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Master Thesis

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Conservation of the transboundary breed Danish Shorthorn Cattle using Optimal Contribution Selection

Developing a breeding strategy for managing the Danish National Gene Bank

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Preface

This thesis was conceptualized as part of a project commissioned by the Danish Agency for Agriculture and Fisheries (DAAF) to construct a mating plan for the critically endangered breed, Danish Shorthorn Cattle, to optimally utilize genetic material imported from foreign sires. The objective of the project was agreed upon during an ERFA group meeting on December 12th, 2024, hosted by Aarhus University and the DAAF. Present were representatives from the university and the agency, the Danish conservation committee, and local shorthorn breeders.
This thesis was supervised by project lead Alban Bouquet (Aarhus University) and co-supervised by Morten Kargo (Viking Genetics, Aarhus University). This thesis presents preliminary results using only pedigree information. Results have not been presented to project partners yet and will be complemented by analyses of genomic data in order to emit final recommendations.

As the author, I would like to thank my supervisors, Alban Bouquet and Morten Kargo, for their collaboration in this thesis, and also the researchers at the Center for Quantitative Genetics and Genomics for being welcoming during my time at the office. I would like to thank the breeders for their openness, willingness to cooperate, and their commitment to the conservation of Danish Shorthorn Cattle. I would also like to thank my colleagues at the Agency of Gran Transition and Water-environment and at the Agency of Agriculture and Fisheries for cheering me on.

Lastly, my friends and family for their support, unyielding faith in my capabilities when my self-confidence failed me, and for their presence when life was just too hard.

"Perseverance is not a long race; it is many short races one after the other."

- Walter Elliot

Abstract

In 2024, the Danish Agency of Agriculture and Fisheries (DAAF) approved the import of genetic material from a British Dairy Shorthorn population in an effort to increase genetic diversity in the Danish Shorthorn population, which suffers greatly from inbreeding depression caused by small population size and high relatedness. As part of a conservation effort for this critically endangered breed, DAAF commissioned a project intending to investigate how to best utilize the imported bulls and provide a mating plan aimed at sustainable breeding. This thesis analysed pedigree information from 221 individuals and their quality. The mean PCI was 0.87 over 6 generations, and the generations equivalent was 6.91, deeming the pedigree quality sufficient for robust calculation of inbreeding and kinship coefficients. The mean inbreeding was 16.3% and ranged as high as 32.7%. The analysis showed that the mean inbreeding had increased with the equivalent of 0.61% per year. The mean kinship was 16.3% , the effective population size was 19.3, and the genetic diversity was 78%. Using information on the latest reproductive events, a list of expected active breeding animals was constructed as a list of potential mating candidates. Individuals with poor pedigree quality ($\mathrm{PCI}(6) < 0.6$) were disqualified as potential mating candidates. For potential sires, the list included 12 of 13 sires from the gene bank and 3 natural service sires. When applying OSC, mating allocation was strongly skewed towards the use of sires from the gene bank, while only 1 natural service sire was selected. It was not possible to apply pedigree-based OCS while including the imported sires, but kinship coefficients of the dams that had been inseminated were calculated and ranked (see Appendix). Overall, the pedigree information was useful in gaining an understanding of the population statistics and structure, but when creating an impactful mating plan, the pedigrees must be complemented by genomic data when applying OCS, both for allocation of native sires and imported sires. Genomic information will also be needed for further investigating hybrid offspring and their use within the population.

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1. Introduction

1.1. Animal Genetic Resources

1.1.1. Importance of genetic resources

Indigenous breeds contain a valuable gene pool as they are adapted to local environmental factors, encompassing, for example, feed resources, climate features, and endemic pathogens. This includes diseases if the local environment is characterized by a high pathogenic load (Gradinaru et al., 2018). Over the last decades, crossbreeding and breed replacement with more productive breeds have often been used to increase farms' productivity and income. These specialized breeds are often poorly adapted to local low-input environments, thereby challenging the sustainability of their usage (Leroy et al., 2016).

As climate change negatively impacts not only the natural ecosystems (Ishida et al., 2015; Phinchongsakuldit et al., 2013) but also in the livestock sector, animal diversity will decline as production will become more demanding and requiring more specialized production animals, affecting food security and the livelihood of smaller marginal farmers (Malik et al., 2015).

1.1.2. International agreements and obligations

The Commission on Genetic Resources for Food and Agriculture was established under the Food and Agriculture Organization of the United Nations (FAO) in 1983, originally working with plant genetic resources, and later, in 1995, the Commission's mandate was expanded, covering all biodiversity of relevance to food and agriculture, including animal genetic resources (FAO, 2025). In 1997, the Commission established its first working group for animal genetic resources (WG AnGR), which has since worked on reviewing and reporting on the world situation.

At the World Food Summit in 1996, world leaders and their representatives reaffirmed the right of all humans to have access to safe and nutritious food and to be free from hunger as a fundamental right. In their declaration, known as the Rome Declaration, the summit affirmed that investing in research, cataloguing, and conservation of genetic resources is essential to food security (FAO, 1996).

1.2. The Danish National Animal Gene Bank

In the 1980s, the first few farmers and animal breeders actively started working to preserve the native breeds and breeds considered of historic and cultural importance. This resulted in the identification of five original Danish cattle breeds, including the Danish Dairy Shorthorn, for keeping in the national gene bank. The gene bank is managed cooperatively by the Danish Agency of Agriculture and Fisheries DAAF). As the link between the Minister of Food, Agriculture and Fisheries and the breeders, the agency creates and maintains policies that support the subsidy-based conservation work of the breeders (Landbrugsstyrelsen, 2023).

1.3. Danish Shorthorn Cattle

1.3.1. History and Breed Description

The transboundary Shorthorn breed was first introduced in Denmark in the 1800s, and by 1922, the breed was one of the most common breeds on the Jutland peninsula, as one-third of the entire cattle population was of the Shorthorn breed (Fransen, 2014; Landbrugsstyrelsen, 2025). Until the 1950s, breeding was mainly local but allowed import from foreign lines, which have since then been restricted to British Shorthorn breeds, that are considered the original Shorthorn cattle, and the remaining population was mainly crossed with red and white dual-purpose cattle from Germany and the Netherlands. Today, few individual females remain from the original breeding line (Fransen, 2014; Sørensen & Nielsen, 2017).

In 1986, Laurits Lynge presented some of the last remaining individuals from pure shorthorn lines, and animals descended from these lines are the ones considered the original Danish Dairy Shorthorn cattle today (Fransen, 2014).

The breed is described as a sturdy breed of small stature. Originating from the British Isles, the breed is well adapted to the colder and wetter climate of Northern Europe, as well as the moorlands seen all over the continent. As a dual-purpose breed, shorthorn cattle were historically fit for both dairy and beef production (Landbrugsstyrelsen, 2025; Sørensen & Nielsen, 2017).

1.3.2. Current population

In 2019, the Ministry of Food, Agriculture, and Fisheries commissioned a study into the genetic structure and diversity of the current shorthorn population using genomic data. The study found that the population was genetically distinct from other shorthorn populations. Moreover, compared to other European shorthorn breeds investigated in the study, the Danish population had the lowest heterozygosity and alarmingly high inbreeding levels (Ravn, 2020). These results suggested a high risk of inbreeding depression that could seriously compromise the survival of the breed. In this project it was concluded that genetic rescuing could be an option to introgress new genetic variation from other Shorthorn populations. However, authors insisted that there is no consensus on optimal practices and no single indicators to determine which animals should be imported and from which populations. Indeed, the use of genomic data or phenotypic data would lead to different choices in the case of the Danish Shorthorn population. They also stressed that more efforts should be put into improving mating decisions in the conservation program to minimize the loss of genetic diversity (Ravn, 2020).

In 2023, it was decided to import semen of two bulls from the Northern dairy Shorthorn population through a collaboration with the British breed association (Bevaringsudvalget, 2023).

1.4.Breeding Strategies for Breed Conservation

Herdbooks are nowadays greatly supported by genomic data to verify parentage, but also get a finer description of genetic diversity present in the population. The overall goal is sustainable maintenance of genetic diversity within a population (Fioretti et al., 2020).

Using genomic data can improve conservation of diversity in specific genome regions because we can access detailed information about the allelic diversity of each individual. However, for some chromosomes, the conserved diversity may be higher when selection is pedigree-based, because pedigree-based approaches tend to distribute contributions more evenly, whereas genomic-based selection may focus contributions on individuals appearing superior based on genomic data, which may potentially reduce variation of certain allele regions (Engelsma et al., 2011).

Inbreeding is often used as an indicator of loss of diversity, as it increases homozygosity. In conservation programs, we aim to minimize the increase in inbreeding by minimizing the relationship between parents (Liu et al., 2017).

Meuwissen (1997) proposed a method to optimize the choice of parents and their genetic contributions to the next generation and to maximize genetic gain while constraining the average co-ancestry among selected parents, the equivalent of constraining the rate of inbreeding in the next generation, to a predefined value. He showed that minimal loss of genetic gains could be achieved with this approach while dramatically limiting the rate of inbreeding, thereby ensuring the long-term sustainability of breeding programs. This method, called *Optimal Contribution Selection*, contrasts with traditional truncation selection, where only top-performing individuals are selected to produce the next generation.

Meuwissen (1997) demonstrates that if G_{t+1} is the genetic level of the next generation, c_t is a vector of genetic contributions of the selection candidates, and EBV are the estimated breeding values of the selection candidates, then

$$G_{t+1} = c_t{'}EBV$$

The contributions of each sex equal 1/2;

$$Q{'}c_t = 1/2,$$

where Q is the matrix of known incidence for sexes, and the average co-ancestry is restricted

$$\bar{C}_{t+1} = c_t' A_t c_t / 2,$$

where A_t is the additive genetic relationship matrix among selection candidates. In conservation, however, there would not be any weight on genetic gain but only on the average relationship.

The benefits of this method have been demonstrated in multiple species and situations, and can also be used to update populations in selection programs (Eynard, Croiseau, et al., 2018; Gourdine et al., 2012; Henryon et al., 2019). This approach can also be applied to conservation programs in which we only aim to minimize the increase in inbreeding. Olsen et al. (2013) applied OCS to the Norwegian and the North-Swedish cold-blooded trotter populations, and concluded the method was feasible to select sire candidates. Nielsen and Kargo (2020) observed good prospects for conservation of the Jutland Horse when OCS and preselection of sires were applied. Successful conservation actions were prompted by applying OCS to the Faroese Horse population, which presented an exceptionally high average inbreeding (26.8%) and low effective population size (8) (Kettunen et al., 2022).

The use of older individuals through cryopreserved germplasm can enhance genetic diversity by restoring some alleles that have been lost over the last generations. Thus, using gene bank material from older, and possibly deceased individuals, can support long-term maintenance of breeds (Eynard, Windig, et al., 2018). However, when there's a high amount of relatedness in the population, applying optimum contribution selection alone cannot reduce the rate of inbreeding, and the addition of foreign breeds is necessary for improving the breed's chances of continuation (A. Schönherz & Guldbrandtsen, 2019-2021; Kettunen et al., 2017). In populations that experience inbreeding depression due to extremely high relatedness, cross-breeding will be necessary (Kettunen et al., 2017). Clark et al. (2013) observed that rotational crossbreeding can be beneficial to cattle production and that applying OCS can balance genetic gain and diversity. Ravn (2020) showed that genetic diversity, which has already been lost, cannot be regained by applying OCS with only the existing sires. However, choosing sires least related to the Danish population, of breeds most phenotypically similar to the Danish population, showed the possibility of increasing genetic diversity with little introgression (Schönherz & Guldbrandtsen, 2021).

Without genomic information on migrant donors, evaluation of their potential genetic contribution to the population is difficult. Therefore, with only pedigree information currently available, this thesis will perform a preliminary analysis of the population's genetic diversity, potential allocation of native sires by applying OCS, and discuss the future use of hybrid offspring that have already been produced.

2. Objective

The Danish Dairy Shorthorn Cattle breed is one of the 5 identified original cattle breeds in Denmark and is considered a conservation breed. However, as the population size has significantly decreased since the agricultural revolution and industrialization, the breed now suffers from severe inbreeding rates, resulting in low fertility and robustness. As part of conservation efforts, the Danish Ministry of Food, Agriculture and Fisheries approved the inclusion of two British Northern Dairy Shorthorn bulls in the Danish national gene bank, by recommendations from researchers and the Danish Conservation Committee. There is a critical need to provide breeders with tools to actively minimize the rise in inbreeding and its unfavourable associated effects.

This thesis aims to fill this gap by developing a mating plan to most effectively select and use Danish Shorthorn animals and discuss strategies to use offspring of the two British bulls in a sustainable way. The objective was to use existing software and include considerations for implementation by the breeders to guarantee the flexibility needed to make the plan realistic in practice.

The project will explore the following:

1. Evaluate the genetic diversity of the current Danish Shorthorn population using pedigree information.
2. Identify individuals of possible interest for cryo-conservation in the gene bank by performing optimal contribution selection, and provide an example mating plan.
3. Evaluate the cows inseminated with British sires in 2024 and discuss the possible use of the offspring.

3. Materials and Methods

3.1.Pedigrees and Pedigree Analysis

At the start of this thesis, 15 remaining Danish Shorthorn herds had been identified, with a total of 221 animals. This includes 175 females, 40 bulls, and 6 steers. From this, a subset pedigree of individuals confirmed as of the conservation breed by the farmers, which included 122 females and 23 males. Pedigrees and data on ongoing pregnancies, last inseminations, and last calvings for most recent reproduction events were extracted by SEGES Innovation P/S from the Danish Cattle Database, and then analysed using the R package “OptiSel” (Wellmann, 2019). Selection of breeding candidates was done using OptiSel (Wellmann, 2019). The retrieved full pedigree contained 2299 individuals spanning 24 generations.

3.1.1. Registration systems and data availability

It is to be noted that the Danish national cattle registration system categorized all Shorthorn cattle as being the same breed, regardless of whether the individual cattle can be defined as Conservation (Dairy) Shorthorn or Beef Shorthorn, based on publicly available information. Therefore, data collection heavily relied on the breeder's information and reports, as well as the cattle database. Some animals in the living population were excluded from the analysis due to farmers' reports of plans for future culling, either due to reproductive failure or age.

3.1.2. Population demographic structure

To gain a better understanding of the population structure, data on inseminations, natural services, and ongoing pregnancies were utilized to identify the active breeding individuals within the population, which was then used to construct a list of potential candidates. Information about bulls in the gene bank was also received and used to evaluate their usage over the last years.
Information on ongoing pregnancies was also used to investigate the future hybrid offspring that will be or have already been born in 2025.

3.2.Pedigree Evaluation

Pedigree data provide relevant information to characterize how the genetic diversity of a population evolves. However, diversity measures heavily depend on the exhaustivity of pedigree information. In this paragraph, we will first introduce the different indicators used to evaluate the quality of pedigree information and then describe the different measures of genetic diversity used in this study.

3.2.1. Pedigree quality and breed composition

The pedigree completeness index (PCI) is the harmonic mean of the paternal and maternal indices (Maccluer et al., 1983), and was calculated using the following formula:

$$PCI = \frac{2C_f \cdot C_m}{2C_f + C_m}$$

where $C_f$and C_m are the proportions of the maternal and paternal ancestors estimated based on:

$$C = \frac{1}{d}\sum_{i=1}^{d} a_i$$

where d is the number of generations and a_i is the ratio of known to unknown ancestors in each generation (Kasap et al., 2021). In the present study, PCI were calculated considering 6 generations back in time (Sørensen et al., 2005). Individuals presenting PCI < 0.6 over $d = 6$ generations were excluded from selection. PCI is commonly used in conservation genetics to quantify the available information on the ancestry of individuals, as well as to give higher accuracy of inbreeding coefficients and estimates on relatedness, which depend on the amount and accuracy of the information available (Maccluer et al., 1983).

The number of equivalent complete generations (equiGen) (Maignel et al., 1996) is a measure of pedigree depth and was calculated using the following formula:

$$equiGen = \sum_{i=1}^{n_j} \frac{1}{2^{gij}}$$

with n_j being the number of ancestors of individual j, and g_{ij} being the number of generations between individual j and ancestor i.

These statistics were computed with the function *summary()* of the OptiSel package, which also computes the number of fully traced generations and the number of maximum generations traced for each individual (Wellmann, 2019).

Breed composition was obtained by computing for each individual the proportion of founders coming from the different breeds found in the pedigree with the function *pedBreedComp()*. The contribution of each breed to age cohorts was then computed using the function *conttac()* (Wellmann, 2019). The thesis investigated the influence of foreign Shorthorn lines by differentiating the country of birth, but for the objective of the overall project, the breed of reference was defined only by Shorthorn Cattle for the rest of the analysis.

3.2.2. Inbreeding and Kinship

Inbreeding coefficient ($\boldsymbol{F}$) is the probability that two alleles at the same locus are identical by descent (IBD) through ancestor A, and is calculated for each individual by the following formula:

$$F = \sum\nolimits_i \frac{1}{2}^{n_i-1} (1 + F_{Ai})$$

where n_i is the number of meiosis (or generations) traced in loop i, and F_{Ai} is the inbreeding coefficient of (shared) ancestor A in loop i (Wright, 1922). The inbreeding coefficient was computed with the function *pedInbreeding()* (Wellmann, 2019).

The kinship coefficient (Wright, 1922) is the probability that two alleles at a neutral locus sampled from two individuals i and j come from common ancestors in the pedigree. The coefficient of kinship of two parents is therefore equal to the inbreeding coefficient of their offspring.

$$f_{ij} = \frac{1}{2}\left(f_{sires(i),j} + f_{dams(i),j}\right).$$

The formula above defines the kinship coefficient where f_{ij} is the kinship coeffiecient between i and j, $f_{sires(i),j}$ is the kinship coefficient between the sire of i and j, and $f_{dams(i),j}$ is the kinship coefficient between the dams of i and j (Falconer & Mackay, 1996).

Kinship coefficients were computed by the function *pedIBD* (Wellmann, 2019).

Genetic diversity is defined as the probability that two alleles randomly sampled from the population are not identical by descent (IBD). It corresponds to the expected heterozygosity (Nei & Li, 1973) and can be derived directly from the mean kinship $\bar{f}$ (Ballou & Lacy, 1995), and can be expressed in terms of the mean kinship, $\bar{f}$, as

$$Gene\ diversity = 1 - \bar{f}.$$

(Ballou & Lacy, 1995).

The **diversity at native alleles** is expressed with the same method, using the mean kinship restricted to native alleles.

3.2.3. Evolution of genetic diversity over time

The inbreeding coefficient strongly depends on the number of generations accounted for in the calculation. Indeed, the farther we track genealogies back in time, the higher the probability of finding a common ancestor. The rate of increase in inbreeding is a much more relevant indicator quantifying how genetic diversity evolves over time. This rate of increase in inbreeding is often presented as the effective population size.

The effective population size N_e is the size of an idealized random mating population for which the genetic diversity decreases at the same rate as the studied population (Cervantes et al., 2011), and is estimated as:

$$N_e = \frac{1}{2\Delta f}.$$

With Δf is the rate of increase in inbreeding (or kinship between parents) per generation.

The **native effective size** of the population is the size of an idealized random mating population for which the genetic diversity at native alleles decreases at the same rate as the studied population (Wellmann et al., 2012), and the value is stored as an attribute in the output when using the function *pedIBDatN()* (Wellmann, 2019).

The native effective population size can be used in breeding programs as a constraint when using optimal contribution selection to balance genetic gain against loss of native alleles (Wang et al., 2017; Wellmann et al., 2012). Comparing the native effective population size to the effective population size can reveal introgression from migrant influence (Wang et al., 2017).

3.3. Choice of breeding animals with Optimal Contribution Selection

In this population, the choice and genetic contribution of breeding animals were optimized for minimizing the average relationship among breeding animals in the next generation. The optimization problem was to find:

$$\min_{c} c'Ac$$

with the constraint:

$$\sum_{i} c_i = 1, \ \ c_i \geq 0.$$

The solution becomes a set of contributions that spreads genetic representations optimally.

This algorithm accounts for three things:

1) If individuals are closely related, their combined contributions are reduced.
2) If an individual is more genetically unique (less related to other candidates), its contribution is increased.
3) Over multiple generations

The optimal contribution of the selection of candidates was computed using the function *opticont()* in OptiSel (Wellmann, 2019).

The list of candidates was constructed using information on insemination, pregnancies, and calvings, creating a subset of all active males and females, as well a the bulls stored in the gene bank, except for the bull *Thy Ajs whose semen has been declared dead in the gene bank*. Each female could contribute up to 1 mating for the next generation (timestep) while bulls could contribute up to 8 matings. Two bulls, *Thy Texas* and *Kræp Adam*, were further restricted to a maximum of two matings due to the limited number of available semen doses. Bulls were not differentiated between natural service and the gene bank. The limit of the number of matings was chosen as a compromise to give enough flexibility to the algorithm to give more emphasis to the bulls from underrepresented lines, whilst ensuring that a sufficient number of bulls are used in the population. The target number of matings was fixed at 59, reflecting the number of calves either already born or anticipated in 2025. We used the function *opticont()* to calculate the optimum contributions of selection candidates and the function *matings* to generate mating plans based on these contributions.

4. Results

4.1. Population demographic structure

Based on records of inseminations and natural matings, the current population was born between 2011 and 2025. Figure 1 shows the age distribution of males and females according to their birth year. The age distribution of the population is strongly skewed toward younger individuals, with the majority of animals born in recent years. The figure shows the distribution of males to be heavily skewed toward young (1-year) individuals, but this is most likely due to the culling of bull calves not having been performed at the time of data extraction.

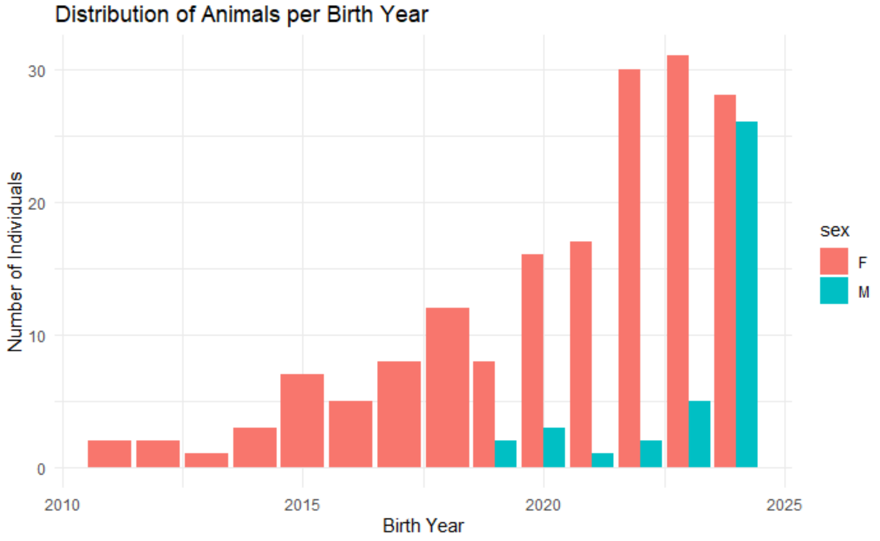

Figure 1: Age distribution of animals based on year of birth.

Insemination records indicate that at least 59 calvings are expected in 2025. Of these, 22 cows were inseminated with semen from the British bulls *Samson* and *David*, while the remainder were sired through natural service. Figure 2 illustrates the number of living animals or animals in the pedigree sired by a bull from the gene bank over the past 25 years. It’s shown that the number of offspring ranged between one and eight, but for almost 14 years (2000-2014), only one to five offspring were born. A relatively substantial increase happened in 2015, before one significant decrease, to then increase again before an overall decreasing trend.

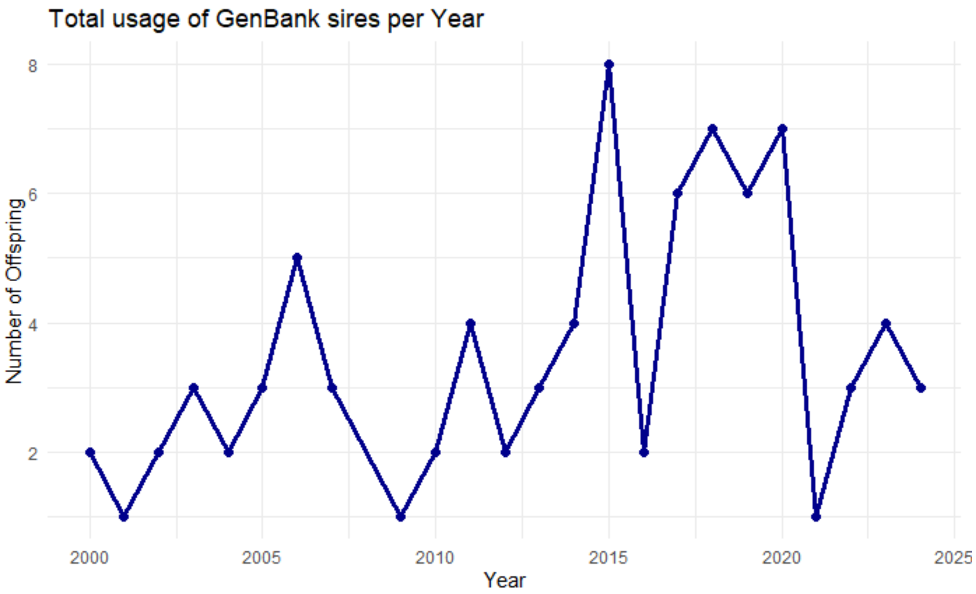

Figure 2: Total usage of bulls from the gene bank per year from 2000 to 2025.

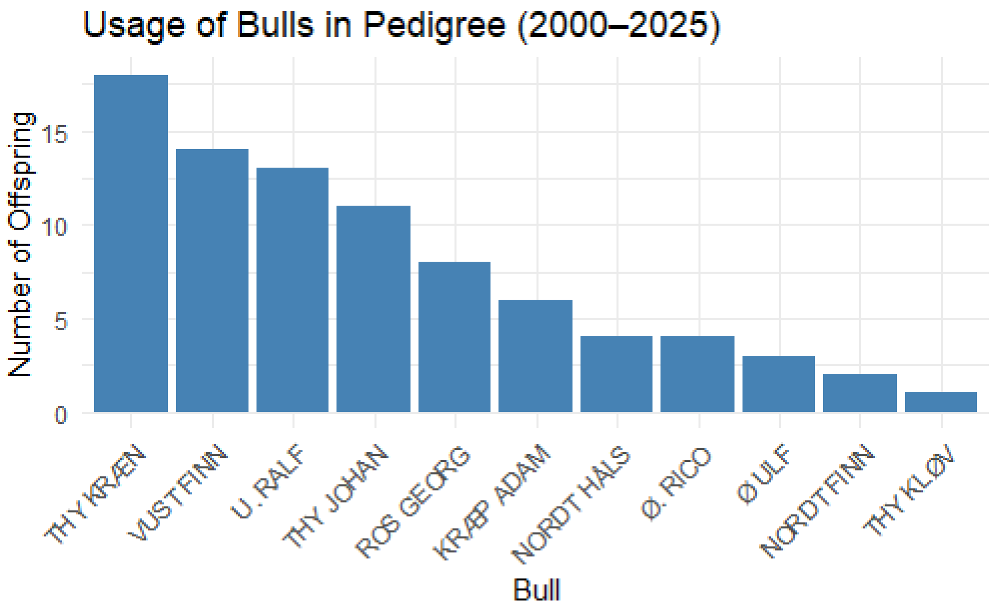

Figure 3: Total number of offspring in the pedigree file sired by each gene bank bull between 2000 and 2025.

Figure 3 shows the number of offspring in the pedigree file sired by each bull between 2000 and 2025. The bull *Thy Kræn* has sired the largest number of offspring, followed by *Vust Finn* and *U. Ralf*. Several bulls from the gene bank, such as *Kræp Adam* and *Nordt Hals*, have also been used, but to a lesser extent. Overall, the figure illustrates that while a few bulls have contributed substantially to the pedigree, many others have been used far less consistently, reflecting both the limited availability of semen doses and the reliance on natural service in recent years.

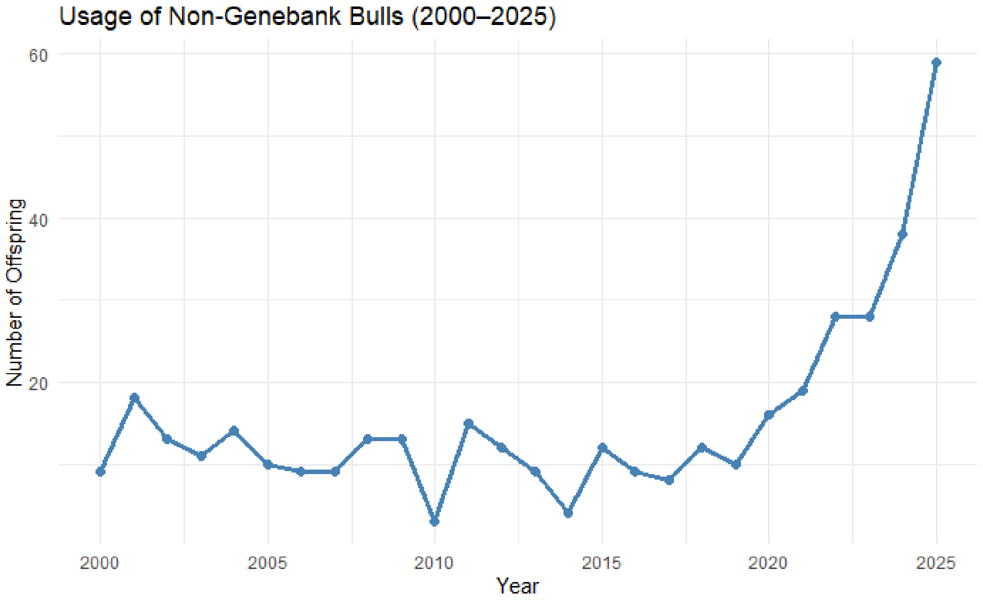

Figure 4: Number of individuals in the pedigree file sired by natural service bulls per year from 2000 to 2025.

Figure 4 shows the number of individuals in the pedigree file sired natural service bulls between 2000 and 2025. From 2000 to around 2018, the number of offspring from these bulls remained relatively low and fluctuated, typically ranging between 5 and 20 offspring per year.

4.2.Pedigree-based Evaluation

4.2.1. Pedigree quality

Indicators of pedigree completeness are summarized in Figure 5. The number of traced generations varied from 0 to 24, while the number of fully traced generations ranged from 0 to 6. The equivalent complete generations (EquiGen) ranged from 0 to 9.74, with a mean of 6.91. The pedigree completeness index (PCI) was calculated mean of 0.866 over 6 generations. In total, 186 out of 209 individuals had a PCI greater than 0.6 when tracing genealogies 6 generations backwards.. Overall, these results indicate that the pedigree information was of high quality for all breeding individuals included in this study.

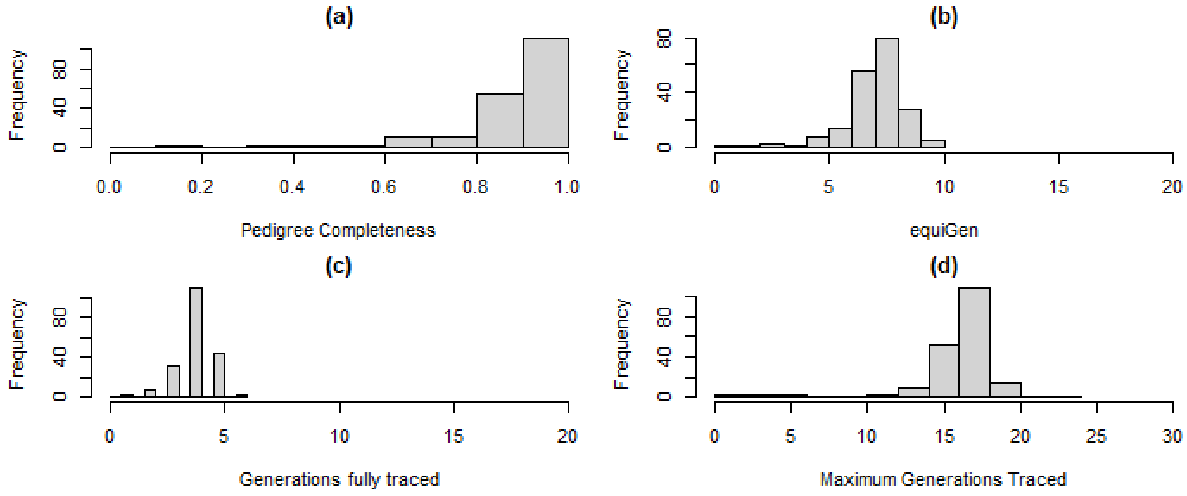

Figure 5: (a) Distribution of PCI of the population. (b). Number of equivalent Complete Generations. (c) Number of Generations fully traced. (d) Number of maximum generations traced per individual.

Figure 6 illustrates PCI over generations, which is an indication of the improvement in registrations of genealogies in more recent times, as there is more information on younger animals. The pedigree completeness index starts declining after 3-4 generations. The difference between the PCI of females and the PCI of males is relatively small, but consistent over generations females having slightly higher PCI than males between generations 4 to 10.

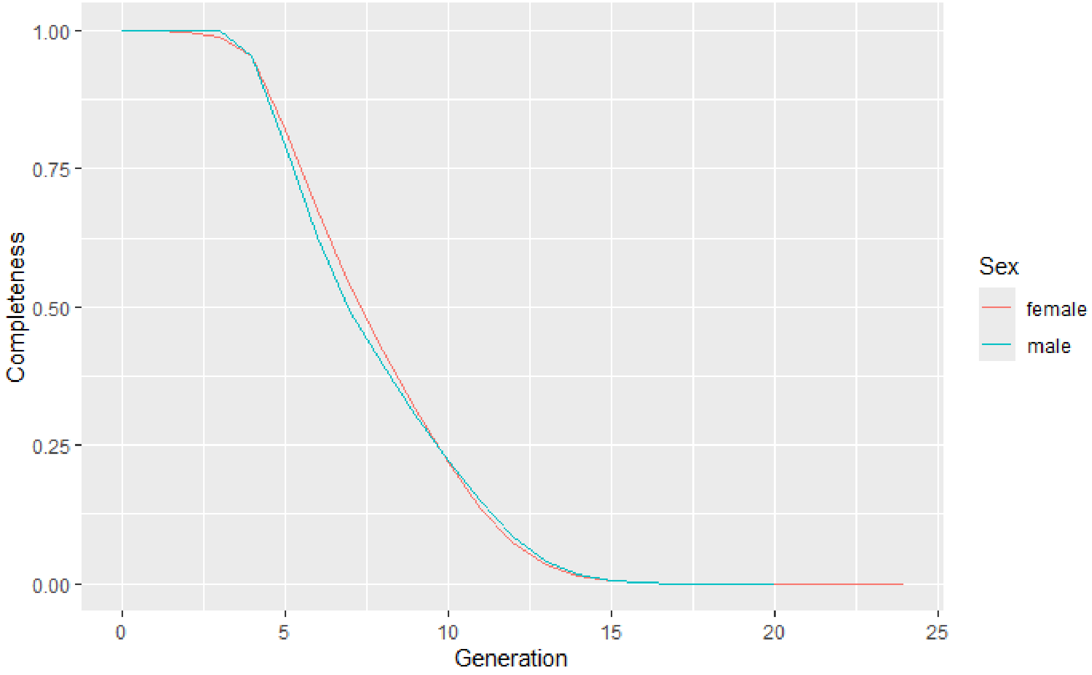

Figure 6 PCI per generation

4.2.2. Breed composition

Figure 7 shows the breed composition of animals in the pedigree based on birth year and illustrates that the influence of other breeds besides shorthorn is minimal. The small influence originates from common breeds, i.e., Holstein-Friesian, Jersey, Nordic Red, and Red Holstein, as common dairy breeds. Some minimal influence from beef breeds such as Hereford and Belgian Blue and the dual-purpose Maine Anjou breed was detected in the pedigree as well.

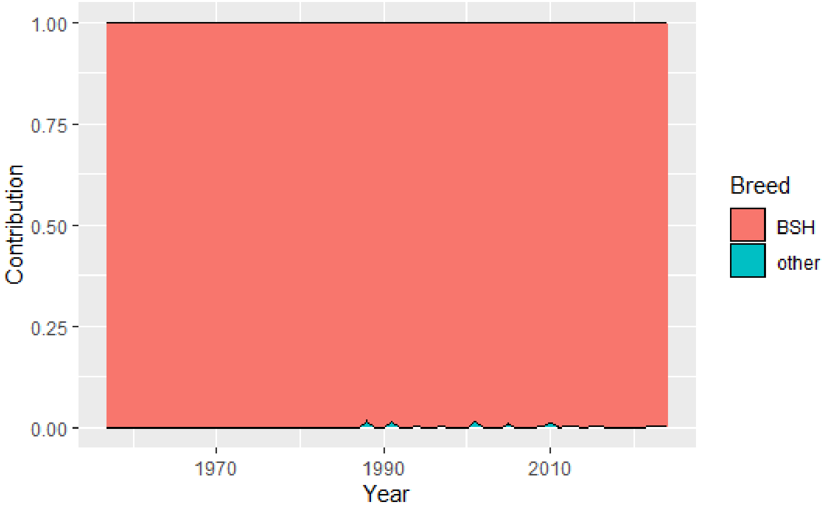

Figure 7: Breed contribution with no differentiation of country of birth, from 1917 to 2024.

As mentioned earlier, there is no distinction between the different Shorthorn lines in the Danish Cattle database. To get a clearer visualization of the influence from other Shorthorn populations, we considered Danish Shorthorn as the native breed, and we individualized/split Shorthorn animals based on their birth country. Figure 8 and Figure 9 shows that even though the influence from other breeds is minimal, the presence of other Shorthorn populations is noticeable, yet has decreased with import restrictions over time.

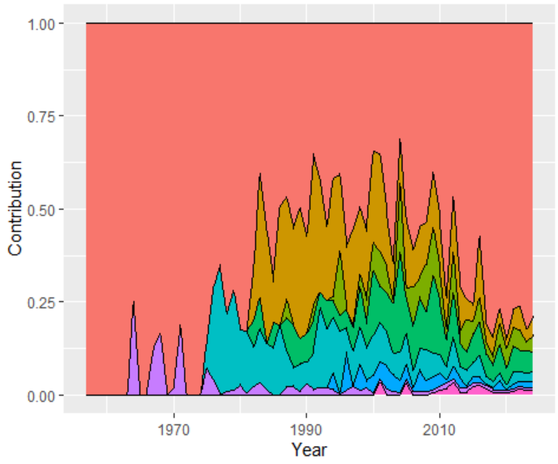

Figure 8:Breed contribution from year 1917 to 2024, showing the contribution from different imported Shorthorn populations.

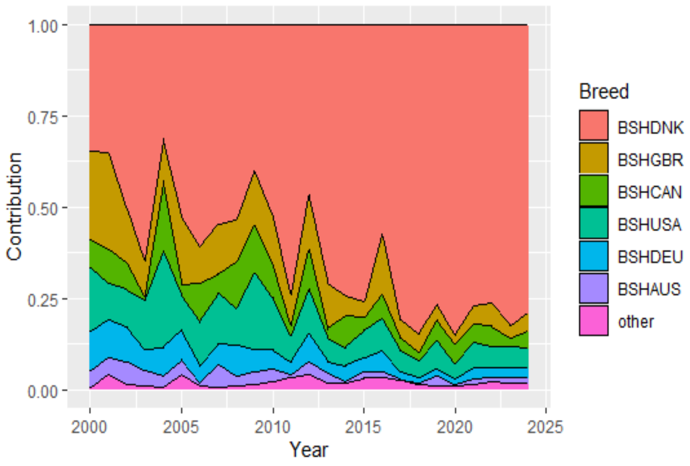

Figure 9: Breed contribution from year 2020 to 2024, showing the contribution from different imported Shorthorn populations.

Along with the 8 different Shorthorn breeds, 34 different populations have been crossed into the Danish Shorthorn population within the last 100 years. As the breed is transboundary, and for the purpose of this thesis, the contribution of different Shorthorn populations will not be explored further. There is, however, an ongoing debate as to whether conservation programs should primarily aim to preserve the genetic pool of the native population or the characteristic traits of the breed. This will be discussed further in the Discussion section.

4.2.3. Inbreeding coefficients and their evolution over time

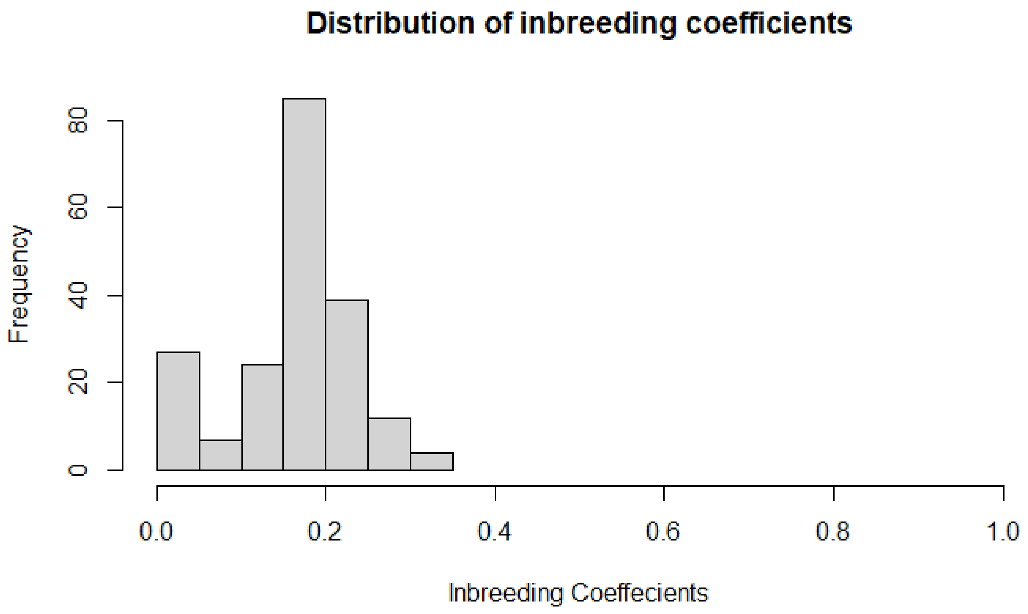

Figure 10: Distribution of inbreeding coefficients

The mean inbreeding coefficient of active breeding animals was 0.163 (Figure 10), and the inbreeding coefficients ranged between 0.0 and 0.327. The mean kinship between all breeding individuals was 0.163, and the resulting genetic diversity was 0.775.

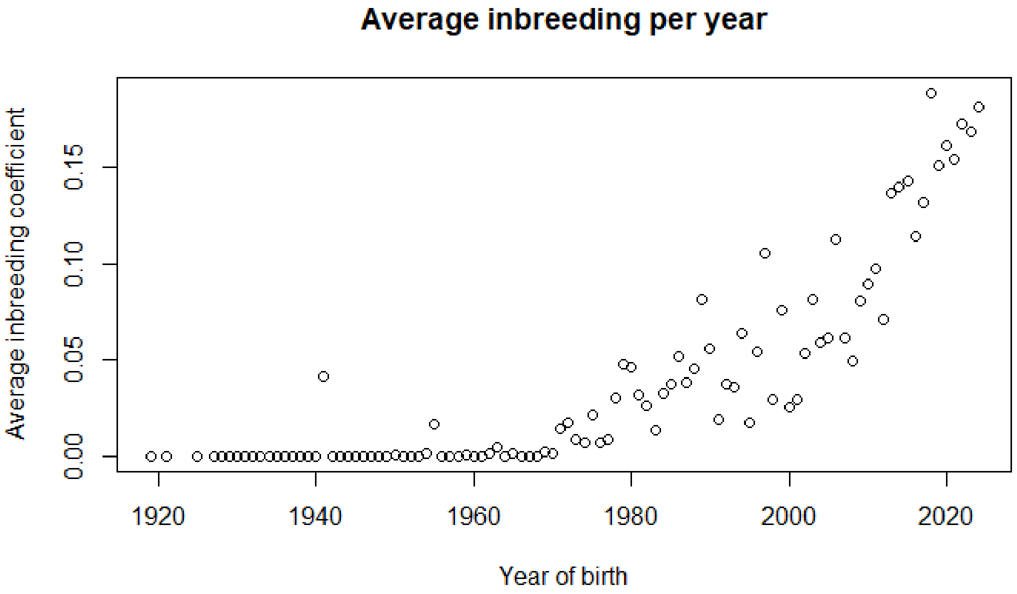

Figure 11: Average inbreeding coefficient based on year of birth

Figure 11 illustrates the mean inbreeding coefficient of all animals known in the pedigree per birth year. We can see a steady increase since 1970, with a lot of variation from year to year due to the limited number of ancestors recorded in some years. Over the last 20 years, the average inbreeding coefficient of the population has increased by 12.1 percentage points, equivalent to an increase of 0.61% per year. The effective population size estimated from trends in kinship was 19.29, which means that the overall genetic diversity of the population decreases at the same rate as a panmictic population of 19.29 individuals.

We performed the same analysis, but considering Danish Shorthorn animals as the native breed, to estimate how the genetic diversity of this subpopulation evolved in comparison to other Shorthorn breeds.

4.2.4. Bull contribution

In the national gene bank, there are currently 13 bulls used for both cryo-conservation and artificial insemination. This thesis explored the genetic contribution of these 13 bulls in the current population. As the material from the bull *Thy Ajs* is confirmed dead, it is not available for inseminations and therefore also shows no contribution in the graphs below.

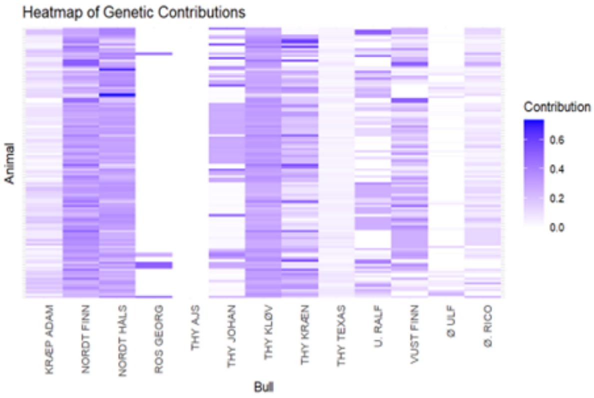

Figure 12: Total contribution of each bull to the current population. Each horizontal line represents an individual in the population.

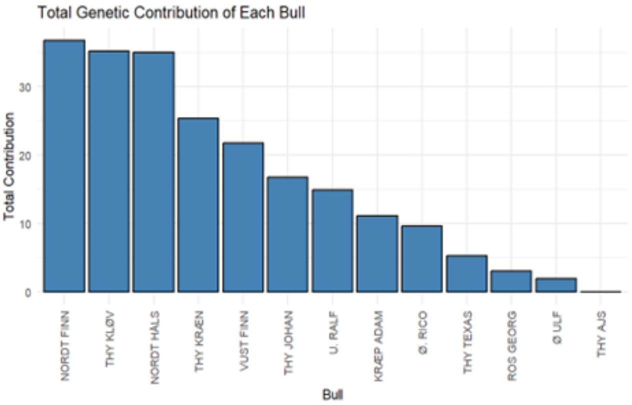

Figure 13: Genetic contribution of gene bank bulls in the current population based on pedigree information.

In Figure 12 it is clear that three of the bulls (*Nordt Håls*, *Nordt Finn*, and *Thy Kløv)* all make major contributions to the population, ranging between 35.0 pct. and 36.9 pct. This is further emphasized in Figure 13, where these three bulls all exceed a total genetic contribution of 40 pct. These large contributions are explained by pedigree relationships between these three bulls, the contribution of a sire being redundant with the contribution of their sons or grandsons.

The bulls in the gene bank are known to be highly related, and their average kinship was calculated as 0.156.

In the current population, 60 individuals have been sired by still living natural service bulls. Figure 14 illustrates their genetic contributions.

Table 1: Number of offspring in the current population per alive natural service bull.

Sire	Number of Offspring	Breed	Born
BSHDNKM000005743500930	33	BSH	2020
BSHDNKM000009207400493	16	BSH	2016
BSHDNKM000009207400380	4	BSH	2015
BSHDNKM000005743500899	3	BSH	2018
BSHDNKM000005743500924	3	BSH	2019
BSHDNKM000009207400511	1	BSH	2020

Table 1 shows that only a handful of males sired offspring to the current population. The dominant contributor is bull BSHDNKM000005743500930, born in 2020, which has already sired 33 offspring despite its relatively young age. In contrast, BSHDNKM000009207400493, born in 2016, has produced 16 offspring, while older bulls such as those born in 2015, 2018, and 2019 have sired only a few offspring each (1–4).

Figure 14 further illustrates this imbalance, with genetic contributions originating from mostly younger sires. While BSHDNKM000009207400380 may only have had 4 offspring, the figure shows that it must be the grandsire of multiple individuals. The figure also shows that two bulls in the population have either had no offspring or have no living offspring.

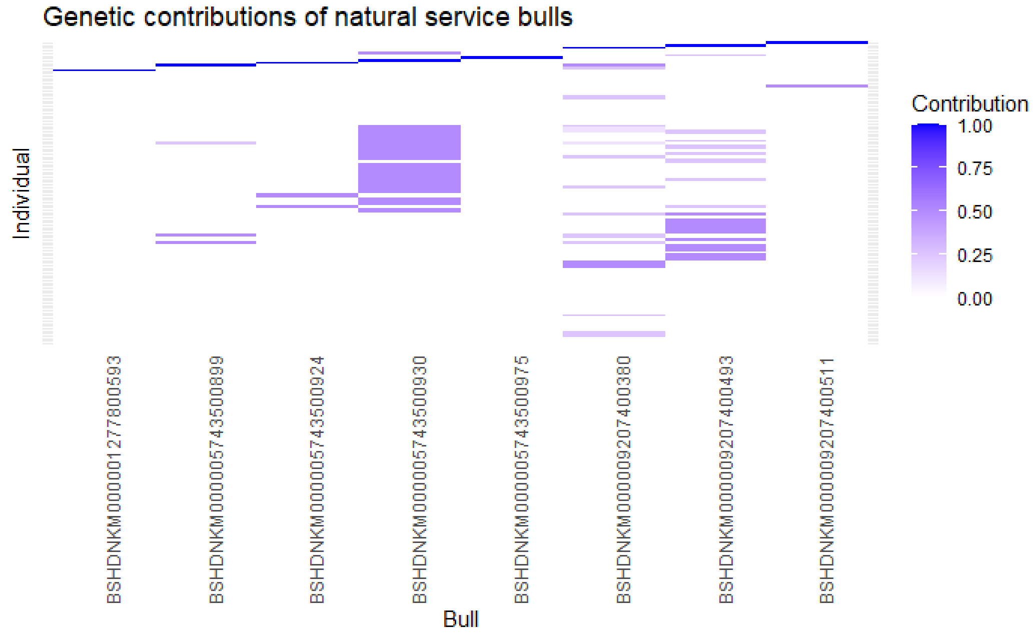

Figure 14: Genetic contributions of natural service bulls to the current population.

4.2.5. Offspring of British bulls born in 2025

It was not possible to compute relatedness between the imported bulls and the Danish population, as there were no declared pedigree relationships between them. It was, however, possible to calculate the kinship coefficients between the dams, between the dams and the other pregnant dams, and between the dams and the rest of the population, which were 0.24, 0.18, and 0.22, respectively, and the mean kinship between all 56 offspring and the current population was calculated to be 0.11.

The mean kinship between the dams pregnant by other sires and the rest of the population was 0.17.

In tables in Appendix 2. and 3. show the average kinship between each dam of hybrids and the rest of the population, and average kinship between each dam of hybrids and other dams of hybrids, respectively.

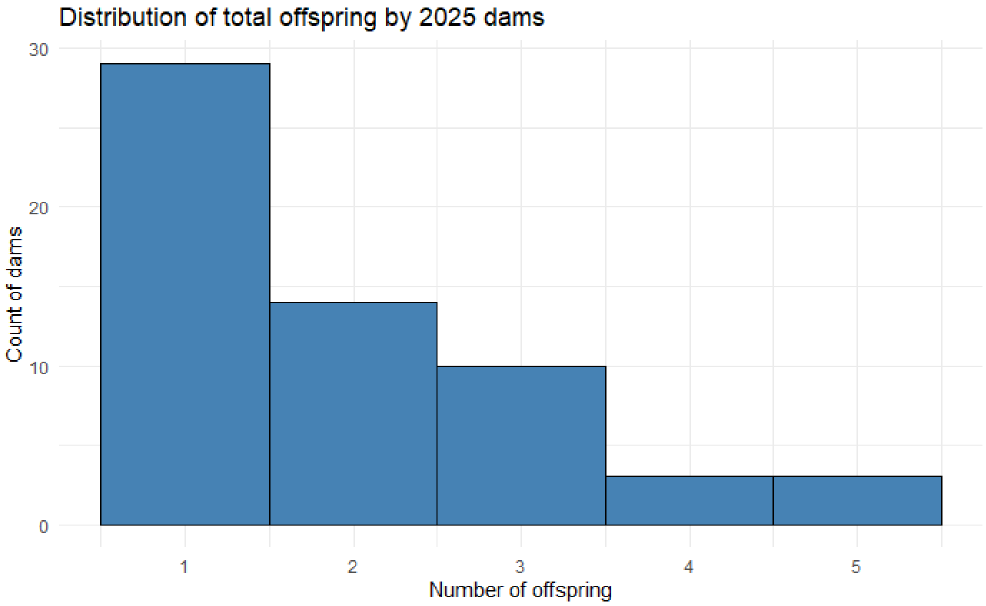

Figure 15: Distribution of the total number of offspring in the pedigree file per dam.

Figure 15 shows the distribution of the total number of offspring per dam with offspring in 2025. The majority of the dams have only one recorded offspring, while fewer have two or three, and only a small number of dams have produced four or five.

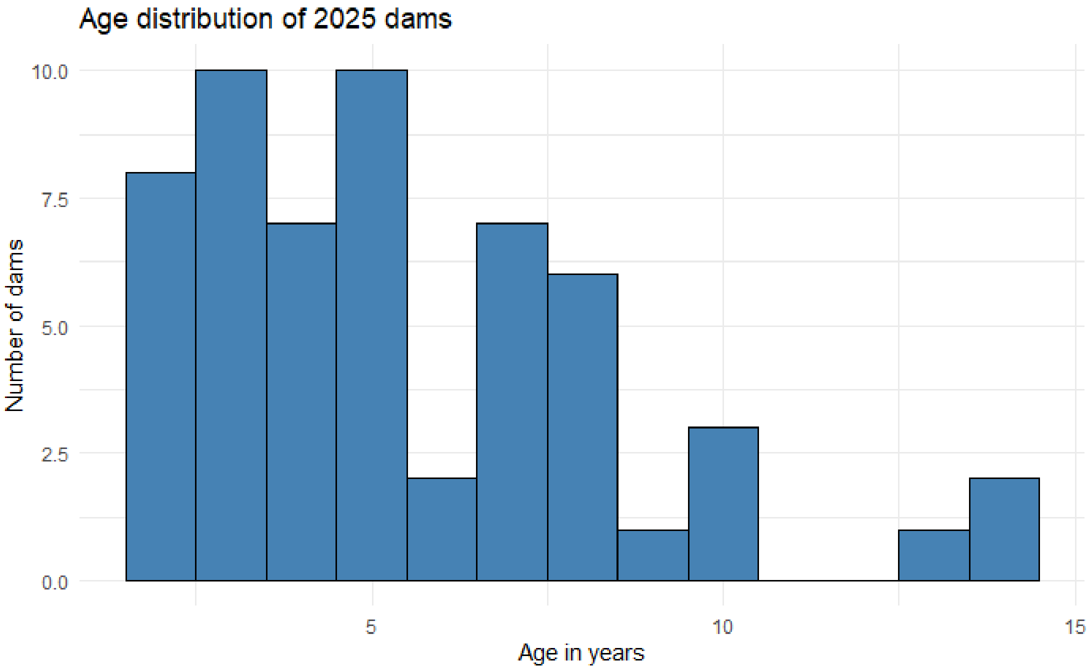

Figure 16: Age distribution of dams with offspring in 2025.

The age distribution of the dams is illustrated in Figure 16, where the distribution is clearly skewed toward younger animals. The majority of the dams are between ages of 2 and 5. A small proportion of older dams is also represented; however, they are very few.

4.3. Optimal Contribution Selection

4.3.1. Age contributions and generation interval

The generation interval was again 6.41 years. Because we are dealing with a population with overlapping generations, OptiSel calculates the expected genetic contributions of each sex in each age classes to the next generation considering genetic contributions observed over the recent years.

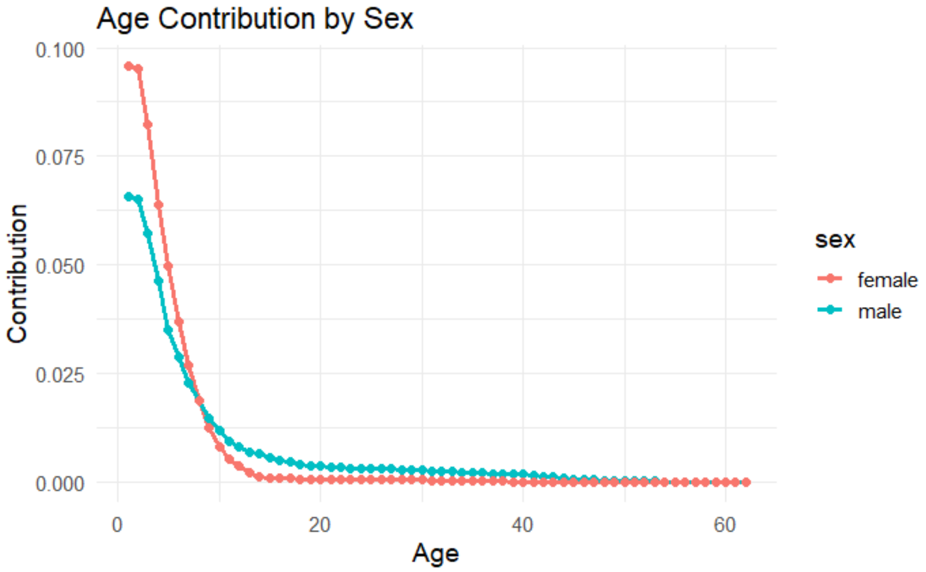

Figure 17: Contribution of age groups 1-61 by males and females

Figure 17 illustrates that the majority of genetic contributions of both sexes is dominated by young parents, with females showing a steeper decline after early reproduction, while males maintain some influence over a longer age range.

4.3.2. Optimal Contributions

The optimal contributions for all sire candidates were computed. Table 2 shows the results of the optimal contribution analysis for candidate sires. The distribution of contributions was highly uneven, with only a small subset of sires assigned significant genetic value. Five gene bank (GB) bulls and one natural service (NS) bull received the largest contributions, each accounting for approximately 0.07 of the total genetic input. One additional GB bull was assigned a moderate contribution (0.044), while two further GB bulls contributed at a lower level (0.018 each). The remaining sires, both from the gene bank and natural service, were excluded from the selection, with contributions close to zero.

Table 2: Optimal contribution for each candidate sire. The third column indicates whether the sire is a natural service bull (NS Bull) or a gene bank bull (GB Bull).

Optimal contributions for each sire

Sire	OC	Type
BSHDNKM000006293300074	0.0701753231580	GB Bull
BSHDNKM000000198604057	0.0701753051606	GB Bull
BSHDNKM000006293300076	0.0701752304382	GB Bull
BSHDNKM000006293300228	0.0701751444598	GB Bull
BSHDNKM000008048700128	0.0701747900609	GB Bull
BSHDNKM000001277800593	0.0701746572766	NS Bull
BSHDNKM000008048700073	0.0438024890761	GB Bull
BSHDNKM000006293300249	0.0175438061318	GB Bull
BSHDNKM000006878500024	0.0175425269022	GB Bull
BSHDNKM000006293300230	0.0000376369171	GB Bull
BSHDNKM000005291001694	0.0000184989587	GB Bull
BSHDNKM000009207400511	0.0000024828728	NS Bull
BSHDNKM000008887300018	0.0000009184218	GB Bull
BSHDNKM000008887300054	0.0000008517055	GB Bull
BSHDNKM000005743500930	0.0000003384697	NS Bull

Table 3 shows an outtake from the optimized mating plan, showing the 10 pairings with the highest average kinship coefficients. Kinship values in these top pairings range from 0.173 to 0.193, indicating that while the optimization has aimed to reduce relatedness across the whole population, some matings still involve relatively close relatives. This is expected when the pool of available sires and dams is limited.

Notably, a few sires appear multiple times within the highest-kinship pairings. For example, BSHDNKM000008048700128 and BSHDNKM000001277800593 occur repeatedly, reflecting their relatively high overall contribution potential in the optimized plan. However, even for these sires, the kinship levels remain moderate, suggesting that the optimization successfully avoided highly inbred matings.

Overall, while these top 10 pairings represent the less desirable part of the mating plan based on kinship, they still fall within an acceptable range.

Table 3: Outtake from mating plan. Pairings with the 10 highest average kinships between pairings.

Mating plan

Sire	Dam	n	Kinship
BSHDNKM000008048700128	BSHDNKF000005743500995	1	0.1931592
BSHDNKM000008048700073	BSHDNKF000005743501020	1	0.1905165
BSHDNKM000001277800593	BSHDNKF000008048700934	1	0.1883842
BSHDNKM000001277800593	BSHDNKF000005743501001	1	0.1869529
BSHDNKM000001277800593	BSHDNKF000008048700815	1	0.1819491
BSHDNKM000008048700073	BSHDNKF000005743501015	1	0.1810886
BSHDNKM000006878500024	BSHDNKF000005743500977	1	0.1757307
BSHDNKM000008048700128	BSHDNKF000005291001859	1	0.1755155
BSHDNKM000008048700128	BSHDNKF000009207400495	1	0.1733615
BSHDNKM000008048700128	BSHDNKF000005291001770	1	0.1732162

In contrast, the lowest-kinship pairings (Table 4) demonstrate how the optimization has identified pairings between sires and dams with minimal genetic relatedness. Kinship values as low as 0.0047 were observed, with the top 10 lowest values all below 0.092. Again, certain sires recur across these pairings, particularly BSHDNKM000000198604057 and BSHDNKM000008048700128, highlighting their flexibility in producing both low- and higher-related offspring depending on the chosen dam.

Table 4: Outtake from mating plan. Pairings with the 10 lowest average kinships between pairings

Mating plan

Sire	Dam	n	Kinship
BSHDNKM000008048700128	BSHDNKF000004902100058	1	0.004689276
BSHDNKM000008048700128	BSHDNKF000009011700207	1	0.008506924
BSHDNKM000001277800593	BSHDNKF000004902100056	1	0.016209465
BSHDNKM000008048700128	BSHDNKF000009011700211	1	0.016262040
BSHDNKM000000198604057	BSHDNKF000005743500994	1	0.064888000
BSHDNKM000000198604057	BSHDNKF000005743500880	1	0.066619873
BSHDNKM000000198604057	BSHDNKF000005743500947	1	0.077304840
BSHDNKM000000198604057	BSHDNKF000005894101284	1	0.090393066
BSHDNKM000000198604057	BSHDNKF000005894101357	1	0.090393066
BSHDNKM000000198604057	BSHDNKF000005743500993	1	0.091270447

Looking at these results together, there is an indication that the optimized mating plan effectively spreads contributions across sires while avoiding highly inbred pairings. Although some matings necessarily involve moderate kinship levels due to the population structure and contribution constraints, the presence of very low-kinship pairings confirms that the plan maintains genetic diversity and minimizes inbreeding wherever possible. This will be further discussed in the section Discussion.

The full mating plan is shown in Appendix.

Table 5: Mean values compared between the population (reference) and the potential offspring produced in the mating plan.

Comparison of mean inbreeding, breeding value, and kinship

Scenario	Inbreeding	BV	Kinship
Reference	0.151394	0	0.131944
Offspring	0.145256	0	0.137361

Table 5 shows the comparison of mean inbreeding and mean kinship in the “parent” population, and the mean inbreeding and mean kinship in the offspring population. The results show that the optimized mating plan is expected to reduce the average inbreeding level slightly, from 0.151 to 0.145, while at the same time increasing the mean kinship from 0.132 to 0.137. This reflects the trade-off between controlling inbreeding and maintaining genetic connectedness within the population, which is a common outcome in optimal contribution and mating strategies.

Table 6: Optimized number of matings for each selected sire.

Sire Usage

Sire	Matings
BSHDNKM000000198604057	9
BSHDNKM000001277800593	8
BSHDNKM000006293300074	8
BSHDNKM000006293300076	8
BSHDNKM000006293300228	9
BSHDNKM000006293300249	2
BSHDNKM000006878500024	2
BSHDNKM000008048700073	5
BSHDNKM000008048700128	8

Lastly, Table 6 shows the optimized number of matings for each sire candidate. It should be noted that even though optimal contribution selection was constrained to 8 matings per sire, 2 of the sires have been allocated 9 matings each, and 1 sire has been allocated 5 matings, which will be discussed in the next section.

5. Discussion

5.1. Pedigree analysis

5.1.1. Pedigree quality

As early herd bookings are not included in the pedigree file, some individuals had pedigree completeness indices (PCI) as low as 0.4—a level usually considered too low for reliable pedigree analyses (Johnson et al., 2011; Kasap et al., 2021; Tahmoorespur & Sheikhloo, 2011). However, the mean PCI was 0.866 over 6 generations. Thus, the low extreme values can be regarded as negligible, since the majority of individuals exceeded the commonly accepted threshold of 0.6 (Johnson et al., 2011; Machová et al., 2020).

In common practice, equivalent complete generations (equiGen) of at least 3–4 are considered the minimum acceptable depth for pedigree analyses(Gutiérrez et al., 2008; Kasap et al., 2021) whereas values of 5–8 or more are generally regarded as indicative of high pedigree quality (Gutiérrez et al., 2008). In the studied population, the mean value of equivalent complete generations was 6.91, reflecting adequate pedigree depth. The range of values (4.24–8.59) also lies within thresholds typically considered sufficient for robust calculations of relatedness and inbreeding.

The analysis revealed high levels of inbreeding and kinship, which is expected and aligns with the findings in Schönherz and Guldbrandtsen (2021).

5.1.2. Breed composition

The analysis highlighted two key aspects of the breed's history. First, the population has been adequately managed, with introgression from non-Shorthorn cattle kept to a minimum since the 1970s. Second, the breed is transboundary, sharing genetic material with other Shorthorn subpopulations through importation, which has been both permitted and necessary for its continued survival. These results also align with the conclusions by Schönherz and Guldbrandtsen (2021), and similar trends have been observed in other shorthorn breed populations, such as Japanese Shorthorn Cattle (Uemoto et al., 2021).

5.1.3. Inbreeding and kinship

(Schönherz & Guldbrandtsen, 2021)estimated high levels of inbreeding within the population at the genomic level, and therefore, the high level of pedigree-based inbreeding found in this study was not unexpected. Trinderup et al. (1999) calculated the mean inbreeding coefficients in 1999 at 4.1%, which means the mean inbreeding in the population has become four times as high over the span of 25 years.

The high level of kinship observed in the population is consistent with small populations, where limited numbers of animals and strong relatedness lead to high homozygosity (Liu et al., 2021; Mastrangelo et al., 2017).

Overall, the high level of kinship and low level of genetic diversity, and more importantly, the high rate at which they evolve, indicate both high relatedness within the current and limited variation in the total gene pool, once again affirming the need for genetic replenishment and broadening of the gene pool (Sponenberg, 2020).

5.1.4. Bull contribution

The results demonstrated a substantial contribution of bulls from the gene bank, with the exception of a few individuals that exhibited limited or no utilization by breeders. This distribution aligns with the elevated levels of inbreeding and genetic relatedness detected within the population. It should be noted that some of the bulls are highly related, even as sire-offspring relationships, which explains why their added contribution exceeds 100% (Figure 13). This also aligns with the findings in (Schönherz & Guldbrandtsen, 2021). The contributions from natural service bulls varied, as expected, due to differences in age and breeding availability. Logistical constraints, such as the movement of animals between farms and the collection of semen for artificial insemination, present challenges for some farmers and may be unfeasible in certain cases. This may explain why certain sires are underrepresented in the population.

5.2. Optimal contribution selection and mating plan

At the time of writing this thesis, it was only possible to analyse pedigree information and perform optimal contribution selection without including genomic information. Therefore, the mating plan was carried out with only Danish individuals, excluding the imported British sires, as they would have been allocated the maximum number of matings due to null kinship coefficient with Danish animals.

It was, however, possible to perform optimal contribution selection on the latest breeding animals based on their pedigrees. During the selection process, 3 natural service bulls and 12 gene bank bulls were included as potential sires and evaluated. From the calculated optimum contributions and the resulting mating plan, it was apparent that the software deems it necessary to utilize the material in the gene bank, as the mating allocations were heavily skewed toward their use. Inaccuracies of pedigree-based kinship may cause a heavier emphasis on gene bank sires, whereas a genomic-based calculation is likely to provide more accuracy on their relatedness with the population, which can potentially skew the mating differently (Clark et al., 2013; Galla et al., 2020; Zhang et al., 2020).

Only one natural service bull (*BSHDNK000001277800593*) was selected in this process and was allocated the maximum of 8 matings. This indicates that this particular bull, or one of its offspring, is a possible candidate for cryo-conservation. This should be studied further with genomic information

The majority of the bulls in the gene bank have generally been minimally utilized, which makes it reasonable to assume low kinship with the population based on utilization alone, depending on how their offspring are utilized in the population. However, the results presented in this report showed that three bulls had a high genetic contribution to the current population. It is therefore unexpected that the allocation of matings is so skewed towards the gene bank, as was shown in Table 6. Two of the bulls were even allocated 9 matings each, exceeding the limit of 8 matings maximum per bull, possibly to compensate for the mating limit on *Thy* Texas and *Kræp* Adam while attempting to reach the goal of 59 desired matings. One explanation could be the extremely low number of natural service bulls. It should be mentioned that one out of four sires was discarded due to poor PCI. The next step should be to include younger animals and investigate whether some of them would be interesting to keep for breeding.

It should be emphasized that at the time of this thesis's conception, 6 months have passed after the extraction of pedigree information, which creates gaps and grey areas in information, as we cannot be sure that the information available at this time accurately represents the population demographic (Wang et al., 2014). The proposed mating plan should be regarded as a preliminary example until it has been reassessed and validated using genomic information (Blackburn et al., 2024; Galla et al., 2020). Henryon et al. (2019) argues that pedigree-based optimum contribution selection is not without merit, as it can prove to realise more true genetic gain than the genomic-based counterpart. While this thesis does not include genetic gain in its objective, the merit of using pedigree cannot be completely disregarded.

It has also been reported that there are uncertainties about the fertility of the gene bank sires, and while *Thy Texas* and *Kræp Adam* have been limited to 2 matings each due to usage restrictions, it is uncertain if the material is viable.

5.3. Use of imported genetic material

From the information on dams, inseminated with the British bulls, average kinship between the dams and between the dams and the rest of the population was computed. The dams were ranked (Appendix) and when choosing which offspring to keep for breeding, it may be beneficial to further investigate the dams presenting with lower kinship. While there doesn't seem to be an exact threshold on parameters to decide how foreign material should be introduced, the general recommendations are to:

1. Use individuals with the lowest mean kinship to the rest of the population and use sparingly.
2. Capture unique alleles carried by the foreign donors.
3. Inseminate females from multiple lineages.
4. Conform to breed standards.

(Leroy et al., 2011; Oldenbroek & Windig, 2022)

As of now, 22 cows have been inseminated, which accounts for approximately one-third of the number of active females within a year. Their mean kinship to the rest of the population was 0.22, which was higher than the mean kinship between the other pregnant dams and the population.

To identify unique alleles, genomic information will be necessary, which was not possible to include in this thesis but will be included in the continuation of the project.

The cows are kept in different herds, but those are few in number, and it seems improbable for them to be of much different lineages when we account for the general high kinship and kinship at native alleles, as well as the small population size.

Lastly, conforming to breed standards to conserve breed identity, defining traits will be much more relevant when information on the offspring themselves is available. It does, however, align with the question of which offspring to keep for breeding, which is difficult to answer without knowledge of sex distribution. It also provokes questions of how selective breeders can afford to be with such a low population number and level of diversity. If an individual shows high conformity but also has a high average kinship with the population, will it still be more desirable for breeding? Lampi et al. (2020) and Oliehoek et al. (2009) caution that placing too much emphasis on phenotypes in breeding programs can lead to loss of genetic diversity due to selection pressure.

Finally, the ages of the dams were examined, and the analysis showed the majority of the dams are in their first, second or third parity, and only a few are in their fourth or fifth, which aligns with the recommendations to use the dams as young as possible to secure offspring, but also to use some older individuals to retain a balanced age structure (FAO, 2013; Oldenbroek & van der Waaij, 2014).

Therefore, when deciding which offspring to prioritize, the balance of these parameters (dam kinship with the population, genetic diversity between dams, age distribution of dams, etc.) must be considered.

5.4. Integrating the wishes of breeders into the breeding strategy

One of the main challenges in constructing a mating plan for livestock breeds is the need to move animals between herds. This is particularly difficult when using natural service sires, since moving a bull to multiple locations to cover the selected matings is both resource-intensive and logistically complex (Baruselli et al., 2018; Overton & Sischo, 2005). For this reason, the selected bulls would be especially valuable for producing male offspring that could later serve as donors to the gene bank.

The breeders have previously expressed their wish to have a flexible mating plan that allows for autonomy of their herds and the agency to make decisions, such as sire and dam selection. One suggested solution is to construct a mating plan that contains ranked options that would need to be further investigated. Mueller et al. (2015), Wurzinger et al. (2021) and Leroy et al. (2017) evaluated stakeholder involvement, breeder autonomy, and local decision-making and discovered positive effects when built into breeding schemes.

Existing software such as AlphaMate (Gorjanc & Hickey, 2018) are capable of performing optimization of breeding plan with ranked mating options, and it is therefore not impossible to develop a method that gives the flexibility and autonomy desired by the breeders (Akdemir & Sánchez, 2016). Finally, recent studies support prioritizing production of male offspring as future donors to the gene bank, reducing the necessity to move live bulls between herds, but can also prove expensive and full of constraints (Blackburn et al., 2023; Oldenbroek & Windig, 2022).

5.5. Future management of the Gene Bank

5.5.1. International collaboration to conserve transboundary breeds

Strengthening international collaboration through shared databases, coordinated breeding strategies, and cross-border cryo-conservation will possibly be critical to safeguard the long-term viability of transboundary breeds such as Dairy Shorthorn. Shared coordination on native breeds and databases (Ovaska et al., 2021), and even safety duplication of germplasm across borders (Jacques et al., 2024) are shown to be beneficial.

5.5.2. Updating the national population and breeding plan, and coordinating breeders

To achieve a meaningful impact, the mating plan will need to be continuously revised and informed by updated data on newly born offspring, as well as the removal of older or deceased individuals from the breeding population. The main challenge lies in the limited availability of data, as pedigree information and related records are privately owned and subject to restrictions on public access Burrow et al. (2021) documented multiple examples of datasets being inaccessible due to ownership, privacy, and poor metadata.

The revision of the mating plan should be performed by advisors with expertise in animal production systems, cattle reproduction, quantitative genetics, and data analysis (Segelke et al., 2014). Furthermore, ongoing collaboration between the appointed professional advisors and the animal breeders is essential to ensure effective implementation. Therefore, a protocol for information sharing between participating parties should be explored (Burrow et al., 2021; Delavenne et al., 2025).

5.6. Future work with Danish Dairy Shorthorn

The involvement of local breeders and livestock producers continues to be of great importance in developing and managing conservation programmes around the world (Leroy et al., 2017). Community-based approaches (Leroy et al., 2017) and social values (Cicia et al., 2003) should be at the forefront to increase the value of conserving native animal breeds.

Further development of the gene bank should incorporate better utilization of information systems to integrate and store genomic data, as well as data on cryo-conservation, phenotypes, and environmental conditions (Paiva et al., 2016).

Samples have already been genotyped, but the resulting genomic information has yet to be analysed at the time of writing. A proper mating plan and strategy will be constructed following this thesis, using the collected data to provide a strategy for future use of imported sires. It is expected that the analysis will provide a more accurate evaluation of the population, as missing ancestry information may be provided by genotyping (Meuwissen, 2009).

Finally, further development of financial and policy incentives for breeders, and raising public awareness of the values of native breeds, could be key actions for promoting the breeds’ survival (Ovaska et al., 2021).

6. Conclusion

In this thesis, pedigree information for Danish Shorthorn Cattle was used to assess the pedigree quality and investigate the evolution of inbreeding and kinship in the population over time. The analysis showed pedigree quality to be substantial for the calculation of inbreeding and kinship coefficients, and there was an overall high level of relatedness and a high rate of inbreeding within the population. The genetic contribution of sires from the gene bank was observed to be substantial, and the investigation showed that their usage has decreased in recent years.

Analysing dams inseminated with imported sires provided an understanding of their demographic structure and their kinship with the rest of the population. The range of kinship was substantial, and for further decisions on offspring to be kept for breeding, potentially as donors to the gene bank, it would be beneficial to investigate the dams presenting with lower levels of kinship. However, to include their offspring and the imported sires in the mating plan, OCS must be applied with genomic information.

Applying pedigree-based OCS resulted in heavy usage of gene bank sires, while only one natural service sire was selected for mating. This thesis argued that the selected natural service bull may be of interest for donation to the gene bank, or more likely as a grandsire to a potential donor. Meanwhile, to gain proper allocation of matings, pedigree information alone will not be adequate for allocating either native sires or imported sires, and OCS should be performed using genomic information.

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Appendix

1. Mating plan in full

Mating plan

Sire	Dam	n	Kinship
BSHDNKM000008048700128	BSHDNKF000004902100058	1	0.004689276
BSHDNKM000008048700128	BSHDNKF000009011700207	1	0.008506924
BSHDNKM000001277800593	BSHDNKF000004902100056	1	0.016209465
BSHDNKM000008048700128	BSHDNKF000009011700211	2	0.016262040
BSHDNKM000000198604057	BSHDNKF000005743500994	1	0.064888000
BSHDNKM000000198604057	BSHDNKF000005743500880	2	0.066619873
BSHDNKM000000198604057	BSHDNKF000005743500947	1	0.077304840
BSHDNKM000000198604057	BSHDNKF000005894101284	1	0.090393066
BSHDNKM000000198604057	BSHDNKF000005894101357	1	0.090393066
BSHDNKM000000198604057	BSHDNKF000005743500993	1	0.091270447
BSHDNKM000006293300249	BSHDNKF000005743501003	1	0.099422455
BSHDNKM000006293300249	BSHDNKF000005743501011	1	0.104496479
BSHDNKM000006293300074	BSHDNKF000005743500960	1	0.111038208
BSHDNKM000006293300076	BSHDNKF000008048701015	1	0.116500854
BSHDNKM000000198604057	BSHDNKF000005743500837	1	0.121307373
BSHDNKM000006293300074	BSHDNKF000005743500934	1	0.121932983
BSHDNKM000006293300074	BSHDNKF000005743500961	1	0.121932983
BSHDNKM000006293300228	BSHDNKF000005743500867	1	0.123817444
BSHDNKM000006293300228	BSHDNKF000005743500854	1	0.123817444

Sire	Dam	n	Kinship
BSHDNKM000006293300076	BSHDNKF000005291001783	1	0.124114990
BSHDNKM000006293300074	BSHDNKF000005743500922	1	0.126861572
BSHDNKM000006293300074	BSHDNKF000005743500966	1	0.126861572
BSHDNKM000006293300074	BSHDNKF000012473800029	1	0.126945496
BSHDNKM000006293300228	BSHDNKF000005743500983	1	0.128852844
BSHDNKM000006293300074	BSHDNKF000005743500929	1	0.128982544
BSHDNKM000006293300074	BSHDNKF000010018400103	1	0.130622864
BSHDNKM000006293300228	BSHDNKF000012473800012	1	0.131340027
BSHDNKM000006293300076	BSHDNKF000005743500795	1	0.133148193
BSHDNKM000006293300228	BSHDNKF000005743500946	1	0.133510590
BSHDNKM000006293300228	BSHDNKF000005743500943	1	0.134954453
BSHDNKM000006293300228	BSHDNKF000005743500892	1	0.136165619
BSHDNKM000006293300228	BSHDNKF000012473800011	1	0.137023926
BSHDNKM000006293300076	BSHDNKF000005743500990	1	0.137847900
BSHDNKM000006293300228	BSHDNKF000005743500894	1	0.138996124
BSHDNKM000006293300076	BSHDNKF000008048701094	1	0.148559570
BSHDNKM000008048700073	BSHDNKF000004551102380	1	0.150949709
BSHDNKM000006293300076	BSHDNKF000005743501010	1	0.155044556
BSHDNKM000006293300076	BSHDNKF000005743500927	1	0.155456543
BSHDNKM000006878500024	BSHDNKF000005743500984	1	0.157303810
BSHDNKM000008048700073	BSHDNKF000005743501002	1	0.162187502
BSHDNKM000001277800593	BSHDNKF000003702000205	1	0.165955030
BSHDNKM000001277800593	BSHDNKF000004607900342	1	0.166197434

Sire	Dam	n	Kinship
BSHDNKM000001277800593	BSHDNKF000004607900288	1	0.166319471
BSHDNKM000001277800593	BSHDNKF000004607900343	1	0.166319471
BSHDNKM000006293300076	BSHDNKF000005743501000	1	0.167907715
BSHDNKM000008048700128	BSHDNKF000005291001864	1	0.170179844
BSHDNKM000008048700073	BSHDNKF000005291001851	1	0.172856539
BSHDNKM000008048700128	BSHDNKF000005291001770	1	0.173216224
BSHDNKM000008048700128	BSHDNKF000009207400495	1	0.173361540
BSHDNKM000008048700128	BSHDNKF000005291001859	1	0.175515473
BSHDNKM000006878500024	BSHDNKF000005743500977	1	0.175730705
BSHDNKM000008048700073	BSHDNKF000005743501015	1	0.181088567
BSHDNKM000001277800593	BSHDNKF000008048700815	1	0.181949054
BSHDNKM000001277800593	BSHDNKF000005743501001	1	0.186952902
BSHDNKM000001277800593	BSHDNKF000008048700934	1	0.188384193
BSHDNKM000008048700073	BSHDNKF000005743501020	1	0.190516546
BSHDNKM000008048700128	BSHDNKF000005743500995	1	0.193159163

2. **Mean kinship between dams of hybrids to the rest of the population ranked lowest to highest.**

Dam	Mean Kinship
BSHDNKF000005743500880	0.1777000
BSHDNKF000005743500990	0.1902690
BSHDNKF000004551102380	0.1927691
BSHDNKF000005743500984	0.1973976

Dam	Mean Kinship
BSHDNKF000005743501001	0.1975240
BSHDNKF000005743501011	0.2073114
BSHDNKF000005743501015	0.2079180
BSHDNKF000005743501020	0.2125740
BSHDNKF000008048700815	0.2156843
BSHDNKF000008048701015	0.2172238
BSHDNKF000009207400495	0.2274292
BSHDNKF000005743500947	0.2274292
BSHDNKF000005743501003	0.2301915
BSHDNKF000005743500943	0.2326594
BSHDNKF000005743500983	0.2332342
BSHDNKF000005743500994	0.2348594
BSHDNKF000005743500977	0.2376808
BSHDNKF000005743500995	0.2391812
BSHDNKF000005743501000	0.2409765
BSHDNKF000005743501002	0.2431920
BSHDNKF000005743501010	0.2435075
BSHDNKF000005743500993	0.2475916

3. **Mean kinship between dams of hybrids ranked lowest to highest.**

Dam	Mean Kinship
BSHDNKF000008048700815	0.2006386

Dam	Mean Kinship
BSHDNKF000008048701015	0.2016893
BSHDNKF000005743500993	0.2123953
BSHDNKF000004551102380	0.2146356
BSHDNKF000009207400495	0.2151868
BSHDNKF000005743500947	0.2229298
BSHDNKF000005743500943	0.2256187
BSHDNKF000005743500984	0.2265577
BSHDNKF000005743501010	0.2301764
BSHDNKF000005743500983	0.2369869
BSHDNKF000005743500990	0.2421721
BSHDNKF000005743501001	0.2468839
BSHDNKF000005743501015	0.2468839
BSHDNKF000005743501003	0.2491218
BSHDNKF000005743501000	0.2534168
BSHDNKF000005743501002	0.2604967
BSHDNKF000005743500995	0.2608852
BSHDNKF000005743500994	0.2631035
BSHDNKF000005743501020	0.2633160
BSHDNKF000005743500977	0.2646965
BSHDNKF000005743501011	0.2712206
BSHDNKF000005743500880	0.2780178