



Norwegian University
of Life Sciences

Master's Thesis 2023 30 ECTS
Fakultet for biovitenskap

Longevity of ewes in Norwegian sheep production: descriptive study of breeds and genetic analysis of Norwegian White sheep

Ida Madelen Larsen
Institutt for husdyr- og akvakulturvitenskap (IHA)

Acknowledgement.....	2
Abstract	3
1.0 Introduction	4
1.1 The Norwegian sheep breeding system	4
1.2 Longevity in Norwegian sheep breeds	5
2.0 Materials and Method.....	7
2.1 Datasets and criteria for inclusion	7
2.2 Statistical Methods	8
3.0 Results	10
3.1 Breed comparison	10
3.2 Genetic Analysis.....	14
3.2.1 Fixed effects model.....	16
3.2.2 The Sire model.....	16
3.2.3 Sire model including the permanent environmental effect of dam.....	16
3.2.4 Sire model with the maternal genetic effect	17
3.2.5 Equal variance components model	18
3.3 Model comparisons.....	18
4.0 Discussion	19
4.1 Model criteria – is it adequate?.....	19
4.2 Breed comparison	19
4.3 The dataset and the model	20
4.4 The additive genetic analysis of Norwegian white.....	20
4.5 Future possibilities	21
5.0 Conclusion.....	21
6.0 Referances	22

Acknowledgement

This study is a part of the NMBU financed PhD project “Robust, resilient and sustainable ruminant production for future resource constraints and climatic conditions”.

First and foremost, I would like to give my thanks to my supervisors Geir Steinheim and Gunnar Klemetsdal. Thank you Geir for teaching me a completely new coding program and Gunnar for your patience when I struggled with modelling in R. Thank you to both of you for many long meetings and answers at random times of the day.

Thank you Hafrún Huld Hlinadóttir for being a companion through the whole process, being there, struggling with me and drinking way too much bubbletea. Thank you, Ida and Thea, for surviving my constant complaining about the zombie sheep and thank you Ellen and Johanne for reading everything. Finally thank you to family and friends for the support and the motivation to keep going.

Ida Madelen Larsen

Norwegian University of Life Sciences
Faculty of Biosciences
Animal Breeding and Genetics

Abstract

Longevity in breeding ewes is a complex trait affected by many factors both genetic and environmental. From an economic, environmental, and animal welfare perspective it is favourable to increase longevity. Norway has many breeds with distinctive differences, but the dominating production breed is the Norwegian White sheep (NWS). The two goals of this thesis are to first look at differences in longevity between breeds and, second, to do a genetic analysis of the longevity of Norwegian White sheep using data collected from Sauekontrollen: can longevity in NWS ewes be selected for.

Two different datasets were generated, one for the breed comparisons and one for the genetic analysis. The breed comparison dataset included information about nine breeds from all of Norway between 2001 and 2022 and had mean ages between 2.7 and 3.1 years. The genetic analysis dataset with NWS had information from sheep farm municipalities in Viken county between 2001 and 2022.

The different breeds showed quite similar longevity despite some breeds being more of a modern high-producing breed, while others were more traditional breeds. No clear patterns or change of mortality rate over the years.

The five models used for the genetic analysis was based on a sire model which was expanded into including the permanent environmental effect of the dam and the maternal genetic effect of the dam. The most complex model show heritability's estimates around 0.055 ± 0.008 on single year and 0.141 ± 0.020 for the average lifetime of the ewe, but results were similar for all models.

Introducing longevity into a Norwegian sheep breeding scheme could be a low-cost implementation since the data is already available and the heritability is on par with growth traits.

1.0 Introduction

Sheep farming in Norway is strongly connected to nature's seasonality, being based on natural, unfenced pastures (Eikje et al., 2008). Normally the sheep are moved indoors as the plant growing season ends and the frost arrives, with some exceptions depending on breed, location, and housing possibilities (Lovdata, 2005; Mattilsynet, 2022; NSG, 2023a). In 2022 41,3% of the sheep flocks were registered into the national database for sheep; Sauekontrollen. The proportion has increased from 25.9% in 2003 to 41.4% in 2022. In Sauekontrollen it is possible to register sheep as one of 22 acknowledged breeds. In 2022 65.2% of the registered animals were Norwegian White Sheep (Animalia, 2022b); a composite, crossbred sheep, with the main recent contributions from the breeds Dala, Rygja and Steigar, and through these breeds influenced by several other UK breeds (Eikje et al., 2008). Other common breeds are White Spæl, old Norwegian Spæl, coloured Spæl and Norwegian pelt sheep (Animalia, 2022b).

1.1 The Norwegian sheep breeding system

The Norwegian Sheep and Goat Organisation (NSG) is responsible for breeding schemes and index calculations of four different breeds; Norwegian White Sheep (NWS), Norwegian Spæl, Cheviot, and Norwegian pelt-sheep. NSG and its breed-specific sub-organisations provide genomic testing for Norwegian White Sheep and Norwegian Spæl, distribute semen (artificial insemination) between flocks and import supplementary semen from other countries, and thus contribute to genetic connections and increase spread of genetic gain between flocks (Avlstrådet, 2022a).

Index calculations are based on Best Linear Unbiased Prediction (BLUP), a common method to acquire breeding values. In Norway the BLUP information is transformed into indexes. The breeding value of an individual may change across its lifetime. New index calculations was available 20 times in 2022 (Avlstrådet, 2022a). After the indexes have been calculated, each index is generated into an overall-O-index. In this transformation, every trait is given weights, depending on progress demands and economic importance. These percentages change somewhat over time (Avlstrådet, 2022a). In this index, some traits are considered optimum traits (e.g., birth weight and litter size) where a specific optimum is considered, and the objective is to reduce variation by applying non-linear economic weights (Blichfeldt, 2020).

An important tool used in Norwegian breeding is the database Sauekontrollen provided by Animalia. Sauekontrollen is a registration platform for farmers who want to receive an improved overview of their flocks, including animal indices (Animalia, 2022a). In 2022 53.8% of Norwegian sheep was registered in Sauekontrollen (Animalia, 2022b). Another provider of information used in the index calculations is the slaughterhouse information about slaughter carcass weight, EUROP classifications, wool weight, and wool class (Avlstrådet, 2022a).

Each year, young test rams with the highest index (or breeding value) and that by experts are found to have qualifying phenotype will be selected as test rams or be sold to production flocks to increase the genetic gain (Avlstrådet, 2022a). Phenotypic traits evaluated differ by breed, but Norwegian White Sheep and Norwegian Spæl are evaluated for usage characteristics; these include feet position, wool quality, wool length, number of teats, and normal testicular growth. Every trait judged is believed to be heritable, which might vary between breeds and traits (Eikje & Blichfeldt, 2020).

The only breed currently possessing a genomic breeding value is the Norwegian White Sheep with a plan to be implemented in The Norwegian Spæl in 2023. The genetic parameters are re-estimated every 3-4 years unless any drastic changes occur, or a new trait is introduced

(Avlsrådet, 2022a). Genomic breeding values are especially important for traits that normally would be measured late in life or after death (e.g., the EUROP scale for meat quality), traits registered on only one gender (e.g., number of lambs), traits registered later in life (e.g., longevity) or traits that are difficult or costly to measure (e.g., methane emission). The traits with genomic breeding value will have a higher accuracy than traditional breeding values, especially at young age (Blichfeldt, 2016).

In 2020 NSG started a project to acquire more reliable data on birthing status, teat size, spring weight and adult weight. Concerning birthing status, the main goal is to include how much help the ewe needs and the birthing position of each lamb. They also want to implement registrations on extra teats, udder shape and exterior (Avlsrådet, 2022a). Selected farms from the ram circles were invited to be part of the registration flocks for Norwegian White sheep and 181 accepted. However, not every farm completed the required registration requirements in 2022 and it is therefore anticipated that approximately 130-151 will remain (Avlsrådet, 2022b). The goal is to have around 100 flocks with approximately 10 000 sheep (Avlsrådet, 2023).

Correspondingly, 57 Norwegian Spæl flocks were invited to become a registration flock in 2022 (Avlsrådet, 2022a). The new registration flocks involved free genome testing of their ewes as compensation, since the extra registration work is on a voluntary basis.

Genome testing is a tool to provide genetic breeding value, secure paternity, and compile information about unwanted mutations, including the two myostatin mutations variants for Norwegian White and Spæl, yellow fat and the Finnsheep gene (Avlsrådet, 2020; Blichfeldt, 2018). The data collected from genomic testing of the registration flocks will be used to link genomic data to phenotypic traits. The goal is to use the information to estimate genetic values for every trait in the breeding goal and develop a new breeding scheme with new traits (Avlsrådet, 2022a).

1.2 Longevity in Norwegian sheep breeds

Longevity is a complex trait with a base in numerous different traits and environmental effects. This constitutes a challenge for including longevity in a practical breeding scheme. Even though the trait is challenging, it is coveted to include the trait in a breeding scheme. Sheep breeding in Norway has tried to include longevity since 2008 but have not been able to find a useable heritability (Avlsrådet, 2008; McLaren et al., 2022). Increased longevity is regarded as economically beneficial due to reduced replacement costs. Longevity is also considered an environmental and an animal welfare trait (Hoffman & Valencak, 2020; McLaren et al., 2022).

Longevity can be defined in various ways. For example, the probability of survival to a specific age or how many years the animal can stay in production (Borg et al., 2009; McLaren et al., 2022), but in this study two different definitions were used for different parts. For the descriptive part of longevity in between the breeds it was defined as how many years the sheep stay in a traditional production setting and for the estimation of breeding value it was defined as the possibility to survive one more year at any given age.

Information regarding culling is available in the national database, but the reason behind it is often lacking (McLaren et al., 2022). The currently top recorded culling reasons in Norway (2022) are *mastitis* (20%), *age* (14.3%), *udder injury* (9.3%) and *non-breeder* (9.1%) ((Animalia, 2022b; McLaren et al., 2022).

Since production animals will be culled when they stop producing, little is known about the natural aging process of the animals. They have been bred for high economic value production traits which are often negatively genetically correlated with health traits (Hoffman & Valencak, 2020). Since the natural aging process is an uncommon occurrence, age related sickness and other complications are unknown (e.g. teeth loss is a common problem in UK-

sheep production) and new complications may arise with increased longevity (Hoffman & Valencak, 2020; McLaren et al., 2022). However, at lower ages one may anticipate that increased longevity will be negatively genetically correlated with disease traits, in correspondence with what has been found in dairy cattle (Holtmark et al., 2008). Selection for increase longevity is therefore an alternative strategy to genetically improve health and other functional traits in species where disease recording is not possible or difficult, like the sheep.

The objective of this master thesis was to first describe the present situation, describing longevity of ewes of different Norwegian breeds and then estimate genetic parameters (variances and heritability) of longevity in the main breed, Norwegian White Sheep to evaluate the possibility of selecting for the trait.

2.0 Materials and Method

The main data wrangling and basic statistics was done in SAS and the modelling in the ASReml-R package on the on-campus Linux OS computing cluster “Orion” for R studio 4.1.0 (RStudioTeam, 2020).

The original dataset had information from 2001 to 2021. The dataset included more than 13 million animals and with variables on production (e.g., litter size, weight, carcass qualities, and wool) and identification (e.g., animal id, farm id, sex, and breed). The data was collected by Sauekontrollen nationwide and included all breeds.

2.1 Datasets and criteria for inclusion

The thesis looks at “normal” production sheep, i.e., animals in commercial systems that had experienced a common pasture-based production cycle. The criteria set for the ewe were to be born between March and May (99%), being born in a litter with between 1 and 5 siblings (99.9%), being weaned between July and November (99.9%) and recruited for breeding having had at least one litter. Further, to be included the dam would need to produce at least one litter in the first two years of life and stay at the same farm across her lifetime. For each herd year the farm would need to have at least 10 winterfed ewes on record to be included. Ewes were removed in case of logical errors such as registering of having lambs after her recorded time of death.

After the criteria were implemented two subsets were made. One containing every breed from the whole country with 4 451 315 observations and one with Norwegian White sheep from farms in Viken county with 56 196 observations. Further, the breed dataset had 775 578 dams, 86 486 sires and 1 358 908 animals. The data was from 394 municipalities and included data from 6 765 farms between 2001 and 2021. The number of unique herd-years were 68 353 with a mean of 101 ewes and a standard deviation of 76. The minimum number of ewes in a herd in a year was set to 10 and the maximum was 957. After the criteria was implemented, the data had 9 breeds remaining Dala, Rygja, Spæl, Steigar, Norwegian White sheep, Pelt sheep, Old Norwegian, Old Norwegian Spæl and coloured Spæl.

The Norwegian White dataset contained 56 196 observations from 125 farms spread across 21 different municipalities. The observations were made of 18 026 different ewes with 1 605 sires and 10 473 dams. For the 125 farms it was 1 032 unique herd-years with different number of observations between the restriction of 10 and 233 with a mean of 84.88 observation per herd-year.

With this in mind this thesis will focus on describing the present situation for common breeds in Norway, while investigating possible heritability for longevity for the biggest production breed Norwegian white with a sub-dataset from municipalities in Viken County collected from Sauekontrollen.

2.2 Statistical Methods

The models used was a general linear mixed model

$$Y = Xb + Zu + e$$

where Y is the vector of the observed binary trait for longevity, where 0 depicts ewes still producing litters and 1 depicts ewes no longer producing litters. Moreover, where X is a matrix linking observations to appropriate fixed effects, b is the vector of fixed effects, Z is a matrix linking the observations to appropriate random effect, u is the vector of the random effect, and e is the residual effect.

The model was used for both datasets, with some modifications. For both models a known X and various Z incidence matrices were included, depending on model. For the breed dataset a Z_{HY} were inserted to link herd-years (HY) to the observations while for the Norwegian White sheep dataset three different Z matrices were used: Z_s , Z_{pe_d} and Z_d . Where Z_s ($s \sim N(\theta, A\sigma_{sire}^2)$) is the additive genetic effect of the sire, Z_{pe_d} ($Pe_d \sim N(\theta, A\sigma_{pe_d}^2)$) is the permanent environmental effect of the dam, and Z_d ($dam \sim N(\theta, I\sigma_{dam}^2)$) is the maternal genetic effect of the dam. Above, u denotes the vector of the random effects, and, finally, the e is a vector of the residual effect. A pedigree matrix containing pedigree data from 32 553 ewes, 16 893 dams and 3 609 sires over 7 generations were generated and the Z_s and Z_d matrices. The A matrix was made from, pedigree-based estimates of additive genetic relationships and linked to sire and dam information by ASReml, respectively.

The b is a vector for the fixed effects. For the breed dataset the fixed effect included breed, and an interaction term between the ewe age and breed. The fixed effects used for the Norwegian White dataset were age of ewe and HY, where ewe age is the age where the ewe got the litter. Each dam got one line for each year she had a litter and one for the year she died.

The Norwegian White model an expansion the simple fixed effect model (Model 1) into a sire model (Model 2), and further to include the permanent environmental effects of the dam (Model 3) to finally including the maternal genetic effect of the dam (Model 4). At the end an equal variance component model was also run where the additive genetic effect of sire and maternal genetic effect of the dam were assumed σ_{SD}^2 (Model 5).

The permanent environmental effect of dam allows for the inclusion of possible difference between dams in the same environment e.g., disease on the dam with a permanent effect on the offspring (e.g., dam had been diseased).

In the equal variance component model, the variance components were constrained for sire and dam to become equal. This model was an alternative version of the linear mixed model that attempted to include the permanent environmental effect of the dam in addition to genetic sire and maternal effect. However, with the inclusion, the additional did not converge.

The random models were tested against each other with a likelihood-ratio test (LRT). Models 3 and 4 were tested against model 2 since the model can be considered nested (the same model with one more random term).

Heritability estimates for longevity was obtained as shown in Table 1 for model 2 through 5 where calculated based on the traditional heritability formula (Table 1). The Table shows that estimates were obtained both annually and on an average lifetime basis, the average calculated from only ewes with a fulfilled potential to die (ewes born between 2001 and 2011).

Table 1: Formulas used to calculate the annual and average lifetime heritability of longevity in various models. All models estimated the additive genetic variance of sire (σ_s^2), model 3 also a permanent environmental effect of dam ($\sigma_{pe_{dam}}^2$), and model 4 a maternal effect of dam (σ_d^2). In model 5, a joint sire and dam genetic variance (σ_{SD}^2) was estimated. The average lifetime was estimated as 2,696 years, on basis of ewes that had a registered death.

Heritability			
Annual			Average lifetime
	Sire	Dam	
2	$\frac{4\sigma_s^2}{(\sigma_s^2 + \sigma_e^2)}$		$\frac{4\sigma_s^2}{(\sigma_s^2 + \sigma_e^2/2.696)}$
3	$\frac{4\sigma_s^2}{(\sigma_s^2 + \sigma_{pe_{dam}}^2 + \sigma_e^2)}$		
4	$\frac{4\sigma_s^2}{(\sigma_s^2 + \sigma_d^2 + \sigma_e^2)}$	$\frac{4\sigma_d^2}{(\sigma_s^2 + \sigma_d^2 + \sigma_e^2)}$	$\frac{4\sigma_s^2}{(\sigma_s^2 + \sigma_d^2 + \sigma_e^2/2.694)}$
5	$\frac{4\sigma_{SD}^2}{(2\sigma_{SD}^2 + \sigma_e^2)}$		

3.0 Results

3.1 Breed comparison

The mean age for each breed per year is illustrated in Figure 1. The analysis indicated that there was little change in the mean ages between 2005 and 2017, however, mean ages appeared to show a decreasing trend between 2018 and 2021 because of the ewes in the most recent data have not had the opportunity to die yet. Note that the Old Norwegian sheep experienced a mean ewe age numerically above the others, however not between 2001 and 2004 and a greater mean compared to the other breeds except in 2014 to 2017 (Figure 1).

The age of breeding ewes ranged between 1 and 21 year(s), with a mean age of 2.78 years across all breeds and years (Table 2). The mean ewe age within breed ranged between 2.65 and 3.09, and the breed with the numerically least average age was Norwegian White Sheep, while the breed holding the corresponding largest average was Old Norwegian Sheep.

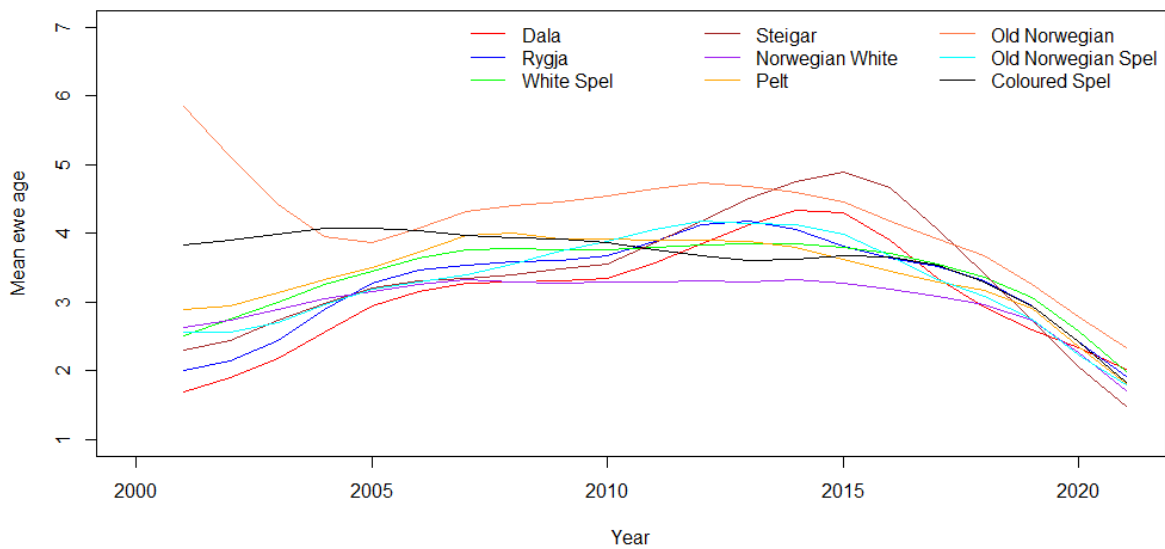


Figure 1: The mean ewe age between 2001 and 2021 by breed, using data from all counties.

Table 2: Descriptive statistics from the breed comparison sub-dataset with nine breeds, with total number of ewes per breed, number, and percentage of ewes per age, and the mean age for each breed.

Age	Dala	Rygja	White Spæl	Steigar	Norwegian White Sheep	Pelt sheep	Old Norwegian	Old Norwegian Spæl	Coloured Spæl
1	39 462 (29.57%)	10 989 (27.13%)	151 078 (27.83%)	31 748 (27.67%)	1 046 906 (30.58%)	19 814 (29.78%)	4 064 (25.70%)	13 616 (29.44%)	20 654 (29.62%)
2	34 107 (25.56%)	9 907 (24.46%)	126 856 (23.37%)	27 322 (23.81%)	849 053 (24.80%)	16 056 (24.13%)	3 589 (22.70%)	12 140 (26.25%)	16 794 (24.09%)
3	23 911 (17.92%)	7 341 (18.13%)	96 279 (18.13%)	20 500 (17.86%)	610 716 (17.84%)	11 558 (17.37%)	2 722 (17.21%)	8 325 (18.00%)	12 251 (17.57%)
4	16 012 (12%)	5 156 (12.73%)	70 900 (13.06%)	14 969 (13.04%)	419 652 (12.26%)	8 190 (12.31)	1 966 (12.43%)	5 461 (11.81%)	8 583 (12.31%)
5	10 454 (7.83%)	3 441 (8.50%)	49 013 (9.03%)	10 352 (9.02%)	267 324 (7.81%)	5 505 (8.27%)	1 369 (8.66%)	3 386 (7.31)	5 619 (8.06%)
6	6 206 (4.65%)	2 161 (5.34%)	30 591 (5.64%)	6 576 (5.73%)	150 997 (4.41%)	3 275 (4.92%)	936 (5.92%)	1 845 (3.99%)	3354 (4.81%)
7	2 516 (1.89%)	1 075 (2.65%)	13 540 (2.49%)	2 559 (2.23%)	60 694 (1.77%)	1 583 (2.38%)	605 (3.83%)	889 (1.92%)	1588 (2.28%)
8	631 (0.47%)	326 (0.80%)	3 644 (0.67%)	588 (0.51%)	14 505 (0.42%)	447 (0.67%)	324 (2.05%)	397 (0.86%)	583 (0.84%)
9	128 (0.10%)	83 (0.20%)	725 (0.13%)	114 (0.10%)	2 571 (0.08%)	87 (0.13%)	165 (1.04%)	136 (0.29%)	207 (0.30%)
10	21(0.02%)	21(0.05%)	136(0.03%)	17(0.01%)	436(0.01%)	17(0.03%)	54 (0.34%)	38 (0.08%)	62(0.09%)
11	5(0.00%)	2(0.00%)	34(0.01%)	2(0.00%)	74(0.00%)	4(0.01%)	16 (0.10%)	16(0.03%)	23(0.03%)
12	1(0.00%)		6(0.00%)	5(0.00%)	22(0.00%)		3 (0.02%)	6(0.01%)	11(0.02%)
13			1(0.00%)		3 (0.00%)				3 (0.00%)
14					2 (0.00%)				2 (0.00%)
15			1(0.00%)						1 (0.00%)
16					1 (0.00%)				
17					2 (0.00%)				
21				1(0.00%)	1 (0.00%)				
Mean	2.68	2.83	2.83	2.81	2.65	2.74	3.09	2.68	2.75
SUM	133 454	40 502	542 804	114 753	3 422 959	66 536	15 813	46 255	69 738

The corresponding average for longevity of ewes by breed shows the mortality rates per age-class (Figure 2). The mortality rate stays around 20% from age 1 to age 5, and then increase for every breed to between 40% and 60%. Each breed had different mortality reaching 100% mortality between the ages of 12 and 21 years old.

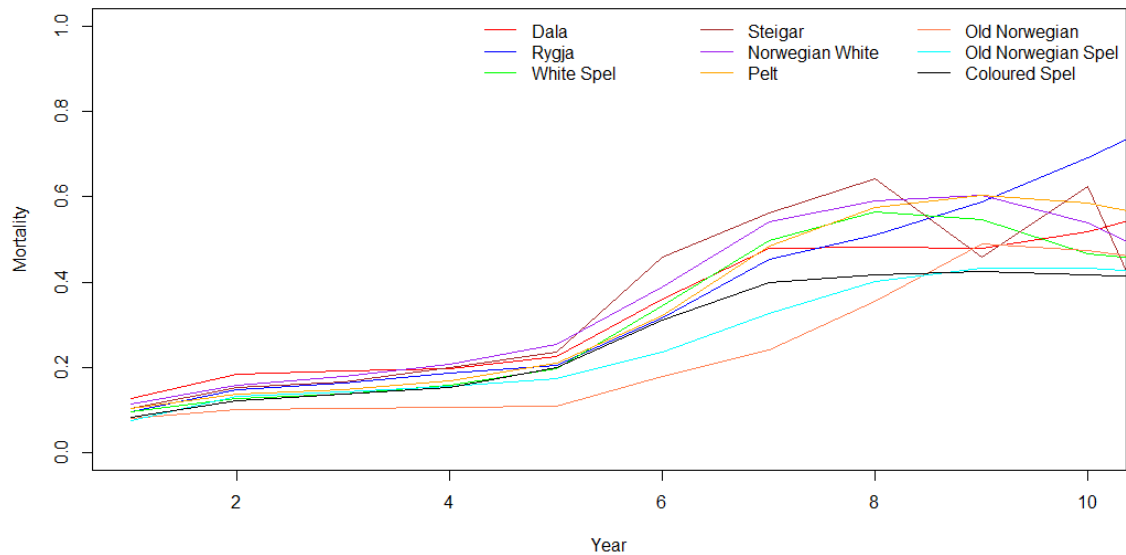


Figure 2: Mean longevity by ewe age for each breed using data from all counties.

The mortality per breed was calculated for the years 2001 to 2021. The mortality rate recorded is around 10% to 20% of every sheep breed each year, except Steigar had a mortality of close to 40% in 2015 (Figure 3).

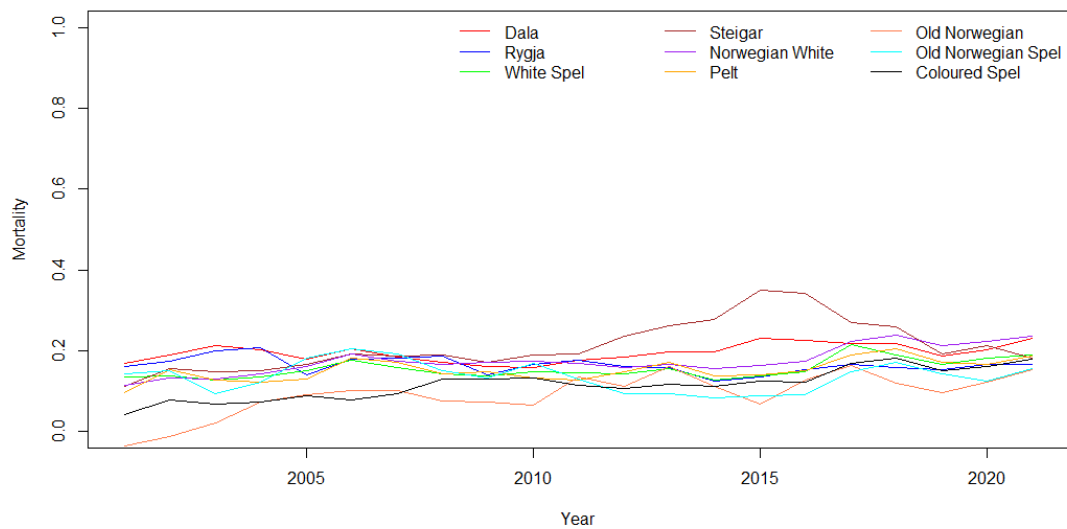


Figure 3: Mean mortality rate by year for each breed using data from all counties.

The variance components for the breed comparison model with random HY to easily compute least-squares mean for longevity by age of ewe within breed is shown in Table 3. The z.ratio was considerably larger than 2, indicating significant variance components.

Table 3: Estimated variance component for the breed comparison model with herd-year effects considered as random, with standard error, confidence interval and the Z.ratio.

Variance components – Breed comparison model			
	Component	SE	Z.ratio
HY	0.0173	1.1e-04	154.5
Error	0.1251	8.5e-05	1479.9

The predicted value for the estimated fixed effect, age of ewe within breed, for every breed moved towards 1 with similar results across ewe ages with standard errors between ± 0.0006 and ± 0.3604 (Figure 4).

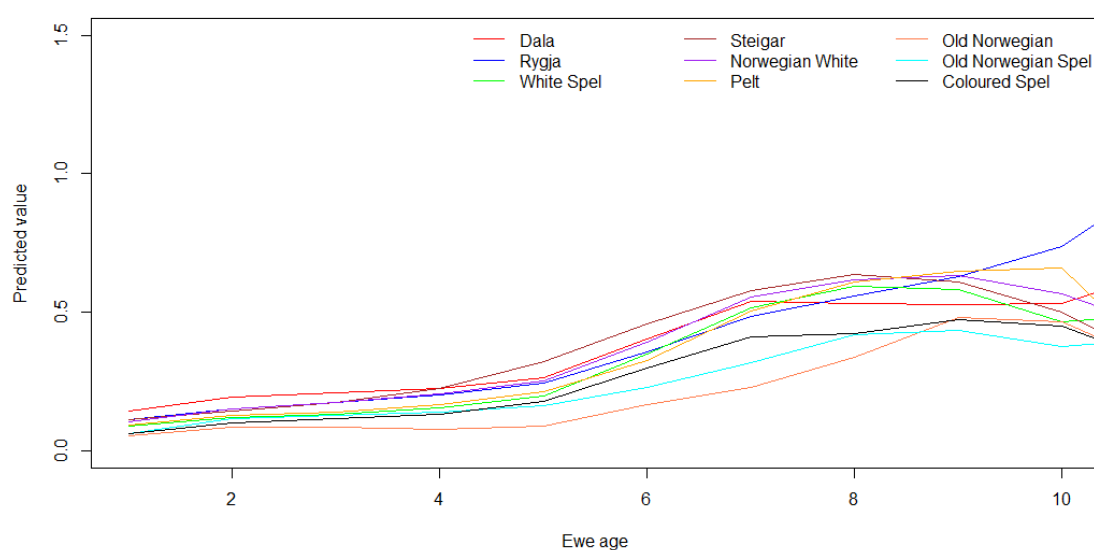


Figure 4: The predicted value of the fixed effects for each ewe age between breeds.

The Wald test indicate that breed is important for longevity with a constrained Wald F statistics value of 572.9. The interaction term between age of the ewe within breed had higher constrained F statistics value of 2359.0 (Table 4).

Table 4: Wald test for the breed description model of longevity, for the variables breed and the variable ewe age within breed, with degrees of freedom and constrained Wald F statistics.

Wald Test – Breed comparison model		
	DF	F.con
Breed	8	572.9
Ewe age within Breed	107	2359.0

3.2 Genetic Analysis

In the data used for genetic analysis, the age of the ewes were between 1 and 10 years of age with a mean of 2.64 (Figure 5), in correspondence with the mean for Norwegian White sheep from the whole country at 2.65 (Table 2).

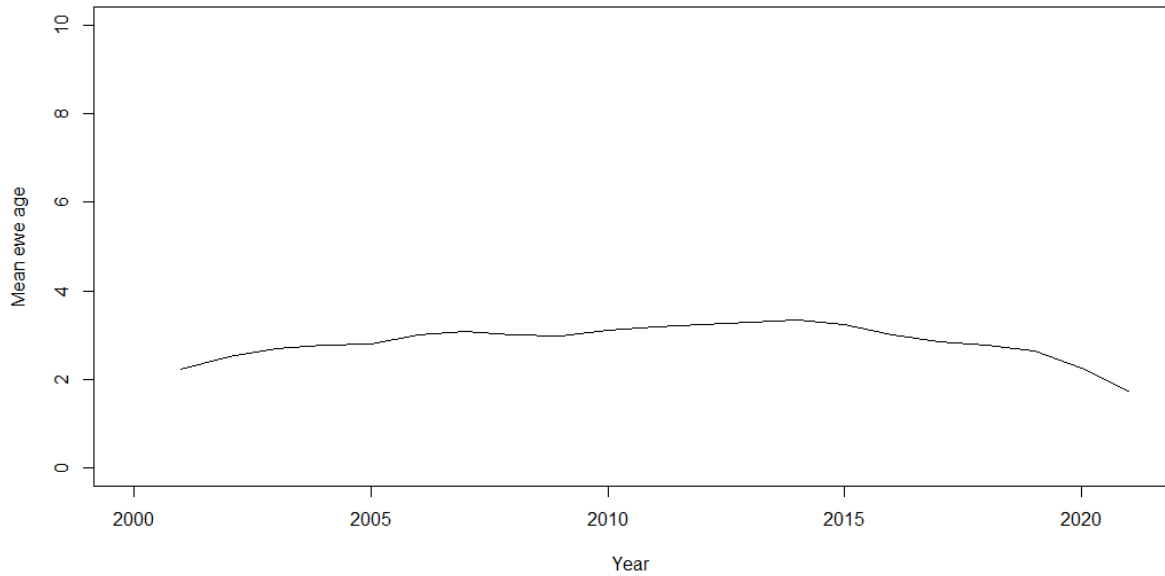


Figure 5: The mean ewe age between 2001 and 2021 for Norwegian White Sheep using data from municipalities in Viken county.

The mortality across each ewe age (Figure 6) was similar to the results for the breed dataset one for each breed with the mortality risk increasing from age 5 and stabilize at age 7 at around 60%. At 11 years of age the mortality is a 100%.

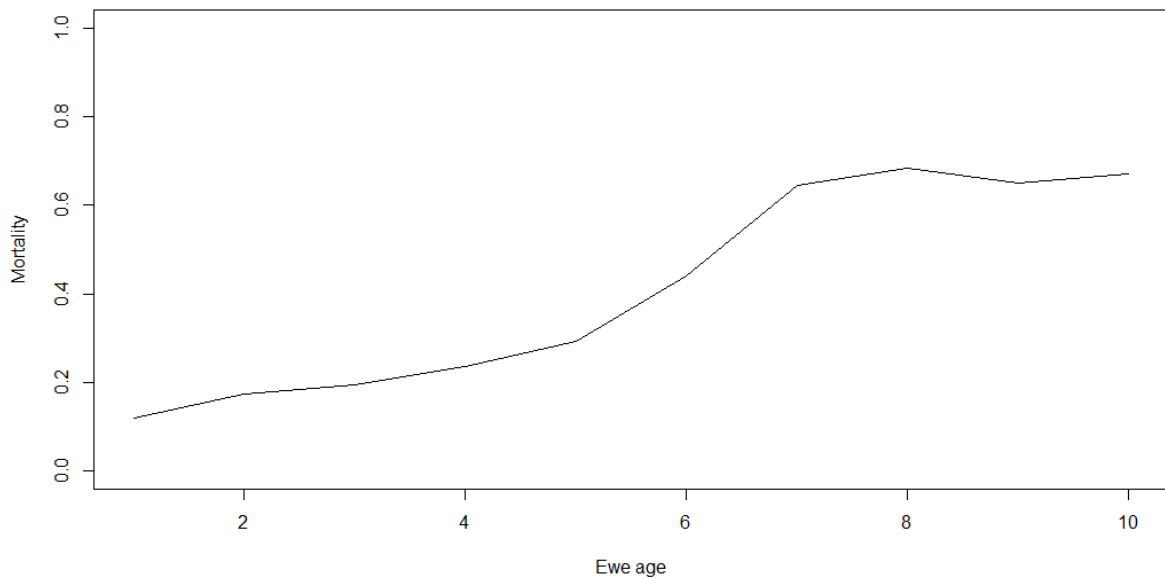


Figure 6: The mortality for every ewe age for Norwegian White sheep between 1 and 10 years.

The mortality rate of the total amount of sheep by year was close to stable between 10% and 25%, however some years the mortality rose above 25% (Figure 7). This corresponds with the results for the breed results across counties.

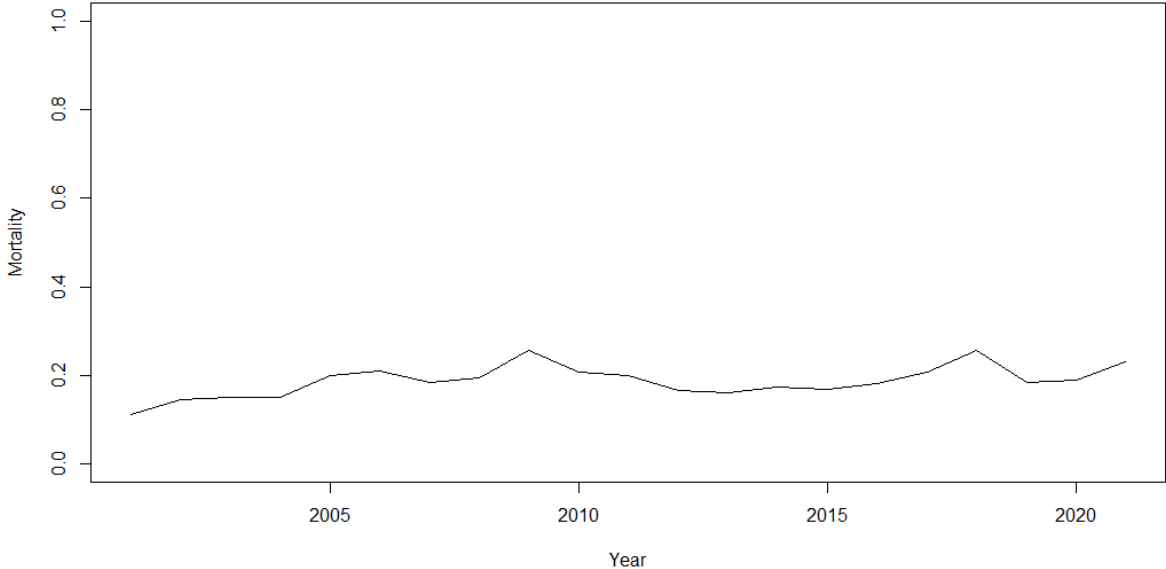


Figure 7: The mortality by year for Norwegian White sheep, using data from municipalities in Viken county.

3.2.1 Fixed effects model

The fixed effect model, model 1, included the fixed effects of herd-year and age of the ewe, i.e., age of ewes, and had no random effects. Both herd-year and ewe age had high constrained Wald F statistics (Table 5) and were therefore included in the up-and-coming models. The estimated error variance component in this model was 0.1340 ± 0.0008 .

Table 5: Wald test of model 1 for herd-year and ewe age with degrees of freedom and f increments results.

Wald Test – Model 1		
	DF	F.con
Herd Year	1025	5.8
Ewe age	9	324.3

3.2.2 The Sire model

In model 2 the estimated variance components with standard errors and Z ratio were provided (Table 6). Again, these the z. ratios were larger than 2.

From model 2, the heritability was estimated at 0.057 ± 0.008 . Additionally, the heritability calculated for an average lifetime of an animal (2.694 years) at 0.149 ± 0.002 .

Table 6: Estimated variance components for the sire effect and error term in model 2, with standard errors and the Z.ratio.

Variance Components – Model 2			
	Component	SE	Z.ratio
Sire	0.0019	0.0027	7.2
Error	0.1328	0.0008	161.5

3.2.3 Sire model including the permanent environmental effect of dam

Model 3, the sire variance was reduced relative to model 2, and both variance components were seemingly significant with respect to size of the Z.ratio (Table 7). With the inclusion of the permanent effect of dam the standard error of the sire variance was reduced. The heritability was estimated at 0.055 ± 0.008 . The mean heritability across an average lifetime (2.694 years) was 0.141 ± 0.028 .

Table 7: Estimated variance components for sire, permanent environmental effect of the dam (Pe_{dam}) and error term in model 3, with standard errors, and Z.ratio.

Variance Components – Model 3			
	Component	SE	Z.ratio
Pe_d	0.0018	0.0004	4.9
Sire	0.0018	0.0003	6.9
Error	0.1311	0.0009	150.4

3.2.4 Sire model with the maternal genetic effect

Model 4, the estimated variance component, and standard error for sire were, respectively, similar to the model containing the permanent environmental effect of dam. The maternal genetic variance was similar to the sire results (0.0015 vs 0.0018; Table 8). The heritability for the sire effect was 0.055 ± 0.008 and the maternal genetic effect of dam was 0.0449 ± 0.009 . Over an average lifetime (2.694 years), the heritability was estimated at 0.141 ± 0.020 .

Table 8: Estimated variance components for sire, maternal genetic effect of dam and error term in model 3, with standard errors, and Z.ratio.

Variance Components – Model 4			
	Component	SE	Z.ratio
Sire	0.0018	0.0003	6.9
Dam	0.0015	0.0003	5.1
Error	0.1315	0.0008	155.6

Figure 7 shows the increasing heritability estimate with repeated longevity records between 2 and 9. The heritability increased from 0.10 at two to 0.40 with 9 records.

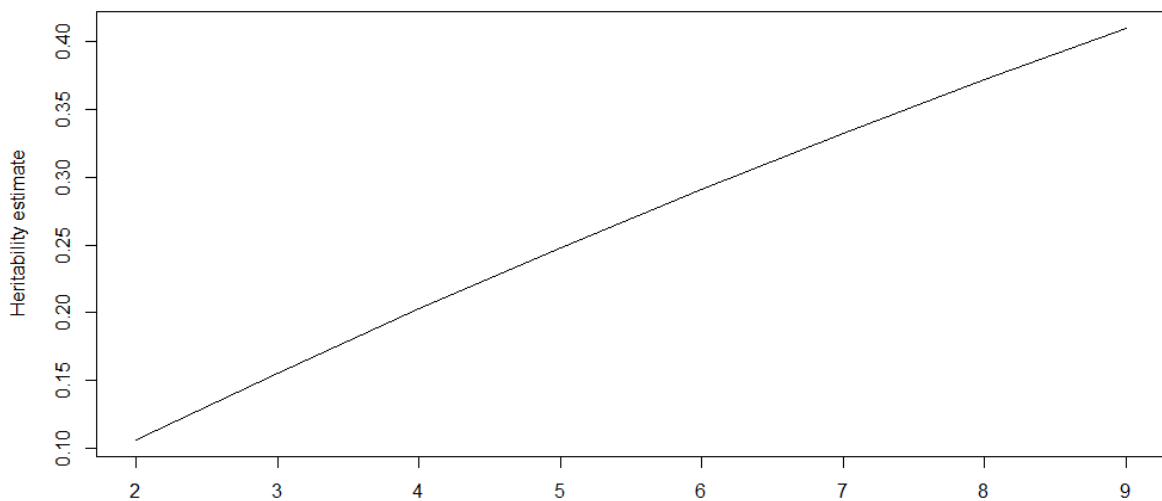


Figure 7: The heritability estimates with increasing repeated records between 2 and 9 records.

3.2.5 Equal variance components model

With the equal variance component model, the estimated components were constrained to be equal to 0.0017 ± 0.0002 for both the sire and dam genetic effects (Table 9). The heritability for this model was estimated at 0.050 ± 0.006 .

Table 9: Estimated variance components of model 5 with equal results for Sire and Dam effect for the component, standard errors and Z.ratio.

Variance Components Model 5			
	Component	SE	Z.ratio
Sire	0.0017	0.0002	8.9
Dam	0.0017	0.0002	8.9
Error	0.1314	0.0008	156.8

3.3 Model comparisons

Model 3 and 4 could be estimated compared with model 2. Every model shows a significance with $P < 0.001$ and an increase in the log likelihood > 19 . This means the included terms (maternal environmental effects with genetic and environmental components) in models 3 and 4 had a significant improvement (Table 10).

Table 10: The results of the Likelihood-ratio Test with the log likelihood results, log likelihood increases and p value when tested against model 2.

Likelihood ratio test			
	Log likelihood	Log likelihood increase	P value
Model 2	24997.65		
Model 3	25009.92	24.54	7.33E-07
Model 4	25016.02	36.74	1.35E-09

4.0 Discussion

Longevity is a complex trait and is challenging to use in a breeding scheme. The trait is heavily reliant on numerous environmental and genetic factors. Some examples include farm management, predator occurrence and disease resistance. How long the ewe survive in a production setting is very much up to the farmer. The farmer chooses animals for the next generation, but they do not all choose based on the same principles. One farmer will chose only based on indexes provided from Sauekontrollen or look at data collected from production traits, while another chooses the daughter of his favourite friendly sheep or the one that always find the best pasture during summer. Since every farmer has his/hers own choice the heritability of longevity will be difficult to measure, but with the inclusion of herd-year as a variable in the evaluation model it is possible to take this into account. Using a longitudinal model with one phenotype per year makes it possible to include herd-year in the genetic evaluation model, the biggest change from previous attempts to estimate heritability for longevity in Norwegian sheep.

4.1 Model criteria – is it adequate?

The base criteria regarding the normal production sheep included 99% of the original ewes and was responsible for eliminating outliers. This included ewes not born between March and May, not in a litter between 1 to 5 or weaned outside of July to November. The principal of a normal production sheep is based in the criteria for being included into the o-index by NSG (Blichfeldt, 2020).

With the implementation of at least 10 sheep for each herd, every year the probability for eliminating nonproduction farms increased. Less than 10 winterfed animals could be an indication of a hobby farmer. This number could have been increased, but since the average sheep farm in Norway includes around 40 winterfed ewes with some variation, 10 was chosen to not delete too many of the flocks.

In regard of the choice of sheep from municipalities from Viken county there were several alternatives, but Viken has low predation and a sufficient number of observations in the time period. If the goal was to look at the highest number of observations it would have been natural to choose Rogaland or Vestland (SSB, 2023), but in this instance the main goal was to get the model working with herd-year and the age of the ewe as fixed effects. Herd-year takes censoring into account and makes it possible to include animals not yet culled and corrects for the mean of every herd-year. While the age of the ewe corrects for the age of the ewes.

4.2 Breed comparison

The nine breeds studied were Dala, Rygja, Spæl (White and coloured), Steigar, Norwegian White, Pelt sheep, Old Norwegian sheep and GNS sheep.

These breeds had approximately the same mean age, between 2.65 and 3.09 years (Table 2), but since they were not raised in the same environment (e.g., same farm), they cannot be directly compared to each other. However, the numerical differences in mean age are small between breeds. This might be because of similarities in the breeding schemes for each breed or the long-time effect of breeding for the same traits (e.g., production related traits). Farmers will learn from each other and implement a lot of the same criteria for their flocks, sometimes independent of breeds.

Several aspects of farm management have an impact on mortality. The treatment provided by the farmer in form of e.g., feed and disease prevention will impact longevity. Even though some breeds have different criteria for being kept over time (e.g., difference between production- and preservation breeds), the resulting difference in mean age is low.

It could have been expected that the less production heavy breeds would present with a higher numerical mean age, but the numerical difference between the highest and the lowest was under 1 year. A possible reason could be the dataset do not represent the true average mean of every breed. For example, not every sheep is registered into Sauekontrollen (59,7%) and some of the smaller farms (under 10 winterfed ewes) were deleted under the selection criteria.

Age is the second most prominent registered culling reason (14%.3), after mastitis (20%), but the mean age of every breed is low compared to the highest recorded (21 years) for each breed (Table 2). This could indicate that we remove the sheep from production prematurely when they could have been kept longer. The high replacement cost and the low price for older sheep's meat should be encouragement for the farmer to increase the mean age of their flocks.

Other culling reasons were udder injury and non-breeder, but 13.3% of the information is recorded as either unknown cause (7%) or other known cause (5.8%) (Animalia, 2022b). Unknown and other do not give sufficient data for evaluation and the definition of udder injury could also include mastitis even though it is not supposed to. The recording of why a sheep was culled are sub-par but might improve with the new registration flocks.

4.3 The dataset and the model

The models run were all based on a sire model instead of an animal model. In the sire model, only the sires will be modelled with equations based on their progeny data, which makes it easier to compute since the number of sires are much lower than that of the whole pedigree, utilised in the animal model. In this case there were 1 605 sires compared to 10 473 dams for the 18 026 individuals. It compares sires against each other. Since the model only considers the additive genetic effect off the sire, the accuracy of the sire (in a sire model) might be lower than for the sire effect in an animal model. However, the sire model was chosen because the aim was to estimate variance components that were not influenced by common environment factors, which they would have been in an animal model. Still, for predicting of breeding values, fitting an animal model instead of a sire model could be advantageous, since it would make it possible to include all genetic relationships in calculations of breeding values. This would be advantageous when selecting new candidates of both sexes (van der Werf, 2012).

The sire model can have maternal effect included. Including maternal effects makes it possible to estimate and correct for biases regarding the ewe (van der Werf, 2012), and this was done by either including permanent environmental effect of the dam or the genetic maternal effect. In either way, the variance components were similar, supporting consistent results. Maternal traits are important and also included in the breeding goal for Norwegian White sheep (NSG, 2023b). Important maternal traits include milk production, fertility, udder conformation, lambing difficulties, and mastitis (Lillehammer et al., 2020).

One problem facing the models was the inclusion of the permanent environmental effect of the dam in addition to additive genetic effect of sire and the maternal genetic effect of the dam. Adding in the permanent environmental effect was attempted both in model 4 and 5 to make additional models, but computer resources were not sufficient.

4.4 The additive genetic analysis of Norwegian white

Given the results of the likelihood-ratio test (Table 10) the superior model would be the sire model with the inclusion of the maternal genetic effect of the Dam. The heritability for annual longevity was approximately 5%, but over an average lifetime of the ewe the lower standard error led to a heritability estimate of 14%. Since longevity is a complex trait highly influenced by the environmental, a heritability estimates of 14% could be viewed as high. The

model itself was only run with two different variables which were herd-year and the ewe age for each litter, but attempts were made to include different variables, with little to no change in the overall heritability and variance components.

Many different traits affect longevity including how well animals survive against predators. In the municipalities the data are collected from the biggest threat is the wolf, but attacks are not frequent. Another trait related to longevity is disease resistance where mastitis is the biggest concern for Norwegian White sheep. NSG is currently working towards estimating breeding values for mastitis with correlation to longevity, but without published results as of now. The biggest problem for estimating heritability for mastitis is the lack of good information. The registration flocks are supposed to give more and superior information on mastitis and other udder deformities.

4.5 Future possibilities

The possibility to keep the average ewe in production for a longer period is high and will give economic-, environmental- and welfare benefits. The present situation of the average age of 2.64 for Norwegian White is lower than the results for average age in other countries (e.g., Ireland, United Kingdom)(McLaren et al., 2022), however the mean could increase in the coming years if selection on longevity is implemented into the breeding scheme. Alongside the implementation of longevity into the breeding scheme, reducing the culling reasons, might also show results. The new registration flocks may provide a higher level of information and therefore provide better understanding, but this improved information is not yet available.

As mentioned before new problems might arise with an increased average age, so breeding for better health alongside increased longevity will increase in importance. Possible problems if the mean age increase could be ageing related sickness, teeth loss and fertility problems(McLaren et al., 2022). To implement longevity into a practical breeding scheme correlations with other traits need to be estimated. Especially relationships with growth traits need to be estimated, since health related traits are often negatively correlated with growth traits (Hatcher et al., 2009; Safari et al., 2005).

This type of genetic analysis can be performed on every breed and for bigger parts of the country. It is also expected if both the permanent environmental effect of the dam and the maternal genetic effect of the dam was included into the same model the results would improve.

5.0 Conclusion

The current numerical difference between breeds longevity is not large, even though some of the breeds are not modern high-producing animals. Longevity could be a low-cost implementation in the Norwegian sheep breeding scheme. The model produces heritability results on par with those for growth traits and is something that could be applied sooner rather than later.

6.0 Referances

- Animalia. (2022a). *Saukontrollen*.
<https://www.animalia.no/no/Dyr/husdyrkontrollene/saukontrollen/>
- Animalia. (2022b). *Årsstatistikk Saukontrollen*.
- Avlsrådet. (2008). *Referat fra møte nr 1/2008 i Avlsrådet for sau*.
- Avlsrådet. (2020). *Referat fra møte nr 2/2020 i Avlsrådet for sau*.
- Avlsrådet. (2022a). *Referat fra møte nr 4/2022 i Avlsrådet for sau*.
- Avlsrådet. (2022b). *Referat fra møte nr 5/2022 i Avlsrådet for sau*.
- Avlsrådet. (2023). *Referat fra møte nr 1/2023 i Avlsrådet for sau*.
- Blichfeldt, T. (2016). Genomisk seleksjon: Vil øke avlsframgangen betydelig. *Sau og Geit*, nr. 6/2016.
- Blichfeldt, T. (2018). Gentesting gir bedre avlsarbeid. *Sau og Geit*, nr. 6/2018.
- Blichfeldt, T. (2020). Saueindeksene: Fra tung teori og omfattende registreringer til nyttig informasjon. *Sau og Geit*, nr. 6/2020.
- Borg, R. C., Notter, D. R., & Kott, R. W. (2009). Genetic analysis of ewe stayability and its association with lamb growth and adult production. *Journal of Animal Science*, Volume 87(Issue 11). <https://doi.org/https://doi.org/10.2527/jas.2008-1623>
- Eikje, L. S., & Blichfeldt, T. (2020). Kåring som avlstiltak: Nyttig, men kan forbedres. *Sau og Geit*, nr. 4/2020.
- Eikje, L. S., Ådnøy, T., & Klemetsdal, G. (2008). The Norwegian sheep breeding scheme: description, genetic and phenotypic change. *Cambridge University Press*, 2(2), 167-176. <https://doi.org/https://doi.org/10.1017/S1751731107001176>
- Hatcher, S., Atkins, K. D., & Thornberry, K. J. (2009). Survival of adult sheep is driven by longevity genes. *Proceedings of the association for the advancement of Animal Breeding and Genetics*, 18, 580-583.
- Hoffman, J. M., & Valencak, T. G. (2020). A short life on the farm: aging and longevity in agricultural, large-bodied mammals. *GeroScience*, 42, 909–922.
<https://doi.org/https://doi.org/10.1007/s11357-020-00190-4>
- Holtmark, M., Heringstad, B., Madsen, P., & Ødegård, J. (2008). Genetic Relationship Between Culling, Milk Production, Fertility, and Health Traits in Norwegian Red Cows. *Journal of Dairy Science*, 91(10), Pages 4006-4012.
<https://doi.org/https://doi.org/10.3168/jds.2007-0816>
- Lillehammer, M., Sonesson, A. K., Klemetsdal, G., Blichfeldt, T., & Meuwissen, T. H. E. (2020). Genomic selection strategies to improve maternal traits in Norwegian White Sheep. *Journal of Animal Breeding and Genetics*. <https://doi.org/DOI:10.1111/jbg.12475>
- Lovdata. (2005). *Forskrift om velferd for småfe*.
<https://lovdata.no/dokument/SF/forskrift/2005-02-18-160>
- Mattilsynet. (2022). *Du må ha tillatelse fra Mattilsynet for å holde dyr ute hele året*. Retrieved 13.06.2023 from <https://www.mattilsynet.no/dyr/produksjonsdyr/sau-og-geit/soke-om-a-holde-sauene-ute-hele-aret>
- McLaren, A., McHugh, N., Lambe, N. R., Pabiou, T., Wall, E., & Boman, I. A. (2022). Factors affecting ewe longevity on sheep farms in three European countries. *Small Ruminant Research*, 189.
<https://doi.org/https://doi.org/10.1016/j.smallrumres.2020.106145>
- NSG. (2023a). *Beiterett- og beitebruksspørsmål*. <https://www.nsg.no/beitebruk/beiterett/beite-og-bruksrett/>
- NSG. (2023b). *Egenskaper i avlsarbeidet hos NKS*.
<https://www.nsg.no/sau/saueavl/avlsmal/nks-avlsmal/>

- RStudioTeam. (2020). *RStudio: Integrated Development for R. RStudio*. In PBC, Bosten. MA
URL <http://www.rstudio.com/>
- Safari, E., Fogarty, N. M., & Gilmour, A. R. (2005). A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. *Livestock Production Science*, 92(3), 271-289.
<https://doi.org/https://doi.org/10.1016/j.livprodsci.2004.09.003>
- SSB, S. S. (2023). *Husdyrhald*. Retrieved 09.07 from <https://www.ssb.no/jord-skog-jakt-og-fiskeri/jordbruk/statistikk/husdyrhald>
- van der Werf, J. (2012). *Mixed Models for Genetic Analysis*. In A. University of New England, Australia (Ed.): VSN International Ltd.



Norges miljø- og biovitenskapelige universitet
Noregs miljø- og biovitenskapelige universitet
Norwegian University of Life Sciences

Postboks 5003
NO-1432 Ås
Norway