Villanueva de la Cañada, 28691 Madrid, Spain

² Departamento Estadística e Investigación Operativa, Universidad de Oviedo, 33007 Oviedo, Spain

³ Departamento de Producción Animal, Facultad de Veterinaria, Universidad Complutense de Madrid, 28040 Madrid, Spain

⁴ Federación de Razas Autóctonas de Galicia-BOAGA, 32152 Fontefiz, Spain

⁵ Centro Tecnológico de la Carne de Galicia, 32900 San Cibrao das Viñas, Spain

* Correspondence: ocortes@vet.ucm.es; Tel.: +0034-913943757

Abstract: Characterization, inventory and monitoring trends of animal genetic resources of local breeds are crucial factors for the development of conservation strategies. Using genealogical information, the genetic diversity of five Spanish local bovine breeds located in the northwest of Spain in the region of Galicia, and called in the past Morenas Gallegas (Cachena, Caldelá, Frieiresa, Limiá and Vianesa), has been analysed. The results achieved a good quality of pedigree records in terms of integrity and deepness. In spite of the low census of the five breeds, (no more or even less than one thousand animals), the strategies developed for genetic diversity conservation since the end of the last century revealed positive results. An increase of generation intervals, the use of reproductive technologies and a higher animal exchange between herds are some strategies suggested to preserve the genetic diversity of the five Galician bovine breeds analysed.

Keywords: Cachena; Caldelá; Frieiresa; Limiá; Vianesa; pedigree analysis; genetic diversity; effective size; inbreeding



Citation: García-Atance, M.A.; Carleos, C.; Andrino, S.; Justo, J.R.; Rivero, C.J.; Fernández, M.; Cañon, J.; Cortes, O. Genetic Diversity of Five Galician (Northwestern Spain) Local Primitive Bovine Breeds Using Pedigree Records. *Diversity* **2023**, *15*, 252. <https://doi.org/10.3390/d15020252>

Academic Editor: Luc Legal

Received: 4 January 2023

Revised: 8 February 2023

Accepted: 8 February 2023

Published: 10 February 2023



Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

The knowledge of the genetics factors that increase the risk of extinction of a population and the strategies to minimize such risks are crucial factors in the conservation of the Animal Genetic Resources (AnGR) [1]. Main factors to be considered in genetic conservation programs are the inbreeding depression, that mainly affect to reproductive and survival traits, the loss of genetic variability, that decreases the ability of the populations to adapt to environmental changes, or particularly in small size breeds the genetic drift that reduces the genetic variability of the populations [2]. Other non-genetic factors can have a negative impact on the conservation of AnGR, such as the global spread of a few highly productive breeds especially in the last 50 years, like the Holstein-Frisian dairy breed. This global diffusion is endangering many local populations which are less productive but well adapted to the local environment [3]. Interest in these local breeds has grown in recent years because their local adaption will become more important for the adaption to climate change, for food supply or as a principal component of many farming systems [4].

In the northwest of Spain, in the region of Galicia, there are located a racial group of five local cattle breeds called in the past Morenas Gallegas (Figure 1), with a long process of local adaption to a particular orography and environmental conditions, and linked to the history of their habitation [5]. Since the first archaeological evidence of pastoral activities in Galicia, approximately five to six thousand years ago, the pastoral practices reflect their adaption to the specific Galician geography [6]. In the 17th century there were more than

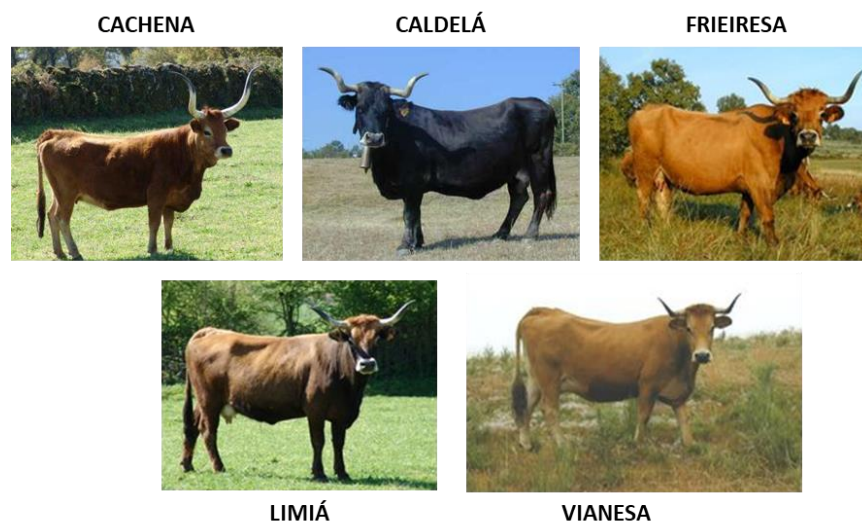


Figure 1. Individuals of the five Galician bovine breeds Cachena, Caldelá, Frieiresa, Limiá and Vianesa.

2. Materials and Methods

Pedigree records were obtained from the official studbooks (Federacion de Razas Autoctonas de Galicia (BOAGA)) of the five analysed breeds Cachena, Caldelá, Limiá, Frieiresa and Vianesa for those animals born until 2021. A reference population was defined as the calves born after 2017. After editing the complete genealogical information, the total number of genealogical records for each breed and for the reference population is shown in Table 1. The analyses were grouped as follows.

2.1. Pedigree Quality and Generation Interval (GI)

The quality of the pedigree was estimated with the Index of Completeness (IC), defined as the proportion of ancestors known in each ascending generation [18]. The number of the Equivalent Complete Generations (ECG) is defined as the sum of overall known ancestors of the terms computed $(1/2)^n$, where n is the number of generations separating the individual to each known ancestor [19]. The generation intervals were calculated for the four pathways (father-son, father-daughter, mother-son and mother-daughter) following the procedure describe by Lacy (1989) [20]. The average generation interval for each population is defined as the average of the 4 pathways.

2.2. Inbreeding Coefficient (F), Average Relatedness (AR), Increase in Inbreeding (ΔF) and Effective Population Size (N_e)

The inbreeding coefficient is defined as the probability that two alleles of an individual at any locus was identical by descent. Relatedness is the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal. The increase in inbreeding was estimated as $(F_t - F_{t-1}) / (1 - F_{t-1})$, where F_t is the average inbreeding coefficient of the animals born in the las generation. F_{t-1} was calculated as $F_t - b \times GI$, where b was the regression coefficient of the individual inbreeding on the year born (ΔF_y), or on the equivalent complete generation (ΔF_{ECG}). Finally, the effective population size then was computed as:

$$N_e = \frac{1}{2\Delta F} \quad (1)$$

The inbreeding coefficient after 50 years was estimated as:

$$F_{50} = 1 - (1 - \Delta F)^g \quad (2)$$

where g is the resulting number of generations after 50 years. F_{50} was computed based on ΔF_y and ΔF_{ECG} .

An Analysis of Variance (ANOVA) for the inbreeding coefficient of the entire and reference population, for the inbred animals, for the animals with $F > 6.25$ and for the average relatedness was done using the SAS proc general linear models. Means were separated following the method of Duncan multiple range test and differences at a $p < 0.05$ were considered to be statistically significant.

2.3. Probability of Gene Origin

The effective number of founders that equally contribute to produce the same genetic diversity as the population under study was computed:

$$f_e = \frac{1}{\sum_{k=1}^f q_k^2} \quad (3)$$

where q_k^2 is the probability origin of k ancestor [14].

The effective number of ancestors is the minimum number of ancestors, founders or not, that explain the total genetic variability of the population and was estimated:

$$f_a = \frac{1}{\sum_{j=1}^n q_j^2} \quad (4)$$

where q_j^2 is the marginal contribution of j ancestor [14].

The number of founder genome equivalents (f_g) represents the number of founders with equal contributions, that explain the genetic diversity of the population under study and no occurring loss of alleles [21]. It was computed following Caballero and Toro (2000) [22] procedures as the inverse of twice the average co-ancestry of the animals of the reference population.

The influence of the different sources that explain the loss of genetic diversity from the founder population to the present day (bottlenecks) can be estimated from the parameters previously describe: f_a , f_e and f_g .

The ratio f_a/f_e measures the effects of the bottlenecks from the founders to the present population. Values close to 1 indicate low genetic diversity losses due to bottlenecks. Furthermore, from f_e and f_g parameters, different diversity parameters can be estimated given information about the main causes of genetic diversity losses.

The loss of genetic diversity since the founder population due to bottlenecks and genetic drift was estimated as 1-GD (Genetic Diversity), GD being:

$$GD = 1 - \frac{1}{2f_g} \quad (5)$$

The loss of genetic diversity due to the unequal contribution of founders was computed as 1-GD*:

$$GD^* = \frac{1}{2f_e} \quad (6)$$

Finally, the loss of genetic diversity due to genetic drift over non founder generations is GD^*-GD , and can also be estimated as the inverse of twice the effective number of non-founders (f_{ne}) [20,22,23].

The software packages PEDIG [24] and ENDOG V4.8 [25] were used to analyse the pedigree information.

3. Results

The evolution of the animals registered in the studbooks evidenced a positive tendency since 2000, except for the period 2011 to 2014 that decreased proportionally to their census in the five breeds analysed (Figure 2). During this period, agricultural subsidies of the EU disappeared, and it is well known that local breeds are dependent on those subsidies. In such conditions, farmers replace their animals with others from more productive breeds, and also increase the non-registration of births.

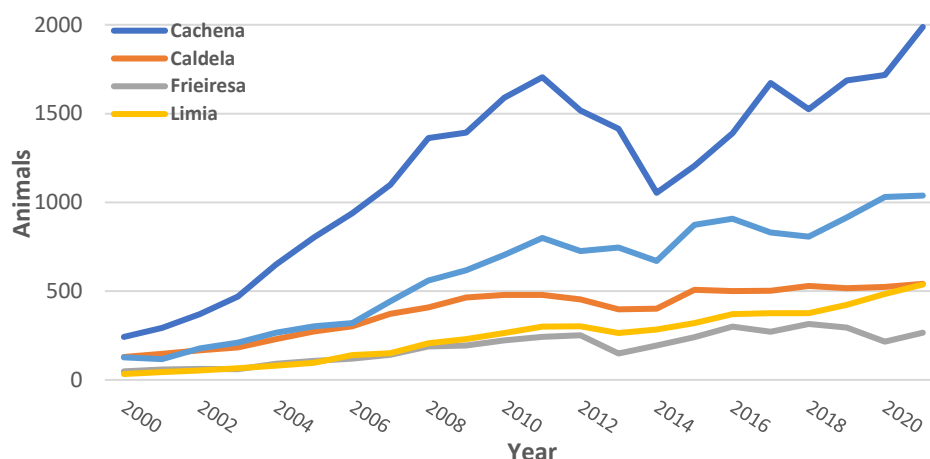


Figure 2. Census evolution of the five Galician bovine breeds.

The IC ranged from 96% to 75% for the entire population and from 100% to 89% for the reference population in the fourth first generations. The Cachena breed showed the highest ECG value of 5.3, and Limiá the lowest of 4.5 (Table 1).

The GI ranged from 5.8 in Cachena to 6.6 in Limiá and Frieiresa. For the reference population, the GI was similar for all the breeds (≈ 7), except for Frieiresa which was higher (8) (Table 1). The GI was higher for the reference population than the total population, with few exceptions, and for the Limiá breed which decreased in three of the four pathways.

The inbreeding coefficients ranged from 4.2 to 5.6 for the reference population, being relatively similar to co-ancestry values for Cachena, Caldela and Vianesa, and slightly higher for Fieiresa and Vianesa (Table 2; Supplementary Table S1). In all the breeds, more than two thirds of the animals show inbreeding coefficients different than 0, and ranged from 14 to 24% when higher than 6.25%. The percentage of high inbred matings was higher than 6% for all the populations, and Caldela achieved the highest value (7.9%).

Table 2. Different Inbreeding and average relatedness parameters. Percentage of highly inbred mating in the five Galician bovine breeds. Different letters indicate statistically significant differences at $p < 0.05$. Reference population refers to those animals born since 2017 to 2021.

	Cachena	Vianesa	Caldela	Limiá	Frieiresa
Inbreeding (%) Total Population	3.1 ^c	3.1 ^c	4 ^a	4.1 ^a	3.7 ^b
Inbreeding (%) Reference Population	4.3	4.2	5.6	5.2	5.1
Percentage of Inbreeding Animals	77.4	69.8	79.2	73.2	76.4
Inbreeding (%) Inbred Animals	4 ^a	4.5 ^b	5.1 ^c	5.6 ^d	4.8 ^e
Percentage Animals F > 6.25	14.4	16.0	20.5	24.1	19.5
Inbreeding Animals F > 6.25	17.5 ^a	17.3 ^a	15.5 ^b	14.7 ^c	14.1 ^c
Average Relatedness (%)	3.5 ^e	4 ^d	5.6 ^c	7.3 ^a	6.8 ^b
Matings (%)					
Half-sibs	2.2	2.4	3.2	2.9	2.1
Parent-offspring	4.6	3.6	4.7	4.7	4.6
Total	6.8	6.0	7.9	7.6	6.7

The effective population size considering the pedigree content (ΔF_{ECC}) was below 50 on all the breeds analysed, and was higher than 50 in Cachena, Caldela and Vianesa when was calculated from ΔF_y . The increase in inbreeding after 50 years achieved higher differences when was estimated from ΔF_y (range: 6.3–9.1) than with ΔF_{ECC} (range: 8–9.8) (Table 3).

The four parameters of gene origin (f_a, f_e, f_g and effective number of non-founders) show a similar pattern in the breeds analysed. Cachena showed the highest values, while Limiá and Frieiresa showed the lowest values, and were very similar among them. Caldela

and Vianesa achieved intermediate values, but Caldelá was closer to Cachena, and Vianesa was closer to Limiá and Frieiresa (Table 4).

Table 3. Effective population size based on year of birth and on Equivalent Complete Generations of the five Galician bovine breeds.

	N_e		F50	
	ΔF_y	ΔF_{ECC}	ΔF_y	ΔF_{ECC}
Cachena	52	45	7.2	8.3
Vianesa	58	48	6.7	8
Caldelá	65	46	6.3	8.8
Limiá	42	40	9.1	9.5
Frieiresa	40	37	9.1	9.8

Table 4. Probability of gene origin parameters and ancestor contribution of the five Galician bovine breeds.

	Cachena	Vianesa	Caldelá	Limiá	Frieiresa	
f_e	45	43	32	26	26	
f_{ne}	18.9	15.7	10.9	8.4	8.7	
f_a	41	33	25	22	22	
f_g	13.3	11.2	7.9	6.3	6.4	
f_a/f_e	0.9	0.8	0.9	0.9	0.9	
1-GD	3.8	4.5	6.3	7.9	7.8	
1-GD*	1.1	1.3	1.7	2.0	2.1	
GD-GD*	2.6	3.2	4.6	5.9	5.7	
Ancestors contribution	25%	6	4	4	3	4
	50%	14	12	9	8	8
	75%	32	35	18	18	16
	90%	68	76	30	38	26

In all the breeds analysed, the ratio f_a/f_e was closer to 1, suggesting similar contributions of ancestors and founders, and no evident signal of bottlenecks effects. However, the differences among f_g with respect to f_a , and f_e would highlight genetic drift effects on the loss of genetic diversity. In addition, the loss of genetic diversity due to non-founder generations was at least twice than that of founder generations. Furthermore, Limiá and Frieiresa were the breeds with higher losses of genetic diversity from founder generations. Cachena and Vianesa were the breeds with a higher number of ancestors contributing to the gene pool of the current reference population (Table 4).

Robertson (1953) [26] classified the herds of a breed according to their genetic flow. Those herds that use their own sires and also sell them are classified as “nucleus”, and are the drivers of the genetic progress, with the remaining herds reflecting the genetic composition of the nucleus herd. The “multipliers” herd multiply the genes of the nucleus herd and pass them to other herds, so there are herds that use purchased sires, sell them, and also have the option to use their own sires. Finally, the “commercial” herds never sell their own sires, so they use purchased and owned sires. The Robertson herd classification of a breed can evidence to what extent a breed followed the model nucleus-multiplier-commercial model of genetic progress. Within each breed, the herd management evidenced that none of them can be considered as nucleus or isolated (Table 5). Among the herds that sell males, the number of herds that also use their own males is greater than the ones that never use their own males (nucleus type A and B), except for the breed Limiá which is the opposite. However, in Cachena breed this difference is higher than in the other three breeds (Caldelá, Frieiresa and Vianesa). Among the commercial herds (no selling of males and purchase them) those that use their own males are fewer in number than those that use them, in all the breeds analysed. It is remarkable that in Caldelá, Limiá, Frieiresa and Vianesa the most common management of the herds entails no selling, and use their own males, so the male genetic progress comes from the purchase of males from other herds.

In Cachena, more than 50% of their herds use their own males and also sell and purchase them (Table 5).

Table 5. Number of herds of the five Galician bovine breeds classified as Nucleus, Multiplier, Commercial and Isolated, according to Robertson (1953). UPB: Herds using purchased sires; UOB: Herds using their own sires; SB: Herds selling bulls used as sires; NH: Number of herds per herd type; PPB: Percentage of purchased sires.

Type	UPB	UOB	SB	Cachena		Caldelá		Frieiresa		Limia		Vianesa	
				NH	PPB	NH	PPB	NH	PPB	NH	PPB	NH	PPB
Nucleus	No	Yes	Yes	0	0	0	0	0	0	0	0	0	0
Multipliers_1	Yes	Yes	Yes	171	0.45	26	0.67	10	0.51	11	0.70	30	0.67
Multipliers_2	Yes	No	Yes	25	1	15	1	6	1	17	1	24	1
Commercial_1	Yes	Yes	No	40	0.61	9	0.80	3	0.4	2	0.74	11	0.83
Commercial_2	Yes	No	No	79	1	43	1	30	1	37	1	50	1
Isolated	No	Yes	No	0	0	0	0	0	0	0	0	0	0

4. Discussion

The programs for conservation of Morenas Gallegas bovine breeds that began in the 1980s have favoured a greater completeness of the pedigree records than in other Spanish autochthonous bovine breeds that later began such activities [6]. As a consequence, the genetic diversity parameters that are sensitive to the quality and quantity of the information, e.g., inbreeding coefficient can be considered reliable. It is remarkable that the ECG of the five cattle breeds is higher than that in other autochthonous Spanish beef cattle breeds, as the nine cattle breeds analyses by Cañas-Alvarez et al. (2014) [27] and González-Cano et al. (2022) [13] ranged from 1 in Bruna dels Pirineus to 4.6 in Pirenaica.

The increase of the generation interval (GI) from the total population to the reference population shown a good tendency in the last years for the Mother-Son, Mother-Daughter and Father-Daughter paths. However, the Father-Son path has decreased in the five Galician bovine breeds (except for Caldela), revealing an earlier substitution of breeding males for their sons. So, for the short term, two approaches that could improve the conservation of the genetic diversity should be (1) an increase of the Father-Son path, and (2) the development of strategies to avoid matings between close relatives, and as a consequence decreasing the current percentage of high inbred matings, as well as increasing the generation intervals. It is well known that an increase of GI negatively affects the genetic gain per unit of time, but also increases the effective population size and decreases the annual rate of inbreeding, which are more relevant parameters for conservation programs. However, the marketability of their products (as labelling schemes that increase consumer confidence) associated with extensive systems and use of local resources could minimize the effect of the lower genetic gain on cost effectiveness.

Average relatedness (AR) and inbreeding coefficients (F) are main indicators of the genetic health of a population. The five Galician bovine breeds achieved F and AR values higher than those in other Iberian Peninsula bovine breeds [28], but lower than the majority of Portuguese bovine beef breeds [11]. The comparison between breeds must be done with caution due to differences in the integrity and quality of the pedigree records between them. Low pedigree integrity and quality favour the underestimation of F and AR values, and could explain the differences among the five Galician cattle breeds and other Iberian Peninsula bovine breeds which are similar in terms of census or management systems. However, F, AR, percentage of inbred animals or high frequency of inbred mating values in the five Galician bovine breeds suggest the need to control the inbreeding evolution. In addition, the Ne and ΔF show worse values than those of other Iberian Peninsula bovine breeds when the pedigree content was taken into consideration [11,27,28]. Furthermore, all the Ne are below 50, so ΔF per generation is higher or equal to 1%, which is the

limit recommended by the FAO to avoid, at least in the midterm, the negative effects of inbreeding depression [29]. As expected, the breeds with a higher census, Cachena and Vianesa, achieved the highest values for N_e among the five Galician bovine breeds. It is remarkably that Limiá has lower N_e than Caldelá, in spite of their having a similar census. Historically, Limiá has had a lower census than Caldelá, and since the year 2000 has increased significantly but from a smaller population than in Caldelá, which has remained constant, explaining that N_e result.

A recent analysis of the genetic diversity of the five Galician bovine breeds using Single Nucleotide Polymorphisms (SNP) evidenced equal or higher levels of genetic diversity than other Iberian Peninsula bovine breeds, except for Frieiresa which showed higher inbreeding coefficients ($\approx 11\%$) [10]. The most common parameter used to estimate the inbreeding coefficient from SNP molecular markers is based on Runs of Homozygosity (ROH), and several authors have concluded that inbreeding based on genealogical records are moderately to lowly correlated with ROH inbreeding estimations when the pedigree is relatively complete [30–33]. Furthermore, ROH has been described as more accurate in estimating the proportion of a genome shared by two individuals than genealogical records [34]. However, genealogical information is a powerful tool to analyse the genetic diversity of livestock populations, as molecular markers, and both are mutually supportive.

The probability of gene origin parameters assesses how an original gene pool has been maintained across generations and it is not so dependent on quality pedigree depth [14]. Additionally, the relationship among such parameters can explain the main reasons for the genetic diversity losses through generations. The effective number of founders and ancestors of the five Galician bovine breeds is lower than those in other autochthonous Iberian Peninsula bovine breeds [11]. However, the relationship among both parameters is close to one, and higher in the five Galician bovine breeds. While among the Galician bovine breeds the N_e effective size is a consequence of a low number of founders (but have contributed in a balanced way to next generations), in other Iberian Peninsula breeds the N_e is a consequence of an unequal contribution of founders through generations, as revealed by the ratio f_a/f_e , which is greater than one. The existence of a conservation program and the lack of a selection program has probably favoured the balanced contribution of founders in the five Galician bovine breeds. As a consequence, the main reason for genetic variability losses is the genetic drift due to the low census of the five Galician bovine breeds, rather than bottlenecks. The low number of founder genomes is a common result, even in cosmopolitan breeds with a higher census [35,36].

The genetic herd structure of the breeds shows a certain degree of genetic exchange among them, as reflected by the fact that the number of herds that use their own breeding animals is lower than those that do not, except for Cachena. However, in Frieiresa the number of herds selling breeding animals is lower (33%) than those that do not (67%), while the remaining breeds are balanced. A strategy that favours an increase in herds selling breeding animals should slow down the inbreeding ratios, being especially profitable in Frieirisa breed, evidenced by the higher inbreeding coefficients.

Since the last quarter of the 20th century, the five Galician bovine breeds analysed (Cachena, Caldelá, Limiá, Frieiresa and Vianesa) have been included in the past in a racial group called Morenas Gallegas. Our results, in agreement with those from molecular markers, have evidenced a certain degree of uniqueness of each of the five breeds. Cachena and Vianesa showed higher levels of genetic diversity as a consequence of their higher census, Caldelá intermediate values and Limiá and Frieiresa lower values. It is remarkable that, as has been mentioned previously, Limiá has a census similar to Caldelá but lower genetic diversity due to a recent demographic expansion from a smaller population than Caldelá (Figure 2). Also, management of the herds resulted in differences among them. In Cachena breed the exchange of genetic material among herds is assured as reflect by the fact that more than 50% of the herds use their own breeding animals, but also purchase and sell them. In the remaining bovine breeds analysed (Caldelá, Limiá, Frieiresa and Vianesa), more than 50% of the herds not use their own breeding animals and must purchase them.

This strategy of exchanging genetic material among herds could slow down the increase of the inbreeding rate of the next generations. More herds selling their breeding animals will positively affect the evolution of the inbreeding rate. While in Caldelá, Limia and Vianesa, the number of selling herds is approximately 50%, in Frieiresa the number decreases to 33%. As is well known, strategies promoting the exchange of genetic material among herds could be a suitable method of AnG conservation.

5. Conclusions

In summary, the genetic diversity of the five Galician bovine breeds estimated from pedigree records achieved higher values than expected, even in breeds with a census lower than one thousand animals. The main reason for genetic diversity losses is genetic drift, so in order to increase the effective size and to slow down such losses, several actions could be implemented or strengthened: (1) increase the generation interval, as it has been in the last generations, (2) use reproductive technologies, such as artificial insemination to increase genetic exchange among herds and the number of sires used, (3) increase the number of herds that sell breeding animals, and (4) promote breeding practices among animals with minimum relatedness.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/d15020252/s1>, Table S1: Frequencies of the inbreeding coefficients of the five bovine breeds analysed: Cachena, Caldelá, Limiá, Frieiresa and Vianesa.

Author Contributions: Conceptualization, J.C. and O.C.; methodology, M.A.G.-A., J.C. and O.C.; software, C.C.; validation, C.C. and S.A.; formal analysis, M.A.G.-A. and C.C., writing—original draft preparation M.A.G.-A. and O.C., writing—review and editing C.C., S.A., J.R.J., C.J.R., M.F. and J.C. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Data Availability Statement: The data that support these findings are available from the breeding associations upon reasonable request.

Acknowledgments: The authors thank the collaboration of breeders, breed associations and the Federación de Razas Autóctonas de Galicia (BOAGA) for the genealogical records provided.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Hedrick, P.W.; Miller, P.S. Conservation Genetics: Techniques and Fundamentals. *Ecol. Appl.* **1992**, *2*, 30–46. [[CrossRef](#)] [[PubMed](#)]
2. Leroy, G.; Carroll, E.L.; Bruford, M.W.; DeWoody, J.A.; Strand, A.; Waits, L.; Wang, J. Next-generation metrics for monitoring genetic erosion within populations of conservation concern. *J. Evol. Appl.* **2018**, *11*, 1066–1083. [[CrossRef](#)]
3. FAO. *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture*; Scherf, B.D., Pilling, D., Eds.; FAO Commission on Genetic Resources for Food and Agriculture Assessments: Rome, Italy, 2015; Available online: <http://www.fao.org/3/a-i4787e/index.html> (accessed on 15 November 2022).
4. Ligda, C.; Casabianca, F. Adding value to local breeds: Challenges, strategies and key factors. *Anim. Genet. Resour. Ressour. Genet. Anim. Recur. Genet. Anim.* **2013**, *53*, 107–116. [[CrossRef](#)]
5. Vázquez Moreira, J. Breve noticia sobre el estado actual de la agricultura y ganadería en la provincia de Orense. *Ed. Rev. Galega Estud. Agrar.* **1975**, *5*, 363.
6. Rivero, C.J. Aportaciones a la Caracterización de las Razas Bovinas Autóctonas de Galicia en Peligro de Extinción. Ph.D. Thesis, University of Santiago de Compostela, Santiago de Compostela, Spain, 2015.
7. Fernández, M.; Rivero, G.; Alonso, M.; Rivero, C.J.; Pose, H.; Justo, J.R.; Adán, S.; Díaz, R.; Rois, D.; Carril, J.A. *Razas Autóctonas de Galicia en Peligro de Extinción*, 1st ed.; Consellería de Agricultura e Desenvolvemento Rural: A Coruña, Spain, 2001.
8. *PIMX: Plan Integral de Mellora Xenética: Ganado Vacún*; Consellería de Agricultura, Gandería e Montes: Santiago de Compostela, Spain, 1991; p. 83.
9. Gicquel, E.; Boettcher, P.; Besbes, B.; Furre, S.; Fernández, J.; Danchin-Burge, C.; Berger, B.; Baumung, R.; Feijoo, J.R.J.; Leroy, G. Impact of conservation measures on demography and genetic variability of livestock breeds. *Animal* **2020**, *14*, 670–680. [[CrossRef](#)] [[PubMed](#)]
10. García-Atance, M.A.; Carleos, C.; Dunner, D.; Eusebi, P.G.; Rivero, C.J.; Justo, J.R.; Fernández, M.; Cañón, J.; Cortés, O. Genomic characterization of a set of Iberian Peninsula bovine local breeds at risk of extinction: Morenas Gallegas. *Animals* **2020**, *10*, 1956. [[CrossRef](#)] [[PubMed](#)]

11. Carolino, N.; Vitorino, A.; Carolino, I.; Pais, J.; Henriques, N.; Silveira, M.; Vicente, A. Genetic Diversity in the Portuguese Mertolenga Cattle Breed Assessed by Pedigree Analysis. *Animals* **2020**, *10*, 1990. [[CrossRef](#)]
12. Cortés, O.; Sevane, N.; Baro, J.A.; Cañón, J. Pedigree analysis of a highly fragmented population, the Lidia cattle breed. *Livest. Sci.* **2014**, *167*, 1–8. [[CrossRef](#)]
13. González-Cano, R.; González-Martínez, A.; Muñoz-Mejías, M.E.; Valera, P.; Rodero, E. Analyses of Genetic Diversity in the Endangered “Berrenda” Spanish Cattle Breeds Using Pedigree Data. *Animals* **2022**, *12*, 249. [[CrossRef](#)]
14. Boichard, D.; Maignel, L.; Verrier, E. The value of using probabilities of gene origin to measure genetic variability in a population. *Genet. Sel. Evol.* **1997**, *29*, 5–23. [[CrossRef](#)]
15. Melka, M.G.; Stachowicz, K.; Miglior, F.; Schenkel, F.S. Analyses of genetic diversity in five Canadian dairy breeds using pedigree data. *J. Anim. Breed. Genet.* **2013**, *130*, 476–486. [[CrossRef](#)] [[PubMed](#)]
16. Menezes, L.M.; Sousa, W.H.; Cavalcanti Filho, E.P.; Cartaxo, F.Q.; Viana, J.A.; Gama, L.T. Genetic variability in a nucleus herd of Boer goats in Brazil assessed by pedigree analysis. *Small Rumin. Res.* **2015**, *131*, 85–92. [[CrossRef](#)]
17. Nyman, S.; Johansson, A.M.; Palucci, V.; Schönherz, A.A.; Guldbbrandtsen, B.; Hinrichs, D.; de Koning, D.-J. Inbreeding and pedigree analysis of the European red dairy cattle. *Genet. Sel. Evol.* **2022**, *54*, 70. [[CrossRef](#)]
18. MacCluer, J.; Boyce, B.; Dyke, L.; Weitzkamp, D.; Pfenning, A.; Parsons, C. Inbreeding and pedigree structure in Standardbred horses. *J. Hered.* **1983**, *74*, 394–399. [[CrossRef](#)]
19. Maignel, L.; Boichard, D.; Verrier, E. Genetic variability of French dairy breeds estimated from pedigree information. *INTERBULL Bull.* **1996**, *14*, 49–54.
20. Lacy, R.C. Analysis of founder representation in pedigrees: Founder equivalents and founder genome equivalents. *Zoo Biol.* **1989**, *8*, 111–123. [[CrossRef](#)]
21. Ballou, J.D.; Lacy, R.C. Identifying genetically important individuals for management of genetic variation in pedigreed populations. In *Population Management for Survival and Recovery: Analytical Methods and Strategies in Small Population Management*; Ballou, J.D., Gilpin, M., Foose, T.J., Eds.; Columbia University Press: New York, NY, USA, 1995; pp. 76–111.
22. Caballero, A.; Toro, M.A. Interrelations between effective population size and other pedigree tools for the management of conserved populations. *Genet. Res.* **2000**, *75*, 331–343. [[CrossRef](#)]
23. Nei, M. Analysis of gene diversity in subdivided populations. *Proc. Natl. Acad. Sci. USA* **1973**, *70*, 3321–3323. [[CrossRef](#)]
24. Boichard, D. PEDIG: A fortran package for pedigree analysis suited for large populations. In Proceedings of the 7th World Congress of Genetics Applied to Livestock Production, Montpellier, France, 19–23 August 2002.
25. Gutiérrez, J.P.; Goyache, F. A note on ENDOG: A computer program for analysing pedigree information. *J. Anim. Breed. Genet.* **2005**, *122*, 172–176. [[CrossRef](#)]
26. Robertson, A. A numerical description of breed structure. *J. Agric. Sci.* **1953**, *43*, 334–336. [[CrossRef](#)]
27. Cañas-Álvarez, J.J.; González-Rodríguez, A.; Martín-Collado, D.; Avilés, C.; Altarriba, J.; Baro, J.A.; De la Fuente, L.F.; Díaz, C.; Molina, A.; Varona, L.; et al. Monitoring changes in the demographic and genealogical structure of the main Spanish local beef breeds. *J. Anim. Sci.* **2014**, *92*, 4364–4374. [[CrossRef](#)] [[PubMed](#)]
28. Gutiérrez, J.P.; Altarriba, J.; Díaz, C.; Quintanilla, R.; Cañón, J.; Piedrafita, J. Pedigree analysis of eight Spanish beef cattle breeds. *Genet. Sel. Evol.* **2003**, *35*, 43–63. [[CrossRef](#)] [[PubMed](#)]
29. FAO. *Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans: Management of Small Populations at Risk*; FAO: Rome, Italy, 1998.
30. Cortés, O.; Eusebi, P.; Dunner, S.; Sevane, N.; Cañón, J. Comparison of diversity parameters from SNP, microsatellites and pedigree records in the Lidia cattle breed. *Livest. Sci.* **2019**, *219*, 80–85. [[CrossRef](#)]
31. Silió, L.; Rodríguez, M.C.; Fernandez, A.; Barragan, C.; Benitez, R.; Ovilo, C.; Fernandez, A.I. Measuring inbreeding and inbreeding depression on pig growth from pedigree or SNP-derived metrics. *J. Anim. Breed. Genet.* **2013**, *130*, 349–360. [[CrossRef](#)] [[PubMed](#)]
32. Wang, J. Pedigrees or markers: Which are better in estimating relatedness and inbreeding coefficient? *Theor. Popul. Biol.* **2016**, *107*, 4–13. [[CrossRef](#)]
33. Zhang, Q.; Calus, P.L.; Guldbbrandtsen, B.; Mogens, S.L.; Goutam, S. Estimation of inbreeding using pedigree, 50k SNP chip genotypes and full sequence data in three cattle breeds. *BMC Genom.* **2015**, *16*, 88. [[CrossRef](#)]
34. Howard, J.T.; Pryce, J.E.; Baes, C.; Maltecca, C. Invited review: Inbreeding in the genomics era: Inbreeding, inbreeding depression, and management of genomic variability. *J. Dairy Sci.* **2017**, *100*, 6009–6024. [[CrossRef](#)]
35. Honda, T.; Fujii, T.; Nomura, T.; Mukai, F. Evaluation of genetic diversity in Japanese Brown cattle population by pedigree analysis. *J. Anim. Breed. Genet.* **2006**, *123*, 172–179. [[CrossRef](#)]
36. Stachowicz, K.; Sargolzaei, M.; Miglior, F.; Schenkel, F.S. Rates of inbreeding and genetic diversity in Canadian Holstein and Jersey cattle. *J. Dairy Sci.* **2011**, *94*, 5160–5175. [[CrossRef](#)] [[PubMed](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.