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Estimation of heritability for the most common calf-hood diseases affecting Norwegian Red calves

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Abstract

Calf health has been gaining attention in the industry as it is the backbone of a successful dairy cattle enterprise. Calves that have been exposed to one or more calf diseases have been known to have compromised performance in later life. This study is the first to estimate heritability of Calf diarrhoea (CD), Joint disease (JD) alongside Respiratory diseases (RD) which has only been estimated once in 2008 in Norwegian Red calves. The main aim of the study was to estimate heritability for the most common calf diseases in the Norwegian Red calves.

The data consisted of 748 624 Norwegian Red calves from 3 437 herds in Norway from the period of 1 January 2014 to 31 December 2019. Records for treatments of the diseases before 180 days of age were 22 873 for respiratory disease, 8 410 for calf diarrhoea, 8116 for joint disease. The traits were defined as binary (0 = not treated, 1= treated). With the use of the three diseases a composite trait was created where each calf was scored based on being treated for any of the three diseases and the records amounted to 39 399. The data editing and descriptive statistics was done using RStudio version 2022.07.1.0 and genetic analyses were performed in DMU software. The estimated breeding values from 782 sires with progeny more than 200 were used to calculate correlation between the disease traits. The mean frequency of RD, CD and JD in the population were 3.05 %, 1.12 %, and 1.08% respectively. The overall calf disease frequency based on the most common diseases in the Norwegian Red population was 5.25 %.

The variance components and breeding values for the calf disease traits were estimated using a univariate linear animal model. Heritability of RD was 0.014 (0.0011), respiratory disease is the highest frequent diseases in Norwegian calves. The estimate for CD was 0.002 (0.0004) and the disease is the second highest recorded frequent diseases in the Norwegian Red calves. Joint disease was the third highest frequent disease with heritability of 0.004 (0.0005). The correlations between the disease traits are approximations of genetic correlations, RD and CD

had 0.16, RD and JD had 0.29 and JD and CD had -0.05 correlation. Calves born in months under winter and autumn had an increased risk of RD, CD and JD as compared to calves born in spring and summer. Larger group size had a tendency of increasing the risk of calves having respiratory, diarrhoea and joint diseases. Estimates were, however, not significantly different between group sizes for all disease traits. There was no significant difference between bull and heifer calves on RD, CD, JD, and the composite trait.

The Norwegian Red breed has been known for its excellent health status and this is also observed in calf diseases frequency reported in this study which is low compared to other calf diseases frequency reported in the European region and other regions in the world. The heritability obtained for all the three diseases RD, JD and CD are low hence there is not much room for genetic improvement. However, when heritability was first estimated in Norwegian Red calves for RD not many herds were participating in the calf health recording system, but now most herds participate, and the frequencies obtained are reliable to safely prove that the Norwegian Red calf health management is good.

Table of Contents

ACKNOWLEDGEMENT.....	I
ABSTRACT.....	II
TABLE OF CONTENTS.....	IV
LIST OF FIGURES.....	V
LIST OF TABLES.....	VI
LIST OF ABBREVIATIONS.....	VII
1.INTRODUCTION.....	1
2. LITERATURE REVIEW.....	3
2.1 NORWEGIAN RED BREED.....	3
2.2 NORWEGIAN DAIRY HERD RECORDING SYSTEM.....	4
2.3 CALF DISEASES.....	5
2.3.1 Respiratory diseases.....	5
2.3.2 Calf Diarrhoea.....	7
2.3.3 Joint Diseases.....	7
2.4 ESTIMATION OF HERITABILITY.....	8
3. MATERIAL AND METHOD.....	9
3.1 DATA.....	9
3.1.1 Description of variables.....	10
3.2 DESCRIPTIVE STATISTICS.....	11
3.3 STATISTICAL ANALYSIS METHOD.....	14
4. RESULTS.....	17
4.1 VARIANCE COMPONENTS AND HERITABILITY.....	17
4.2 FIXED EFFECT SOLUTIONS FOR GENDER, GROUPSIZE, BIRTH MONTH YEAR ON CALF DISEASES.....	18
4.3 ESTIMATED BREEDING VALUES.....	22
4.4 CORRELATION BETWEEN BREEDING VALUES.....	22
5. DISCUSSION.....	23
6. CONCLUSION.....	29
7. REFERENCES.....	30

LIST OF FIGURES

Figure 1. Mean frequency of diseases by birth year.....	12
Figure 2. Mean frequency of diseases by month of birth.....	13
Figure 3. Distribution of calves by month of birth.....	13
Figure 4. Distribution of records by age in months at first treatment until six months.....	14
Figure 5. Fixed effect solutions for group size on (a) respiratory (b) diarrhoea (c) joint diseases (d) composite.....	19
Figure 6. Fixed effect solutions for birth month-year effects for (a) respiratory (b) diarrhoea (c) joint disease (d) composite.....	20
Figure 7. Distribution of Estimated BLUP breeding values for (a) respiratory (b) diarrhoea (c) joint (d) composite.....	22

LIST OF TABLES

Table 1. Description of variables in the data set.....	10
Table 2. Mean frequency of calf diseases respiratory (RD), diarrhoea (CD), joint disease (JD) and composite grouped by gender in the Norwegian Red population.....	11
Table 3. Description of fixed and random effects.....	15
Table 4. Estimated herd year variance (σ^2_{HY}), additive variance (σ^2_A), residual variance (σ^2_e) and heritability (h^2) of calf diseases in Norwegian Red calves (Standard Error (SE) in parentheses)	17
Table 5. Estimated effect of gender on respiratory, diarrhoea, joint disease, and composite (solution for fixed effects)	18
Table 6. Correlations among estimated breeding values (EBV) from sires with ≥ 200 progeny for calf disease.....	23

LIST OF ABBREVIATIONS

RD	Respiratory Diseases
CD	Calf Diarrhoea
JD	Joint Disease
NDHRS	Norwegian Dairy Herd Recording System
EBV	Estimated Breeding Value
SE	Standard Error
BLUP	Best Linear Unbiased Prediction
BLUE	Best Linear Unbiased Estimate
EBVs	Estimated Breeding Values

1. Introduction

Calf health is key to herds' long-term health and productivity through healthy replacements. Records for health are key in animal health improvement, they allow key players to monitor trends of the most important diseases and the estimation of genetic and environmental factors affecting diseases (Egger-Danner et al., 2013). Health traits generally have a low heritability but are of high economic importance, thus justifying the attention given in the last two decades (Hu et al., 2020). In a review paper that was reported by Shook (1998), it was pointed out that genetic and economic studies for calf-hood diseases were needed for inclusion in breeding programs. Genetic variation of calfhood diseases is of potential economic importance and will assist in evaluating breeding programs.

The Norwegian Dairy Herd Recording System (NDHRS) has ensured recording of all health data concerning dairy cattle, this includes recording of all veterinary treatments for all individuals, including calves. Studies for common diseases of dairy cattle have been mainly focused on cows, and little research has been done on calf-hood diseases. One of the few genetic research studies that has been published on calf diseases focused on Respiratory Diseases (RD) in Norwegian Red (Heringstad et al., 2008). During the time the research was done, not all herds reported calf diseases, and the assumption is years later, many records for other diseases could be available for more research on calf-hood diseases.

The most common calf-hood diseases besides RD are calf diarrhoea and joint diseases such as arthritis (Gulliksen & Østerås, 2009; Marcé et al., 2010; Svensson & Liberg, 2006). The presence of calfhood diseases in herds have a major impact on the economics of cattle enterprises because of the direct calf losses through death and treatment costs and lastly the long-term effects on performance of the calves in their adult life (Lorenz et al., 2011). Thus, it is of interest to know more about the genetics of calfhood diseases, estimate heritability and

examine the potential for including these traits in the breeding program of Norwegian Red. The focus of this project is to estimate heritability for the most common calf diseases in Norwegian Red. Estimation of heritability can enlighten key players in breeding programs to decide if there is potential for genetic improvement of the trait.

2. Literature Review

2.1 Norwegian Red breed

Norwegian Red is a dual-purpose cattle breed dominating in Norway. The bull calves are used for meat production and the heifer calves are used for dairy production. The average annual milk production of the Norwegian Red cow is 8673 kg Energy Corrected Milk (ECM) with approximately 4.28 % fat and 3.56 % protein (Tine, 2022). The Norwegian Red breeding goal is focused on production, fertility, health, and udder conformation. Prior to selection of elite bulls, evaluation using a Total Merit Index (TMI) with 14 traits with respect to the breeding goal is carried out. Production, udder health, udder conformation and fertility are the traits that receive the highest relative weights in the breeding program.

The Norwegian Red breed is known for its high health and fertility status which are a proof that it is possible to improve low heritability traits through selection. Most of the Norwegian Red cows are not treated for diseases like clinical mastitis, metritis, milk fever, ketosis, and each disease percentage range between 83.9% to 99% cows free of treatments (Tine, 2022). The progress done for the breed in terms of health traits in cows can be implemented to the improvement of calf health and incorporated into the breeding program to ensure that calf treatments and losses are reduced.

According to (Tine, 2022) the total population for dairy cattle in Norway is 213 190 with an average herd size of 31, the Norwegian Red population size is around 180 000 with a calving interval of 12.3 months. This means that the Norwegian Red holds more than 84.5% of the total

population showing how the breed is of importance in Norway. The current total number of Norwegian Red calves born per year is 180 000 with a 50% proportion between bull calves and heifer calves. The national dairy cooperative TINE certified by International Committee for Animal Recording (ICAR) runs the Norwegian Dairy Herd Recording System (NDHRS), ensuring the collection of relevant data to be used for genetic evaluations and for research and development.

With the Norwegian Red accommodating the greater part of dairy cattle, (Tine, 2022) reported that 55% of the cows are milked by the Automatic Milking System (AMS). This makes the breed one of the dairy breeds with a large proportion of cows in AMS. This can be used as an indicator to confirm that if most of the cows are managed in an automated system, the calves are also likely to be raised in an environment with automatic management systems which influence the decision of raising calves in group systems to ensure productivity and profitability.

2.2 Norwegian Dairy Herd Recording System (NDHRS)

Recording dairy cattle data has provided data required for genetic evaluation in herds for a long time. The Norwegian Dairy Herd Recording System (NDHRS) was established in 1898, with information being collected for milk yield (Østerås, et al., 2007). This information has formed the foundation of the breeding program of the Norwegian Red, which currently now has fourteen traits grouped as production, health, and fertility traits. After seven decades, the NDHRS introduced a system called the Norwegian Cattle Health Recording System (NCHRS). The NCHRS began in 1975, involving the entire country, and was based on a partnership between GENO, Veterinary Association, TINE, and the Artificial Insemination Association (Østerås, et al., 2007). Advancements on NCHRS since its establishment included disease records being used to estimate breeding values for udder health, claw health, reproduction

related disorders, advisory services, and herd management purposes for improving production in Norwegian Red (Østerås, et al., 2007).

The data collected into the system comes from various sources such as veterinarians, artificial insemination technicians, advisors, claw trimmers, farmers, laboratories, and slaughterhouses. Data is recorded on each animal individually and can be accessed even if the cow is moved to another farm. In 2012 around 99% of Norwegian Red cows participated in the health recording system (Espetvedt et al., 2013). When the NCHRS was established, its progression was mainly toward cows, and there was less focus on the recording of calf health. According to (LeBlanc et al., 2006), reports about the monitoring of calf diseases in many countries on national levels were seldom reported. In the early decade of the 20th century, the NCHRS made efforts to improve calf health recordings in Norway (Gulliksen & Østerås, 2009). This improvement would ensure that herd health preventative work, genetic improvement, and research would be established (Egger-Danner et al., 2013). The use of calf health data from NCHRS for the Norwegian Red can help increase the longevity of cows as calf health has an impact on performance in the latter life (Gulliksen, et al., 2009).

2.3 Calf Diseases

Calf diseases have a major impact on the profitability of dairy farms. According to (Østerås, et al., 2007) death among calves causes annual losses of up to 100 million Norwegian kroner for Norwegian dairy farmers. Research on calf mortality indicated that RD, CD and JD were the most common diseases in Norwegian dairy herds (Gulliksen, et al., 2009). There has been limited genetic research for calf diseases in Norwegian Red; not much literature on a genetic study of specific diseases was found except for genetic analyses of RD in Norwegian Red calves (Heringstad et al., 2008).

2.3.1 Respiratory diseases

Respiratory disease is a multifactorial respiratory tract infection caused by different pathogens which can show mild to very severe different levels of infection. RD infections can be induced by stress, inhalation of high-level toxins, and reduced immunity in calves (Kirchhoff et al., 2014). The RD is an inflammation that can cause damage to lung tissues leading to poor performance and death in calves. The most common pathogens related to RD in the Norwegian population are bovine respiratory syncytial virus (BRSV) and parainfluenza-3 virus (Gulliksen, et al., 2009). In Norway some of the pathogens have been eradicated for instance since 2007 the country has been declared free from infectious bovine rhinotracheitis (Kampen et al., 2007). In Nordic countries, the incidence of RD is mainly in autumn and winter and peak in calves RD is around 35 and 49 days of age (Svensson et al., 2006). Clinical signs for RD include coughing, weeping eyes, running nose, breathing difficulties, and calves can also show concurrent respiratory signs and diarrhoea (Saif, 2010). Some pathogens that cause RD can be found in the calf's respiratory tract without causing disease until the calf is stressed, then they are triggered to cause noticeable symptoms. Respiratory disease may be infectious hence it can be transmitted from one calf to another.

Losses due to RD are mainly due to mortality and treatment costs (use of antibiotics) and vaccination (Phill, 2009). Calves with RD are likely to suffer from reduced weight gain, as seen through reduced daily gain, and there is a risk that the animal's performance will be reduced its entire life (Sacco et al., 2014). (Buczinski et al., 2021) meta-analyses reported that effect of RD loss on average daily gain was 0.067 kg/ day. RD can cause a decrease in daily gain by half, for instance, the Holstein average calf's daily gain is around 0.8kg/day and can be reduced to 0.4kg/day (Statham, et al., 2018). A recent study reported that cows that were diagnosed with lung consolidation as calves showed reduced milk yield during the first lactation (Dunn et al., 2018). One of the reasons for increased antibiotic treatments in calves is

related to RD, the disease is likely to cause a concern on antibiotic resistance, welfare, and profitability of dairy production systems (Toftaker et al., 2020).

2.3.2 Calf diarrhoea

Calf diarrhoea is still problematic even though the dairy industry has improved greatly in animal health and management (Cho & Yoon, 2014). Calf diarrhoea is also a multifactorial disease caused by bacteria, viruses, protozoa, and the pathogenesis of these include the fusion of villi in the small intestines (Boileau & Kapil, 2010). Clinical signs of diarrhoea are watery stools followed by dehydration, sunken eyes, weakness, and inability to stand. Diarrheic calves in herds are often infected by one pathogen, even though co-infection exists. Main pathogens known to cause CD are bovine rotavirus (BRV), bovine coronavirus (BCoV), bovine viral diarrhoea virus (BVDV, salmonella (S), Escherichia (E) coli and other emerging enteric pathogens (Cho & Yoon, 2014). CD can be treated by administering antimicrobial and anti-inflammatory drugs in conjunction with oral rehydration treatments. In Norway, CD is the second most reported disease after RD, and it causes profitability losses in dairy enterprises through treatment costs or death (Gulliksen, et al., 2009).

2.3.3 Joint disease

(Gulliksen, et al., 2009) defined joint diseases as warmth, swelling or pain in one or several joints and possibly accompanied by lameness and fever. Joint disorders are mostly seen in calves as secondary infections to naval infections, and commonly affected joints are the hock, knee (carpus), and stifle joints (Maunsell et al., 2011). Clinical signs include painful and swollen joints with the calves appearing unthrifty; most infection of joints arises from

gastrointestinal (*E. coli* and *Salmonella*) or respiratory diseases (Maunsell et al., 2011). Joints will be inflamed because bacteria enter the joint from other sites in the calf's body through traumatic injury or infection from the cow while the calf's blood system is still joined in the uterus (Lorenz et al., 2011). The bacteria attach to the synovial membrane tissue lining the bone and releases harmful chemical that breaks down the cartilage at the ends of the bone.

Calves affected develop slowly and might have long-term lameness. Antibiotic and aggressive therapy (surgical) treatments, along with long-term lameness, result in heavy direct losses to the farmer. In most cases, affected calves must be euthanized due to permanent damage to joint cartilage (Pardon et al., 2013). There is not much literature pertaining joint diseases in Norwegian Red cattle breed.

2.4 Estimation of heritability

Falconer and Mackay (1996) defined heritability as the proportion of additive genetic variance to phenotypic variance. In other words, heritability is the phenotypic variation that can be explained by genetic variation among individuals in a population (Ge et al., 2017). Heritability is classified as a population parameter, it depends on population specific factors, and it changes over time. When traits have low heritability, it means most differences in the trait are not genetic, and health traits are known to have low heritability (<0.15), thus making it difficult and expensive to improve them (Bennett et al., 2014). However, it is important to develop breeding strategies for the health traits as they are important for a successful production system. The Norwegian Red breeding program has proven that genetic improvement in low heritable traits, such as health traits, is possible if they are given enough weight in the total merit index (TMI) (Heringstad et al., 2007). It is also important to have a large amount of data to ensure accurate breeding values from estimating low heritable traits (Pal & Chakravarty, 2020).

Previous estimates of heritability in calfhood diseases in Norwegian Red were only reported for respiratory diseases (0.05) using threshold model by (Heringstad et al., 2008). Considering calf health recording has since improved, estimating heritability for the common calf diseases such as respiratory diseases, diarrhoea and joint diseases could precisely help in the breeding program of Norwegian Red. Heritability estimates are the first step to help breeders decide if a trait will or will not be included in a breeding program, and they also determine evaluation and selection methods (Getabalew et al., 2019).

3. Material and Method

3.1 Data

The data was attained from the Norwegian Dairy Herd Recording System. The data contained calves born between January 1st, 2010, and December 31, 2020, belonging to different breeds and all records of veterinary treatments up to one year of age. Only Norwegian Red calves were selected for this study. A total of three data sets were used, the first data set had 2 535 862 records of general information about calves; calf-id, birthdate, sex, herd, date of entry and exit from the herd, reason for enrolment and leaving the herd. The second data set had 1 460 911 records of all health records for calves within the period of the study until the age of one year. Treatment records had one record per treatment; calf-identification, birthdate, age at treatment, treatment date, treatment code and code for the veterinarian that treated the calf. The third data set was a pedigree file for the Norwegian Red calves traced back for five generations with a total of 3 158 994 animals.

Data cleaning was performed separately for the first two datasets, repeated records for treatments were removed and only the first record per animal was retained for each disease. After data cleaning the first and second data sets were merged, and new variables such as herd-year, month-year, group size and herd-month-year were created. Group size was developed by

counting the number of calves born in the same herd by year by month, followed by recoding group sizes to 6 classes. Group size 1 had calves less than 5, group size 2 (5-9 calves), group size 3 (10-20 calves), group size 4 (19-30 calves), group size 5 (31- 40 calves) and lastly group size 6 (>40 calves). In order to reduce the dataset further restrictions were imposed by keeping calves only from herds with at least 30 calves per herd-year, and records from the period between 2014 and 2019. A total of 748 624 calves from 3 437 herds was used for further analysis.

The three diseases were defined as binary traits with coding 1 for treated and 0 for not treated calves based on whether the calf had at least one treatment before they reached 180 days of age. In this study any veterinary treatments related to respiratory tract are considered as RD, this constitutes calves with contagious respiratory tract infections and unspecified respiratory tract infections. In the case of calf diarrhoea infections related to the gastrointestinal tract were considered as CD, stomach or intestinal inflammation, gastritis or enteritis and traumatic gastritis constituted the trait. Joint diseases encompassed all infections related to joints such as arthritis and lameness. The three disease traits developed were further used to create a composite trait based on if a calf had at least one of the three diseases.

3.1.1 Variables

A total of 23 variables were in the data set including the ones developed from the original data sets. Each of the diseases had its own columns for age at first treatment and treatment dates except for the composite trait leading to disease information having ten columns. Herds and animals have unique numbers in the Norwegian Dairy Herd Recording System.

Table 1. Description of variables in the data set

Variable	Code	Description
Respiratory Disease, Diarrhoea, Joint Diseases and Composite	0/1	Traits with binary codes for a calf being treated or not treated
Animal ID	Numeric coding	Unique number to each animal
Dates	y-m-d	Birth, treatment, entry and exit date
	y-m	Month-year calf born
Gender	1 or 2	Bull = 1, Heifer = 2
Age	days	Age at first treatment
Herd	Continuous numeric	Herd coding in the system
Herd-month-year	Numeric coding	Calf's herd, month, and year it was born
Group size	6 levels	Size of the group the calf was born in.

3.2 Descriptive Statistics

Data editing and descriptive statistics was done in RStudio version 2022.07.1.0.

The mean frequency of the disease traits and the total number of calves grouped by gender is shown in (Table 2). Calves treated for RD, CD and JD were 22873, 8410, and 8116, respectively. Respiratory disease shows the highest frequency in the population for a six-year period. Calf diarrhoea and Joint disease showed similar low disease frequency in the population. The frequency of the composite trait was higher because it totalled all infections of the three disease traits. Bull calves had a slightly higher mean frequency of RD, CD and JD than heifer calves.

Table 2. Mean frequency of calf diseases respiratory (RD), diarrhoea (CD), joint disease (JD) and composite grouped by gender in the Norwegian Red population.

	Number of Records	RD	CD	JD	Composite
Bull	386 473	3.17	1.08	1.16	5.19
Heifer	362 151	2.93	1.17	1.00	4.90
Total	748 624	3.05	1.12	1.08	5.26

The overall mean disease frequency for each birth year was calculated and visualised through plot shown in Figure 1. The mean frequency ranged from slightly above 1% – 3.5 % throughout the six years with RD having the highest frequency in the population. From the year 2017 an increase in RD disease frequency is an indicator of the improvement of calf records submitted to NDHRS or increased diseases in the population.

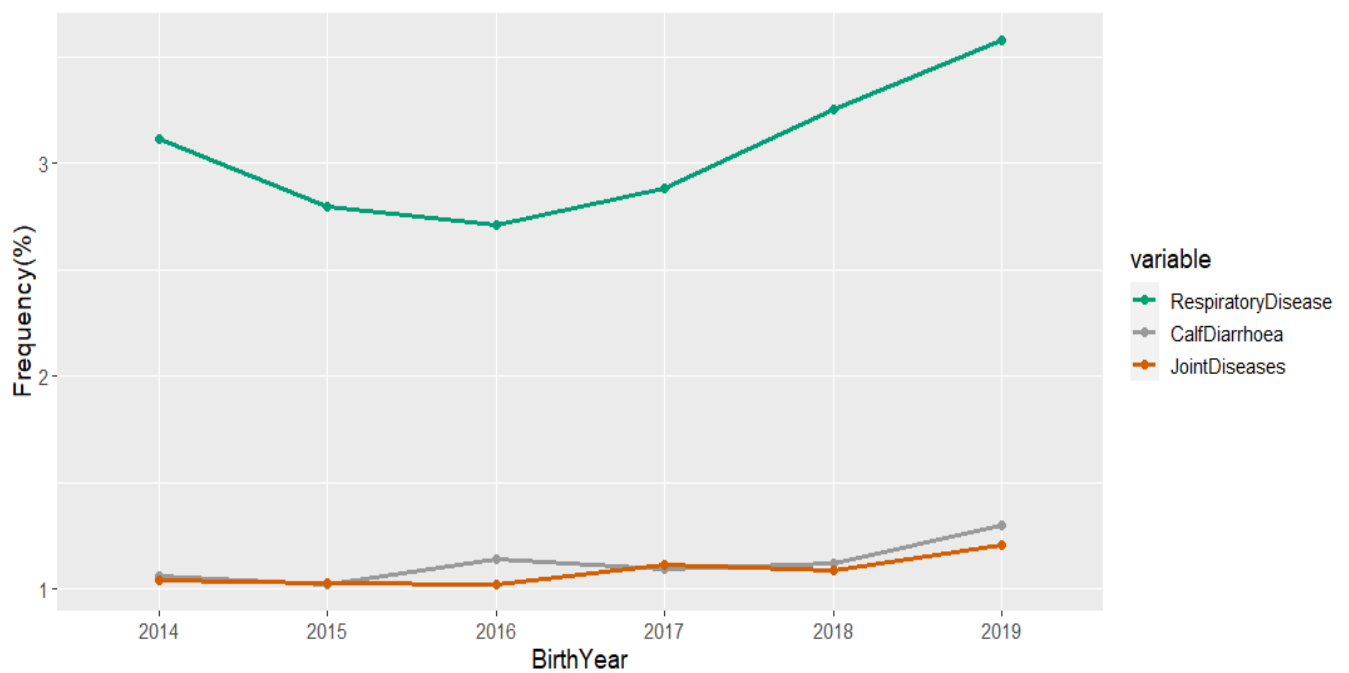


Figure 1. Mean frequency of the disease by birthyear

The birth-month of the calves fall into four seasons namely winter, spring, summer, and autumn which have different climatic conditions ranging from high and low temperatures. The mean temperature differences between the coldest month and warmest month in the country is around 10 to 15°C (Hanssen-Bauer et al., 2017). The warmest temperature Norway has experienced is 35.6°C and the coldest has been -51.4°C (Hanssen-Bauer et al., 2017). Outdoor and indoor temperature has huge differences in cold months; however, calves are housed in barns that are more comfortable. Winter in Norway is around the month of December, January, and February whereas spring is experienced between the month of March, April, and May. Summer starts from the month of June through July, and August whilst autumn starts from the month of September to October and November. The Figure 2 below shows the mean frequency of diseases for each birth-month in total for the six years in study.

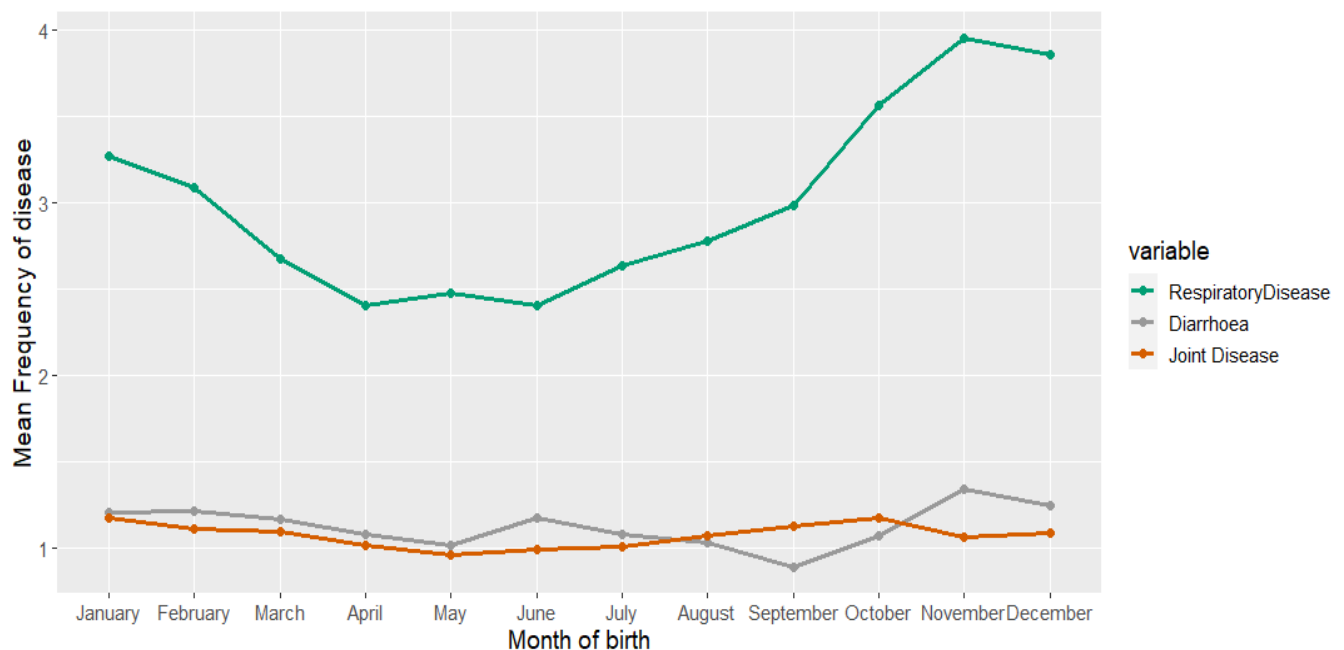


Figure 2. Mean disease frequency by month of birth

The distribution of calves by birth month is shown in Figure 3. The highest number of calves are recorded in the September, a month that falls in autumn season and the lowest number of calves is recorded in April and May which fall in spring season.

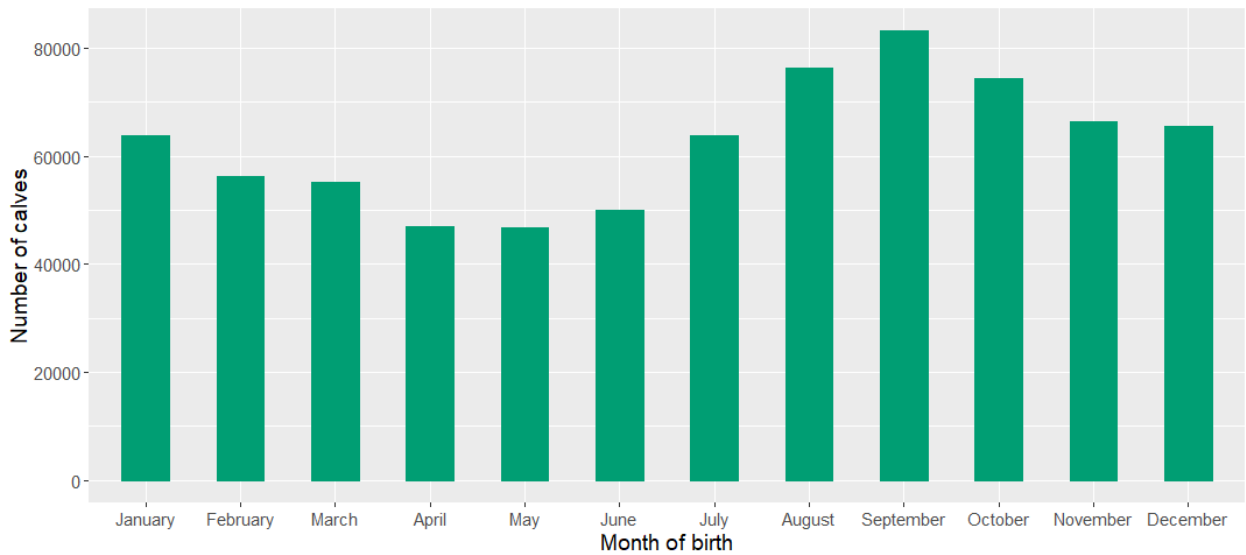


Figure 3. Distribution of calves by birth month

The distribution of records by age of the first treatment are shown in Figure 4. The highest number of treatments are recorded at 2 months for RD whereas for JD and CD the peak is recorded at 1 month of age. There after the number of treatments decrease for all the three diseases and reach a plateau at the age of 6 months and above.

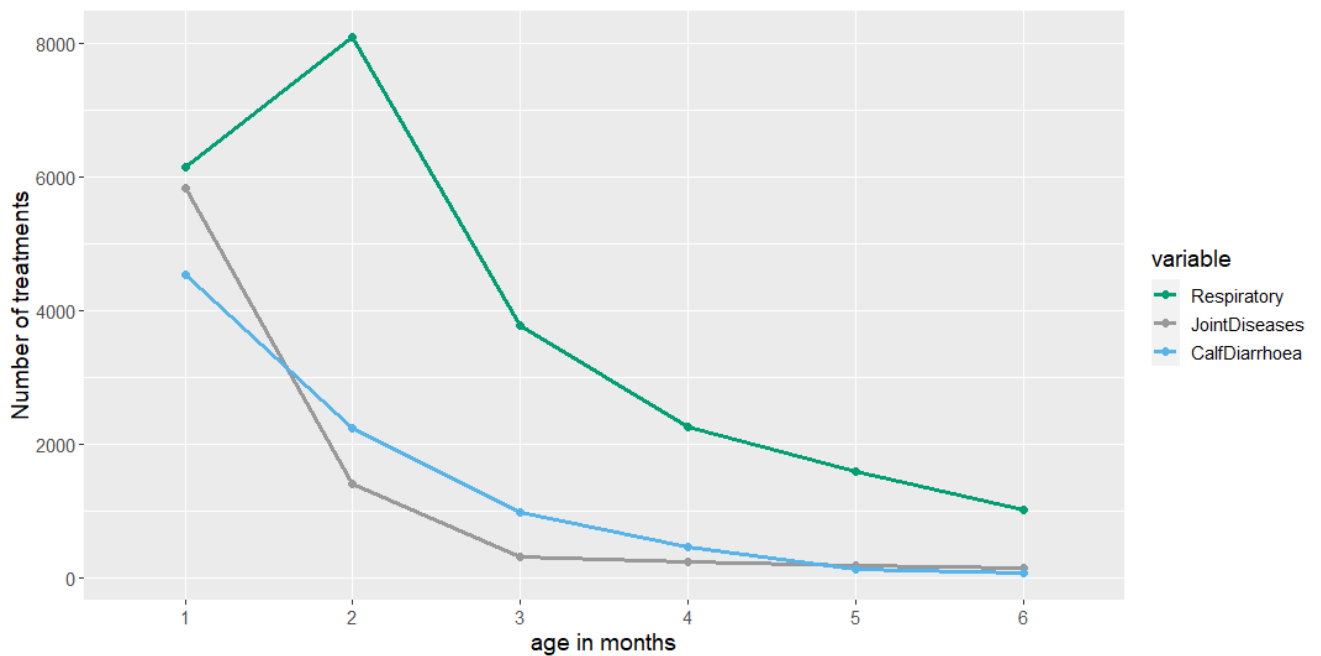


Figure 4. Distribution of records by age in months at first treatment until six months

3.3 Statistical Analysis

The analysis of the data and estimation of variance components was done using a linear animal model using the Average Information Restricted Maximum Likelihood (AI-REML) algorithm implemented in the DMU package (Madsen and Jensen, 2013). Estimation of heritability was done using single-trait animal models. The fixed effects included in the model were sex of the calf, birth-month-year, and group-size as shown in (Table 3). The fixed effects had a total of 80 levels with sex having 2 levels, birth-month-year 72 levels and 6 levels for group size. The variable group size was developed to describe the number of calves born in the same herd, year, and month (HYM) and it had 6 classes. The number of calves born per HYM ranged from 1 calf to 63 calves, the following was used to create fewer group-size levels: with 0-5 being in group 1, 6-10 group 2, 11-20 group 3, 21-30 group 4, 31-40 group 5, and lastly calves raised in greater than 40 calves as group 6.

Table 3: Description of fixed and random effects

Effect	Classes (n)	Minimum	Maximum
Birth-month-year	72	2014	2019
Sex of calf	2	Bull	Heifer
Group size	6	1	>40
Herd-year	15 165	-	-

Analysis model for calf diseases:

$$Y_{ijklm} = \mu + \text{Sex}_i + \text{GS}_j + \text{MY}_k + \text{Hy}_l + a_m + e_{ijklm}$$

where Y_{ijklm} is an observation of the trait (RD, CD, JD or composite, μ is the overall mean, Sex_i is the fixed effect of gender of the calf, GS_j is the fixed effect of group size the calf was

raised in, MY_k is the fixed effect of birth-month-year, Hy_i is the random herd-year effect, a_m is the random additive genetic effect of animal with relationship matrix A derived from pedigree information and e_{ijklm} is the residual variance. In matrix notation the model can be described as

$$\mathbf{Y} = \mathbf{Xb} + \mathbf{Z}_1\mathbf{hy} + \mathbf{Z}_2\mathbf{a} + \mathbf{e}$$

where \mathbf{Y} is a vector of 748 624 observations for each calf health trait, \mathbf{X} , \mathbf{Z}_1 , \mathbf{Z}_2 are design matrices relating the observations to fixed effects, random herd-year effects and animal effects, \mathbf{b} contains the fixed effects, \mathbf{hy} is a vector of random herd-year effects with 15 165 levels, \mathbf{a} is a vector of random animal effects and \mathbf{e} is a vector of random residual effects.

The following variance structure was assumed for the random effects:

$$\mathbf{a} \sim N(0, \mathbf{A}\sigma_a^2), \mathbf{hy} \sim N(0, \mathbf{I}\sigma_{hy}^2), \text{ and } \mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2),$$

where σ_a^2 is the additive genetic variance, σ_{hy}^2 = herd-year variance, σ_e^2 = residual variance, \mathbf{A} is the additive relationship matrix, and \mathbf{I} is an identity matrix. The \mathbf{A} matrix had a total of 1 412 885 animals, where pedigree of the calves with data were traced back up to the fifth generation.

The estimated variance components were used to calculate heritability(h^2) using the formula:

$$h^2 = \frac{\sigma_A^2}{\sigma_{HY}^2 + \sigma_A^2 + \sigma_e^2}$$

Due to low frequency of all disease traits, it was not possible to estimate genetic correlations. However, correlations between estimated breeding values (EBV) were used instead to calculate an indicator of genetic correlations. For these correlations only sires with most accurate EBVs were used. Breeding values for 782 sires with 200 or more progeny were selected and used in the correlation analysis.

4. Results

4.1 Variance components and heritability

The estimated variance components and the corresponding heritability for respiratory, diarrhoea, joint and lastly the composite trait created from the three diseases are given in (Table 4). Respiratory disease had the highest heritability of 0.014 (0.001) whilst the diarrhoea had 0.002(0.0003) and joint illness had 0.004 (0.0006) heritability. The new composite trait developed had a heritability of 0.011 (0.001) which was lower than heritability for respiratory disease. All variance components were estimated with small standard errors and despite low numbers all heritabilities were significantly different from 0.

Table 4: Estimated herd year variance (σ^2_{HY}), additive genetic variance (σ^2_A), residual variance (σ^2_e) and heritability (h^2) of calf diseases in Norwegian Red calves (Standard Error (SE) in parentheses)

	Respiratory	Diarrhoea	Joint disease	Composite
σ^2_{HY}	0.0023 (0.00003)	0.0007 (0.00001)	0.0002 (0.000005)	0.0036 (0.00005)
σ^2_A	0.0004 (0.00004)	0.00003 (0.000004)	0.00005 (0.000006)	0.0005 (0.00005)
σ^2_e	0.0267 (0.00005)	0.0104 (0.00002)	0.0104 (0.00002)	0.0435 (0.00008)
σ^2_T	0.0293	0.0111	0.0107	0.0476
h^2	0.014 (0.001)	0.002 (0.0003)	0.004 (0.0006)	0.011 (0.001)

4.2 Fixed effect solutions for gender, group size and birth month year on calfhood diseases

The genetic analysis of the most common calfhood diseases showed that some fixed effects had a significant effect on each trait. However, the gender of the calf had no significant effect on all the disease traits including the composite trait. There was no significant difference between bulls and heifers for all the disease traits as the standard errors were overlapping. The bulls had higher fixed effect solutions for all the diseases except CD compared to heifers (Table 5), indicating that bull calves are likely to be more susceptible to disease than the heifers.

Table 5: Estimated effect of gender on respiratory, diarrhoea, joint disease, and composite (solutions for fixed effects)

Trait	Bull: Estimate ±SE	Heifer: Estimate ±SE
Respiratory	0.0295 ± 0.0076	0.0271 ± 0.0076
Diarrhoea	0.0069 ± 0.0045	0.0077 ± 0.0045
Joint diseases	0.0258 ± 0.0038	0.0243 ± 0.0038
Composite	0.0631 ± 0.0096	0.0602 ± 0.0096

The number of calves housed together may influence the health and welfare of the animal. The solutions for fixed effects of group size showed an increasing tendency on RD and JD as shown in Figure 5. Estimates were however not significantly different between group sizes for all the disease traits. Larger group size (number of calves born in the same month) had the highest fixed effect solutions for RD and JD.). Group size 5 which represented calves raised in 30-40 calves per group had highest unfavourable effect solution for all the disease traits.

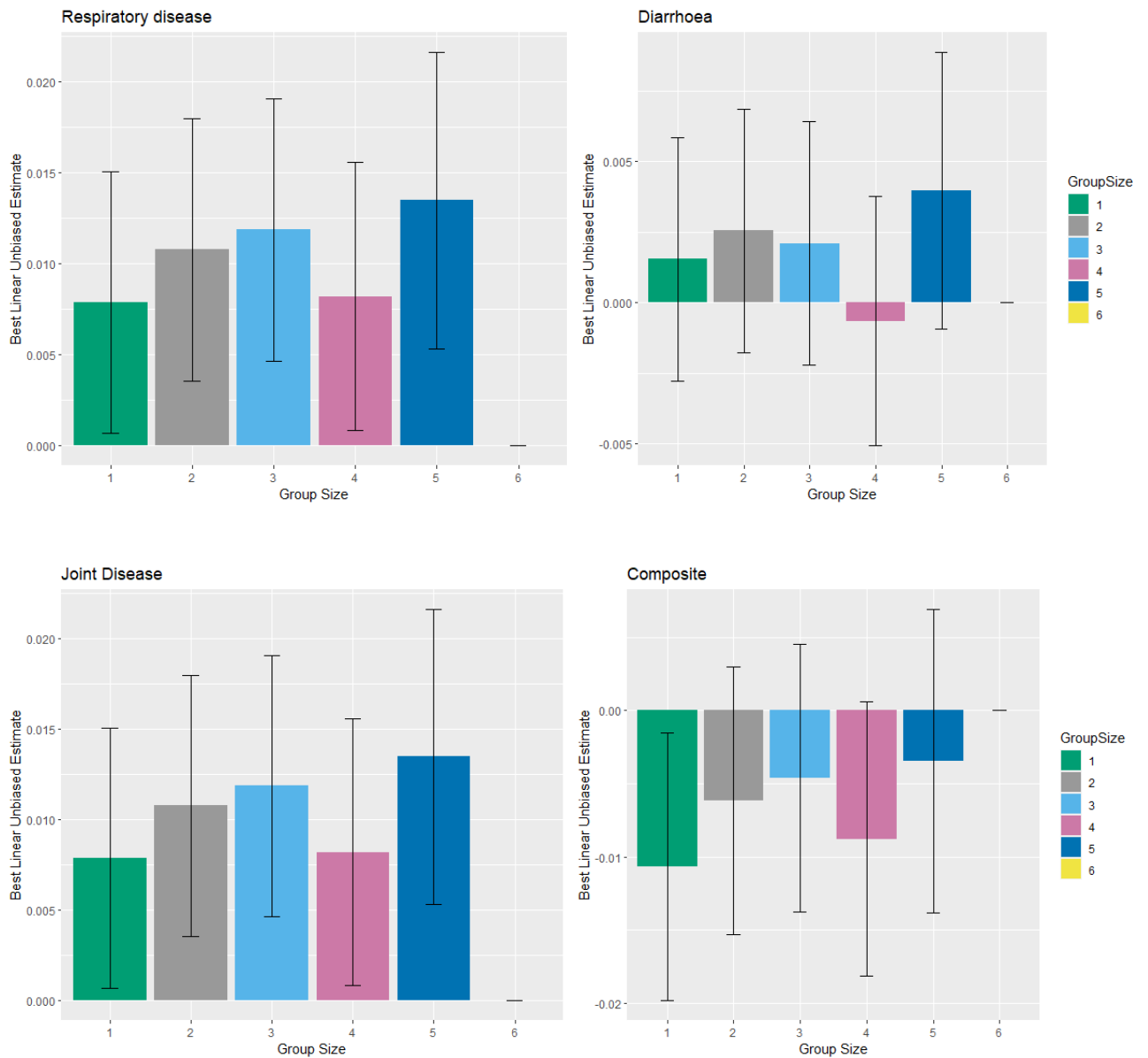


Figure 5: Fixed effect solutions for Group size on (a) respiratory (b) diarrhoea (c) joint disease (d) composite

The birth month-year had a significant effect on the calf diseases. There are also variations between years and tendency of seasonal variation especially for RD which is lower in summer and higher in winter. Calves born in months which are categorised as winter and autumn had a higher risk of being affected by the diseases compared to calves born in months which fall under summer and spring as shown in Figure 6. The lower risk for months in spring and summer indicate that calves are less likely to be affected by diseases due to warmer temperatures or

because they are spending time outdoors where they have abundant fresh air and more space. Standard errors for birth month-year solutions throughout the study years range from zero to RD (0.003), CD (0.002), and JD (0.001).

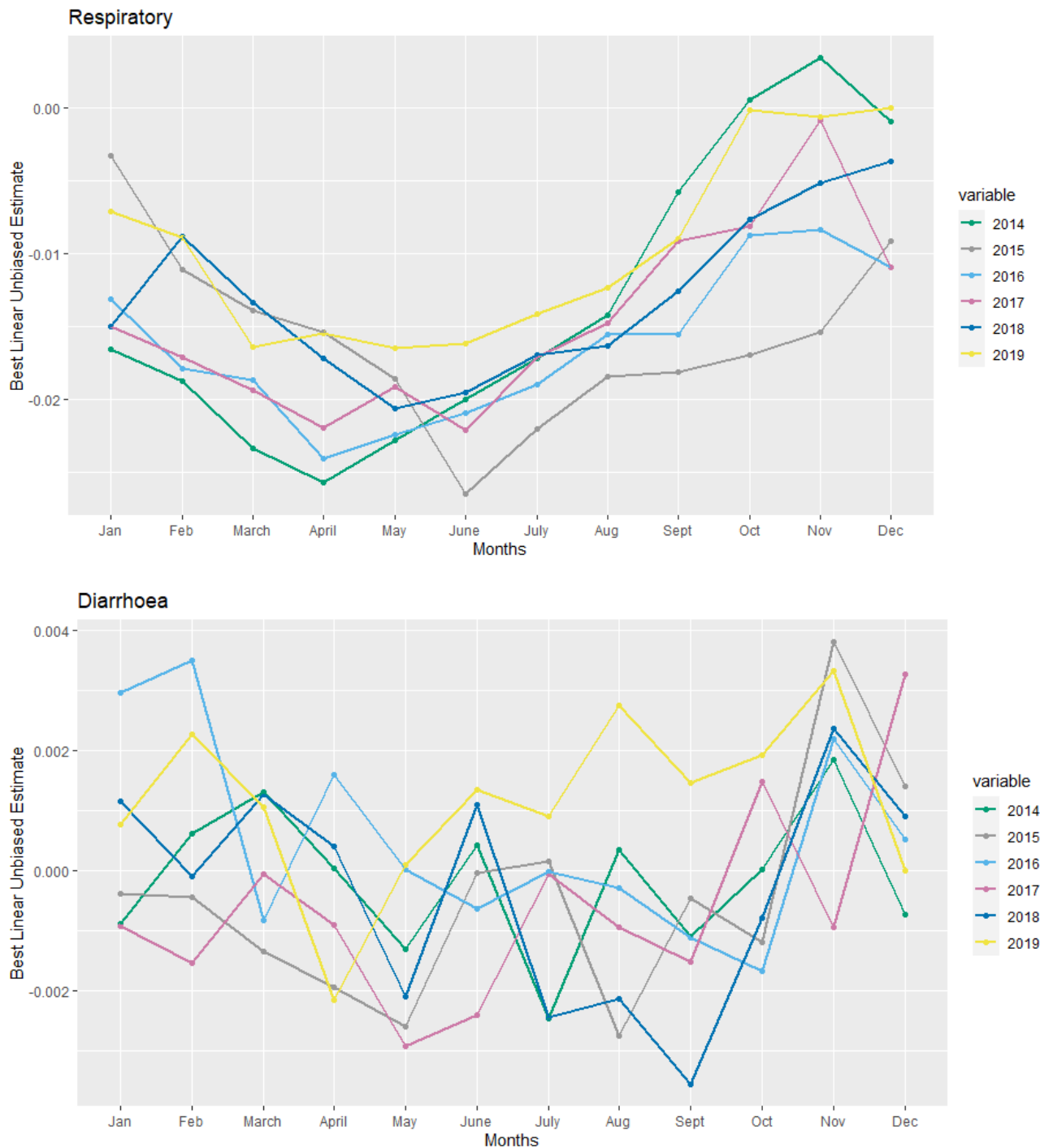


Figure 6a Fixed effect solutions for birth month-year effects for (i) respiratory (ii) diarrhoea

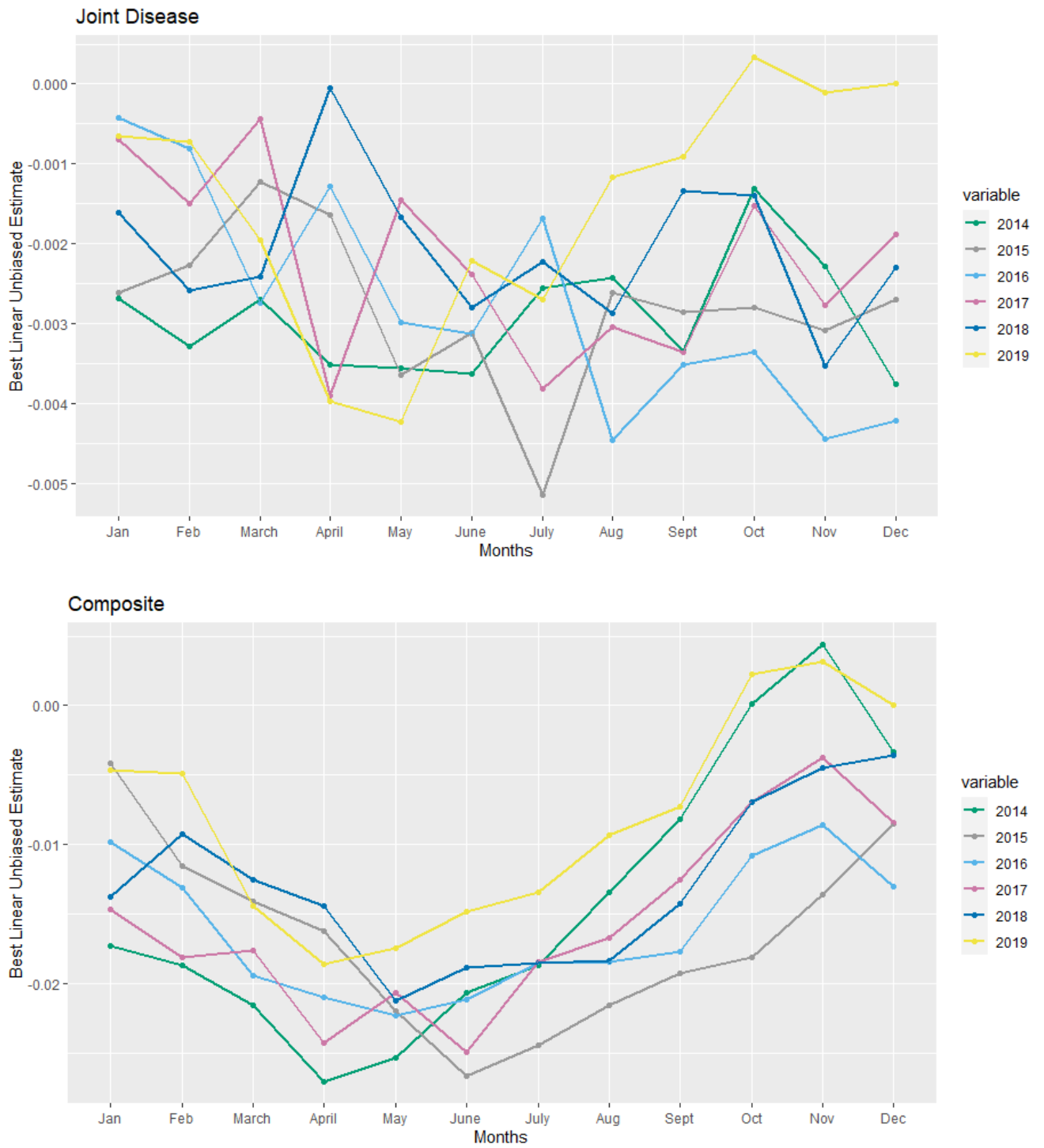


Figure 6b. Fixed effect solutions for birth month-year effects for (i) joint diseases (ii) composite

4.3 Estimated Breeding Values

The distribution of breeding values for the disease traits RD, CD, JD, and the composite are shown in the histogram plots Figure 7. The shape shows an approximate normal distribution curve for the three common calf disease traits and the composite trait. The breeding values for each disease's trait range from -0.031 to 0.07, -0.006 to 0.01, -0.009 to 0.03 and -0.03 ± 0.09 , for RD, CD, JD, and composite, respectively.

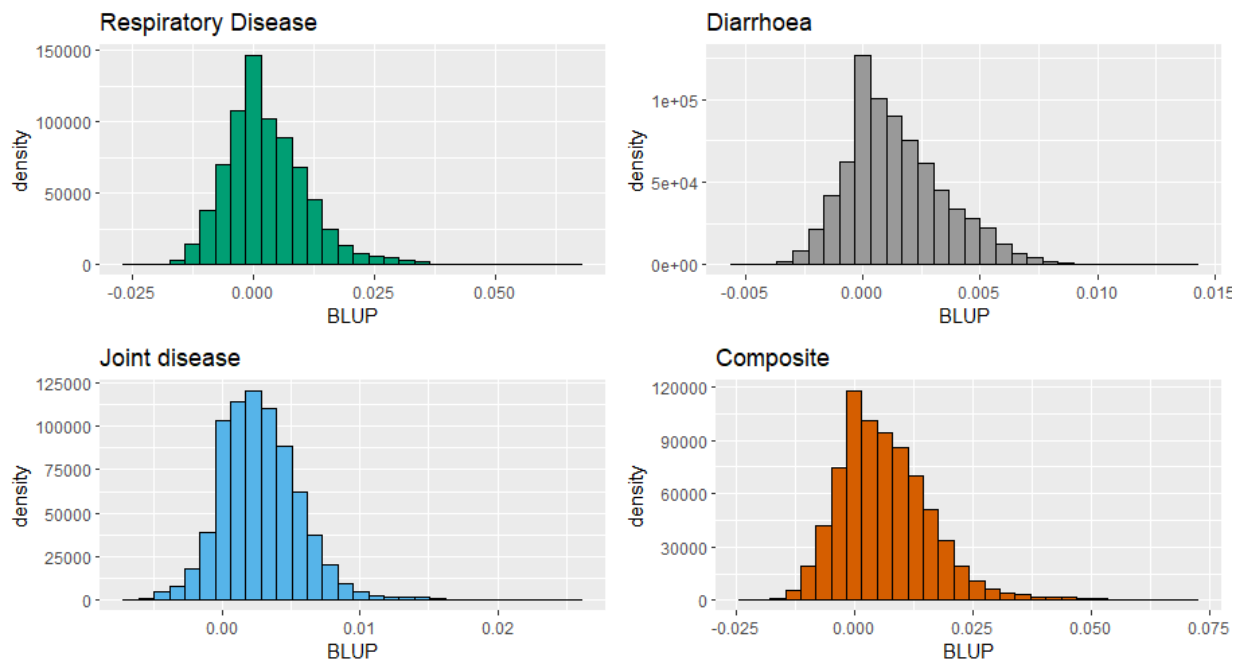


Figure 7. Distribution of BLUP breeding values for animals with records (a) respiratory (b) calf diarrhoea (c) joint disease (d) composite

4.4 Correlations between breeding values

Correlations between EBV for RD, CD and JD are presented in (Table 6). The correlations computed from EBV of sires with at least 200 progeny. These correlations can be used as an indication or approximation for genetic correlations. Respiratory diseases had a low positive correlation with diarrhoea (0.15) and joint diseases (0.29). Regarding JD and CD the correlation was -0.05. The correlations were significantly different from zero (p-value: 2.2×10^{-16}).

Table 6: Correlations among estimated breeding values (EBV) from sires with ≥ 200 progeny for calf disease

	Respiratory	Calf Diarrhoea
Calf Diarrhoea	0.15	
Joint diseases	0.29	-0.05

5. Discussion

This study is the first to report heritability for the three most common calf diseases in Norwegian Red calves. Norway has been known for breeding health traits for cows which are associated with low heritabilities and have been known to be difficult to incorporate in breeding programs. Estimating heritability for calf health is the first step considered when aiming to improve calf health traits.

Disease Incidences

The study showed that RD, CD and JD mean incidences in Norwegian Red were 3%, 1% and 1% respectively for calves before they reach the age of 180 days, and this is low as compared to other studies. In the United States of America (USA) (Urie et al., 2018) reported the incidence of RD to be 11.3% for pre-weaned calves and 5.9% for weaned calves. (Gonzalez-Peña et al., 2019) reported the incidence of RD from birth until 365 days of age to be 21%. RD incidence in the Norwegian Red herds is low as compared other countries as reported by (Heringstad et al., 2008) who observed a frequency of 0.7% and 3% as reported from this study. The increase in the frequency after the first study conducted in Norway in 2008 can be explained by the increase in calf health data reporting as time progressed or increase in diseases. Norwegian herds have small average herd sizes of 31 cows per herd, hence an important explanation to the low frequencies observed since RD is more frequent in larger herds.

However, environment factors such as climate, pathogens, nature of the data used can also explain the huge differences in the frequency of RD between studies (Heringstad et al., 2008).

Genetic studies of calf diarrhoea and joint diseases have not been conducted for the Norwegian Red calves hence an incidence of 1% is the first to be reported for these two traits and the frequency is low as compared to other studies. (Haagen et al., 2021) reported an incidence of 44.4%, this incidence has been higher against the digestive diseases incidence of 18.9% reported by (Urie et al., 2018) and (Gonzalez-Peña et al., 2019) who also reported an incidence of scours or diarrhoea to be 26.1% using producer recorded calf health data. The low incidences reported for Norway can be explained by small average herd sizes of 31 cows leading to the calves raised in smaller groups as compared to other herds in both the Nordic region and with other continents (Rajala-Schultz et al., 2021). The larger the calf herds the more susceptible to diseases due to increased direct contact between calves and faecal matter. The records used for this study are veterinary treatments hence they also include the more severe cases for the diseases.

Joint disease incidence has been reported for older animals in the Nordic region, there no reports on the incidences of the disease for calves. (Jalal et al., 2016) reported an average incidence of joint diseases of 2.25% based on farmer data. The JD mostly arises from primary infections from navel, wounds, and pathogenic bacteria. This explains the low frequency in this case 1% reported from this study as most farmers have mastered how to carry out navel dipping, dehorning, and providing clean environments for new-born calves. Once infection of these primary activities is ruled out, the probability of joint diseases becomes low. (Rao et al., 2020) reported an incidence of 8.35% for septic arthritis which is a form of JD in calves aged 20 to 155 days of age.

Group size

Larger group sizes had a tendency of increasing the risk of RD, CD and JD, however the group sizes reported in this study are considered small in most other studies carried out in other regions. Similar reports by (Godden & Knauer, 2021) state that large group sizes are associated with higher incidences of diseases. In Sweden, (Svensson & Liberg, 2006) reported that calves raised in groups of 12-18 calves had a higher incidence of respiratory disease than those raised in smaller groups. (Svensson et al., 2003) reported that calves raised in larger groups together had 2.8 times more risk of respiratory diseases. (Gulliksen et al., 2009) reported that large Norwegian dairy herds tend to have larger calf groups thereby increasing the risk for respiratory infection. (Abdelfattah et al., 2013) in the USA reported that a group size of 8 and below does not lead to increased health problems thus the small effect of smaller group size to diseases incidences as reported in this study. This supports the results of this study showing smaller group sizes having a smaller effect on diseases than larger groups.

The effect of group size on diarrhoea was not significant, but it showed that larger groups had an increasing tendency. Studies in Swedish dairy calves shows no significant difference in large and small group sizes on diarrhoea (Svensson & Liberg, 2006). Most calf diarrhoea infections are predisposed from increased contact with faecal matter and calves raised in larger groups are mostly susceptible to this condition (Curtis et al., 2016). Maunsell and Donovan, 2008) reported that rearing calves in smaller group sizes minimizes the risk for infection from carrier animals and contamination from the environment through faecal contact.

Group size affects calf health in two ways, firstly on the process of identifying or recording infected calves and lastly on how large groups have an increased risk of infection. Norway has smaller average herds of 31 throughout the country thus a greater number of calves housed between 1-10 calves, and with this indication 75% of respiratory infections were registered in

the smaller groups than larger groups which are not common in the Norwegian herds. (Conboy, 2021; Swartz et al., 2017) highlighted the problem of large group of calves in detecting diseases such as respiratory diseases as opposed to calves reared in small groups. Raising calves in large groups considers the welfare perspective raised, in addition group rearing has been adopted due to the increased automation in dairy farms. However, despite the advantages that come with group rearing studies have shown that detection of diseases has become more difficult (Svensson & Liberg, 2006). This also supports the pattern discovered in this study where large calf groups with 20 or more calves accounted for 2% of the respiratory infections registered in this study as compared to groups with less than 20 calves accounted for 98% of the infections. This can highlight that the small percentage registered from large calf groups could be because of infections that go unnoticed because of the difficulty in identifying infected calves due to large group rearing numbers. Diarrhoea and joint diseases presented the same pattern, the greater number of infections were reported in small group sizes than large group sizes. Smaller groups are associated with less direct contact and increased air volume thus the less risk of infection, however the group size effect does not act alone but it is highly connected to other management factors such as stocking density and resource availability which could be more important in influencing the risk of disease (Abuelo et al., 2019).

Birth month-year

The effect of birth month-year showed a significant effect on RD, CD and JD. Calves born in autumn (September, October, November) and winter season (December, January, February) showed an increased susceptibility to developing disease as compared to summer and spring months. The variation could be explained by temperature differences amongst the seasons with autumn and winter having low temperatures. When calves are born, they are more susceptible to cold stress and if calves are born in summer and spring the high temperatures will reduce the risk of cold stress (Uhrincat et al., 2022). Calves born in autumn are likely to have their

first 6 months of life in prolonged cold temperatures hence the increased susceptibility to develop respiratory, diarrhoea and joint diseases (Reiten et al., 2018). (Küçük Baykan & Özcan, 2019) also reported that birth season affects the incidences of diseases in Swiss and Simmental calves. Studies conducted by (Samolovac et al., 2019) also reported that a higher risk of respiratory diseases was in autumn and winter, for calf diarrhoea the probability to occur in autumn and winter was 3 times higher than in spring and summer months. A conducive environment for pathogens is created by wet and cold conditions thereby calves born in winter and autumn season are likely to be infected by respiratory, diarrhoea and joint diseases (Gulliksen, et al., 2009; Hordofa et al., 2021). (Gulliksen, et al., 2009) reported that cows calving in winter produce colostrum with lower immune quality than that produced in any other season, thereby predisposing the calves born to risk of infection hence the effect of birth-month-year to incidence of disease.

Gender

In this study the effect of gender on RD, CD and JD was not significant. This is in agreement with (Küçük Baykan & Özcan, 2019) who reported that sex of the calf had no significant effect on disease incidence. (Marcato et al., 2022) reported sex of the calf did not affect its health, no significant difference was found in terms of treatments between bull and heifer calves. However other studies reported sex linked differences in immune system of animals adding to a larger extent disease susceptibility of males against females (Baxter et al., 2012).

Heritability

The heritability for RD was 0.014(0.001) and it is smaller than the estimate of 0.05(0.018) reported by (Heringstad et al., 2008) using threshold model for Norwegian Red calves. In a case-controlled study in the USA (Neiberger et al., 2014) estimated a heritability of 0.13 and (McCorquodale et al., 2013) in Canada using a linear model estimated a heritability of 0.04 for

RD when recorded from birth until 90 days of age. (Gonzalez-Peña et al., 2019) found a heritability estimate of 0.04 from farmer recorded data of animals from birth up to 1 year of age and recently (Haagen et al., 2021) reported an estimate of 0.10 for respiratory disease using threshold models. However, a direct comparison of these heritabilities is difficult because of the different models used for estimation.

Calf diarrhoea had an estimated heritability of 0.002. This estimate is lower than a heritability of 0.075 for Holstein calves reported by (Haagen et al., 2021). (Gonzalez-Peña et al., 2019) using a threshold model estimated a heritability of diarrhoea for Holstein calves up to 50 days of age to be 0.045 and 0.084 for US Jerseys. (Mahmoud et al., 2017) reported a heritability of 0.06 for CD in German Holstein calves using a generalised linear model. Joint diseases had a heritability of 0.004, variance components estimate in literature were not found hence there was no similar findings to compare with in dairy calves. For diarrhoea and joint diseases herd-year effect accounted for the larger amount of the total variance, similar findings were reported by (Haagen et al., 2021) suggesting that herd management are likely to play a huge role in phenotypic variation.

The heritability estimates for binary traits calculated using linear models depends on the frequency. Therefore, the low heritability estimated for the calf diseases traits are to be expected considering the low frequencies. Differences in heritability estimates for the three calf health traits across studies can be explained by various reasons such as different rearing environments, differences in records used and lastly the definition used to develop traits. Veterinary or farmer reported health events tend to have lower estimates than heritability from studies coupled with clinical and genome analyses (Quick et al., 2020). These recent estimates reported in this study show that there is genetic difference in susceptibility of calves to the most common calfhoo diseases. (Berry et al., 2011) noted out that for low heritability traits if large progeny group sizes are used accurate estimates of genetic value are obtained and considering

the number of records used for the current study the genetic evaluations were reasonably accurate.

In this first analysis of calf diseases, a decision to analyse all traits using a linear animal model was made although a threshold liability model would have been theoretically more appropriate for the binary traits. Linear models are robust and often the model of choice for routine genetic evaluations and we therefore used this approach for initial genetic analyses of new traits, to explore their potential. In addition, the ability of linear models to analyse large amount of data and provision of direct values of heritability after analyses aided the decision in comparison to threshold models which results in a scale of heritability and can be difficult to interpret.

Correlation

The correlation between EBVs of RD and CD was 0.16, it is closer to a value of 0.13 reported by (Mahmoud et al., 2017) using linear model EBVs from German Holstein calves. (Mahmoud et al., 2017) research also reported on genetic correlations between RD and CD of 0.29 (0.09), however these cannot be directly compared to the results from this study. There was no literature about JD correlations with other calf diseases hence the correlation of 0.29 with RD is the first reported in Norwegian calves. The small positive correlations among the diseases could be explained by all infections being controlled partly by the same immune system thus having one disease influencing the other diseases positively. The negative 0.05 correlation between CD and JD could be attributed to the fact that one disease mainly affected the gastrointestinal and the other one affects the bones or joints, with the later one being a secondary infection prior to other primary causes such as injuries. Despite these low correlations from EBVs of sires, an anticipation that if genetic correlations are computed they can be higher is expected as reported by (Henderson et al., 2011; Mahmoud et al., 2017) that genetic correlations can be higher than correlations computed from EBV.

6. Conclusions

Health traits are known for their low heritability, this study showed the estimated heritability of respiratory diseases, calf diarrhoea and joint diseases ranging from 0.002 to 0.014 using linear animal model. Although heritability was low, all the diseases showed significant genetic variation. Correlation between EBVs for respiratory diarrhoea, and joint diseases was low but positive suggesting selection for one would result in a correlated response in the other. However, the frequency of calf diseases is low in the Norwegian Red population posing a challenge to improve them genetically. An alternative use of these results is to use them as indicators of calf health and welfare.

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