

Article

Turopolje Pig: Between Conservation and Sustainability

Dubravko Škorput ¹, Ana Kaić ^{1,*} , Marija Špehar ² , Danijel Karolyi ¹  and Zoran Luković ¹

¹ Division of Animal Science, Faculty of Agriculture, University of Zagreb, Svetošimunska cesta 25, 10000 Zagreb, Croatia; dskorput@agr.hr (D.Š.); dkarolyi@agr.hr (D.K.); lukovic@agr.hr (Z.L.)

² Croatian Agency for Agriculture and Food, Svetošimunska cesta 25, 10000 Zagreb, Croatia; marija.spehar@hapih.hr

* Correspondence: akaic@agr.hr

Abstract: The Turopolje pig is a fatty-type pig breed created during the Middle Ages in the Turopolje region in Central Croatia. Although the population of the Turopolje pig is stable today, this breed is still one of the endangered breeds that are severely threatened by inbreeding. The aim of this work was to evaluate the genetic diversity parameters of the recent Turopolje pig population in Croatia and to consider mating strategies to limit the increase in inbreeding in the population using algorithms within an optimal contribution selection frame. The pedigree of 1155 individuals was analysed. In addition to the basic pedigree structure, the following population parameters were analysed: average coefficient of inbreeding; mean rate of increase in coancestry; increase in coancestry between any individuals; effective population size. Based on obtained parameters, mating optimization using estimated kinship between candidates in several scenarios was carried out, restricting maximal kinship between candidates on a minimal possible value 0.07, as the least possible level of kinship, candidates on a value of 0.10, and candidates on a value of 0.25. The average inbreeding coefficient (F) in the population was 0.03, while the average F of inbred animals was 0.10. The effective population size obtained from pedigrees based on the increase in coancestry (0.17) was 29.14. Mating plans were created from 5 active boars and 120 sows in different scenarios with constraint on the level of kinship between candidates. The least possible level of kinship was 0.07, and no available solutions were under this level. With the increase in the allowed kinship between candidates, the level of inbreeding increased from 0.01 to 0.06 in the next generation. Under practical conditions, mating between ideal individuals in local pig populations is not always possible, and the use of optimisation algorithms allows alternative mating within existing populations to be considered. Finally, this approach opens up the possibility of potentially improving sustainable breeding through selection by considering breeding values for economically important traits. This approach can help to differentiate the Turopolje pig breed from other commercial and local breeds, e.g., for meat quality traits.

Keywords: Turopolje pig; conservation; genetic diversity; sustainability; local breeds



Citation: Škorput, D.; Kaić, A.; Špehar, M.; Karolyi, D.; Luković, Z. Turopolje Pig: Between Conservation and Sustainability. *Sustainability* **2024**, *16*, 1786. <https://doi.org/10.3390/su16051786>

Academic Editor: George K. Symeon

Received: 11 January 2024

Revised: 12 February 2024

Accepted: 19 February 2024

Published: 21 February 2024



Copyright: © 2024 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 Turopolje pig is a fatty-type pig breed that originated in the Middle Ages in the Turopolje region in Central Croatia and is one of the oldest European pig breeds (Figure 1). The pigs of this breed are well adapted to the natural environment, especially to continental climate conditions and lowland forest ecosystems. The predominant form of rearing Turopolje pigs is outdoor farming with low production intensity. The production performance of the Turopolje pigs is also low, with low fertility and modest fattening performances, but with excellent meat quality traits [1]. Due to its long genesis, isolated breeding area, and specific low-input rearing technique, the Turopolje pig has preserved its genetic uniqueness, as confirmed by Zorc et al. [2]. Moreover, the Turopolje pig in Croatia is differentiated from other pig breeds from the broader geographical area. However, the rapid penetration of imported highly selected lean pigs in the second half of the twentieth

century, as well as the ban on forest grazing, significantly reduced the interest in this breed and decreased the number of pigs over decades.



Figure 1. Turopolje pigs in natural environment.

The conservation of the Turopolje pig breed began after the Croatian War of Independence in the 1990s during the 20th century. However, conservation efforts have led to a small increase in the population (Figure 2) and an improvement in the genetic diversity of the Turopolje pig. The majority of the population is located in the Turopolje region, southeast of the capital Zagreb. This could be the result of various events during the conservation period, including natural causes such as the occurrence of brucellosis in 2008, but it could also be due to a lack of selection and marketing programmes aimed at more sustainable breeding of this breed. Therefore, several research projects on the Turopolje pigs have been carried out in recent years, leading to a comprehensive analysis of production and reproduction data [1], as well as of the breed products, which is a prerequisite for future steps needed to move from conservation to sustainability of the breed.

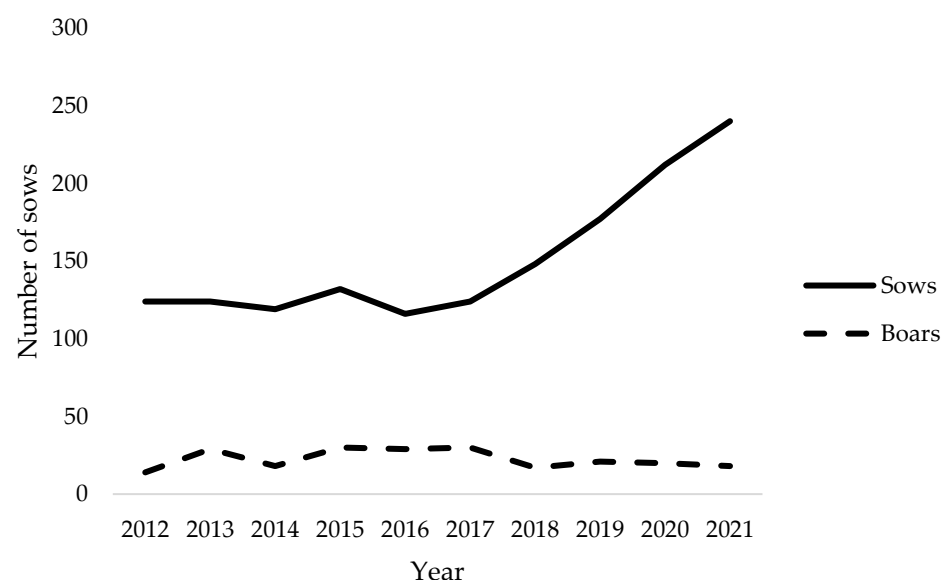


Figure 2. Trends in the number of sows and boars in the Turopolje pig.

The ultimate preservation goal for local breeds is to achieve sustainability [3] and reduce dependence on government subsidies. In addition, the impact of pig production on the environment is highly dependent on production systems. Local pig breeds are reared in extensive semi-outdoor or outdoor systems, and their environmental impact

can be controlled by controlling the amino acid and crude protein content of the feed, as these breeds have lower nutrient requirements compared to modern conventional breeds reared under intensive production systems [4]. This is especially obvious in the case of Turopolje pig, where pigs are usually provided with only a simple shelter, water, and some supplemented feed (e.g., 0.5–2 kg of corn per animal daily), while the majority of the animals' diet is supplied from natural resources (e.g., acorn, grass, worms, snails, shellfish, etc.). This is especially important in the context of locally produced feed supplied to animals and low nutritional demands that reduce the direct competition between pigs and humans for available crops [5]. Indoor housing and intensive production are rarely practiced. Thus, the Turopolje pig has been part of a well-preserved and sustainable local ecosystem for centuries, and a source of meat and dried meat products for centuries. As such, the Turopolje pig plays an important role in the local population, not only as a source of food, but also as a part of local tradition and cultural identity, and, finally, an important source of biodiversity. Thus, the Turopolje pig within its natural ecosystem is a good example of how local and autochthonous pig breeds can contribute to sustainable pig production adapted to local conditions and preserve the environment, local societies, and traditional livestock farming in rural areas. Local and autochthonous breeds are usually suitable for alternative breeding systems that become popular due to their low expenses and good market position among products from systems with increased welfare and a low ecological footprint. Moreover, due to their resilience to harsh conditions, including unfavourable climates, such as extremely warm or extremely cold weather, these breeds might play an important role in the adaptation to increasingly pronounced climate changes [6]. Considering all the above-mentioned advantages of such systems and the role of local breeds in alternative pig breeding, they have an important place in preserving rural areas, which is one of the pillars of the Common Agricultural Policy of the European Union and part of the European Green Deal that aims to achieve sustainability in using natural resources [7]. Since the genetic resources of livestock ensure food security, availability, and the sustainable development of rural areas, genetic diversity is indispensable for the sufficient flexibility of future animal husbandry in adapting to changing market demands and climate changes [8].

Mating systems in the breeding population have a key role in maintaining genetic diversity. In breeds under conservation, the main goal of breeding programmes is to preserve genetic diversity, with very little or no possibility for selection for economically important traits, due to small genetic variances in the population [9]. Thus, mating plans in such populations are designed with the purpose of reducing the inbreeding rate in the population, which is one of the main indicators of genetic erosion in the population. The absolute value of the inbreeding coefficient is not always completely informative, due to shallow and incomplete pedigree, and the inbreeding rate provides more insight into the state of genetic diversity in the population. The control of the inbreeding rate in the population is usually in conflict with genetic improvement by selection, since the selection methods in use are based on pedigree and tend to choose related animals [10]. Thus, the conflict between these breeding goals might be solved by using algorithms within an optimal contribution selection (OCS) frame [11]. However, to achieve both breeding goals, i.e., to maintain genetic diversity and to improve the desired trait(s), comprehensive and accurate data recording is required, which is a common problem with local breeds. In cases where pedigree and data records are scarce, insufficient, or omitted, methods based on genomic information might be helpful.

The aim of this study was to analyse the population parameters of the Turopolje pig using genealogical data and to provide an insight into the current status of the genetic diversity of the population. In addition, the application of algorithms in the context of optimal contribution selection for the creation of mating plans with the aim of inbreeding control was investigated in various practical scenarios depending on the level of kinship between the candidates.

2. Materials and Methods

2.1. Data and Pedigree Structure

Genealogical data parameters for the analysis of the Croatian native Turopolje pig population were provided by the Croatian Agency for Agriculture and Food. The final pedigree data set contained 1155 individuals from the years 1996 and 2023. The reference population for the analysis was set for animals without a culling record. The basic pedigree structure and statistics were determined using contribution, inbreeding (F), and coancestry (CFC) software (v 1.0) [12].

2.2. Pedigree Completeness

The pedigree quality and completeness were evaluated using following parameters:

- Number of fully traced generations (NTG)—this represents the number of generations separating an individual from its furthest ancestor;
- Maximum number of complete generations (NCG)—this identifies the furthest generation with two known ancestors;
- Number of equivalent complete generations (NECG)—this expresses the sum of all known ancestors, counting how many generations have been traced. It is calculated for those individuals having at least one known parent [13]. Also, pedigree completeness is visualized graphically by the mean completeness of the pedigrees of specified individuals within sexes.

2.3. Population Parameters

The following population parameters were estimated for the reference population that included live animals:

- Coefficient of inbreeding (F)—this was determined by calculating F using Cholesky factorisation of the relationship matrix as proposed by [14];
- Mean rate of increase in coancestry [15];
- Increase in coancestry between any pair of individuals i and j calculated as

$$\Delta c_{ij} = 1 - \frac{g_i + g_j}{2} \sqrt{1 - c_{ij}}$$

where c_{ij} is the kinship between i and j , and g_i and g_j are the numbers of equivalent complete generations of individuals i and j ;

- Effective population size calculated as

$$N_e = 1/2\Delta c_j$$

The OptiSel (v 2.0.7) package [16] in the R programming environment (v 4.3.1) [17] was used to analyse the above-mentioned parameters.

2.4. Genetic Parameters

The data set for the estimation of genetic parameters contained 1588 litter records from 697 sows. In order to increase the reliability of the estimation, a season was defined as a three-month season corresponding to the natural year seasons: winter, spring, autumn, and summer. Genetic parameters for NBA were estimated using the following single-trait repeatability model:

$$y_{ijklmno} = \mu + S_i + P_j + B_k + H_l + p_{im} + a_{mn} + e_{ijklmno}$$

where the effects of mating season ($S_i = 242$), parity ($P_j = 13$), service boar ($B_k = 100$), and herd ($H_l = 38$) were considered as fixed class effects. Permanent environmental (p_{im}) and

direct additive genetic effects (a_{mn}) were included in the model as random effects. The matrix notation of the repeatability model can be written as follows:

$$y = \mathbf{Xb} + \mathbf{Z_p p} + \mathbf{Z_a a} + \mathbf{e}$$

where y is a vector of observations, \mathbf{X} is the incidence matrix for fixed effects, \mathbf{b} is a vector of unknown parameters for fixed effects, $\mathbf{Z_p}$ and $\mathbf{Z_a}$ are incidence matrices for permanent environmental and additive genetic effects, \mathbf{p} and \mathbf{a} are the corresponding vectors of parameters for random effects, and vector \mathbf{e} presents residuals. The following covariance structure was assumed:

$$\text{var} = \begin{bmatrix} p \\ a \\ e \end{bmatrix} = \begin{bmatrix} I_p \sigma_p^2 & 0 & 0 \\ 0 & A \sigma_a^2 & 0 \\ 0 & 0 & I_e \sigma_e^2 \end{bmatrix}$$

where \mathbf{A} is the numerator relationship matrix, while $\mathbf{I_p}$ and $\mathbf{I_e}$ are identity matrices, and σ_a^2 , σ_p^2 , and σ_e^2 are the variances in additive genetic, permanent environmental, and residual effects, respectively. Covariances between random effects were assumed to be zero. The estimation of the variance components for NBA was based on the residual maximum likelihood method using the VCE-6 software (v 6.0) package [18].

2.5. Optimization of Mating Plans

Animals with more than three generations of ancestors in the pedigree were used as mating candidates in order to create mating plans with reliable information about the kinship of the candidates. The optimization problems were solved using the CCCP (cone constrained convex problems) solver from the R package OptiSel [16]. The package contains routines for solving cone constrained convex problems using interior-point methods that are partially ported from Python's CVXOPT and based on Nesterov–Todd scaling [19]. Although the solver allows optimization of genetic contributions taking account of breeding values, the only scenario considered in the study was minimizing kinship without accounting for breeding values in order to find optimal bounds on kinship between candidates. For that purpose, different bounds on kinship were tested (0.07, 0.10, and 0.25), and average inbreeding in the offspring was analysed in order to evaluate the mating plans. The total number of breeding candidates was 5 boars and 120 sows.

3. Results

3.1. Basic Pedigree Structure

The pedigree contained 135 founders, 160 sires with progeny, and 271 dams with progeny. The basic pedigree structure (Table 1) showed that 23% of 1155 individuals in the pedigree were inbred.

Table 1. Basic pedigree structure.

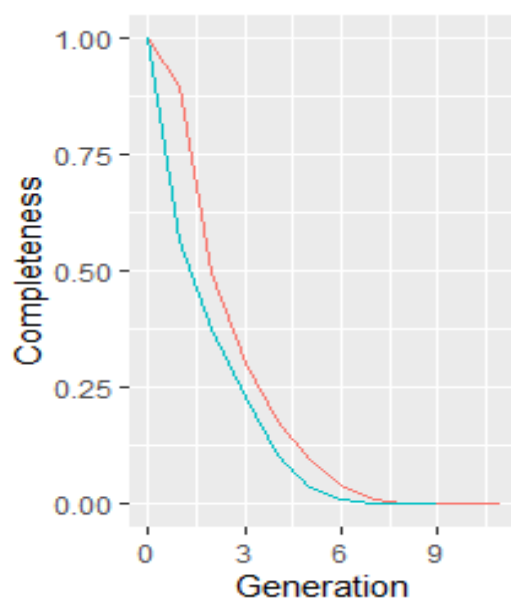
Individuals in total	1155
Inbreds in total	260
Sires	160
Dams	271
Founders	135
Non-founders	1020

3.2. Pedigree Completeness

Pedigree completeness was characterized by relatively low numbers of maximum and full generations (Table 2). The mean completeness of the pedigrees of specified individuals within sexes is shown in Figure 3 and indicated the quick loss of information with every further generation. For 481 individuals, the longest ancestral path was one generation, while the maximal ancestral path was 11 and was found in four animals.

Table 2. Pedigree completeness parameters in the Turopolje pig.

Parameter	Value
Number of maximum generations	1.96
Number of full generations	1.35
Number of equivalent generations	3.45

**Figure 3.** Mean completeness of the pedigrees of specified individuals (red color = female animals, blue color = male animals).

3.3. Population Parameters

The average inbreeding coefficient obtained through pedigree analysis in the population was 0.03 or 3%. However, the average inbreeding coefficient of inbred animals was higher, with a value of 0.10. The more informative measures of genetic diversity than the inbreeding coefficient alone, the increase in relatedness in the population, and the effective population size showed unfavourable values (Table 3), which indicates an impaired genetic diversity in the population.

Table 3. Main population parameters of the Turopolje pig.

Parameter	Value
Inbreeding coefficient	0.03
Average F* in inbred animals	0.10
Average relatedness	0.06
Effective population size	29.14
Δc_{ij}	0.17

* Inbreeding coefficient.

3.4. Genetic Parameters

The estimated genetic parameters showed low additive genetic variance and low heritability (Table 4). Also, the variance in permanent environmental effect was negligible. The total phenotypic variance as a sum of all estimated variance components was 3.43.

Table 4. Genetic parameters of the Turopolje pig.

	σ^2_{ph}	σ^2_p	σ^2_a	σ^2_e
Variances	3.43	0.00	0.05	3.39
Ratio of phenotypic variances		p^2	h^2	e^2
		0.00	0.01	0.98

σ^2_{ph} —phenotypic variance; σ^2_p —permanent environmental variance; σ^2_a —additive variance; σ^2_e —residual.

3.5. Mating Optimization

Mating optimization by restricting kinship among candidates showed that there was no possibility of choosing candidates with a kinship of less than 0.07 (Table 5), and this was the lowest possible value that might be used in the optimization process.

Table 5. Number of selected breeding pigs, average inbreeding in offspring generation, minimum and maximum male and female contribution calculated by minimizing the average kinship of the population without taking account of breeding values.

Upper Bound on Kinship	Selected Number of Candidates	F	Average Kinship among Candidates	Maximal Male Contribution	Maximal Female Contribution
<0.7			No solution		
0.07 *	5/31	0.01	0.74	0.12	0.07
0.10	5/120	0.02	0.09	0.12	0.01
0.25	5/120	0.06	0.11	0.11	0.01

* The lowest possible kinship.

With the increase in the lower upper bound of kinship among mating candidates, average inbreeding in the offspring increased from 0.01 for the lowest possible upper bound to 0.06 for an upper bound of 0.25. In the first scenario, the average kinship among candidates was 0.74, in the second scenario it was 0.09, and it was 0.11 in the last scenario.

4. Discussion

In small local and autochthonous pig populations, genealogical information is the standard source of information about population parameters. The pedigree of the analysed Turopolje pig population was characterized by low completeness, which is to be expected in small pig populations where the systematic recording of data is not fully recognized as it is in commercial herds. Higher values of inbreeding coefficient were obtained for other local breeds, such as the Croatian Banija spotted pig [20], where the average coefficient of inbreeding was 6.67%, three strains of the Hungarian Mangalitza pig ($F = 4.07$ – 5.87%), and the Retinto line (5.80%) of the autochthonous Spanish Iberian pig [21]. A similar inbreeding coefficient to the one obtained in our study was found in the Entrepelado line ($F = 2.50\%$) of the Iberian pig. A shallow pedigree can lead to an underestimation of key population parameters, such as the inbreeding rate, or an overestimation of the effective population size. However, the completeness of the pedigree in the Banija spotted pig was lower than for other local breeds, such as the Hungarian Mangalitza pig [22]. Despite the low pedigree depth, pedigree analysis showed reduced values of genetic diversity in the Turopolje pig population, especially considering the fact that 25% of active animals were inbred and that the average inbreeding coefficient of inbreds was almost 10%. However, a more informative measure than the inbreeding coefficient alone is the change in the inbreeding rate or average coancestry and the effective size of the population. According to the Food and Agriculture Organisation of the United Nations, proposed values for the change in inbreeding between generations should not exceed 1%, and the effective population size should be larger than 50 [23]. Considering these values, results obtained in this study show an impaired genetic diversity of the Turopolje pig population in Croatia that classifies it as an endangered breed, together with other local breeds where low genetic diversity was obtained through the

analysis of effective population sizes, such as Italian local pig breeds, Cinta Senese (40.32), and Mora Romagnola (7.68) [24].

Previous studies on the genetic diversity in the Turopolje pig population were based on molecular information. Druml et al. [25] found dramatically low genetic diversity in the Turopolje pig in Croatia using microsatellite markers and obtained low values for the observed heterozygosity. Low genetic diversity of the Turopolje pig was also found in the study by Schiavo et al. [26]. Zorc et al. [2] used genomic data in the most recent study and showed that the genetic diversity of the Turopolje pig breed was very low compared to five other local breeds: the Black Slavonian pig, the Banija spotted pig, the Krškopolje pig, the Moravka pig, and the Serbian swallow-bellied Mangalitza population. Numerous studies have confirmed that low genetic diversity resulting from a high increase in inbreeding in the population can have harmful effects on reproductive traits. The small negative effect of inbreeding on litter size in Large White and Landrace pigs was established by Koeck et al. [27], for example, using genealogical data. Significant effects of inbreeding on the reproductive traits of the Iberian pig were found by Saura et al. [28] using genome-wide data.

The estimated additive genetic variance was lower than in other local pig breeds, such as the Iberian pig [29] or the Bisaro pig [27]. Expectedly, the additive genetic variance was dramatically lower than in global breeds such as the Large White [30]. The obtained results are as expected and could be explained by the small population size and several historical events that have caused a genetic bottleneck and a reduction in additive genetic variance. The low additive genetic variance for litter size is an indicator of slow future genetic improvement through selection. The negligible value for the permanent environmental variance is a consequence of the parity distribution with a high frequency of low order parities. In future work, data recording and accuracy should be improved to obtain more reliable estimates of variance components. Litter size is a trait that is strongly dependent on environmental factors. This is even more evident for breeds in alternative production systems, such as the Turopolje pig, where there is no possibility of controlling environmental factors [31]. Such systems are characterised by more space for the pigs, access to additional roughage, year-round free-range housing, and, often, limited use of antibiotics and vitamins. Environmental influences could therefore significantly determine the variations in litter size. However, achieving a large litter size is not the main breeding goal in such populations, and the balance between achieving better production results and the welfare of the animals is the main advantage of such systems [32]. As the Turopolje pig breed is adapted to a harsh environment and based on a low-input system, intensive management of this breed will not lead to a significant improvement in reproductive and production traits, but could significantly affect the welfare of the animals in areas such as the availability of space and the expression of natural behaviour, and, consequently, alter the meat quality characteristic of the breed. Improving housing conditions could be considered for breeding sows and boars to control environmental conditions and to limit the impact of the environment on litter size.

The increase in coancestry in the population is a measure similar to the inbreeding rate of the population that is usually used in genetic diversity analysis. However, an estimation of the increase in the coancestry in the population is useful because it identifies the individuals with high average coancestry with the other members of population. Since the inbreeding is a result of the mating of related individuals, those identified in this way can be selected for plans that will avoid the mating of related animals [16]. This might be useful in future analysis and for the inclusion of estimated breeding values for economically important traits in breeding programmes. The set of procedures based on algorithms that optimize the genetic contribution of selection candidates, known as optimal contribution election [11,33], might be a tool of choice when creating mating plans that will result in simultaneous genetic improvement and a restricted increase in inbreeding in the population. Sustainability of the breed can be achieved only if the breed is competitive with other breeds, and selection for traits that are better expressed than in commercial herds,

such as meat quality, might be an adequate tool for achieving that goal [34]. Breeding programmes for local and autochthonous pig breeds usually have a primary objective of maintaining genetic diversity, and there are rare examples of breeding programmes that include selection for economically important traits, such as in the Iberian pig in Spain [4,18]. The low genetic diversity of the Turopolje pig population is a consequence of several historical events that occurred and affected the population census and breeding activity, such as the brucellosis outbreak in 2008. Although the Turopolje pig is considered one of the oldest pig breeds in Europe, the population size and breeding activities have still not reached a self-sustaining level. One of the main reasons for this is the lack of value-added products that are recognized outside the breeding area. In the year 2023, however, the fresh meat of the Turopolje pig was officially recognized as a product with a protected designation of origin (PDO) in the European Union [35], which could be an important step towards broader recognition of the breed and could contribute to its conservation and to achieving development of the breed without significant state interventions.

Changing the level of constraint on kinship caused the changes in the number of mating candidates and would be expected to increase inbreeding in the offspring population. Considering the variation in constraints and using several different kinship levels are important steps in creating mating plans, as breeding conditions in small populations such as the Turopolje pig are affected by various effects. One of the most evident examples is the recent outbreak of African swine fever in Croatia in 2023, which could affect the implementation of mating plans. In such a situation, mating between favourable candidates could be prevented by strict measures (forbidden animal transfer into/from infected and endangered areas) to control African swine fever, which poses a major threat to the survival of local autochthonous breeds, most of which are kept in extensive outdoor systems. The applied approach enables flexible mating systems within practical conditions that can often deviate from ideal conditions. The results of the application of optimisation algorithms are the least possible increase in inbreeding in given circumstances and the preservation of genetic erosion and loss of diversity through the mating of closely related animals. The implementation of breeding techniques such as artificial insemination could contribute to more effective breeding, the selection of breeding candidates, and, ultimately, more effective control of changes in the level of inbreeding in the population.

Moreover, the use of optimisation methods for mating plans is the basis for the future work on sustainable breeding, which should include optimal contribution selection and genetic improvement of the breed. According to Gourdine et al. [9], optimal contribution selection is a useful tool that can be used in small populations for the genetic improvement of traits of interest. Although selection for economically important traits might improve the sustainability of small populations, there are conditions that must be met for effective selection. The amount, accuracy, and quality of data are of key importance in implementing selection procedures. In small populations with shallow pedigrees, a combination of these data with molecular information is beneficial and can improve the reliability of estimated population parameters [36]. The use of selection methods based on pedigree, such as animal models, requires connectedness between breeding units [37] for the reliable comparison of evaluated animals. There is a small number of studies evaluating connectedness in local pig populations, such as the study by Škorput et al. [38], where the authors analysed connectedness between management units in the Black Slavonian pig and possibilities for selection for litter size. In practical conditions, it is challenging to meet all the requirements because achieving genetic connectedness among herds requires the involvement of all stakeholders in the system. Thus, selection work in small populations such as the Turopolje pig might be implemented only when conditions for reliable selection are fulfilled. Achieving sustainability of the breed through the development of mating schemes, including genetic evaluation in the breeding program, demands accurate data recording (pedigree and phenotype) and the consideration of traits of interest for selection. Thus, future work is expected to be focused on establishing and achieving additional breeding goals. An important step in achieving those goals is motivating breeders to take

part in the processes that include creating and conducting mating plans, phenotyping, and genotyping for genetic evaluation, especially for traits that can distinguish the breed and its products on the market. In general, achieving satisfying production and market goals through the sustainable breeding of the Turopolje pig might result in an enriched high-quality meat product supply, preserving the local rural area through the preservation of valuable genetic resources.

5. Conclusions

Genealogical analysis showed impaired genetic diversity of the Turopolje pig population in Croatia. The sustainable breeding of small populations such as the Turopolje pig requires balance between different goals, such as genetic improvement, genetic purity of the breed, and genetic diversity. The Turopolje pig is an endangered pig breed, and practical ways for achieving a sustainable number of individuals and preserving the genetic diversity of the population should be based on appropriate mating systems that will prevent the loss of genetic diversity. In practical conditions, mating between appropriate candidates is not always possible, and the use of algorithms that optimize mating between individuals can be helpful in different scenarios. Future research should focus not only on the preservation of genetic diversity, but also on the realisation of additional breeding goals, such as the evaluation of traits that give the Turopolje pig breed additional value and competitiveness compared to other pig breeds. These traits primarily relate to meat quality, which distinguishes the Turopolje pig from commercial pig breeds and enables a more economically sustainable development of the breed; this will contribute to both the preservation of the breed and the development of rural areas in the Turopolje region.

Author Contributions: Conceptualization, D.Š., A.K., Z.L., and D.K.; methodology, D.Š. and Z.L.; software, D.Š.; investigation, D.K. and Z.L.; resources, D.K. and M.Š.; data curation, M.Š.; writing—original draft preparation, D.Š.; writing—review and editing, D.Š., A.K., D.K., M.Š., and Z.L.; visualization, D.Š. All authors have read and agreed to the published version of the manuscript.

Funding: This project has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No 101000236. This project is part of EuroFAANG (<https://eurofaang.eu>, accessed on 10 January 2024).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Data are available upon request.

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

References

1. Karolyi, D.; Luković, Z.; Salajpal, K.; Škorput, D.; Vnućec, I.; Mahnet, Ž.; Klišanić, V.; Batorek-Lukač, V. Turopolje Pig (Turopoljska Svinja). In *European Local Pig Breeds—Diversity and Performance. A Study of Project TREASURE*; Candek-Potokar, M., Nieto Linan, R.M., Eds.; IntechOpen: London, UK, 2019.
2. Zorc, M.; Škorput, D.; Gvozdanović, K.; Margeta, P.; Karolyi, D.; Luković, Z.; Salajpal, K.; Savić, R.; Muñoz, M.; Bovo, S.; et al. Genetic Diversity and Population Structure of Six Autochthonous Pig Breeds from Croatia, Serbia, and Slovenia. *Genet. Sel. Evol.* **2022**, *54*, 30. [[CrossRef](#)]
3. Barker, J.S.F. Conservation and Management of Genetic Diversity: A Domestic Animal Perspective. *Can. J. For. Res.* **2001**, *31*, 588–595. [[CrossRef](#)]
4. Monteiro, N.T.R.A.; Wilfart, A.; Utzeri, V.J.; Batorek Lukac, N.; Tomažin, U.; Nanni Costa, L.; Čandek-Potokar, M.; Fontanesi, L.; Garcia-Launay, F. Environmental Impacts of Pig Production Systems Using European Local Breeds: The Contribution of Carbon Sequestration and Emissions from Grazing. *J. Clean. Prod.* **2019**, *237*, 117843. [[CrossRef](#)]
5. Godfray, H.C.; Beddington, J.R.; Crute, I.R.; Muir, J.F.; Pretty, J.; Robinson, S.; Thomas, S.M.; Toulmin, C. Food Security: The Challenge of Feeding 9 Billion People. *Science* **2010**, *327*, 812–819. [[CrossRef](#)] [[PubMed](#)]
6. Renaudeau, D.; Collin, A.; Yahav, S.; de Basilio, V.; Gourdine, J.L.; Collier, R.J. Adaptation to Hot Climate and Strategies to Alleviate Heat Stress in Livestock Production. *Animal* **2012**, *6*, 707–728. [[CrossRef](#)] [[PubMed](#)]
7. Fetting, C. *The European Green Deal*; European Sustainable Development Network (ESDN) Office: Vienna, Austria, 2020.

8. Kasprzyk, A.; Walenia, A. Native Pig Breeds as a Source of Biodiversity—Breeding and Economic Aspects. *Agriculture* **2023**, *13*, 1528. [CrossRef]
9. Gourdine, J.L.; Sørensen, A.C.; Rydhmer, L. There Is Room for Selection in a Small Local Pig Breed When Using Optimum Contribution Selection: A Simulation Study. *J. Anim. Sci.* **2012**, *90*, 76–84. [CrossRef] [PubMed]
10. Fernández, J.; Toro, M.A. The Use of Mathematical Programming to Control Inbreeding in Selection Schemes. *J. Anim. Breed. Genet.* **1999**, *116*, 447–466. [CrossRef]
11. Meuwissen, T.H.E. Maximizing the Response of Selection with a Predefined Rate of Inbreeding. Maximizing the Response of Selection with a Predefined Rate of Inbreeding. *J. Anim. Sci.* **1997**, *75*, 934–940. [CrossRef]
12. Sargolzaei, M.; Iwaisaki, H.; Colleau, J.J. CFC: A Tool for Monitoring Genetic Diversity. In Proceedings of the 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, Brazil, 13–18 August 2006; pp. 27–28.
13. Maignel, L.; Boichard, D.; Verrier, E. Genetic Variability of French Dairy Breeds Estimated from Pedigree Information. *Interbull Bull.* **1996**, *14*, 49.
14. Meuwissen, T.H.E.; Luo, Z. Computing Inbreeding Coefficients in Large Populations. *Genet. Sel. Evol.* **1992**, *24*, 305–313. [CrossRef]
15. Cervantes, I.; Goyache, F.; Molina, A.; Valera, M.; Gutierrez, J.P. Estimation of Effective Population Size from the Rate of Coancestry in Pedigreed Populations. *J. Anim. Breed. Genet.* **2011**, *128*, 56–63. [CrossRef]
16. Wellmann, R. Optimum Contribution Selection for Animal Breeding and Conservation: The R Package. *Bioinformatics* **2019**, *20*, 25. [CrossRef]
17. R Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2021.
18. Groeneveld, E.; Kovač, M.; Mielenz, N. *VCE User's Guide and Reference Manual. Version 6.0*; Institute of Farm Animal Genetics: Neustadt, Germany, 2010.
19. Vandenberghe, L. The CVXOPT Linear and Quadratic Cone Program Solvers. 2010. Available online: <https://www.seas.ucla.edu/~vandenbe/publications/coneprog.pdf> (accessed on 1 December 2023).
20. Škorput, D.; Ceranac, D.; Luković, Z. Control of Inbreeding in Banija Spotted Pig Population Using Optimisation Methods. *J. Cent. Eur. Agric.* **2023**, *24*, 53–60. [CrossRef]
21. Casellas, J.; Ibáñez-Escriche, N.; Varona, L.; Rosas, J.P.; Noguera, J.L. Inbreeding Depression Load for Litter Size in Entrepelado and Retinto Iberian Pig Varieties. *J. Anim. Sci.* **2019**, *97*, 1979–1986. [CrossRef]
22. Posta, J.; Szabó, P.; Komlósi, I. Pedigree Analysis of Mangalica Pig Breeds. *Ann. Anim. Sci.* **2016**, *16*, 701–709. [CrossRef]
23. Food and Agriculture Organization (FAO). *Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans: Management of Small Populations at Risk*; Food and Agriculture Organization (FAO): Rome, Italy, 2000.
24. Crovetto, A.; Sirtori, F.; Pugliese, C.; Franci, O.; Bozzi, R. Pedigree Analysis of Cinta Senese and Mora Romagnola Breeds. *Acta Agric. Slov.* **2013**, *2013* (Suppl. 4), 41–44.
25. Druml, T.; Salajpal, K.; Dikic, M.; Urosevic, M.; Grilz-seger, G.; Baumung, R. Genetic Diversity, Population Structure and Subdivision of Local Balkan Pig Breeds in Austria, Croatia, Serbia and Bosnia-Herzegovina and Its Practical Value in Conservation Programs Genetic Diversity, Population Structure and Subdivision of Local Bal. *Genet. Sel. Evol.* **2012**, *44*, 5. [CrossRef]
26. Schiavo, G.; Bovo, S.; Muñoz, M.; Ribani, A.; Alves, E.; Araújo, J.P.; Bozzi, R.; Čandek-Potokar, M.; Charneca, R.; Fernandez, A.I.; et al. Runs of Homozygosity Provide a Genome Landscape Picture of Inbreeding and Genetic History of European Autochthonous and Commercial Pig Breeds. *Anim. Genet.* **2021**, *52*, 155–170. [CrossRef] [PubMed]
27. Paixão, G.; Martins, Â.; Esteves, A.; Payan-Carreira, R.; Carolino, N. Genetic Parameters for Reproductive, Longevity and Lifetime Production Traits in Bísaro Pigs. *Livest. Sci.* **2019**, *225*, 129–134. [CrossRef]
28. Saura, M.; Fernández, A.; Varona, L.; Fernández, A.I.; de Cara, M.Á.R.; Barragán, C.; Villanueva, B. Detecting Inbreeding Depression for Reproductive Traits in Iberian Pigs Using Genome-Wide Data. *Genet. Sel. Evol.* **2015**, *47*, 1. [CrossRef]
29. Noguera, J.L.; Casellas, J.; Rosas, J.P.; Varona, L. Genetic Parameters and Direct, Maternal and Heterosis Effects on Litter Size in a Diallel Cross among Three Commercial Varieties of Iberian Pig. *Animal* **2019**, *13*, 2765–2772. [CrossRef]
30. Sell-Kubiak, E. Selection for Litter Size and Litter Birthweight in Large White Pigs: Maximum, Mean and Variability of Reproduction Traits. *Animal* **2021**, *15*, 100352. [CrossRef]
31. Zaalberg, R.M.; Chu, T.T.; Bovbjerg, H.; Jensen, J.; Villumsen, T.M. Genetic Parameters for Early Piglet Weight, Litter Traits and Number of Functional Teats in Organic Pigs. *Animal* **2023**, *17*, 100717. [CrossRef]
32. Leeb, C.; Rudolph, G.; Bochicchio, D.; Edwards, S.; Früh, B.; Holinger, M.; Holmes, D.; Illmann, G.; Knop, D.; Prunier, A.; et al. Effects of Three Husbandry Systems on Health, Welfare and Productivity of Organic Pigs. *Animal* **2019**, *13*, 2025–2033. [CrossRef]
33. Woolliams, J.A.; Berg, P.; Dagnachew, B.S.; Meuwissen, T.H.E. Genetic Contributions and Their Optimization. *J. Anim. Breed. Genet.* **2015**, *132*, 89–99. [CrossRef] [PubMed]
34. Obšteter, J.; Jenko, J.; Hickey, J.M.; Gorjanc, G. Efficient Use of Genomic Information for Sustainable Genetic Improvement in Small Cattle Populations. *J. Dairy Sci.* **2019**, *102*, 9971–9982. [CrossRef] [PubMed]
35. Commission Implementing Regulation (EU) 2023/2177 of 9 October 2023 on Entering a Name in the Register of Protected Designations of Origin and Protected Geographical Indications (Meso Turopoljske Svinje (PDO)). Available online: http://data.europa.eu/eli/reg_impl/2023/2177/oj (accessed on 8 December 2023).

36. Álvarez, I.; Royo, L.J.; Gutiérrez, J.P.; Fernández, I.; Arranz, J.J.; Goyache, F. Relationship between Genealogical and Microsatellite Information Characterizing Losses of Genetic Variability: Empirical Evidence from the Rare Xalda Sheep Breed. *Livest. Sci.* **2008**, *115*, 80–88. [[CrossRef](#)]
37. Kennedy, B.W.; Trus, D. Considerations on Genetic Connectedness between Management Units under an Animal Model. *J. Anim. Sci.* **1993**, *71*, 2341–2352. [[CrossRef](#)]
38. Škorput, D.; Gorjanc, G.; Luković, Z. Evaluation of Connectedness between the Management Units of Landrace Breed of Pigs in Croatia. *Acta Agric. Slov.* **2012**, *100*, 181–185.

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.