



Master Thesis

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Optimal Contribution Selection in the Endangered Danish Landrace prior 1970

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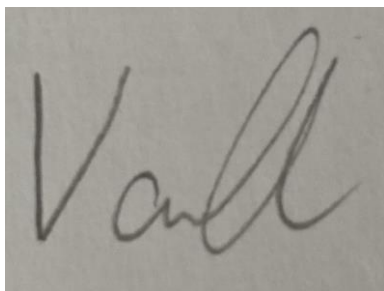
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Signature

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Abstract

The rare pig breed Danish Landrace originating from the period prior to 1970, is critically endangered. The aim of this thesis was to assess the current genetic status of the breed and to evaluate its future prospects under the implementation of optimum contribution selection (OCS) in combination with the use of cryopreserved donor semen.

Pedigree data were analysed and two OCS scenarios were simulated: one including only the currently active breeding animals, and a second scenario incorporating the option to use donor semen.

The pedigree completeness index (PCI) across six generations was estimated at 0.66 and showed pronounced fluctuations over time. The effective population size was calculated to be 18.85.

The mean inbreeding coefficient in the most recent generation was 0.154. OCS without donor semen was predicted to result in an inbreeding coefficient of 0.16 in the subsequent generation, whereas inclusion of donor semen reduced the expected inbreeding coefficient to 0.10. These results indicate that the use of cryopreserved donor semen is strongly recommended to mitigate further inbreeding.

However, the relatively low PCI together with multiple inconsistencies within the pedigree data limited the reliability of the analyses. This highlights the need for improved pedigree recording to enable accurate breeding plans and effective decision-making for breeders.

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1. Introduction

1.1 Genetic resources

The conservation of livestock genetic diversity has become an increasingly urgent priority as many traditional native breeds face rapid declines in population size. Modern breeding programs, while successful in improving production efficiency, have contributed to the genetic homogenization of commercial livestock populations and the marginalization of local breeds. According to the Domestic Animal Diversity Information System (DAD-IS), 53.11% of local European breeds were classified as at risk of extinction as of 31 December 2024. Among European pig breeds, 33.74% are already extinct, 8.64% are categorized as critical or critical-maintained and 16.87% are endangered (20 May 2025). This decline is often attributed to the lower production performance of local breeds compared with modern commercial lines. (Johanna Wider, 2023; Szekeres et al., 2016a).

The potential loss of such breeds presents two major concerns. First, we risk losing our cultural heritage. Second, we may also lose potentially valuable genetic resources that could be reintroduced into modern animal lines should challenges such as inbreeding depression, disease outbreaks, or other demographic bottlenecks arise (Meuwissen, 2009a). Moreover, older breeds may offer adaptive traits useful for coping with changing climatic conditions (Grădinaru et al., 2018).

International and national institutions, including the Food and Agriculture Organization of the United Nations (FAO) and, in Denmark, the Danish Agricultural and Fishery Agency, maintain databases documenting remaining breeds and Population numbers. These organizations also coordinate conservation programs and provide breeding guidelines (FAO, 2011). In Denmark, the national gene bank is managed by the Danish Agricultural and Fishery Agency.

In 2007, Denmark, together with 108 other countries, signed the Interlaken Declaration and adopted the Global Plan of Action for Animal Genetic Resources, which aims to halt the loss of livestock genetic diversity (FAO, 2007).

Conservation approaches include both *in situ* (on-site) and *ex situ* (off-site) strategies. *Ex situ* conservation involves, for example, cryopreservation or the establishment of independent subpopulations using founders from different small groups (Fernández et al., 2016; Kumar

Chandrakar et al., 2016). In situ conservation may include controlled crossbreeding with closely related breeds to alleviate inbreeding (Meuwissen, 2009b).

The Danish Landrace originating from the period prior to 1970 (DL-1970) is currently classified as a critically endangered pig breed in Denmark. The breed traces back to structured Danish breeding programs initiated in 1906 and was historically selected for high bacon production, contributing substantially to Denmark's pork export industry. DL-1970 pigs are pure white, long and slim with slightly arched backs, long ears, straight snouts, and well-developed hams. Their meat is darker, more tender, and more flavorful than that of modern Danish Landrace pigs (Landbrugstyrelsen, 2025, Szekeres et al., 2016a)

Around 1970, breeding objectives shifted toward more intensive production traits, and crossbreeding with landrace populations from other countries became common from the 1980s onward. As a result, only a small number of original purebred DL-1970 animals remained, and the breed became endangered (Szekeres et al., 2016b). DAD-IS reported a maximum population of 43 and a minimum of 28 animals in 2023 (DAD-IS, 2025). However, population estimates vary, with some reports as low as five sires and three dams (Simon Kolind, 2025).

A genetic analysis conducted in 2016 by Aarhus University and the Danish Committee for Animal Genetic Resources found that DL-1970 animals are closely related to modern Danish Landrace, (Szekeres et al., 2016a), The study reported an average inbreeding coefficient of 12%, which is not unusually high in isolation but is concerning given the small population size and the associated rapid increase in the rate of inbreeding. The researchers also identified two genetically distinct DL-1970 groups within the living population and the cryopreserved genetic material: the active population and a group originating from the Tylstrup resource population (Szekeres et al., 2016a)

In 2022, Nielsen & Kargo performed an optimum contribution selection (OCS) analysis on 53 DL-1970 pigs (7 boars, 46 sows). They concluded that OCS could reduce the rate of inbreeding more effectively than random mating however, the living population of DL-1970 has continued to decline in recent years (Nielsen & Kargo, 2022).

1.2 Objective of the thesis

The aim of the thesis is to investigate the current status of DL-1970 with respect to conservation of the breed and to investigate if optimal contribution selection using active boars can reduce rate of inbreeding or if inclusion of semen stored in the genebank is needed.

2. Breeding and Conservation

2.1 Basics of Breeding

Modern quantitative breeding relies heavily on the breeder's equation for predicting genetic gain:

$$\Delta G = \frac{i * r_{IA} * \sigma_a}{L}$$

Where ΔG = annual genetic gain, i =selection intensity, r_{IA} = Accuracy between observed breeding values and true breeding values, σ_a =expected genetic standard deviation of the population, L = generation interval (Lush, 1937)

The breeder's equation emphasizes the connection between genetic gain and parameters of the breeding program such as selection intensity, prediction accuracy and genetic in a population. It is clear from breeder's equation that size of genetic variance is important to be able to obtain genetic gain.

2.2 Inbreeding

Inbreeding is unavoidable in any real diploid population and occurs when an individual inherits alleles that are identical by descent (IDB) through a common ancestor.

Increased inbreeding leads to higher homozygosity and reduced heterozygosity, causing inbreeding depression—manifested as a reduction in the mean performance of traits across the population (Douglas S. Falconer, 1989). Where F is the inbreeding coefficient

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

Where n_i is the number of meiosis traced in loop i , and F_{ai} is the inbreeding coefficient of shared ancestors A in loop i (Wright, 1938)

In pigs, inbreeding depression may result in reduced sperm quality, lower litter weights, decreased growth rate and altered backfat thickness (Tsheten et al., 2023; Zhang et al., 2022). In in other species such as dairy cattle, it affects milk yield and survival (Thompson et al., 2000). The rate of inbreeding (ΔF) is directly linked to the loss of genetic variance according to:

$$Var(a) = (1 - F) * V_a$$

F = inbreeding coefficient, V_a =additive genetic variance, (Douglas S. Falconer, 1989)

Which together with the breeder's equation shows that our genetic variance will decrease in the pursuit of genetic gain.

And can be calculated with the following formula

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}} \quad \text{Equation 1}$$

Where F_t is the inbreeding coefficient in generation t and F_{t-1} the inbreeding coefficient in generation $t-1$.

In conservation the recommended level of inbreeding of each generation is preferably below 1% per generation to minimize the loss of genetic diversity (Charles Smith, 1984).

2.3 Methods for Controlling Inbreeding

Random selection is the simplest breeding strategy, involving the random choice of mating partners. However, it produces no directed genetic improvement and will increase inbreeding because of genetic drift. In small populations with limited mate choice and skewed sex ratio, this process would be even more accelerated. Random selection does not adjust for existing relatedness and is not giving a representable picture for populations under artificial selection programs (M. A. Toro et al., 1988).

Minimum coancestry (MC) is a method where mating pairs with the lowest mutual relatedness are selected for mating (Toro et al., 1988). While MC can delay inbreeding for one generation, its long-term effectiveness is limited, because it often leads to the next generation being highly inbred (M. A. Toro et al., 1988; M. Toro & Pérez-Enciso, 1990).

Optimal contribution selection (OCS) has two different approaches:

(1) Meuwissen's approach, which restricts the rate of inbreeding to predefined levels (Meuwissen, 2009b)

(2) Henryon et al. (2015) approach, which applies penalties to average relationships.

Both are based on the framework proposed by Wray and Goddard (1994).

Meuwissen used the formular

$$G_{t+1} = c'_t EBV_t$$

Where EBV_t =vector of BLUP estimates the breeding values of the candidates for selection in generation t.

Ac_t = vector of genetic contributions of the selection candidates to generation t+1.

G_{t+1} = the genetic level of the next generation of animals.

The optimum c_t for the highest G_{t+1} is given when

$$Q'c_t = \frac{1}{2}$$

Where Q= known incidence matrix for the sex and $\frac{1}{2}$ a vector of halves of the order 2.

And given the constraints

$$\bar{c}_{t+1} = \frac{c'_t A_t c_t}{2}$$

A_t = the matrix of additive genetic relationships among selection candidates in generation t. (T.

H. E. Meuwissen, 1996)

In Henryon's approach are the restrictions within the possible optimisation as of the fixing elements c and P(Henryon et al., 2015).

Henryons approach is maximising the quadratic function, U_t with respect to c

$$U_t = c' \hat{a} - \frac{\omega}{L^2} (c + Pv)' A (c + Pv) \text{ Equation 2}$$

c= vector of genetic contributions to the new cohort and the numbers of matings allocated to each candidate is a linear function of these contributions.

$\hat{a}$ = a vector of BLUP-Breeding values.

ω = penalty applied to the average relationship of the current generation.

L= generation interval

v= vector of lifetime breeding profiles or expected relative contributions to future age-class of animals in the current generation.

A= a matrix of additive genetic relationships.

P = a matrix of contributions to each age-class of animals in the current generation.

OCS avoids selecting a single male excessively because self-relationship, weighted by the number of offspring, will contribute very heavily to the average relationship of the selected parents (T. Meuwissen, 2009b).

Table 1. Pro and contra of MC against OCS

	Pro	Con
MC	Easy to use, fast, no genetic improvement	Not a long-term solution,
OCS	Long-term solution, lower gain than Truncation selection, but possible to still improve the breed	More computational expensive, higher requirements towards the Pedigree

OCS is widely used across species for conservation purposes (Gourdine et al., 2012; T. Meuwissen, 2009b; Škorput et al., 2022, 2023; Tarrés et al., 2006; Zhao et al., 2024). Zhao et al. (2021) investigated the long-term effects of Truncation selection and OCS conservation methods. They compared Random selection, truncation selection and OCS either pedigree data or genome information. They found that OCS in general was the best method of keeping the highest degree of genetic improvement while at the same time minimising the increase in rate of inbreeding. Moreover, OCS with selection based on genomic relationship matrix, was a better choice if the goal was to achieve the best genetic gain and conservation of genetic diversity. Compared to pedigree-based OCS which lead to a higher genetic gain, but at the same time higher increase in the rate of inbreeding.

-Examples of using OCS include the Faroese horse, where Kettunen et al. (2022), quantified the degree of inbreeding, effective population size and probability of gene origin, in order to assess the feasibility to conserve the Faroese horse. They found that the Faroese horse had extremely high average inbreeding (26.87%) and a very low effective population size of 8. They concluded that OCS was a promising tool to control the increase in average relationships in the breed and help to increase the effective population size by lowering the increase in the rate of inbreeding. Other examples include -the Jutland Horse, where Nielsen & Kargo(2020), preselected Sires based on the lowest average relationship to the active breeding females. The conclusion was that preselection of sires using OCS reduced rate of inbreeding.

-in the Black Slavonian pig Škorput et al. (2022), attempted to balance both genetic improvement and maintenance of diversity. where OCS proved effective but noted some practical problems from low pedigree completeness and data accuracy.

2.4 Effective population size

Wright (1938) defined the effective population size (N_e) as “the number of breeding individuals in an idealized population that would show the same amount of dispersion of allele frequencies under random genetic drift or the same amount of inbreeding as the population under consideration.”

A common estimator of N_e based on census numbers of breeding animals is:

$$N_e = \frac{4 * Nm * Nf}{Nm + Nf}$$

Nm = number of breeding males used in the last four years, Nf = number of breeding females in the same period.

This formula highlights the drastic effect of skewed sex ratios on N_e , but does not account for relationships among individuals and therefore often overestimates N_e .

A more accurate estimator uses the rate of inbreeding:

$$N_e = \frac{1}{2 * \Delta F * L} \text{ Equation 3}$$

ΔF = annual increase in inbreeding L = generation interval (Douglas S. Falconer, 1989).

Thus, rate of inbreeding also provides insight into the effective population size and the spread of deleterious alleles with negative implications for future genetic gain (Woolliams et al., 2015).

Estimating effective population size using linkage disequilibrium between marker pairs is another genomic approach which has proven effective (T. Meuwissen, 2009c; Qanbari et al., 2010),

$$E(R^2) = \frac{1}{4N_e * c + 1}$$

c =recombination rate between the markers. R^2 =linkage disequilibrium between the two markers.

Effective population size can also be calculated from the kinship:

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

Where c_{ij} is the kinship between I and j and g_i and g_j are number of equivalent complete generations for individuals I and j, so the effective size is then

$$Ne = \frac{1}{2\Delta c} \text{ Equation 4}$$

Effective population size may differ substantially from the actual population, depending on breeding practices and historical bottlenecks. For example, Ne estimates for Holstein cattle in Denmark and Germany are approximately 49 and 52, (Koenig & Simianer, 2006; Sørensen et al., 2005a), whereas the U.S. Holstein population has been estimated at 71 (Kim & Kirkpatrick, 2009). This despite the total population of Holstein Cattle in Denmark according to Nordisk Avlsværdi Vurdering was 340.000 Cows.

2.5 Possibilities with Genomic Data

Increasingly affordable genetic testing has expanded the use of SNP chips and whole-genome sequencing (WGS) for OCS (Eusebi et al., 2020; T. Meuwissen, 2009c). Dense SNP data typically provide more precise relatedness estimates as well as a generally more precise picture of the state of the breed than pedigree data alone (T. Meuwissen, 2009b). However, SNP chips designed for commercial breeds may introduce ascertainment bias when applied to small or rare breeds, making WGS preferable (Eusebi et al., 2020).

OCS with Genomic data for relationship matrix promises to improve the calculations.

With genomic assessment, it is not only possible to identify the within breed relationships but detect the detection of breeds in a pool of genotyped animals and to estimate the breed proportions in each admixed animal. (Guldbrandtsen et al., 2020)

3. Material and method

3.1 Software and Computational Tools

Optimum Contribution Selection (OCS) was performed using the freely available program EVA(Berg et al , 2006). Pedigree preprocessing and quality control were conducted in R using the package “OptiSel”(Wellerman 2019) which provides functions for pedigree cleaning, relationship matrix construction and inbreeding estimation.

EVA requires the pedigree to be divided into discrete time steps. In this study, a time step length of six months was chosen, starting prior to the birth of the first recorded animal in the pedigree (1 January 1983). Thus, time step 1 covered the period from 1 January 1983 to 2 July 1983, and time step 2 from 3 July 1983 to 1 January 1984. The total number of time steps was selected ad hoc to keep the number as low as possible while ensuring that no offspring was assigned to the same time step as its parents.

3.2 Dataset and pedigree

The dataset and pedigree was extracted from the Danish Agricultural Agency database, where breeders register births of all DL-1970 piglets. The pedigree included 1,466 individuals born between 1983 and 2025. In total there were 1051 dams, 401 Sires and 14 animals with unknown sex.

Each record contained parental information, sex, birth date, farm of origin, and a unique nine-digit identifier composed of the farm ID, date of birth, and a farm-specific individual code. As well as a list over the stored sperm in the Gene bank. The dataset therefore represents the most complete available pedigree snapshot at the time of extraction September 2025. The health and current availability of these animals are unknown, which must be considered when interpreting the results.

3.3 Pedigree cleaning

Quality control revealed several inconsistencies including individuals listed as their own sire, animals with offspring born before their own birth date, missing sex information, and individuals recorded as producing offspring at biologically implausible ages (e.g. one month after birth). These inconsistencies likely resulted from data entry errors by breeders or registry personnel.

A total of 47 individuals were removed to enable reliable downstream analyses, resulting in a final pedigree of 1,419 individuals used for OCS. It should be emphasized that the dataset reflects the state of the registry at the time of extraction; subsequent corrections or updates may have occurred and some of the identified errors may since have been resolved.

3.4 PCI

Pedigree completeness index (PCI) is a measurement of the proportion of paternal and maternal indices (Maccluer et al., 1983). PCI where calculated with the formula:

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

Where C_f and C_m denote the proportions of known maternal and paternal ancestors, respectively. These proportions were computed as:

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

Where a_i was the ratio of known to unknown ancestors in each generation d is the number of generations (Kasap et al., 2021). In this study, PCI was calculated considering 6 generations back in time (Sørensen et al., 2005b) and individuals who had a PCI over 6 generations below 0.6 were excluded from consideration as breeding candidate.

3.5 Inbreeding and effective population size

The inbreeding coefficient for each animal was computed by EVA and found in the output file. Effective population size was computed in 2 different ways

1. with equation 3 (see paragraph 2.3).
2. from the mean increase in coancestry, of the whole population, The coancestry between individual i and j was computed as:

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

With the Optisel call pedIDB. Kinship coefficients where calculatet for all individuals in the pedigree.

Which lead to computing N_e as $N_e = \frac{1}{2\Delta \bar{c}}$ where $\Delta \bar{c}$ is the average increase in kinship

3.6 OCS

The OCS methodology applied in this study follows the framework proposed by Henryon et al. (2015) with modifications reflecting the primary objective of breed conservation rather than genetic improvement. Consequently, optimization based on estimated breeding values (EBVs) was omitted (see Equation 2, Section 2.3), placing full emphasis on penalizing inbreeding. Genetic contributions were therefore optimized to minimize average relationships rather than to maximize genetic gain. This resulted in the following reduced equation as also used by Nielsen and Kargo (2010):

$$U_t = \frac{\omega}{L^2} (c + Pv)'A(c + Pv)$$

c = vector of genetic contributions to the new cohort and the numbers of matings allocated to each candidate is a linear function of these contributions.

ω = penalty applied to the average relationship of the current generation.

L = generation interval

v = vector of lifetime breeding profiles or expected relative contributions to future age-class of animals in the current generation.

A = a matrix of additive genetic relationships.

P = a matrix of contributions to each age-class of animals in the current generation.

Two OCS scenarios were evaluated. In the first scenario, only animals from the current living population were considered for selection. Specifically, animals born in 2023 and 2024 were eligible, comprising 12 sires and 34 dams.

In the second scenario, OCS was performed with the inclusion of boars represented in the national gene bank, adding 10 cryopreserved boars born between 1996 and 2017

(Landbrugstyrelsen, 2025), resulting in a total of 22 sires and 34 dams.

Boars were restricted to a maximum of 34 matings each, corresponding to the number of available dams, while dams were restricted to a single mating.

4. Results

4.1 Breed status and pedigree quality

The PCI over 6 generations mean was 0.66. The trend of PCI over birthyear (see Figure 1) reflects fluctuations in data quality, which may influence the observed patterns of inbreeding over time.

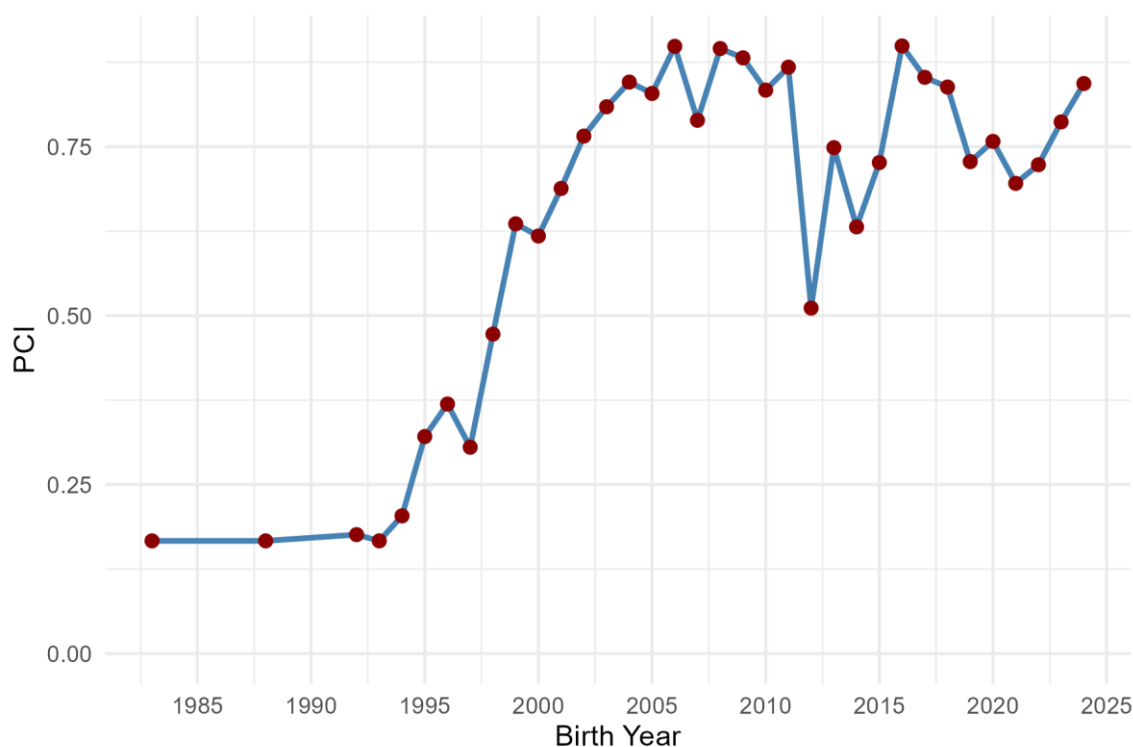


Figure 1 Average PCI by birth year

Overall, these results indicate that the pedigree information was of feasible quality for most of the breeding individuals.

4.2 Average Inbreeding

The pedigree analysis revealed an average inbreeding coefficient of 0.154 for the most recent generation of animals so from the second half of 2024, with the highest individual inbreeding coefficient reaching 0.175. The trend of average inbreeding coefficient, based on birth year, is shown in Figure 2.

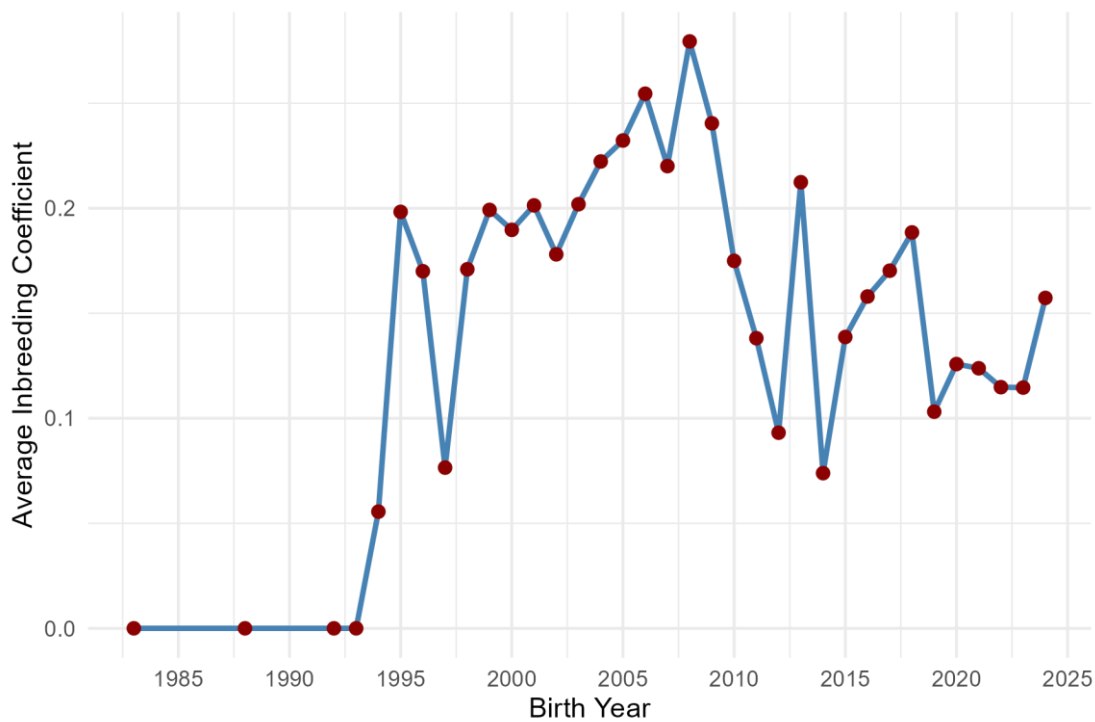


Figure 2, Average inbreeding coefficient over birth year for boars and sows

The average inbreeding coefficient varies a lot over the years, with some down trends, but no clear trend in one direction.

Table 1 shows the last 7 timesteps from the second halve of 2021 up to the end of 2024, their Corresponding average inbreeding coefficients, change in inbreeding and N_e .

Where we can see that they have changed between a state of inbreeding and outbreeding. With no real Trend in the recent timesteps.

Table 2. Timesteps of a 6 month time frame were used to group the animals, N amount of animals, F_a average inbreeding coefficient in the Timestep, dF delta F of the timestep, N_e effective population size calculated with equation 3, page x

Timestep	N	F_a	dF	N_e
78	11	0.18	0.09	5.53
79	34	0.11	-0.09	-5.78
80	6	0.13	0.02	23.49
81	5	0.14	0.02	32.15
82	23	0.11	-0.04	-11.80
83	12	0.16	0.06	8.61
84	11	0.15	-0.01	-76.06

the N_e for the current population calculated via equation 4, paragraph 2.3 was estimated at $N_e = 18.85$.

In Figure 3 can we see that the Average inbreeding coefficient of both sexes are fairly close to each other, apart from a few outliers, like in 2013 where the female inbreeding where significantly higher.

Table 3. Year the birth year of all N animals, with the Sex Male 1 or female 2. And the annual mean inbreeding coefficient Mean F

Year	Sex	Mean F	N	Sex	Mean F	N
2016	1	0.171	7	2	0.155	32
2017	1	0.082	4	2	0.187	21
2018	1	0.185	3	2	0.189	25
2019	1	0.098	10	2	0.105	33
2020	1	0.117	14	2	0.129	44
2021	1	0.110	7	2	0.127	33
2022	1	0.179	5	2	0.106	35
2023	1	0.123	9	2	0.111	19
2024	1	0.150	5	2	0.159	18
total		0.182	390		0.171	1029

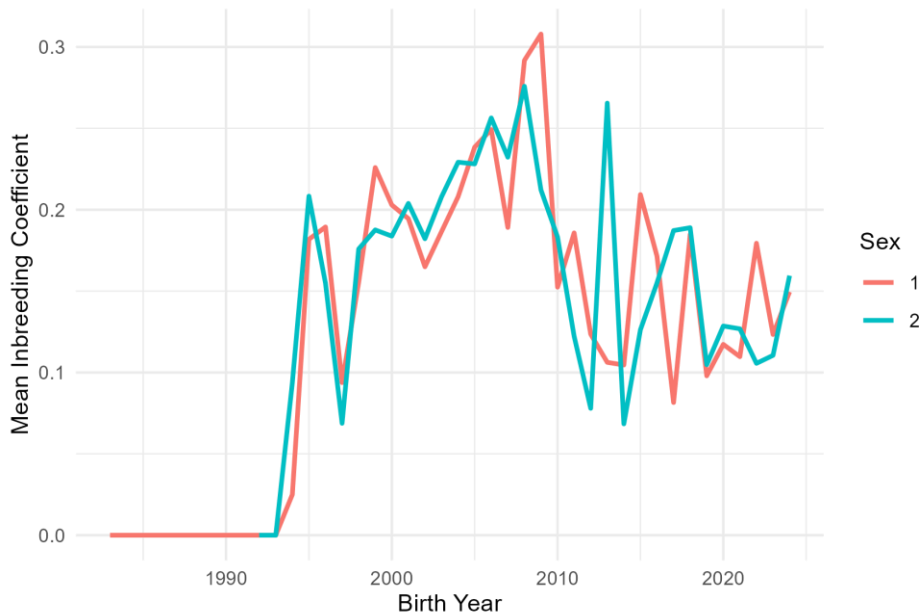


Figure 3. mean inbreeding coefficient over brith year for each sex, where 1 is male and 2 female

4.3 OCS without frozen sperm from the gene bank

By applying OCS with 34 sows available for mating, 8 out of 12 males were selected. Most matings were assigned to the boars with the lowest relationship to all potential females (table 2).

Table 4. No of matings pr Boar (ID) previous offspring (Prev. offspr) and Relationship with all Males and Females

ID	N.matings	Prev.offspr	Rel.males	Rel.females
901000123	3	0	0.5523	0.4497
901000223	3	0	0.5523	0.4497
901001023	3	0	0.5523	0.4497
901001123	3	0	0.5523	0.4497
901001223	3	0	0.5523	0.4497
167008623	0	4	0.5461	0.4425
167008724	4	0	0.5113	0.4302
901001624	3	0	0.4932	0.4461
869001824	12	0	0.386	0.367
901001323	0	0	0.5706	0.4614
907000324	0	0	0.5855	0.4527
907000424	0	0	0.5855	0.4527

Under random mating we would expect an average inbreeding of the progeny corresponding to 0.22, which we could reduce to 0.16 by using OCS.

4.4 OCS with frozen sperm from the Gene bank

Incorporating cryopreserved semen from the national gene bank expanded the pool of male candidates from 12 to 22. With the gene bank donors OCS choose only 6 boars compared to 8 without the gene bank donors (table 3). Again, OCS selected the ones with lowest relation to all females in the population

Table 5. No of matings per boar (ID), previous offspring (Prev. offspr) and Relationship with all Males and Females. Sperm donors from the gene bank are in light grey.

ID	N.matings	Prev.offspr	Rel.males	Rel.females
371002994	5	1	0.3546	0.2098
371003994	5	8	0.3526	0.2071
371004394	6	0	0.3526	0.2071
371006994	6	15	0.3526	0.2071
371007994	0	9	0.3653	0.2247
371009594	6	0	0.3526	0.2071
371009994	6	1	0.3526	0.2071
340034798	0	12	0.396	0.2518
269002614	0	18	0.3886	0.3592
188001015	0	1	0.3729	0.3491
901000123	0	0	0.4106	0.4497
901000223	0	0	0.4106	0.4497
901001023	0	0	0.4106	0.4497
901001123	0	0	0.4106	0.4497
901001223	0	0	0.4106	0.4497
167008623	0	4	0.4411	0.4425
167008724	0	0	0.4221	0.4302
901001624	0	0	0.3729	0.4461
869001824	0	0	0.3058	0.367
901001323	0	0	0.4575	0.4614
907000324	0	0	0.4456	0.4527
907000424	0	0	0.4456	0.4527

With random mating we expect an average Inbreeding of 0.17, which is considerably lower than without usage of donor sperm (0.22). Using OCS reduced the expected average inbreeding to 0.10.

5. Discussion

5.1 Key Challenges and limitations of the Analysis

Several limitations must be considered when interpreting the results of this study. First, the pedigree cleaning process inevitably resulted in the removal of individuals with inconsistent or biologically impossible records(e.g. offspring born before their parents). While necessary to

ensure analytical accuracy, the removal of such individuals may have introduced gaps in the pedigree that artificially reduced estimates of relatedness.

This effect is reflected in the relationship between the PCI and the average inbreeding coefficient, where declines in PCI coincide with decreases in the estimated inbreeding coefficient (Figure 4). The pronounced dip in the inbreeding coefficient around 2012 may be associated with the use of cryopreserved donor semen; however, incomplete pedigree information and the low PCI of several individuals may also have contributed to this pattern.

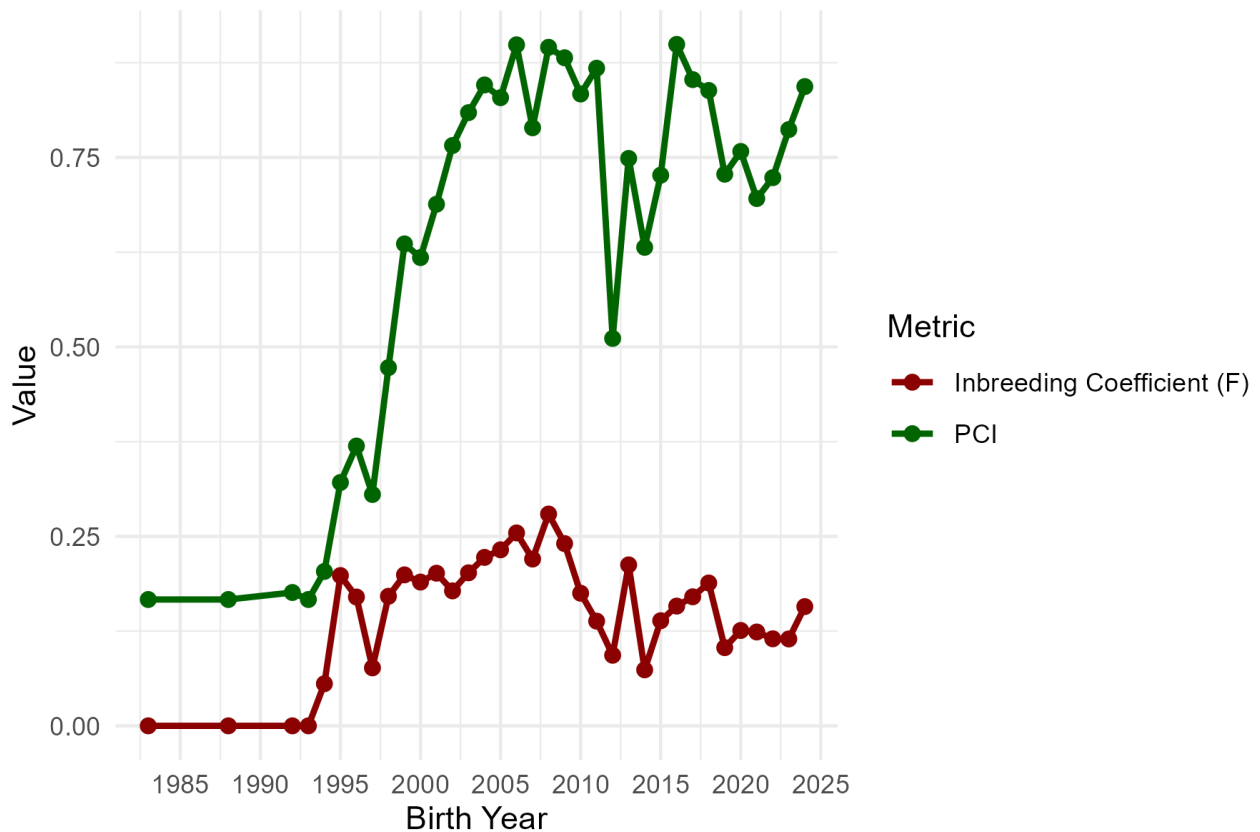


Figure 4. average PCI and Average inbreeding coefficient pr birthyear together

Nielsen & Kargo (2022) reported a substantially higher PCI across eight generations (Figure 5), with markedly less fluctuation compared to the results obtained in the present study. This discrepancy suggests that the observed instability in PCI is more likely attributable to differences in the pedigree dataset at the time of extraction rather than to deficiencies in the pedigree itself. The datasets were extracted at different points in time and it was not possible to investigate the origin of these differences further due to time constraints and limited access to personnel responsible for database maintenance.

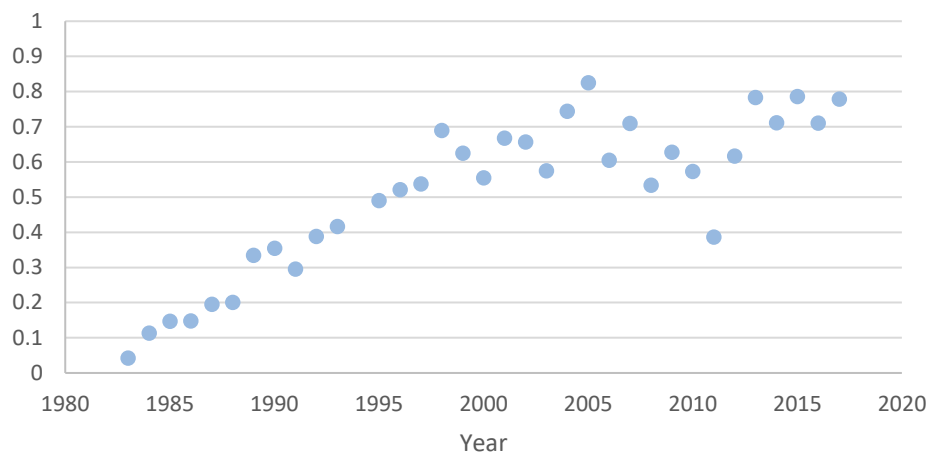


Figure 5. Pedigree completeness index over 8 generations, from year 1983 to 2019 (Copied from Nielsen & Kargo 2022)

The actual reproductive status, health, and availability of the animals included in the pedigree remain unknown, as such information is not recorded in the database. Consequently, the practical implementation of the proposed mating strategies may deviate from the theoretical outcomes presented here.

A further concern relates to the quality of cryopreserved semen. Much of the stored material is approximately 30 years old, originating from periods when freezing protocols were less efficient than today. Fertility rates for frozen boar semen have improved from 60–70% historically to 70–85% with modern methods, (Knox, 2015) because of improvements in freezing methods, as well as thawing and insemination method (Yeste et al., 2017). As a result, the practical usability of certain donor boars identified through OCS may be limited and successful insemination cannot be guaranteed.

Additionally, the estimation of N_e using Equation 3 yielded implausible values, including negative estimates or values exceeding the census population size. This limitation arises from the simplicity of the model, which does not account for overlapping generations and it is a fairly simple model to calculate N_e . Moreover, uncertainty remains in the estimated inbreeding coefficients due to the low PCI_6 observed for a substantial proportion of individuals.

Frozen embryos were not considered in this study and could represent an additional conservation opportunity. Embryos could be transferred to surrogate dams that are not part of the DL-1970

population and fertilized using semen from active or cryopreserved boars. However, embryo transfer involves substantially higher costs and logistical complexity. Fertility and prolificacy rates range between 50% and 80%, with an average of 6–10 piglets per litter (Gil et al., 2024). making this approach both expensive and uncertain compared to conventional breeding.

5.2 implications of Optimal contribution selection in DL-1970

The results of this study are consistent with earlier findings demonstrating that OCS is an effective tool for managing inbreeding in small populations. Similar to the results reported by Nielsen and Kargo (2022), the simulations indicate significant reductions in expected inbreeding compared with random mating.

When OCS was applied without the inclusion of donor semen, all individuals with a PCI below 0.6 were excluded from selection. In contrast, all cryopreserved donor boars exhibited PCI values far below the population mean (0.166), which may have led EVA to overestimate the genetic benefit of donor inclusion while underestimating their true inbreeding coefficients. Despite this limitation, the selection of donor individuals remains relevant for recovering lost genetic diversity. Szekeres et al. (2016a) demonstrated that donor animals stored in the gene bank represent a genetically distinct subgroup capable of broadening the genetic base of DL-1970 (Figure 6). The effectiveness of donor inclusion could be further improved by genotyping the currently active dams and incorporating genomic relationships rather than relying solely on pedigree information. This would reduce the importance of low donor PCI values on OCS outcomes reliability.

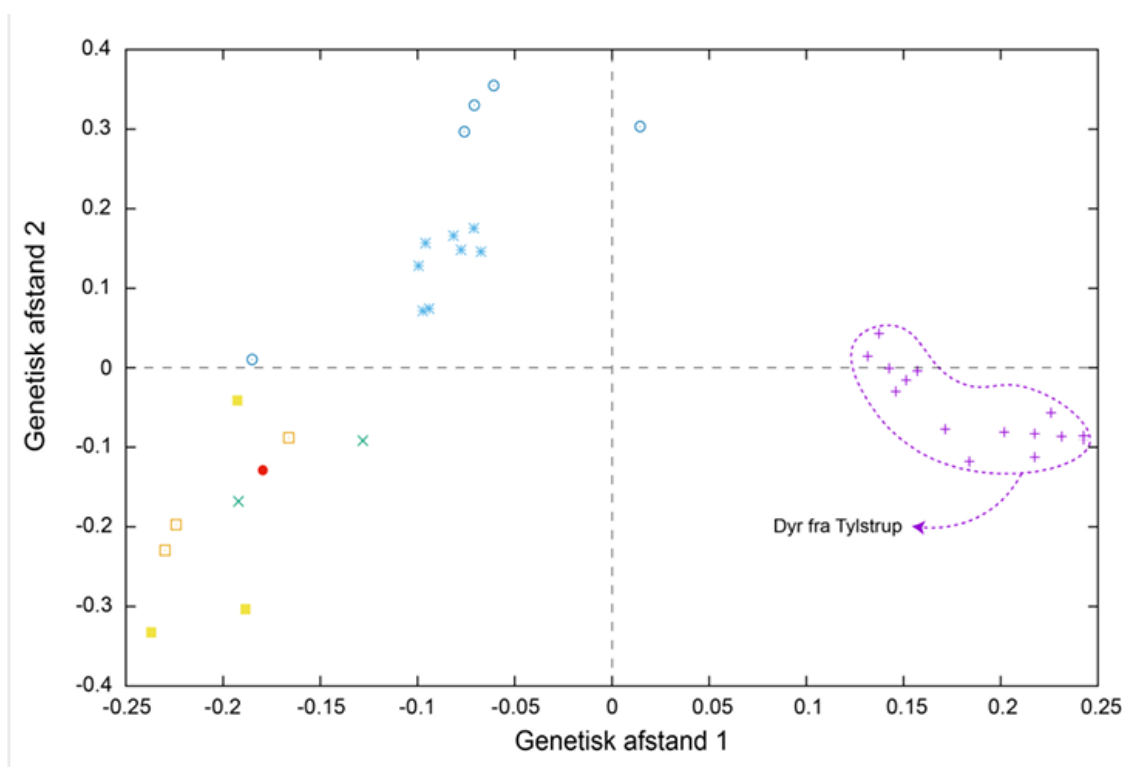


Figure 6: Genetic distance 1 and 2 of the investigated DL1970 pigs each symbol i68s a individual and each farm have its own symbol, the animals in the circle are the group from Tylstrup corresponding to the donors in the genebank (Szekeres et al., 2016a)

Following the same rationale, genotyping the remaining DL-1970 population would improve the reliability of OCS by providing a more accurate assessment of within-breed relationships, inbreeding levels, and effective population size.

Despite the observed reductions in expected inbreeding when donor semen was included, DL-1970 remains critically endangered. Even under optimized OCS scenarios, the breed faces persistent challenges due to its very small census size, low effective population size, and a declining breeder community. Without decisive intervention, including carefully controlled genetic introgression, the long-term survival of the breed remains uncertain.

The decision to exclude genetic improvement from the OCS framework was motivated by the extremely small population size of DL-1970. Nevertheless, some authors argue that maintaining a degree of genetic improvement, even in conservation programs, can enhance economic viability and incentivize breeder participation (T. Meuwissen, 2009c; Škorput et al., 2022). In highly endangered populations, however selection for improvement may not be feasible or desirable due to the associated loss of genetic diversity, as illustrated by the Baniya Spotted Pig with an estimated N_e of 8.47 (Škorput et al., 2023).

Importantly, estimated breeding values in a conservation context need not be limited to production traits. They could instead target traits related to fitness, robustness, or mitigation of existing inbreeding depression, for example by assigning negative breeding values to highly inbred individuals rather than excluding them entirely. While this approach warrants further investigation, it would inevitably narrow the selection pool and may ultimately prove less effective than focusing exclusively on minimizing the rate of inbreeding.

5.3 Future of the Breed

Many of the challenges facing the DL-1970 are structural rather than purely genetic. As of September 2025, only six breeders were officially registered as DL-1970 breeders, of whom only four were actively breeding in 2024 (Simon Kolind, 2025). Encouragingly, breeders have begun to strengthen collaboration and focus on retaining new participants.

One strategy to increase population size and support conservation would be the commercialization of DL-1970 meat as a premium product, analogous to products derived from Iberian or Nustrale pigs (Casabianca et al, 2012; Toro et al, 2000).

Alternatively, products derived from DL-1970 could be considered for Protected Designation of Origin (PDO) status, similar to Iberian pork or Bergues cheese made with milk from Flemish Red. However, PDO designation imposes strict production and breeding requirements, including the exclusion of crossbred animals which may not be feasible for a breed as small and endangered as DL-1970 (Derkimba et al, 2008). Establishing a PDO framework also requires extensive stakeholder coordination and compromise (Müller et al., 2013).

Another potential strategy would be the establishment of a centralized breeding facility, where animals could be distributed to breeders while allowing more efficient monitoring of breed status and pedigree quality. Such a facility could potentially be combined with an educational or exhibition component, similar to Arche Warder in Germany a centre for rare and endangered domesticated animals. With the goal raise public awareness of agricultural heritage and the importance of breed conservation. A multi-species facility encompassing several Danish heritage breeds may be a more realistic approach.

Crossbreeding is highly effective in reducing the negative effects of inbreeding but remains controversial due to both social and genetic considerations (Lauvie et al., 2008). Introgression

inevitably dilutes the remaining gene pool and may alter breed phenotype, potentially compromising breed identity. However, for critically endangered breeds, controlled introgression may represent the only viable option to preserve at least part of the genetic diversity. Bennewitz et al (2008) suggested that limited admixture involving one or two endangered breeds and a non-endangered breed can result in a net gain of conserved diversity. Genomic tools, such as SNP-based breed composition analysis, can further assist in minimizing unwanted admixture and optimizing conservation decisions. Furthermore, Guldbbrandtsen et al (2020) showed that using Genomic assessment using DNA array data could help to choose animals for inclusion in conservation programs, by preventing unwanted admixture from other breeds or at least help to keep it as low as possible.

6. Conclusion

The inclusion and use of cryopreserved donor semen appear to provide a clear benefit for the Danish Landrace 1970 when OCS is applied. While OCS without donor semen would still result in a lower rate of inbreeding increase compared to random mating, the reduction achieved through the inclusion of donor semen is substantially greater.

However, the practical applicability of these results depends strongly on the current availability, reproductive status, and health of the living animals within the population. In addition, the pedigree contains several errors that must be further investigated and corrected, where possible to improve data quality and ensure the reliability and robustness of future analyses. Given the current limitations of the pedigree data, it is not yet possible to provide a fully realistic representation of the present state of the breed. Nevertheless, when considered alongside previous studies, the results clearly indicate that DL-1970 is critically endangered.

These findings highlight the urgent need to establish an accurate and up-to-date overview of the living population, while simultaneously applying all available conservation tools and strategies, such as those discussed in this thesis, to safeguard the long-term survival of the breed. Future steps should include close collaboration with breeders, implementation of OCS based on verified information on the active population and repeated application of OCS across successive generations to maintain long-term control of inbreeding levels.

Literature

- Bennewitz, J., Simianer, H., & Meuwissen, T. H. E. (2008). Investigations on merging breeds in genetic conservation schemes. *Journal of Dairy Science*, 91(6), 2512–2519.
<https://doi.org/10.3168/jds.2007-0924>
- Berg, P., Nielsen, J. & Sørensen, M. K. (2006). *EVA: realized and predicted optimal genetic contributions*. In Proceedings of the 8th World Congress on Genetics. Applied to Livestock Production: 13–18 August 2006, Belo Horizonte; 2006: Communication 27–09.
- Casabianca F., Lauvie A., Muller T., Maestrini O. (2012) *Farmers' Breeding goals and Requirements for PDO Products: The Nustrale Pig Breed in CORSICA*. Proc. of the Annual Meeting of the European Production of Animal Science, Bratislava, Slovakia.
- Charles Smith. (1984). Genetic aspects of conservation in farm livestock. *Livestock Production Science*, 11, 37–48.
- Derkimba, Adeline & Verrier, Etienne & Casabianca, François. (2008). *PDO project for Corsican pork as an innovation for the whole marketing chain*. 10.3920/978-90-8686-726-4_43.
- Douglas S. Falconer, T. F. C. M. (1989). *Introduction to quantitative genetics* (3rd ed.). Longman.
- Eusebi, P. G., Martinez, A., & Cortes, O. (2020). Genomic tools for effective conservation of livestock breed diversity. In *Diversity* (Vol. 12, Issue 1). MDPI AG.
<https://doi.org/10.3390/d12010008>
- FAO. (2007). *COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE GLOBAL PLAN OF ACTION FOR ANIMAL GENETIC RESOURCES and the INTERLAKEN DECLARATION* (1st ed.). FAO.
<https://openknowledge.fao.org/handle/20.500.14283/a1404e>
- Fernández, J., Toro, M. A., Gómez-Romano, F., & Villanueva, B. (2016). The use of genomic information can enhance the efficiency of conservation programs. *Animal Frontiers*, 6(1), 59–64. <https://doi.org/10.2527/af.2016-0009>
- Gil, M. A., Parrilla, I., Cuello, C., & Martinez, E. A. (2024). Current status of nonsurgical embryo transfer in swine. *Reproduction, Fertility and Development*, 37(1).
<https://doi.org/10.1071/rd24137>

- Gourdine, J. L., Sørensen, A. C., & Rydhmer, L. (2012). There is room for selection in a small local pig breed when using optimum contribution selection: A simulation study. *Journal of Animal Science*, 90(1), 76–84. <https://doi.org/10.2527/jas.2011-3898>
- Grădinaru, A. C., Petrescu-Mag, I. V., Oroian, F. C., Balint, C., & Oltean, I. (2018). Milk protein polymorphism characterization: A modern tool for sustainable conservation of endangered Romanian cattle breeds in the context of traditional breeding. In *Sustainability (Switzerland)* (Vol. 10, Issue 2). MDPI. <https://doi.org/10.3390/su10020534>
- Guldbrandtsen, B., Nielsen, V. H., & Schönherz, A. A. (2020). Genomic assessment of suitability of pigs for inclusion in the Pied Danish Pig conservation program—A case study. *Acta Agriculturae Scandinavica A: Animal Sciences*, 69(1–2), 95–100. <https://doi.org/10.1080/09064702.2020.1732455>
- Henryon, M., Ostensen, T., Ask, B., Sørensen, A. C., & Berg, P. (2015). Most of the long-term genetic gain from optimum-contribution selection can be realised with restrictions imposed during optimisation. *Genetics Selection Evolution*, 47(1). <https://doi.org/10.1186/s12711-015-0107-7>
- Johanna Wider. (2023). *Einheimische Nutztierassen in Deutschland und Rote Liste gefährdeter Nutztierassen 2023*. www.ble.de
- Kasap, A., Ramljak, J., & Špehar, M. (2021). Estimation of population-specific genetic parameters important for long-term optimum contribution selection—case study on a dairy istrian sheep breed. *Animals*, 11(8). <https://doi.org/10.3390/ani11082356>
- Kim, E. S., & Kirkpatrick, B. W. (2009). Linkage disequilibrium in the north American holstein population. *Animal Genetics*, 40(3), 279–288. <https://doi.org/10.1111/j.1365-2052.2008.01831.x>
- Knox, R. V. (2015). The fertility of frozen boar sperm when used for artificial insemination. In *Reproduction in Domestic Animals* (Vol. 50, pp. 90–97). Blackwell Publishing Ltd. <https://doi.org/10.1111/rda.12552>
- Koenig, S., & Simianer, H. (2006). Approaches to the management of inbreeding and relationship in the German Holstein dairy cattle population. *Livestock Science*, 103(1–2), 40–53. <https://doi.org/10.1016/j.livsci.2005.12.009>
- Kumar Chandrakar, A., Yadav, K. K., Kumar, V., & Gupta, N. (2016). *Scenario of Biodiversity Conservation in India: An Overview*. <https://www.researchgate.net/publication/311641120>
- Landbrugsstyrelsen. (2025) *Svin - gamle danske racer*. <https://lfst.dk/landbrug-og-planter/husdyr genetiske-ressourcer/gamle-danske-husdyrracer/svin>

- Landbrugsstyrelsen (2025) *beholdninger af ornesæd* <https://lfst.dk/landbrug-og-planter/husdyr genetiske-ressourcer/bestil-genmateriale>
- Lauvie, A., Danchin-Burge, C., Audiot, A., Brives, H., Casabianca, F., & Verrier, E. (2008). A controversy about crossbreeding in a conservation programme: The case study of the Flemish Red cattle breed. *Livestock Science*, 118(1–2), 113–122.
<https://doi.org/10.1016/j.livsci.2008.01.004>
- Maccluer, J. W., Boyce, A. J., Dyke, B., Weitkamp, L. R., Pfennig, D. W., & Parsons, C. J. (1983). Inbreeding and pedigree structure in Standardbred horses. In *The Journal of Heredity* (Vol. 74). <https://academic.oup.com/jhered/article/74/6/394/868877>
- Meuwissen, T. (2009a). Genetic management of small populations: A review. *Acta Agriculturae Scandinavica A: Animal Sciences*, 59(2), 71–79.
<https://doi.org/10.1080/09064700903118148>
- Meuwissen, T. (2009b). Genetic management of small populations: A review. *Acta Agriculturae Scandinavica A: Animal Sciences*, 59(2), 71–79.
<https://doi.org/10.1080/09064700903118148>
- Meuwissen, T. (2009c). Genetic management of small populations: A review. *Acta Agriculturae Scandinavica A: Animal Sciences*, 59(2), 71–79.
<https://doi.org/10.1080/09064700903118148>
- Meuwissen, T. H. E. (1996). *Maximizing the Response of Selection with a Predefined Rate of Inbreeding I*. <https://academic.oup.com/jas/article/75/4/934/4624959>
- Müller, T., Lauvie, A., Casabianca, François, & Maestrini, O. (2013). Managing local breed is a hard way to find a compromise between collective needs and individual aims: the case of the Nustrale pig breed. *Acta Agriculturae Slovenica, Supplement*, 4(4), 211–214.
<https://doi.org/10.14720/aas-s.2013.4.19059>
- Nielsen, HM & Kargo, M 2022, *Conservation of an endangered pig breed using optimum contribution selection. i WCGALP 2022 Programme book*. Wageningen Academic Publishers, World Congress on Genetics Applied to Livestock Production, Rotterdam, Holland, 03/07/2022.
<https://www.wageningenacademic.com/pbassets/wagen/WCGALP2022/72_007.pdf>
- Qanbari, S., Pimentel, E. C. G., Tetens, J., Thaller, G., Lichtner, P., Sharifi, A. R., & Simianer, H. (2010). The pattern of linkage disequilibrium in German Holstein cattle. *Animal Genetics*, 41(4), 346–356. <https://doi.org/10.1111/j.1365-2052.2009.02011.x>
- Simon Kolind. (2025, September). *Danske Husdyr Nyhedsbrev september 2025*. 8–9.
www.dkhusdyr.dk

- Škorput, D., Ceranac, D., & Luković, Z. (2023). Control of inbreeding in Banija spotted pig population using Optimisation methods. *Journal of Central European Agriculture*, 24(1), 53–60. <https://doi.org/10.5513/JCEA01/24.1.3681>
- Škorput, D., Špehar, M., & Luković, Z. (2022). Managing genetic diversity in pig populations: implications of optimal contribution selection in the Black Slavonian pig. *Italian Journal of Animal Science*, 21(1), 1259–1267. <https://doi.org/10.1080/1828051X.2022.2104661>
- Sørensen, A. C., Sørensen, M. K., & Berg, P. (2005a). Inbreeding in danish dairy cattle breeds. *Journal of Dairy Science*, 88(5), 1865–1872. [https://doi.org/10.3168/jds.S0022-0302\(05\)72861-7](https://doi.org/10.3168/jds.S0022-0302(05)72861-7)
- Sørensen, A. C., Sørensen, M. K., & Berg, P. (2005b). Inbreeding in danish dairy cattle breeds. *Journal of Dairy Science*, 88(5), 1865–1872. [https://doi.org/10.3168/jds.S0022-0302\(05\)72861-7](https://doi.org/10.3168/jds.S0022-0302(05)72861-7)
- Szekeres, B., Schönherz, A. A., Nielsen, V. H., & Guldbrandtsen, B. (2016a). *GAMLE DANSKE HUSDYRRACERS GENOMER-RACERNES OPRINDELSE OG SLAEGTSKAB*. DCA - Nationalt Center for Fødevarer og Jordbrug. www.digisource.dk
- Szekeres, B., Schönherz, A. A., Nielsen, V. H., & Guldbrandtsen, B. (2016b). *GAMLE DANSKE HUSDYRRACERS GENOMER-RACERNES OPRINDELSE OG SLAEGTSKAB* (82nd ed.). DCA - Nationalt Center for Fødevarer og Jordbrug. www.digisource.dk
- Tarrés, J., Bidanel, J. P., Hofer, A., & Ducrocq, V. (2006). Analysis of longevity and exterior traits on Large White sows in Switzerland. *Journal of Animal Science*, 84(11), 2914–2924. <https://doi.org/10.2527/jas.2005-707>
- Thompson, J. R., Everett, R. W., & Hammerschmidt, N. L. (2000). Effects of inbreeding on production and survival in holsteins. *Journal of Dairy Science*, 83(8), 1856–1864. [https://doi.org/10.3168/jds.S0022-0302\(00\)75057-0](https://doi.org/10.3168/jds.S0022-0302(00)75057-0)
- Toro, M. A., Nieto, B., & Salgado, C. (1988). A Note on Minimization of Inbreeding in Small-Scale Selection Programmes. In *Livestock Production Science* (Vol. 20).
- Toro, M., & Pérez-Enciso, M. (1990). Optimization of selection response under restricted inbreeding. *Genet Sel Evol*., 93–107. <https://doi.org/10.1186/1297-9686-22-1-93>
- Toro M.A., Rodriga~nez J., Silio L., Rodriguez C. (2000) *Genealogical analysis of a closed herd of Black Hairless Iberian pigs*. *Conserv. Biol.*, 14, 1843–1851
- Tsheten, G., Fuerst-Waltl, B., Pfeiffer, C., Sölkner, J., Bovenhuis, H., & Mészáros, G. (2023). Inbreeding depression and its effect on sperm quality traits in Pietrain pigs. *Journal of Animal Breeding and Genetics*, 140(6), 653–662. <https://doi.org/10.1111/jbg.12816>

- Wellmann, R. (2019). *Optimum Contribution Selection and Mate Allocation for Breeding: The R Package optiSel*. BMC Bioinformatics 20:25
- Wright, S. (1938). Size of population and breeding structure in relation to evolution. *Science*, 87, 430–431. <https://cir.nii.ac.jp/crid/1572543025597175424.bib?lang=en>
- Yeste, M., Rodríguez-Gil, J. E., & Bonet, S. (2017). Artificial insemination with frozen-thawed boar sperm. In *Molecular Reproduction and Development* (Vol. 84, Issue 9, pp. 802–813). John Wiley and Sons Inc. <https://doi.org/10.1002/mrd.22840>
- Zhang, Y., Zhuo, Y., Ning, C., Zhou, L., & Liu, J. F. (2022). Estimate of inbreeding depression on growth and reproductive traits in a Large White pig population. *G3: Genes, Genomes, Genetics*, 12(7). <https://doi.org/10.1093/g3journal/jkac118>
- Zhao, Q., Liu, H., Qadri, Q. R., Wang, Q., Pan, Y., & Su, G. (2021). Long-term impact of conventional and optimal contribution conservation methods on genetic diversity and genetic gain in local pig breeds. *Heredity*, 127(6), 546–553. <https://doi.org/10.1038/s41437-021-00484-z>
- Zhao, Q., Liu, H., Zhang, Q., Qadri, Q. R., Pan, Y., Su, G., Li, P., & Huang, R. (2024). Optimal Combination of Different Selection and Mating Strategies on Exploiting Genetic Diversity and Genetic Gain in Small Pig Conservation Populations. *Journal of Animal Breeding and Genetics*. <https://doi.org/10.1111/jbg.12917>

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List which GAI tools you have used and include the link to the platform (if possible): <i>Example: [Copilot with enterprise data protection (UCPH license), https://copilot.microsoft.com]</i>
Describe how generative AI has been used in the exam paper: 1) <i>Purpose (what did you use the tool for?)</i> 2) <i>Work phase (when in the process did you use GAI?)</i> 3) <i>What did you do with the output? (including any editing of or continued work on the output)</i> <i>Please note: Content generated by GAI that is used as a source in the paper requires correct use of quotation marks and source referencing. Read the guidelines from Copenhagen University Library at KUnet here</i>