
Estimation of genetic parameters for young stock survival in beef x dairy crossbred calves

Master thesis - Agrobiology

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Title page

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Preface and acknowledgement

This master's thesis marks the end of my master's degree in Agrobiological – Animal health and welfare at the University of Aarhus. The thesis corresponds to 45 ECTS and consists of a literature review and a statistical analysis. This Master's thesis is a part of the project *Crossbred calves with a greater potential* funded by The Danish Cattle Levy Fund. The results are generated for future publication and implementation in the Nordic routine genetic evaluation for beef x dairy crossbred cattle. Data was provided by SEGES livestock innovation.

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Abstract

Young stock survival is an important trait as calf mortality leads to economic losses. Furthermore, dead calves are an animal welfare issue. The aim of this Master's thesis was to estimate genetic parameters for young stock survival, in order to evaluate if it is feasible to implement young stock survival in the Nordic routine genetic evaluation for beef x dairy crossbred calves. Data on 101,172 crossbred calves was provided by SEGES. Two traits were defined, young stock survival from 1-30 days and 31-200 days after birth. The traits were analyzed with a univariate animal model using the AI-REML algorithm in the DMU package. Results showed low but significant heritabilities (0.045-0.075) for both survival traits in line with previous studies. Breed combinations with Danish Blue cattle sires outperformed all other sire breeds. The lowest survival rates were found for breed combinations with Jersey dams or Blonde d'Aquitaine sires. Breeding values were calculated using DMU4 and sufficient genetic variation for young stock survival was found. Differences in breeding values ranged from -2.5 to 3.5 % and -5.4 to 4.7 % for survival from 1-30 days and 31-200 respectively. It is therefore feasible to implement young stock survival in the genetic evaluation for beef x dairy crossbred calves. This will increase the survival rate of the calves and hereby increase animal welfare and decrease economic loss for the veal producers.

List of abbreviations

Breed abbreviations

BAQ – Blonde d’Aquitaine

BLK – Danish Blue Cattle

HER – Hereford

HOL – Holstein dairy cattle

JER – Jersey dairy cattle

LIM – Limousine

RDC – Red dairy cattle

SIM – Simmental

XXX – Crossbred dairy cattle

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1 Introduction

Calf mortality is a substantial problem in cattle farming. Losing an animal in the rearing period causes economic losses, both in the form of lost revenue from the slaughterhouse, but also extra expenses for treatment and labour (Carlen et al., 2016). Østerås et al. (2007) calculated the annual total losses due to dairy calf mortality (including stillbirth) to be approximately € 70 million in the Scandinavian countries. Calf mortality is not only an economical issue, but also an animal welfare problem. As the public have become increasingly interested in animal welfare, it is essential that young stock survival should be improved as much as possible.

In Denmark it has been mandatory since 1998 to register all living cattle and record the date of birth, death, slaughter and transfers between herds. This gives nearly 20 years of reliable data on calf mortality. For Danish dairy cattle, the national average calf mortality in 2016 was 3.8 % within the first 30 days after birth and 7.3 % within the first 180 days (Raundal 2017). The average calf mortality is substantially larger for bull calves compared to heifer calves for all breeds. However, there is large variation between both herds and breeds (Østerås et al., 2007).

During the last decade it has become increasingly common in Denmark to inseminate dairy cows with semen from beef sires. When crossing dairy cattle with beef cattle, the meat production capacity of the calf is greatly increased, compared to a purebred dairy calf, which ensures a higher slaughter price for the farmer (Dal Zotto et al., 2009). From 2014 to 2015 the number of Danish dairy cows inseminated with beef semen nearly doubled from 67.740 in 2014 to 120.656 in 2015 (SEGES 2016). It is especially the beef breed Danish Blue Cattle that has become increasingly popular, respectively 67 % and 80 % of the inseminations on dairy cattle in 2014 and 2015 where sired by this breed.

In the Nordic countries, the beef breed sires used for crossbreeding with dairy cattle were initially selected based on their purebred breeding values. However, purebred beef bulls are selected to improve the beef breeds and not for crossbreeding (Fogh 2017). Therefore, a new index for beef sires used for crossbreeding with dairy cattle was developed by the Nordic Cattle Genetic Evaluation. The X-index, as it is called, correlates information from the sire's purebred index with progeny records from crossbred calves. The traits included are calving ease, liveability, EUROP form score and daily gain (Fogh 2016). This only accounts for stillbirth and mortality within the first 24 hours, not postnatal calf mortality.

There are many means of reducing calf mortality in terms of feeding and management, but these improvements are not permanent. By contrast improvements of the additive genotype of a calf is permanent, this is however only possible if genetic variation for the traits exists (Hansen et al., 2003). If there is no variation between individuals for a trait it is not possible to differentiate individuals from each other, which makes selection impossible. Several studies have investigated calf mortality and found genetic variation in both dairy (Hansen et al., 2003, Carlen et al., 2016,

Fuerst-Waltl and Sørensen 2010) and beef cattle (Cundiff et al., 1986), and therefore we expect that there is also genetic variation for calf mortality in cross bred calves.

For dairy cattle, a breeding value for young stock survival was included in the Nordic Total Merit index with economic weights in May 2016 (Carlen et al., 2016). Therefore, it could be relevant to develop a similar index for beef x dairy cross bred calves. This would increase both animal welfare and the revenue for the calf producer. Only the Nordic countries and the Netherlands have a young stock survival index for dairy cattle (Carlen et al., 2016, CRV 2014) and to our knowledge no countries have developed a young stock survival index for cross bred calves.

This Master's thesis is a part of the project *Crossbred calves with a greater potential* funded by the Danish Cattle Levy Fund. The aim of the thesis is to uncover the extent of calf mortality in beef x dairy crossbred calves and which risk factors influence the trait. This knowledge will be used to define a young stock survival trait and estimate the genetic parameters, in order to evaluate if it is feasible to implement young stock survival in the Danish X-index for beef sires used on dairy dams.

2 Background

This section will be used to uncover the current status of calf/young stock survival in dairy, beef and crossbred calves. Following this a short description of the most frequent causes of mortality and the associated risk factors will be presented. The genetic background of young stock survival will then be discussed, with focus on previously calculated genetic correlations and heritabilities. Finally, the basic theory behind cross breeding will briefly be introduced. This will establish background knowledge regarding young stock survival, and what genetic parameters previous research has found in order to evaluate if it is feasible to breed towards increased young stock survival in dairy x beef crossbred calves.

2.1 Calf/young stock mortality

Calf and young stock mortality is a large problem, not only with regards to animal welfare, but also due to economic and genetic losses for the farmer. Animal welfare has in later years become increasingly important for the consumers, and it is therefore very important to ensure that production animals have the best possible welfare, and mortality rates are low, to maintain the goodwill of the consumers (Carlen et al., 2016). If a dairy heifer dies, a replacement animal is lost which causes genetic loss due to reduced possibility of selection, and thereby less genetic gain (Fuerst-Waltl and Sørensen 2010). The genetic loss is very hard to quantify as it accumulates over generations (Henderson et al., 2011). When a bull calf dies, it is an economic loss, as income from slaughtering the animal cannot be obtained (Carlen et al., 2016). For both heifers and bull calves there is an economic loss from treatments and feeding days; the later the calf dies, the greater the loss. Østerås et al. (2007) calculated the annual total losses due to dairy calf mortality (including stillbirth) to be approximately € 70 million in the Scandinavian countries.

Carlen et al. (2016) estimated that the cost of a calf that dies within the first month of life is similar to that of a stillbirth (destruction €21 plus extra work 0.25 hours), but an additional cost of €5 is estimated for additional labour to prevent the death of the calf and rearing costs. The costs of a calf that dies after a month are the same plus an additional €10 in rearing costs (Carlen et al., 2016). For a calf that dies after 2 months and until 6 months for bull calves and 15 months for heifer calves, there is a similar cost of destruction plus extra work 0.5 hours and an extra rearing cost of €10 (Carlen et al., 2016)..

In Figure 1 the average calf mortality each month for calves born in Danish dairy herds from 2014 to 2016 is shown (Raundal 2017). There is a slight decrease in calf mortality during this period but with large seasonal variation. However, the goodness of fit (R^2) is very low, which means that the prediction of the trend line is not very accurate. In practise this means that there is no trend in the average calf mortality in Danish dairy herds.

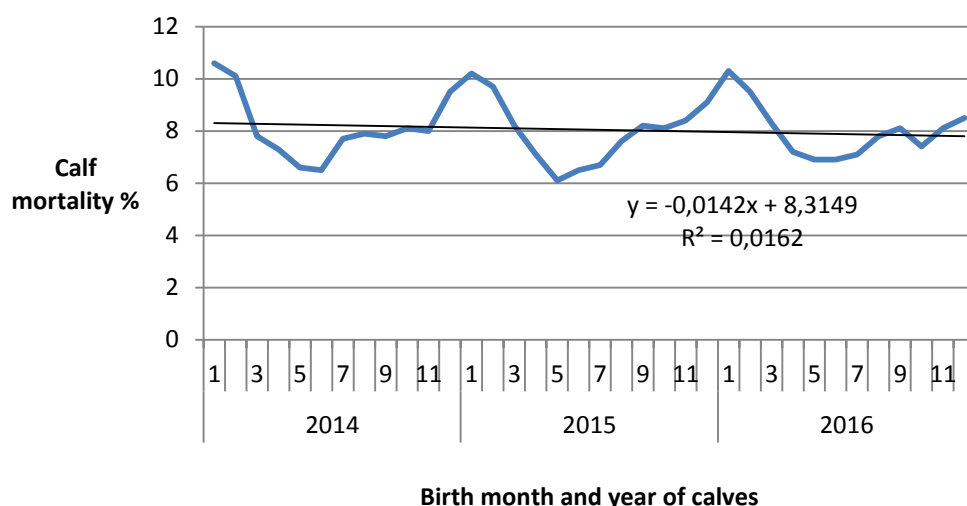


Figure 1- Average calf mortality from 1-30 days after birth in percent for calves born in Danish dairy herds from 2014-2016.

It has been hypothesized that breeding for decreased still birth (death within 24 hours after birth) and increased longevity in the Nordic Cattle Genetic Evaluation (NAV), has contributed to the animal's genetic ability to survive the rearing period (Pedersen et al., 2014). This is due to favourable genetic correlations between the traits. However, it is more efficient to breed directly towards a decreased mortality by including a young stock survival trait.

2.1.1 Breed differences

In dairy production heifer calves are most often kept as replacement animals on farm and bull calves are sold to veal producers (Carlen et al., 2016). For beef x dairy calves both heifers and bulls are commonly sold to a veal producer from 14 days and older. The mortality is to a large degree dependent on the management, and large variations in calf mortality are seen between farms and production systems (Østerås et al., 2007).

In Figure 2 the average Danish calf mortality (1-180 days after birth) from 1999-2016 is shown. Stillborn calves are not included in the averages. The main dairy breeds in Denmark, crossbred dairy cows and an average of all beef cattle are shown. Of the dairy breeds, Holstein calves have the lowest mortality rates and Jersey the highest. Newborn Jersey calves are known to have high mortality rates, which can be partially explained by the common practice of euthanizing young bull calves (Norberg et al., 2013). This has been an area of focus in recent years, therefore the mortality has decreased significantly, but it is still apparent that calf mortality is a greater problem in Jersey cattle compared to other dairy breeds (Norberg et al., 2013).

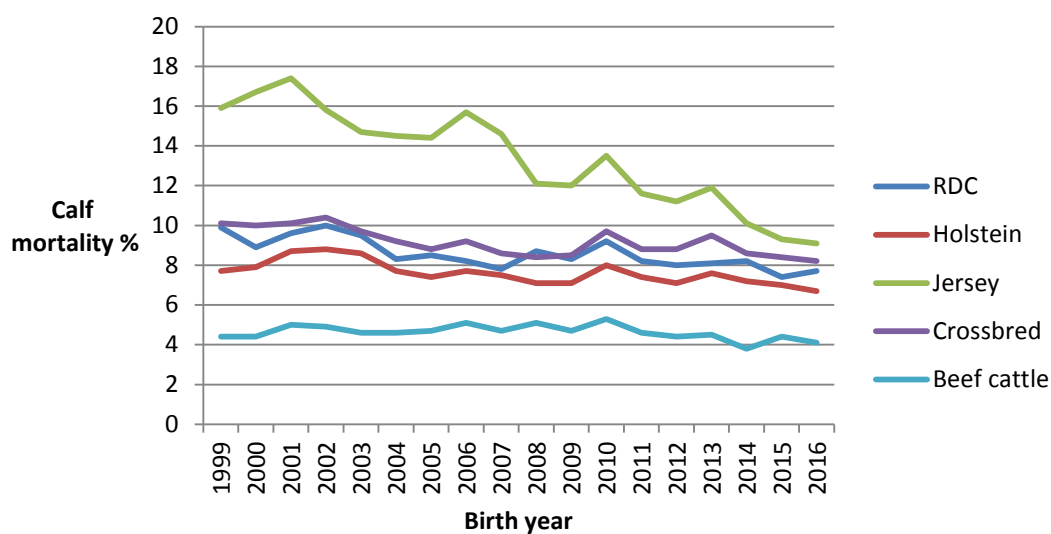


Figure 2 – Average calf mortality from 1-180 days after birth in percent, for calves born in Danish dairy herds, divided by breed.

Fuerst-Waltl and Sørensen (2010) investigated calf and heifer loss in Danish Holstein for animals born from 1998 until 2007. They used 5 different time periods day 1-30, day 31-180, day 181-365, day 366-until the day before first calving and finally day 1 until the day before first calving. They found mortality rates of 3.23, 2.66, 0.97, 1.92 and 9.37 % for the 5 periods respectively. Also in Holstein, for both heifer and bull calves, Hansen et al. (2003) found a mortality rate of 6.6 % within the first 180 days. Norberg et al. (2013) found an increased postnatal mortality rate in Danish Jersey heifer calves of 12.5 % within the first 180 days. van Pelt et al. (2012) reported a survival rate of 97.5 % from 15-180 days in dairy calves raised for veal production.

The average Danish calf mortality for beef cattle is lower than the dairy breeds. However, the calves are raised in different production systems. Calves born in dairy herds are removed from the dam within 12-24 hours after birth, whilst calves born in beef herds are usually kept with their mother until weaning. The average herd size for beef cattle is also lower than that of dairy cattle, which may influence overall calf mortality (SEGES 2016). Furthermore, beef cattle are often raised in extensive production systems whilst dairy cattle are raised under intensive production conditions. The average calf mortality for purebred beef cattle from 1-30 days was 3.6 %, 4.2 %, 4.6 % and 3.0 % for Simmental, Blonde d'Aquitaine, Charolais and Limousine respectively, and from 1-180 days average calf mortality was 5.3 %, 6.4 %, 6.6 % and 4.5 % (Raundal 2017). For beef cattle Østerås et al. (2007) reported a death rate of 3-4 % at birth and an additional 4-5 % from 1-180 days of life.

Crossbred dairy calves have been found to have a better survival rate than purebred calves. However, they tended to have more problems during birth and had a greater frequency of stillbirth (Sørensen 2007). In a Dutch study, van Pelt et al. (2012) found that crossbred dairy calves that expressed 100 % heterosis, had a 0.22 % and 0.61 % higher survival rate for day 3-14 and 15-180 respectively. Heins et al. (2012) found that only 2.6 % of the crossbred heifers did not survive

until the first test day for milking, compared to 8.7 % of the purebred Holstein heifers. Cundiff et al. (1986) conducted a study on 4,639 Hereford x Angus crossbred calves and found a calf survival rate of 91 % from birth to weaning. In white veal production for dairy, beef and Holstein x Belgium Blue calves Pardon et al. (2012) found a total mortality risk of 5.3 %. The study showed that the lowest mortality rates were found for the crossbred calves (3.5 %) followed by dairy (4.9 %) and the highest group were beef calves (7.5 %). This is in contrast to the national Danish average, which could be due to the fact that production in Denmark is based on rosé veal production and not white veal production as is the case for Pardon et al. (2012).

Besides breed variation in calf mortality, there is also a large effect of the sex of the calf. The average calf mortality from 1999-2016 from 1-180 days after birth for dairy calves was 9.9 % and 7.1 % for bull and heifer calves respectively (Raundal 2017). van Pelt et al. (2012) found that dairy heifer calves had a 0.38 and 0.62 % higher chance of survival from day 3-14 and day 15-180 respectively, compared to dairy bull calves. Erf et al. (1990) also observed a higher mortality rate of male compared to female calves during the first week of life in Brown Swiss cattle. Finally, Hansen et al. (2003) found a 2 % higher mortality rate for bull calves compared to heifers from 1-180 days after birth in Holstein dairy cattle. The same tendency is seen for beef cattle, though less pronounced, here the average mortality is 5.3 % and 4.0 % for bull and heifer calves respectively (Raundal 2017). As the genetic variation for calf mortality is small, the difference between studies is believed to arise from differences in management, climate and housing between the countries (Hansen et al., 2003).

It seems that dairy calves have a higher mortality compared to beef calves, and also that bull calves die more often than heifer calves. The low mortality of beef calves could also be an effect of a different production system than the dairy calves. Only a few studies have investigated calf mortality in beef x dairy crossbred calves, and they are conducted in different types of production systems. Therefore, it is difficult to conclude how they perform compared to purebred beef and dairy calves. To understand calf mortality more in depth, the following section will be used to investigate the different causes of calf mortality, and at which age the calves are most at risk.

2.2 Causes of calf mortality

Agerholm et al. (1993) investigated the causes for calf mortality in 65 Danish cattle herds, consisting of both dairy and beef breeds during a 1-year period. They found an average calf mortality rate of 7 % from 0 days to 6 months of age, which is slightly lower than the national average mortality. Of the dead calves 43 % died in connection with calving, 22 % due to abortion and 15 % died within the first week of life. Only 21 % of the total deaths occurred in the period from 1 week to 6 months after birth (Agerholm et al., 1993). There were large breed differences regarding the proportion of stillborn calves out of the dead calves, 40 %, 48 %, 25 % and 63 % for Holstein, RDM, Jersey and beef breeds respectively (Agerholm et al., 1993).

In concordance with Agerholm et al. (1993), Svensson et al. (2006) found in a Swedish study on 8,964 heifer calves born in 122 dairy herds from January 1998 to December 2000 that the risk of dying was highest during the first week after birth. In addition 3.1 % died within the first 90 days, 0.9% between 91 and 210 days and 2.2 % between 211 and first calving. Norberg et al. (2013) reported that mortality was highest in Jersey heifers in the first month after birth (7.8 %). Fuerst-Waltl and Sørensen (2010) also confirmed that the risk of calf mortality was highest during early stages of life.

Svensson et al. (2006) found that pneumonia was the most common cause of death (27 %) overall, but for calves that were less than 31 days old; enteritis was the most common cause. The probability of dying due to enteritis was highest during the second week of life (Svensson et al., 2006). In the study by Agerholm et al. (1993) it was found that at day 0 the majority of the dead calves were registered as stillbirths (81 %). From 1-7 days 78 % of the dead calves were registered as dead due to an infection, most commonly septicaemia (blood poisoning) and enteritis/diarrhoea. In the age group 1 to 4 weeks, 82 % of the calves died due to an infection and from 1 to 6 months all calves died of an infection, of which 46 % died of pneumonia (Agerholm et al., 1993). In the United States scours, diarrhea and other digestive problems were found to be responsible for 57 % of preweaned heifer deaths, followed by respiratory problems (23 %). For weaned heifers 47 % of the deaths were accounted for by respiratory diseases (US Department of Agriculture 2010). Bähler et al. (2012) found in a study of Swiss veal calves that the main cause of death was digestive disorders (52 %) followed by respiratory diseases (28 %), similar results were found under Flemish conditions by Pardon et al. (2014).

From the above it is clear that respiratory and digestive diseases are the main causes of calf mortality. In this thesis the mechanisms behind the diseases and methods of prevention will not be discussed. It seems that calves are most susceptible to disease in the first month of life, and that diarrhoea is the most prevalent cause of death in this period, whilst pneumonia is more prevalent in later periods. Thus, it is different parts of the calf's immune system that ensures its survival depending on how old it is (Hansen et al., 2003). This could indicate that time periods should be differentiated between, as the risk factors are not the same. In the following section different factors that influence calf mortality will be discussed briefly.

2.3 Risk factors that influence calf mortality

Calf mortality is a multifactorial problem, the management of the herd, the dam and the season all have an impact. As described in the previous section the first weeks after birth and the time around calving are the greatest risk periods.

2.3.1 Calving

The degree of calving difficulty did not significantly influence the risk of mortality in the study by Mccorquodale et al. (2013), but both Gulliksen et al. (2009) and Henderson et al. (2011) observed significant associations between calving difficulty and calf mortality. This may be due to negative

associations between calf size and calving ease, as heavier calves experience more dystocia (Sieber et al., 1989b). Henderson et al. (2011) found evidence that the effect of calving difficulty influences survival beyond the first 30 days of life and until maturity. Mccorquodale et al. (2013) also found that low body weight at 0 to 8 days of age, was associated with higher calf mortality. Calves that weighed ≤ 39 kg had an increased risk of death whilst calves that were ≥ 44 kg had a decreased risk. This is in contrast to Henderson et al. (2011), who found that there was an optimum birth weight. They found that both heavy and light calves had an increased risk of death, but calves that were between 38 to 41 kg had a decreased risk. Very light or very heavy weight at arrival, had a negative impact on calf mortality, and heifers were more likely to die with an increasing calving ease score (Henderson et al., 2011).

Another risk factor is twin births. Mccorquodale et al. (2013) found that there was a 1.14 times higher death risk for twins compared to single born calves, this was confirmed by Gulliksen et al. (2009) and Hansen et al. (2003) who similarly found a significantly higher postnatal mortality for all mortality traits for twin calves compared to single born calves.

2.3.2 Parity

Results regarding the impact of parity on calf mortality were ambiguous. Hansen et al. (2003) investigated if there was an effect of the parity of the dam on calf mortality in Holstein calves. They found that the genetic correlations between parities were very high (>0.93). This indicates that the parity of the dam does not have a large effect on calf mortality. Hansen et al., (2003) also found that the effect of repeated observation from the same dam was small. Similarly, Gulliksen et al. (2009) found that there was no effect of parity in Norwegian red cattle. In contrast Norberg et al. (2013) found that the risk of mortality increased with increasing parity of the dam in Jersey cattle. Finally, in a Dutch study by van Pelt et al. (2012), calf mortality was found to decrease with increasing parity number, reaching the lowest level at ninth parity and higher.

Regarding calving age, Hansen et al. (2009) found that there was a limited effect of age at first calving on calf mortality, with the exception of calves born by dams with a low calving age (23 months), which had a significantly higher mortality. Also, a low calving interval (<331 days) resulted in significantly increased calf mortality (day 1-180) compared to cows with a calving interval of 391-450 days (Hansen et al., 2009).

2.3.3 Management

Management varies greatly between herds and has a large impact on the survival of calves and young stock. Hansen et al. (2009) investigated the variance of herds, and found that management differences between sexes increased with the age of the calf. This difference is a consequence of the fact that bull calves are most often transferred to a veal producer to be reared for meat production, whilst the majority of heifer calves are kept on farm and are raised as replacement animals (Hansen et al., 2003). Furthermore, herds with low mortality in the first period (d 1-14) also had a lower mortality rate in the later periods (Hansen et al., 2003). Henderson et al. (2011)

found that calves with more than 2 disease treatments before weaning had a higher risk of mortality compared to calves without any incidence of disease. Therefore, good management and low disease incidence enables low calf mortality throughout the rearing period.

Godden et al. (2008) state that it is essential that the newly born calf receives an adequate amount of good quality colostrum shortly after birth to ensure a sufficient amount of immunoglobulins, which protect them against pathogens until their immune system is fully developed. Calves less than 5 weeks of age do not have an active immune system and therefore, colostral antibodies are the only source of immunoglobulins to protect calves from infectious diseases (Weaver et al., 2000). The level of immunoglobulins in the blood can be indirectly measured by the amount of serum total protein (STP). Henderson et al. (2011) found that calves with a STP concentration of <6.0 g/dL were more likely to die. These results were corroborated by McCorquodale et al. (2013), who found that calves with an STP <5.0 g/dL had a 2.4-time higher chance of dying than calves that had a concentration between 5.0 and 6.0 g/dL.

Gulliksen et al. (2009) and Lance et al. (1992) found that calf mortality increased with increasing herd size. Del Rio et al. (2007) also reported a higher mortality in herds with >1000 calvings a year compared to herds with <100. An explanation could be that cows are more closely monitored in small herds, but it could also be that the larger herds more accurately report calf mortality (Del Río et al., 2007). The average herd size has increased every year, so it is important to take initiatives that will counteract the potential increase in calf mortality that this might result in.

Many calves are transferred early in life, especially calves that are sold to veal producers. When a calf is transferred it is exposed to stress and an increased pressure of infections (Hansen et al., 2003). During the first month the calves are most susceptible to disease, and have the highest mortality risk. Hansen et al. (2003) investigated the effect of transfer on calf mortality, and found that there was a significant effect. Calves transferred at an age of 14-30 and 31-60 days of age, had a significantly higher frequency of mortality compared to non-transferred calves. Norberg et al. (2013) also found higher mortality rates for transferred Jersey heifer calves. Less than <1 % of the calves were transferred in this study, and of the transferred calves 16.5 and 44.4 % died between day 14-30 and day 31-180 respectively. Hansen et al. (2003) stated that if transfer of calves becomes more common, the importance of including postnatal mortality in a breeding programme would increase. This is due to the increased genetic variation for transferred calves.

2.3.4 Seasonal effect

McCorquodale et al. (2013) found in a Canadian study on 1,588 Holstein heifer calves, that there was a significant effect of season of birth on calf mortality. Heifer calves born from October to January were 1.9 times more likely to die than calves born from July to October. Calves born in the spring had a lower risk of mortality compared to all other seasons (McCorquodale et al., 2013). It should be noted that the study was only conducted for a single year and therefore, it could be an expression of that specific year and not a general tendency.

Hansen et al. (2003) found that for Danish Holstein heifers no trend could be found for late mortality, but for day 1-14, for both heifer and bulls, mortality was lower for calves born in the summer and higher for those born in winter. Similarly, Norberg et al. (2013) found that Danish Jersey calves born in the winter period had a higher risk of dying compared to those born in the spring and summer. Svensson et al. (2011) and Gulliksen et al. (2009) both found that the risk of calf mortality increased during the colder months in Southern Sweden and Norway respectively, but the effect was not significant in the Swedish experiment. The season also has an impact on the risk associated with transfer, Hansen et al. (2003) found that transferred calves had the highest mortality when moved during the autumn.

An easy calving of a single calf, a sufficient body weight and an adequate amount of good quality colostrum is imperative to reduce calf mortality. Furthermore, transfer, possibly the parity of the dam and the season are factors that have an effect on calf mortality. There are many more factors that also have an impact, here only the most important have been described. It is essential to know what influences calf mortality in order to include the most important factors in the model used to estimate the genetic parameters.

2.4 Genetic background – Young stock survival

In this section the genetic background for young stock survival will be investigated. In the previous sections the extent of calf and young stock mortality has been uncovered, followed by the different causes of mortality. This unveiled that calf and young stock mortality is a substantial problem, not only in Danish herds, but globally. In the following section, relevant research in genetic parameters such as heritabilities and correlations will be investigated. This will substantiate whether it is feasible to breed for young stock survival, and in what range the genetic parameters could be expected.

2.4.1 Heritabilities

Not many studies have investigated the genetic background of young stock survival and those that have mostly evaluated dairy calves. In Table 1 below, studies that have estimated genetic parameters for young stock survival have been listed. Common for all studies is that the heritability estimates are very low (<0.10), but in general they were higher for beef cattle compared to dairy cattle. The low heritabilities are mainly due to a low frequency of calf mortality, large environmental variation and different causes of death (Pedersen et al., 2014). Norberg et al. (2013), found higher heritabilities for Jersey heifer calves compared to Holstein heifers. This could be explained by the higher frequency of prepubertal mortality in Jersey cattle, as binary traits depend on the frequency (Norberg et al., 2013). Maternal heritabilities were estimated to be very small and insignificant, which indicates that the dam's role in calf mortality is genetically less important than the direct effect (Norberg et al., 2013).

Table 1-Overview of studies that have investigated young stock survival, the estimated heritabilities and what breed the estimates were calculated on. Heritabilities on the underlying scale (U) or the observed scale (O).

Study	Time period	Heritability	Breed
(Erf et al., 1990)	Both sexes Day 1-7	Linear model 0.04 (U)	Brown swiss
(Fuerst-Waltl and Sørensen 2010)	Heifer calves Day 1-30 Day 1-day before first calving	Threshold model 0.017 (U) 0.042 (U)	Holstein
(Hansen et al., 2003)	Bull calves Day 1-14 Day 1-180 Heifers Day 1-14 Day 1-180	Linear model 0.015 (U) 0.030 (U) 0.024 (U) 0.025 (U)	Holstein
(McGuirk et al., 1998b)	Both sexes Dead within 48 hours	Threshold model 0.08 (U)	Beef cattle sires on dairy dams
(Norberg et al., 2013)	Heifer calves Day 1-14 Day 1-180	Linear model 0.097 (U) 0.077 (U)	Jersey
(van Pelt et al., 2012a)	Both sexes Day 3-14 Veal calves Day 15-180 Heifer calves Day 3-365	Linear model 0.006 (O) 0.005 (O) 0.011 (O)	Heifer calves Both sexes Veal calves

2.4.2 Genetic correlations

Significant differences in survival rate between sexes have previously been found. This is also reflected in the genetic correlations found by Buch (2012), the genetic correlations within time period and between sex are fairly high (0.9-0.95), but they are low to moderate between time periods within sex (0.4-0.75). This supports the notion that there are different genes that control the survival of calves and young stock over time, but the genes are the same for both heifer and bull calves (Pedersen et al., 2014). The genetic correlation between sexes was found to be very high (>0.91) by Hansen et al. (2003) for all time periods, and was not significantly different from 1. Therefore, it seems feasible to use the same trait for both bull and heifer calves.

Other studies have also investigated calf mortality and found that early life and late life mortality is probably two different traits (Hansen et al., 2003, Buch 2012, Fuerst-Waltl and Sørensen 2010). Fuerst-Waltl and Sørensen (2010) found a genetic correlation of 0.92 between the period from 31-180 days and 181-365 days. Hansen et al. (2003) reported genetic correlations of 0.73 between

day 1-14 and day 15-60, 0.54 between day 25-60 and 61-180 and low correlations of 0.34 between day 1-14 and day 61-180. Buch (2012) found a genetic correlation of 0.44 between survival from 1-30 days and day 31 until first calving for heifer calves and 0.51 between 1-30 days and 31-183 days for bull calves.

Henderson et al. (2011) found a genetic correlation of 0.58 between survival from arrival date to weaning and from weaning to exit from the heifer facility. van Pelt et al. (2012) found a high genetic correlation (0.85) between the two traits day 3-14 (all calves) and day 3-365 (heifer calves), but a moderate genetic correlation (0.66) between day 3-365 (heifer calves) and day 15-180 (veal calves). All the studies were conducted on Holstein calves (Fuerst-Waltl and Sørensen (2010) and Henderson et al. (2011) only had heifer calves in their investigation). In Jersey heifer calves Norberg et al. (2013) found a genetic correlation of 0.88 between mortality from day 1 to 14 and day 1 and 180, as the first 14 days are the same in both time periods, it is expected that there is a high correlation. These results substantiate that there is a genetic difference between early life mortality and mortality later in the rearing period and it could potentially be different groups of genes that are responsible.

The correlations between the breeding value from day 1 until first calving and the Nordic index for stillbirth at first calving (direct) was 0.09 (Fuerst-Waltl and Sørensen 2010). One of the reasons for the low correlations may be the fact that the index for stillbirth includes both heifer and bull calves. For the Nordic longevity index, low correlations were found for the first period (day 1-30), whilst moderate correlations were found for the whole period (day 1 until first calving) (Fuerst-Waltl and Sørensen 2010).

In an American study by Henderson et al. (2011), associations between young stock survival and routinely evaluated traits in Canada and the United States were investigated. Survival from weaning until calving was positively associated with several feet and leg traits, such as feet and leg composite and rear leg-rear view, whilst survival from birth until weaning was associated with bone quality. The importance of desirable feet and leg conformation is well recognized, and many countries include measures of feet and legs in their selection programmes as a predictor of longevity (Miglior et al., 2005).

Furthermore, bulls with high genetic evaluations for linear body size conformation traits sired calves that were less likely to survive to maturity than calves sired by bulls with a low genetic value for these traits. This could be due to the connection between large calves and decreased calving ease (Henderson et al., 2011). Another interesting association was that bulls that sire daughters with low somatic cell count also sire calves that are more likely to survive maturity. This suggests that general immune function has an impact on survival. As could be expected Henderson et al. (2011) also found positive associations with herd survival traits, which could indicate that there is some general disease resistance factor with a genetic component (Heringstad et al., 2005).

Finally, a positive association between both direct and maternal calf survival with calf survival in the first 24 hours from the Canadian evaluation was established (Henderson et al., 2011). Calves sired by bulls whose offspring are more likely to survive during the first 24 hours, are also more likely to survive to maturity. Likewise, dams sired by bulls whose offspring are more likely to survive to maturity, also get calves that are more likely to survive (Henderson et al., 2011).

2.4.3 Index for young stock survival in dairy cattle

In May 2016, young stock survival was included in the Danish breeding value estimation for dairy cattle (Carlen et al., 2016). Previously calf and young stock survival were only accounted for during the first 24 hours after birth and in cow longevity. These traits do not account for survival during the rearing period (Carlen et al., 2016). Therefore, an index specifically regarding survival in the rearing period was developed.

The index is divided into 4 separate sub-indexes - each sex is divided into two different rearing periods. For both heifers and bulls the first period is from day two after calving until one month of age, the second period differs between the sexes, as heifers are mostly used as replacement animals, and bull calves are fattened for slaughter. Therefore, the second period runs from 2 to 15 months for heifers and 2 to 6 months for bull calves (Carlen et al., 2016). Another reason for splitting the rearing period into two separate time periods is that the calves are typically moved at this age. Some heifers are sent to specialized heifer units, whilst bull calves are sent to a fattening herd (Carlen et al., 2016).

In the Netherlands they have also developed a breeding value for calf survival. The index is developed to improve the survival rate of replacement heifers for dairy cattle (van Pelt et al., 2012). They have defined three different traits, of which two are used as predictor traits for the main trait that is included in the breeding goal. The trait included in the breeding goal is survival from day 3-365 for replacement heifers. The first predictor trait is calf survival from day 3-14 for all calves, both heifers and bulls and the second is veal calf survival from day 15-180 (van Pelt et al., 2012).

2.4.4 Index for young stock survival in beef cattle

Traditionally, the focus in beef breeding programmes is easy calvings of live calves, and high average daily gain and a good meat production to sustain a high slaughter price. Little attention has been shown to calf mortality even though mortality before slaughter reduces income and adds significantly to costs (Goyache et al., 2003). It has previously been found that most reported heritabilities in beef cattle are at least 2-fold those found in dairy cattle (Koots et al., 1994). The higher genetic variability in beef cattle thus suggests that young stock survival could be implemented in beef cattle breeding programmes. Goyache et al. (2003) found low heritabilities for all survival traits despite being analysed as either calf or dam traits. However, they found that the genetic variability for calf survival traits justified the inclusion in beef cattle breeding objectives, especially for the time around calving (Goyache et al., 2003).

As for dairy cattle, not many countries have developed an index for young stock survival in beef cattle. The Danish routine evaluation for beef cattle includes an index for stillbirth, survival the first 24 hours and survival until 200 days. However, the index weights on survival are quite low compared to the production traits (Fogh 2005).

2.4.5 Genetic trend

Carlen et al. (2016) did not find a genetic trend for young stock survival when they implemented the index in the Nordic routine genetic evaluation. Similarly, Norberg et al. (2013) found no deterioration in genetic trend from 1985-2005 for Danish Jersey heifer calves. Fuerst-Waltl and Sørensen (2010) found a significant but small positive trend for day 1 to 30 after birth, but no clear trend for survival from day 1 until first calving. In the Netherlands van Pelt et al. (2012) also found a neutral genetic trend when they investigated young stock survival.

This indicates that there is no development either positive or negative in young stock survival. Presumably, this is due to a long tradition in the Nordic countries to breed towards more live-born calves and increased cow longevity, which has indirectly prevented a decrease in young stock survival (Carlen et al., 2016). There is also an aspect of natural selection in calf mortality traits, as those that die will not have any offspring, therefore the 'bad' genes are not inherited. However, the natural selection for calf mortality is apparently not strong enough to improve the trait, possibly due to negative correlations to other traits.

Despite low heritabilities of young stock survival it has been included in both the Nordic and Dutch routine genetic evaluation for dairy cattle and in the Danish evaluation for beef cattle. Therefore, it seems feasible to introduce such a trait in the evaluation for beef x dairy crossbred calves. In the following section the theory of crossbreeding will be discussed in order to understand the mechanisms behind and what effects it has. This will be related to beef x dairy crossbreeding and the X-index which is used to select the best beef bulls for breeding with dairy cows.

2.5 Crossbreeding

Crossbreeding has become increasingly popular in the last decade, especially the use of beef semen on dairy cattle (Sørensen et al., 2008). In many other production systems such as crops, poultry and pigs crossbreeding has been used for many years with great success (Sørensen et al., 2008). When an animal is cross bred it means that it has parents from two different breeds or lines. There are two main reasons for crossbreeding in livestock. Firstly, breed complementarity between breeds can be utilized to generate offspring with increased economic ability caused by new combinations of additive genetic components. Secondly, crosses between pure breeds and lines express heterosis (Sørensen et al., 2008).

2.5.1 Heterosis

Heterosis can be described as a measure of the degree that the offspring exceeds the average performance of the parents; the magnitude depends on the genetic distance between the parental lines (Ducrocq and Wiggans 2014). The increased performance is due to changes in non-

additive genetic effects of dominance and epistasis (Sørensen et al., 2008). In the first cross individual (F_1) 100 % heterosis is expressed, while in later generations heterosis will be expressed to varying degree depending on the breed combinations. Heterosis or hybrid vigour is the opposite of inbreeding depression and increases fitness lost by inbreeding. Heterosis is like inbreeding depression, most pronounced for traits related to fitness (Mäki-Tanila 2007, Kristensen and Sørensen 2005). The increased fitness is due to changes in non-additive genetic effects from dominance and epistasis. Heterosis effects tend to be greater for functional traits, which have a lower heritability compared to production traits (Sørensen et al., 2008).

When a specific line or breed develops, selection drives it in a different direction than other breeds. This results in a dispersion of gene frequencies between breeds. If the two breeds that are crossed do not differ in gene frequency then there will be no heterosis effects, in contrast, the larger the deviation in gene frequencies, the further the breeds are apart, the more heterosis will be expressed. In general, animals with more heterozygous loci have a higher fitness level compared to animals with more homozygous loci (Sørensen et al., 2008). A result of pure breeding is often an increased degree of homozygosity due to selection and genetic drift. When animals are cross bred the probability that genes are homozygous within loci is much lower, because the genes at a locus originate from different breeds. The more distinct differences that exist in alleles and allele frequencies between the two parental breeds, the more heterozygosity will be expressed (Sørensen et al., 2008). Mäki-Tanila (2007) state that in general heterosis increases with increased genetic distance between and inbreeding in the parental breeds. The greater the probability that two genes within a locus originate from different breeds, the more heterosis is obtained.

The observed heterosis is a sum of the dominance effects (often positive) and the epistatic effects (often negative) of which the dominance effects usually constitute the greatest proportion by far. Dominance effects are caused by gene interaction within loci, whilst epistasis is caused by gene interactions between loci (Falconer et al., 1996). A dominance effect is when one allele is dominant over another (recessive allele) and therefore has a greater effect. Heterosis due to dominance effects is fully expressed in the F_1 generation as all gene pairs consist of a gene from each parental line, however if there are dominance effects that contradict each other, they cancel each other out, and no heterosis is seen for those genes. If the F_1 animals mate, and produce a second cross line (F_2) only half of the heterosis will be expressed (Sørensen et al., 2008). Epistatic single gene interactions are the most important, but also interactions between gene pairs may have an influence. An epistatic effect is when expression of genes on one locus depends on alleles at another locus. Co-adapted positive gene complexes accumulate both under natural and artificial selection. These favourable gene complexes established in the parental

Locus (loci) – The position of a gene on a chromosome

Allele – The DNA sequence located at a given locus

breeds may be lost if animals are cross bred, this is called recombination loss (Falconer et al., 1996).

The degree of heterosis expressed depends on the effective population size of the parental breeds. The effective population size of a breed is an expression of the level of inbreeding within the breed. It is calculated from the rate of inbreeding per generation which is calculated by multiplying the annual rate of inbreeding with the generation interval (Sørensen et al., 2005). The average co-ancestry of animals in a population forecasts the average coefficient of inbreeding in the next generation (Falconer et al., 1996). As both dairy and beef cattle have a small effective population size, and fairly high rate of inbreeding, presumably there is a high degree of homozygosity within the breeds. When crossing a beef breed with a dairy breed it would therefore be expected that a large degree of heterosis would be expressed, both due to the fact that the breeds are genetically distant to each other, but also because both have a small effective population size and a relatively high rate of inbreeding, this should lead to a high level of heterozygosity in the F_1 offspring. Basic theory states that the greatest heterosis estimates are found for survival traits (Sørensen et al., 2008). This could indicate that crossbreeding would increase young stock survival.

Besides heterosis, crossbreeding can be used to exploit breed complementarity. In this way favourable attributes from two or more breeds that are genetically different from each other but have complementary qualities can be utilised. If a specific trait is of interest, then a breed that has a superior genetic level for that trait compared to the original breed should be selected. In dairy cross breeding there are two different reasons for crossbreeding. Firstly, superior production animals from two different dairy cattle breeds of the same genetic level can be produced by utilising the heterosis in F_1 crosses. Secondly, breed complementarity can be utilised by crossing dairy cattle with beef cattle, this ensures offspring with superior meat production compared to a purebred dairy calf (Dal Zotto et al., 2009).

2.5.2 Beef x dairy crossbreeding

In most European countries over 50 % of beef production is from pure dairy or dual purpose breeds, either from cull cows, bull calves or surplus replacement heifers (Kinghorn et al., 2014). Earlier, beef production traits were considered in dairy and dual purpose breeds. However, this is no longer the case for the majority of dairy breeds which has led to a deterioration of these traits (Kinghorn et al., 2014). The reason for this is that there are unfavourable correlations between milk and meat production traits (Pirchner 1986). Therefore, it has become increasingly popular to produce beef x dairy crossbred calves that have increased merit for meat production compared to purebred dairy calves (Kinghorn et al., 2014). It is important that the beef sires selected for crossbreeding combine good growth and carcass characteristics with acceptable calving ease.

Crossing a dairy breed with a beef breed utilises the breed complementarity and the calf becomes an intermediate between the two breeds. The result is an improved meat production compared to

purebred dairy calves, and thereby the farmer can obtain a higher price for the calf (Dal Zotto et al., 2009). Wolfová et al. (2007) confirmed in their study on crossbred Holstein x Charolais animals, that the carcasses of beef x dairy crosses were significantly more valuable than carcasses from purebred animals. In an Italian study by Dal Zotto et al. (2009) it was calculated that the increased value of Limousine sired crossbred calves compared to purebred calves was nearly \$125, whilst for Belgium Blue sired crossbred calves it was \$288.

Kinghorn et al. (2014) evaluated the use of beef breeds for cross breeding. They found that the French breeds (Charolais and Limousine) are popular due to their high growth rates and high lean meat rate, whilst the British beef breeds (Hereford and Angus) are more popular due to the relatively low incidence in calving difficulties. Both in Denmark and the United Kingdom Belgium Blue (in Denmark Danish Blue) are responsible for a large percentage of the inseminations in Dairy cattle, despite only have a small number of purebred cattle (Kinghorn et al., 2014, SEGES 2016). This is due to their ability to produce calves with good conformation at acceptable levels of calving ease when used on dairy cows (Kinghorn et al., 2014).

In a British study of beef sires used for crossing with dairy cows, means were predicted for the average calf mortality within the first 48 hours after birth (McGuirk et al., 1998a). Simmental and Belgium Blue had the lowest mortality rates of 4.82 % and 4.33 % respectively. The highest mortality rates were found for Charolais and Blonde d'Aquitaine of 7.89 % and 7.43 % respectively, whilst Limousine were intermediate at 6.57 % (McGuirk et al., 1998a).

2.5.3 X-index for beef bulls used on dairy cattle

In Denmark an index named the X-index, which describes the breeding value of a beef bull used on a dairy cow, has been developed (Fogh 2016). This index is used solely for terminal sires, and has a different breeding objective compared to a purebred index. The X-index is expressed as DKK per calf and is split into two separate indices: One for the dairy producer and one for the veal producer. The X- dairy producer index includes the additional monetary gain from birth until slaughter of the calf from the respective bull and for the X-veal producer it is an expression of the additional gain from slaughter of the calf from the respective bull (Fogh 2016).

There are 4 sub-indicies that have been included in the X-index: Daily gain, EUROP form score, calf vitality and calving ease. The X-dairy producer includes all 4 sub-indicies, whilst the X- veal producer only includes daily gain and conformation score (Fogh 2016). All the sub-indicies have a mean of 100 and a standard deviation of 10. Before a bull gets a published X-index it has to have at least 100 offspring which are born in at least 10 different herds. Furthermore, they have to have 25 slaughtered offspring that have been raised in at least 10 different herds. As of now only bulls of the breeds Simmental, Charolais, Aberdeen Angus, Blonde d'Aquitaine, Limousine and Danish Blue Cattle receive published indexes, as it is a requirement for publication that the breed must have data on all sub-indicies from minimum 10 bulls in the database (Fogh 2016).

Correlations between the purebred index and the X-index have been calculated. There is a large degree of uncertainty regarding the results as the number of bulls that fulfil the publication criteria is very low (Fogh 2017). The general tendencies are that the correlations between the functional traits are moderate to purebred birth indices, whilst the indices for daily gain and classification are higher (Fogh 2017). This indicates that the purebred index for slaughter traits is highly correlated with the slaughter traits in the X-index, which means that they describe the same traits, whilst the functional traits included in the purebred index are not precisely the same for the crossbred calves. There is however a large variation in correlations between breeds. A reason for the large variation and relatively low correlations is that it is not exactly the same traits that are compared to each other (Fogh 2017). Another reason is that the purebred indices have a low reliability as some of the beef breeds have a very low number of purebred calves.

The X-index, as it is constructed now, aims to increase the calving ease and ensure that the calf survives the first 24 hours. Other than calving traits the only other traits regard the meat production and slaughter qualities (Fogh 2016). This means that there is no index that ensures that the calves survive the rearing period. If the calf survives the first 24 hours after calving, it still must survive for at least 8 months until it can be slaughtered and the veal producer can receive the profit from the calf. It is essential to ensure that as many calves as possible survive until they are ready for slaughter to maximise profit for the veal producer.

The background section has unveiled that calf mortality is a substantial problem for both beef, dairy and crossbred calves. In the first month the calves are most vulnerable and often die from an infection or diarrhoea, whilst after this period it is most often pneumonia that is the reason of death. Many factors influence young stock survival, calving, the dam, management and season are just some of the factors that have an impact. Several studies have found heritabilities for young stock survival, however they are all low. Despite this there is enough genetic variation to make it feasible to breed for increased young stock survival. Crossbreed beef x dairy calves express 100 % heterosis and due to breed complementarity calves have better meat production than purebred dairy calves. Including young stock survival in the X-index seems natural as it would increase animal welfare and economic gain for the farmers. In order to include a new trait in the X-index the genetic parameters must be calculated, how this is done and the data used for this purpose will be presented in the following section.

3 Materials and methods

In the materials and methods section the editing of data and the model that will be used to calculate the genetic parameters for young stock survival will be presented. Legislation introduced in 1998 required Danish farmers to supply all living cattle with a unique identification number, and to record date of birth, death, slaughter and transfers between herds. This makes it possible to follow all cattle from birth to death (or export). All these records and other information regarding Danish cattle are kept in the Danish Central Cattle Database (Hansen et al., 2003). In the database

information regarding pedigrees, production results, diseases, inseminations, death, transfer and dates of the events were available. Records from all beef x dairy crossbred calves born from 2000-2016 were extracted from the Danish cattle database and provided by SEGES in a preliminary dataset.

3.1 Data editing

The data provided contained beef x dairy crossbred calves born from 2000 and onwards in milk delivering herds. Both heifer and bull calves were included. The provider deleted data on calves if they were from multiple births, had unknown sex, unknown parents or if the dam was not from a dairy breed. All further editing of data has been conducted in SAS (SAS Institute 1990) and is shown in table 2.

Table 2 - Data editing steps, the number of deleted animals and total number of animals that fulfil the requirements.

Editing	Deleted calves	Total
Preliminary dataset		145,214
Deletion of stillborn calves	6,489	138,725
Deletion of dam breeds SRB and NRF	12	138,713
Deletion of PIE, HER, and ANG	5,107	133,606
Deletion of calves born after June 2016	17,876	115,730
Deletion of herds with <5 animals in the dataset	10,051	105,679
Deletion of animals slaughtered within the first 200 days	112	105,567
Deletion of exported animals	4,395	101,172

Stillborn calves (dead within the first 24 hours) have been deleted from the dataset, as they are accounted for in the calving traits. Calves that were recorded as dead after 24 hours, but did not have a recording for the date of death were denoted as having died 4 days after birth. Animals out of the two dam breeds Finnish Ayrshire (FAY) and Norwegian Red Cattle (NRF) were also deleted, as there were very few individuals. The same was the case for the sire breeds Piemontese (PIE), Hereford (HER) and Angus (ANG). Only calves from sires of the most used beef breeds have been included in this analysis: Simmental (SIM), Blonde d'Aquitaine (BAQ), Charolais (CHA), Limousine (LIM) and Danish Blue cattle (BLK). On the dam side, there were 3 pure dam breeds: Holstein (HOL), Jersey (JER) and Red Dairy Cattle (RDC) additionally crossbred dams (XXX) that were no more than 12.5 % beef cattle breed were also included.

To ensure that all the calves in the dataset had a fair chance of surviving the time period from 31 - 200 days, all calves born after June 2016 were deleted. In order to avoid any bias, all animals that were slaughtered, exported or sold within 200 days after birth were also deleted. Finally, all herds that had less than 5 animals in the dataset were deleted.

3.2 Descriptive statistics

The SAS programme was used for all preliminary data analysis (SAS Institute 1990). The proc GLM and proc FREQ commands were used to calculate the means and frequencies of the final data set. The average survival rates and calving ease scores for all groups were calculated and will be presented in the results section. Calving ease is scored on a scale from 1 to 4, where 1 is an easy calving without help and 4 is a difficult calving with veterinarian assistance.

The proc FREQ command in SAS were used to calculate the frequencies of birth year, number of calves for each dam and sire breed, number of sires for each sire breed and the distribution of sire breed for each dam breed and finally, the week of death for all dead calves. Figure 3 illustrates the distribution of calves for each birth year in the edited data. From 2000 to 2012 the number of calves born per year was fairly stable and did not exceed 5,000. After 2012 there was a large increase and in 2015 over 20,000 beef x dairy crossbred calves were born.

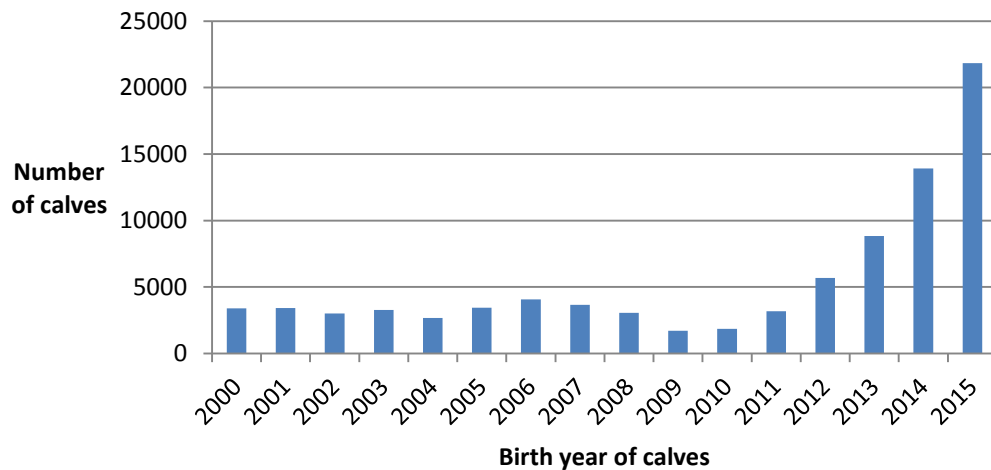


Figure 3 – The distribution of calves in the data set by birth year from 2000-2015

In table 3 the number of calves per sire and dam breed is presented. A large majority of the calves were sired by BLK. The two sire breeds with the least offspring were BAQ and CHA. With regards to the dam breeds the majority of calves had a HOL dam and least had a RDC dam.

Table 3 – Number of offspring (N) and percentage of total offspring (%) in the dataset for sire and dam breeds (January 2000-July 2016)

Sire breed	N	%	Dam breed	N	%
SIM	12,421	12.3 %	RDC	8,305	8.2 %
BAQ	3,893	3.8 %	HOL	61,441	60.7 %
CHA	3,608	3.6 %	JER	17,200	17.0 %
LIM	20,325	20.1 %	XXX	14,226	14.1 %
BLK	60,925	60.2 %			

Table 4 – Number of sires for each sire breed and the average number of offspring

Sire breed	Number of sires	Average number of offspring
SIM	133	93
BAQ	40	97
CHA	43	84
LIM	72	282
BLK	116	525
Total	404	250

In Table 4 the number of sires and the average number of offspring for each sire breed is shown. The number of sires ranges from 40 (BAQ) to 133 (SIM). The average number of offspring also varies greatly from 84 (CHA) to 525 (BLK).

Table 5 – Distribution of sire breeds for each dam breed

Sire breed	Dam breed			
	RDC	HOL	JER	XXX
SIM	14 %	11 %	5 %	19 %
BAQ	4 %	4 %	2 %	6 %
CHA	4 %	3 %	5 %	5 %
LIM	23 %	17 %	23 %	26 %
BLK	55 %	65 %	67 %	45 %

Table 5 shows the distribution of sire breeds for each dam breed. It is evident that there are large differences between the dam breeds. Approximately two thirds of all JER and HOL dams are inseminated with BLK, compared to only 55 and 45 % of the RDC and XXX dams. The use of BAQ and CHA is relatively low for all four dam breeds, whilst SIM and LIM are used more frequently.

The time of death was calculated as the death date minus the birth date. Figure 4 shows the week of death for the dead calves. A large proportion of the calves died within the first weeks after birth. From week 4 after birth and onwards the mortality rates are not as high and decrease slowly. Of the calves that did not survive from 1-200 days after birth, 17 % died within the first week and 48 % within the first 4 weeks. Only 5 % of the calves died in the last 4 weeks.

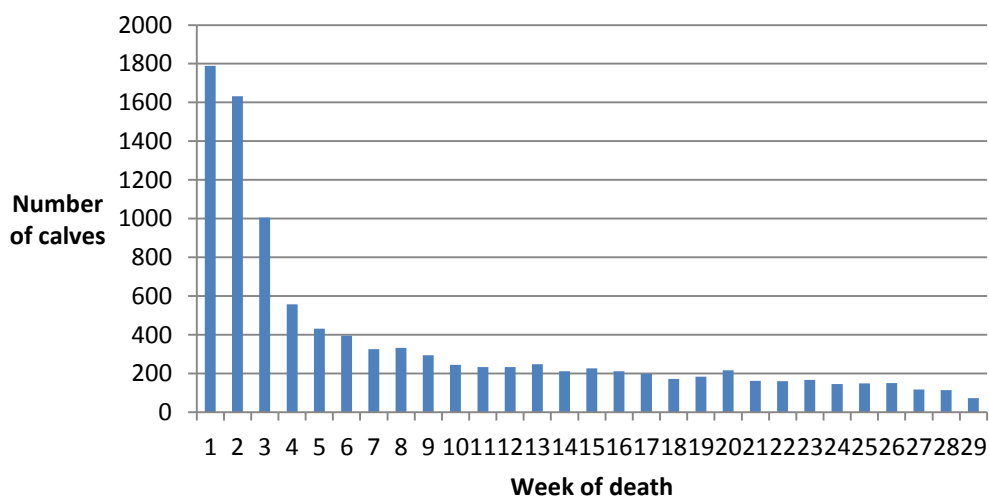


Figure 4 – The week of death for the calves that died from 1-200 days after birth

3.3 Traits of interest

Young stock survival is a binary or “all or none” trait. Either the calf is dead or alive (0 or 1) in a given time period, and therefore it is a categorical variable. It is assumed, that different genes control the survival in different periods as described in the background. Therefore, early and late mortality in the rearing period should be defined as two separate traits. Also most calves are moved at around 1 month of age from the dairy herd to a fattening unit, by splitting the trait into two different time periods the herd effects can be accounted for more precisely in the model. Furthermore, the X-index is split into an index for the dairy producer and one for the veal producer therefore; it would make sense to make the time period at the dairy producer one trait, whilst the time period at the veal producer should be another trait.

This led to the definition of two traits: Young stock survival from 1-30 days (period 1) and from 31-200 days (period 2). Calves that died in the given time period were denoted with a 0, whilst surviving calves were denoted 1. If the animal did not survive period 1, then it did not have the opportunity to survive period 2, and received a missing value for this time period. Bull and heifer calves are treated equally in this paper as it is expected that all beef x dairy crossbred calves are fattened for slaughter, in contrast to purebred dairy calves where the heifers are used as replacement animals, and therefore have a longer rearing period. A third trait; young stock survival in the whole period (1-200 days) was used to calculate correlations and evaluate the other traits.

3.4 Estimation of genetic parameters

The genetic parameters quantify the rate of genetic change that is obtainable and are required for the estimation of genetic merit. The heritability describes the variation that is of genetic origin, whilst correlations among traits describe how change in one trait can affect others. When multiple traits are evaluated co-variances indicate to what degree the information from one trait influences the others. For this project the genetic parameters of interest are: Heritabilities, additive genetic, residual and phenotypic standard deviations and correlations. To estimate the genetic parameters a model that describes the trait of interest must be constructed.

As young stock survival is not only affected by the genetic merit of the sire but also the dam, an animal model was chosen. The advantage of this is that all known relationship information is included in contrast to a sire model. In an animal model, a random effect for the additive genetic merit of each animal is included, both for animals with records and animals with parents only. Another advantage is that the additive genetic variance is estimated as the variance of the animals' additive genetic merit (Mrode 2014).

The animal model is based on a mixed linear model which allows the inclusion of both fixed effects, random animal effects and random residual effects. The linear model is constructed as follows:

$$y = Xb + Zu + e$$

Where:

y = vector of observations

b = vector of fixed effects

u = vector of random animal effects

e = vector of random residual effects

X and *Z* = incidence matrices

Fixed effects are constant across individuals whilst random effects vary. Random effects are commonly used when the variable has many levels with relatively little data at each level that is unevenly sampled. The residual effect is an estimate of the unobservable statistical error.

All phenotypic observations on an animal are determined by environmental and genetic factors, which can be defined by:

$$\text{Phenotypic observation} = \text{environmental effects} + \text{genetic effects} + \text{residual effects}$$

Or

$$y_{ij} = \mu_i + g_i + e_{ij}$$

This relationship is also reflected in the variances:

$$\text{Phenotypic variance} = \text{Additive genetic variance} + \text{residual variance}$$

Or

$$\sigma_P^2 = \sigma_A^2 + \sigma_E^2$$

The relationship between the variances is based on the assumption that there is no covariance between the additive genetic and the environmental effects: $cov(A, E) = 0$. This assumption is commonly used in prediction of breeding values (Mrode 2014).

When calculating heritabilities, the amount of genetic variance that can be explained by the phenotypic variance in the population is estimated. It is therefore derived from the additive genetic variance and the phenotypic variance (Falconer et al., 1996).

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

Because herd x year was included in the model as random effect, the intraherd heritability was used as it expresses the proportion of phenotypic variance that can be explained by additive genetic differences between animals within herd (Van Hulzen et al., 2009). It is calculated as follows:

$$h^2 = \frac{\sigma_A^2}{(\sigma_A^2 + \sigma_E^2)}$$

As young stock survival is a binary trait (0, 1), the heritability depends on the frequency of the trait. In order to express the heritability independently of the frequency, the heritability on the observed scale is transformed to the underlying scale, which gives a more accurate estimate of the true heritability. The transformation is done by using the approximate formula proposed in Dempster and Lerner (1950):

$$h_{pa}^2 = \frac{\bar{z}^2 h_x^2}{\bar{p}\bar{q}}$$

Where:

h_{pa}^2 = the heritability on the underlying scale

$\bar{z}^2$ = the height of the normal distribution curve at the threshold

h_x^2 = the heritability on the observed scale

$\bar{p}\bar{q}$ = the liability

In the following section, the traits that were analysed and the variables that were included in the model will be described.

3.5 Statistical analysis

The programme DMU, specifically the DMUAI module, has been used to analyse the data. DMUAI can be used for estimation of (co)variance components using Average Information Restricted Maximum Likelihood (AI-REML) (Madsen, Jensen 2008). This package includes procedures to do “multivariate analysis by restricted maximum likelihood based on a derivate-free approach”. This enables DMU to solve very complex models in animal breeding such as estimation of genetic parameters and breeding values.

3.5.1 Single trait model

A univariate model was used on a single trait of interest to estimate the fixed effects, heritability and the additive genetic, residual, and phenotypic standard deviation.

The model used for young stock survival from day 1-30 is as follows:

$$Y_{ijklmn} = YM_i + H_j + S_k + BC_l + P_m + a_c + a_h + e_{ijklmn}$$

Where:

Y_{ijklmn} = Binary variable dead or alive at 1 – 30 days

YM_i = Fixed effect of year * month of birth

H_j = Fixed effect of birth herd

S_k = Fixed effect of sex

BC_l = Fixed effect of breed combination

P_m = Fixed effect of parity of the dam

a_c = Random effect of calf

a_h = Random effect of birth herd * year

e_{ijklmn} = Random residual

The model for young stock survival from day 31-200 is as follows:

$$Y_{ijklmn} = YM_i + H_j + S_k + BC_l + P_m + T_n + a_c + a_h + e_{ijklmn}$$

Where:

Y_{ijklmn} = Binary variable dead or alive at 31 – 200 days

YM_i = Fixed effect of year * month of birth

H_j = Fixed effect of slaughter herd

S_k = Fixed effect of sex

BC_l = Fixed effect of breed combination

P_m = Fixed effect of parity of the dam

T_n = Fixed effect of transfer

a_c = Random effect of calf

a_h = Random effect of slaughter herd * year

e_{ijklmn} = Random residual

3.5.2 Multi trait model

When several traits are of interest a multivariate model can be used. The multi trait model can estimate the effects of multiple variables simultaneously and find the genetic and phenotypic correlations. The multi trait model was used to find correlations between young stock survival in both time periods, and with other traits.

$$\begin{bmatrix} y_{1-30 \text{ days}} \\ y_{31-200 \text{ days}} \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where X_1 and X_2 are design matrices that relate the fixed effects b_1 and b_2 to the records $y_{1-30 \text{ days}}$ and $y_{31-200 \text{ days}}$. The design matrices Z_1 and Z_2 relate the random animal effects u_1 and u_2 to the records. Finally, e_1 and e_2 are random residuals. The fixed effects included in the multi trait model are identical to those for the single trait model.

3.5.3 Variables included in the model

Fixed effects

A seasonal effect of year and month of birth was included in the model to take seasonal and annual fluctuations into account. For young stock survival from 1-30 days after birth an effect of the herd the calf was born in was included in the model, whilst for survival from 31-200 days the herd that the calf was registered in the longest period of time within the first 200 days was included in the model. This takes into account any management practises and environmental factors that might affect young stock survival.

The breed combinations were made by merging the dam and sire breeds, generating 20 different breed combinations. This corrects for all breed differences, both from the dam and sire breeds. The parity of the dam was also included in the model. As few cows were older than fourth parity all dams in their fifth or later parity were pooled together.

A large majority of beef x dairy calves are transferred to a fattening unit early in life. Therefore, a transfer variable was defined as transferred (1) or not transferred (0) within 200 days. No matter how many times the calf had been transferred, it was denoted 1. Only transfers from the dairy herd to the veal producer were included in the transfer variable. All transfers to livestock markets, slaughter houses or destruction were disregarded. It is not legal to transfer calves before they are at least 14 days old therefore the majority of calves are transferred between 2-4 weeks after birth. Hence, transfer was only included in the model for young stock survival from 31-200 days, as the effect of the transfer is not expressed until after the transfer.

Random effects

A random effect of the individual and herd x year was also included in the model. The random effect of herd x year was included as there are few individuals in many of the herds each year. All herds with less than 5 animals each year were deleted, and animals from 2000-2005 and 2005-2010 were pooled in one group as the number of observations was low. From 2010-2016 the number of observations was larger, therefore, all years are represented separately.

3.6 Breeding value estimation

Breeding values for the traits of interest were calculated using DMU4. Breeding values were estimated by best linear unbiased prediction (BLUP). The BLUP approach uses mixed model equations, which can be constructed and solved relatively easily. The solutions include estimates of fixed effects corrected for all other factors and estimated breeding values (EBVs) for every individual in the pedigree. The EBV of an individual is a function of the EBVs of the parents, its progeny and own records (Mrode 2014).

When calculating breeding values for sires used for crossbreeding, it is desirable to compare them across breed. When a fixed effect of the breed combination is included, this is not possible, as the

breed effects are accounted for. To account for the pedigree, but not correct for the sire breed effects, phantom parent groups were included as a random effect in the estimation together with a fixed effect of dam breed. This allows dam breed differences to be accounted for, whilst the bulls are ranked independently of breed.

Phantom parent groups

An animal with one or two unknown parents can be assigned so-called phantom parents. Phantom parents are assumed to be unrelated, non-inbred and to have a single descendant, they are not themselves of interest, but facilitate modelling and computations (Westell et al., 1988). When assigning unknown parents to genetic groups, the strategy should be to reflect the average genetic level of the unknown parents, and form sub-populations (Pollak, Quaas 1983). By doing this, the assumption that all base animals belong to a single population is avoided.

The pedigrees of the genetic groups have been traced back 5 generations for the sires and 2 generation for the dams. If a sire or dam does not exist in the traced pedigree file it was set as missing. All the missing parents were defined as phantom parents based on the animals breed and birth year. 25 phantom parent groups were constructed with a sufficient number of animals in each. As not all phantom parent groups are large due to some small breeds, they were included as random effects.

4 Results

The result section will give an overview of the findings in this thesis. Firstly, a section of group means will give an overview of the average survival rates. The phenotypic and genetic trends will be used to detect the development of young stock survival. Finally, the estimated genetic parameters and breeding values will be presented.

4.1 Group means

Overall survival rates independent of breed combination were 94.8, 94.5 and 89.6 % for young stock survival from 1-30, 31-200 and 1-200 days after birth respectively. The average survival rates for all dam breeds are presented in Table 6. JER had the lowest average survival rate from 1-200 days whilst HOL, RDC and XXX were almost equal. In the first time period 1-30 days JER had by far the lowest survival rate, approximately 2.5 % less than all other dam breeds despite having the lowest average calving ease score. In the second time period from 31-200 days the dam breeds were more equal.

Table 6 – The average young stock survival for 1-30, 31-200 and 1-200 days from birth and average calving ease for dams by breed. Number of calves included in parenthesis.

Dam breed	Survival 1-30 days	Survival 31-200 days	Survival 1-200 days	Calving ease
RDC	95.8% (8,298)	94.0% (7,952)	90.4% (8,267)	1.21 (7,579)
HOL	95.6% (61,407)	94.7% (58,697)	91.0% (61,095)	1.32 (54,846)
JER	92.0% (17,187)	94.1% (15,815)	89.3% (16,674)	1.18 (15,637)
XXX	95.6% (14,215)	94.5% (13,591)	91.0% (14,112)	1.25 (11,643)

With regards to the sire breeds the average survival rates are shown in Table 7. BAQ and LIM calves had the lowest survival rate from 1-200 days, whilst BLK had the highest. In the early period (1-30 days) LIM sired calves had the lowest survival rate and SIM the highest. From 31-200 days BAQ were inferior to all breeds and BLK were superior. With regards to calving ease the average score was the highest for SIM and lowest for BLK.

Table 7 - The average young stock survival for 1-30, 31-200 and 1-200 days from birth and average calving ease for sire by breed. Number of calves included in parenthesis.

Sire breed	Survival 1-30 days	Survival 31-200 days	Survival 1-200 days	Calving ease
SIM	95.6% (12,414)	94.7% (11,864)	91.1% (12,341)	1.38 (9,892)
BAQ	93.9% (3,891)	91.4% (3,655)	86.7% (3,856)	1.29 (3,644)
CHA	95.1% (3,604)	94.0% (3,426)	90.4% (3,561)	1.31 (3,174)
LIM	93.5% (20,298)	92.5% (18,976)	87.7% (20,013)	1.29 (17,380)
BLK	95.5% (60,900)	95.4% (58,134)	91.8% (60,377)	1.25 (55,615)

Table 8 shows the distribution of calves for the different breed combinations and the average survival rates and calving ease scores. For all dam breeds the most frequent combination was with BLK. All other combinations except HOL x LIM constituted less than 10 % of the total number of observations. The most superior breed combination for young stock survival from 31-200 days was XXX x SIM and the poorest combination was JER x BAQ. For survival from 1-30 days all dam breeds except XXX had the highest survival rates when inseminated with BLK, this is also the case in the second time period (31-200 days). BLK combinations were also superior with regards to calving ease for all dam breeds.

The lowest survival rates differed more between dam breeds. For RDC and JER the poorest combinations were with BAQ in both the first and second period. In HOL the LIM sire breed had the lowest survival rate in the first period, whilst in the second period and overall it was BAQ. The XXX dams combined with CHA and LIM in the first period and BAQ in the second period and overall had the lowest survival rates. The lowest average calving ease score was obtained by RDC x BLK and highest by HOL x SIM. No significant differences were found between dam breeds within sire breed except for BAQ x RDC and BAQ x HOL crossbred calves.

Table 8 – Average young stock survival for 1-30, 31-200 and 1-200 days from birth and average calving ease for all breed combinations. Number of observations in parenthesis.

Dam breed	Sire breed	%	Survival 1-30 days	Survival 31-200 days	Survival 1-200 days	Calving ease
RDC	SIM	1.2 %	95.7 % (1,173)	94.7 % (1,122)	90.6 % (1,173)	1.31 (1,035)
RDC	BAQ	0.4 %	93.2 % (365)	87.4 % (340)	82.5 % (360)	1.17 (341)
RDC	CHA	0.3 %	95.6 % (294)	92.5 % (281)	89.0 % (292)	1.23 (280)
RDC	LIM	2.0 %	95.3 % (2,072)	93.3 % (1,975)	89.3 % (2,064)	1.27 (1,774)
RDC	BLK	4.3 %	96.4 % (4,394)	94.8 % (4,234)	91.6 % (4,378)	1.16 (4,149)
HOL	SIM	7.1 %	95.5 % (7,140)	95.1 % (6,818)	91.2 % (7,113)	1.41 (5,924)
HOL	BAQ	2.5 %	94.5 % (2,568)	91.9 % (2,428)	87.3 % (2,556)	1.33 (2,398)
HOL	CHA	1.8 %	95.9 % (1,796)	94.4 % (1,722)	91.6 % (1,776)	1.37 (1,592)
HOL	LIM	10.4 %	94.4 % (10,482)	92.4 % (9,897)	87.8 % (10,421)	1.35 (9,104)
HOL	BLK	39.0%	96.0 % (39,421)	95.4 % (37,832)	92.0 % (39,229)	1.30 (35,828)
JER	SIM	0.9 %	91.6 % (934)	91.5 % (856)	86.2 % (908)	1.26 (727)
JER	BAQ	0.3 %	85.2 % (264)	90.7 % (225)	82.3 % (248)	1.24 (235)
JER	CHA	0.8 %	93.2 % (828)	92.4 % (772)	87.9 % (811)	1.29 (719)
JER	LIM	4.1 %	88.9 % (4,099)	92.1 % (3,645)	85.8 % (3,911)	1.17 (3,527)
JER	BLK	10.9 %	93.3 % (11,062)	95.3 % (10,317)	91.0 % (10,796)	1.17 (10,429)
XXX	SIM	3.1 %	96.9 % (3,167)	94.8 % (3,068)	92.4 % (3,147)	1.36 (2,206)
XXX	BAQ	0.7 %	95.4 % (694)	92.0 % (662)	88.0 % (692)	1.22 (670)
XXX	CHA	0.7 %	94.9 % (686)	95.4 % (651)	91.1 % (682)	1.25 (583)
XXX	LIM	3.6 %	94.9 % (3,645)	92.9 % (3,459)	88.8 % (3,617)	1.26 (2,975)
XXX	BLK	6.0 %	95.5 % (6,023)	95.4 % (5,751)	91.9 % (5,974)	1.20 (5,209)

Gender differences

As expected a significant effect of gender was found. Table 9 shows the survival rate for all three time periods and the average calving ease score for bull and heifer calves. The average survival rate is lower for bull calves compared to heifer calves in all time periods. Also the calving ease score is lower for heifer calves, which indicates that the dams have an easier calving when giving birth to a heifer calf than when giving birth to a bull calf.

Table 9 – Average differences between heifer and bull calves for calving ease, young stock survival 1-30, 31-200 and 1-200 days after birth

Sex	N	Calving ease	Survival 1-30 days	Survival 31-200 days	Survival 1-200 days
Bull	53,097	1.34	94.4 %	93.6 %	89.6 %
Heifer	48,075	1.21	95.7 %	95.5 %	91.8 %

Phenotypic trend

In Figure 5 the phenotypic development of young stock survival from 1-30 and 31-200 days is shown. The figure shows that there are large fluctuations between years, but no significant ($P > 0.05$) overall trend for either trait was found, despite the negative tendencies.

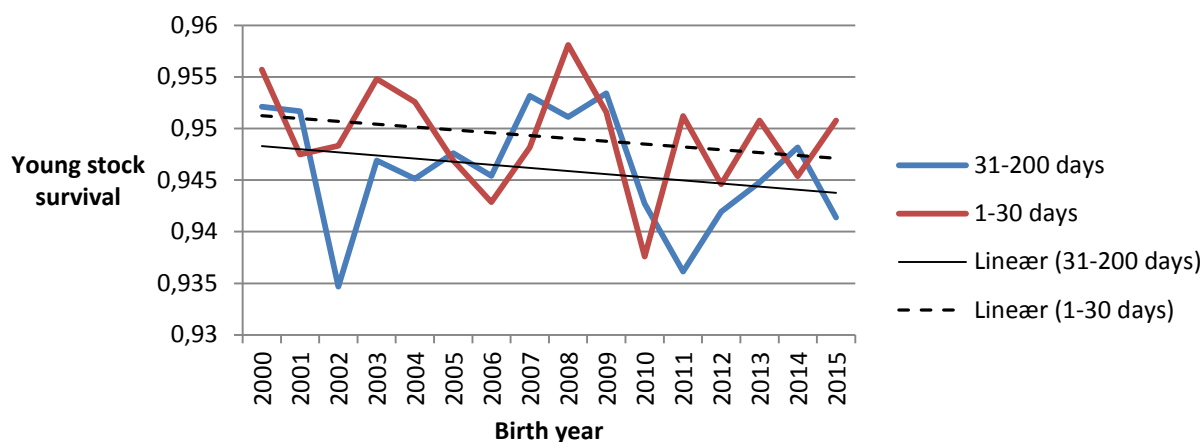


Figure 5 – The phenotypic trend from 2000-2015 for young stock survival from 1-30 and 31-200 days after birth, with the corresponding trend lines.

Seasonal effect

Figure 6 shows the average young stock survival from 31-200 days for calves born from 2012-2014, divided by birth year and month. There is a significantly higher survival rate in the spring, compared to all other seasons. The lowest survival rates are seen in the autumn and winter months, due to cold and damp weather.

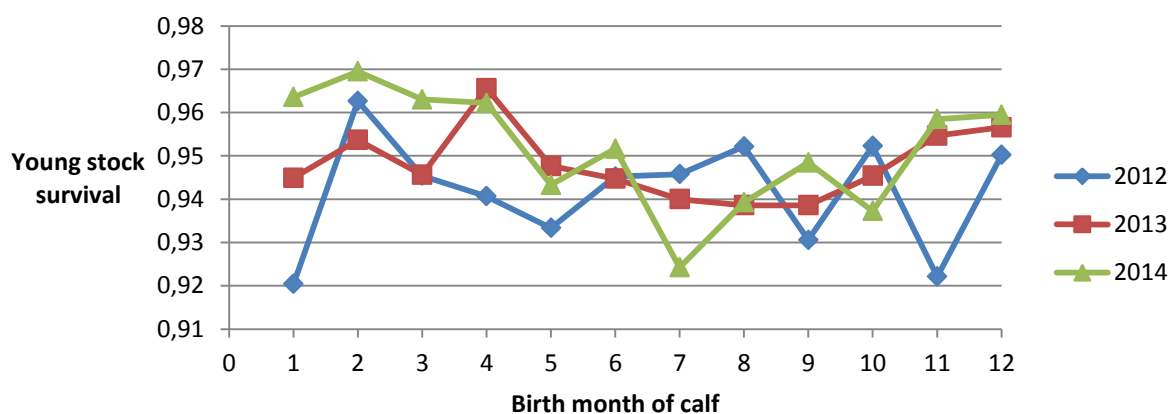


Figure 6 – Average young stock survival from 31-200 days for calves born from 2012-2014, divided by birth year and month

Transfer

It is not legal to transfer calves before they are at least 14 days old in Denmark. Figure 7 shows the time of transfer for the transferred calves (only calves that survived the first 30 days). The majority of the calves are transferred within the first month (50 %). The largest amount of calves were transferred on day 14, from day 14 and onwards the amount of transferred animals declines.

67.1 % of the calves were transferred at least once from 1-200 days after birth. The calves that were transferred had a higher survival rate from day 31-200 than those that were not transferred, 94.9 % and 93.8 % respectively. The reason for this is that non-transferred animals are often dead before they have the opportunity to be transferred.

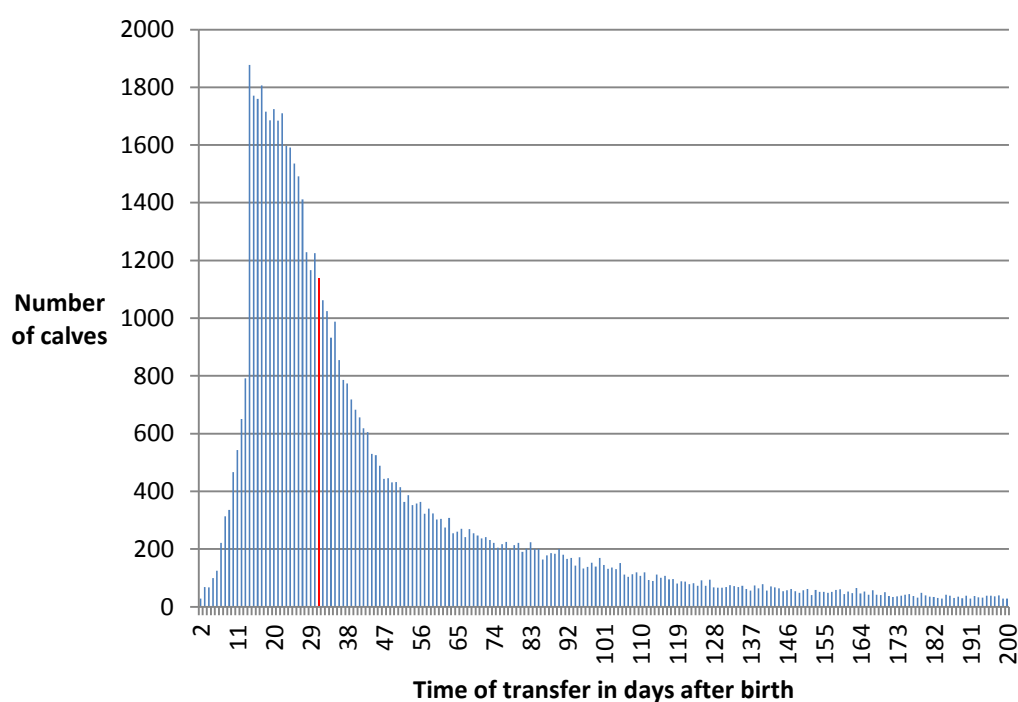


Figure 7 – The number of calves that are transferred divided by time of transfer after birth. The red line indicates day 30.

Parity

All calves born from dams in fifth or greater parity were pooled together. Table 10 shows the distribution of the dam's parity. The survival rate in all periods was quite stable. There was a slightly lower survival rate from 1-30 days for calves from first parity cows, probably due to more difficult calvings which was reflected in a lower average for calving ease. Calves from fifth or older parities had the lowest overall survival rate (1-200 days). This was mainly due to a lower survival rate in the first 30 days, however no significant differences between parity for any time periods were found.

Table 10 – Number of offspring, young stock survival 1-30, 31-200 and 1-200 days after birth and calving ease for parities 1-5

Parity	N	%	Survival 1-30 days	Survival 31-200 days	Survival 1-200 days	Calving ease
1	6,079	6 %	94.8 %	94.3 %	90.7 %	1.53
2	28,577	28 %	95.1 %	94.6 %	90.6 %	1.28
3	28,330	28 %	95.2 %	94.5 %	90.9 %	1.25
4	18,980	19 %	95.2 %	94.6 %	90.8 %	1.25
5	19,206	19 %	94.5 %	94.5 %	90.2 %	1.27

The percentage of sire breeds used within parity is shown in Figure 8. There were large differences between the use of sire breeds in first parity cows compared to all other parities. Only 17.4 % of the offspring had a BLK sire, compared to between 60-65 % in all other parities. Instead of BLK, LIM is used to a much greater extent for the first parity cows compared to later parities. Also SIM is used to a greater extent on first parity cows compared to later parities.

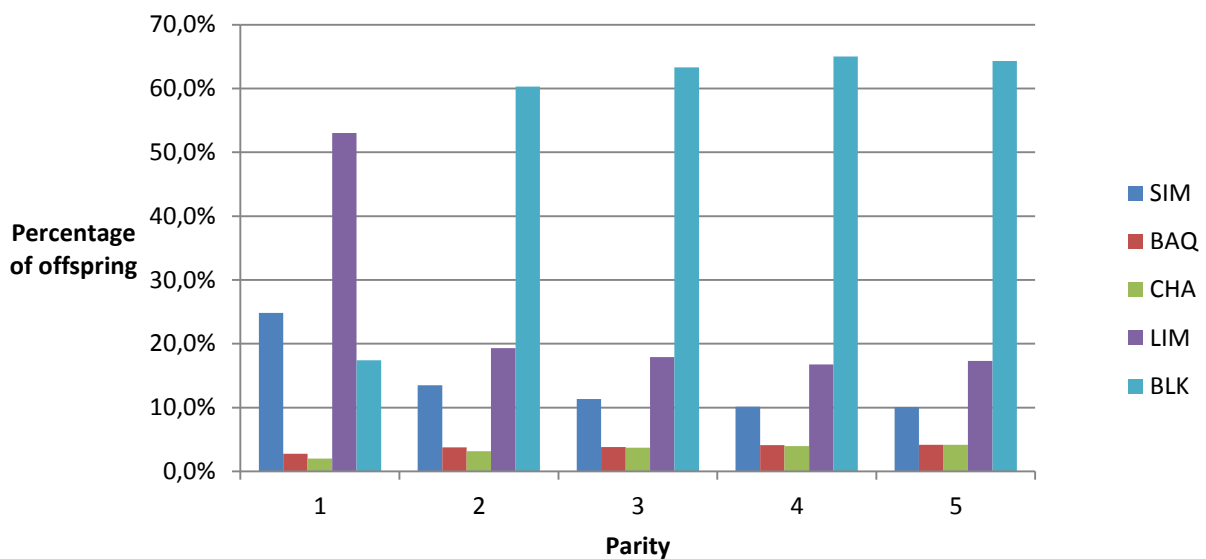


Figure 8 – Percentage of offspring for each sire breed divided by parity of the dam

4.2 Genetic parameters

4.2.1 Heritabilities

Several different models were tested to see which model fitted the data best. A PROC HPMMIXED function in SAS, was used to test the significance of the fixed effects. All the effects except for parity of the dam were significant.

The herd x year effect (HY) was tested both as a random and as a fixed effect. The results are shown in Table 11. The heritabilities are presented on both the observed and the underlying scale. Standard errors and standard deviations are based on the heritabilities on the observed scale.

Table 11 – Different models for young stock survival from 31-200 days (model number in parenthesis), number of calves (N), with the corresponding heritabilities (h^2), standard error (SE) of the heritability and the additive genetic (σ_A), environmental (σ_E) and phenotypic (σ_P) standard deviations.

Model	N	h^2 - observed	SE	h^2 - underlying	σ_A	σ_E	σ_P
HY fixed (1)	101,172	0.0177	0.0033	0.0746	0.0279	0.2073	0.2092
HY random (2)	101,172	0.0170	0.0031	0.0718	0.0275	0.2086	0.2104
HY random + no XXX (3)	85,953	0.0177	0.0034	0.0745	0.0280	0.2085	0.2104
HY fixed + no XXX (4)	85,953	0.0192	0.0037	0.0806	0.0289	0.2071	0.2091

The model where herd x year was included as a fixed effect (model 1), compared to the model where it was included as a random effect (model 2), had a higher heritability, but they were not significantly different from each other. Model 1 had a slightly lower residual and a higher additive genetic standard deviation compared to model 2. The additive genetic standard deviation describes the genetic differences between the animals. The more genetic difference is captured the higher heritability it is possible to obtain.

If the crossbred cows were excluded from the dataset (model 3 and 4), the heritability was increased. Crossbred cows express heterosis which is not passed on to their offspring, furthermore the breed composition can vary greatly; this creates noise in the model. Model 3 had a higher heritability than model 2, but the same as model 1. The standard deviations of model 2 and 3 are very similar; however the additive genetic standard deviation is higher for model 3 which indicates that the model fits the data better. The highest heritability was obtained in model 4, which also had the highest additive genetic standard deviation and lowest residual standard deviation.

A model with herd x year as a fixed effect seems to be the best fit in order to estimate the genetic parameters with the most accuracy, but in accordance with the theory it is best to include herd x year as a random effect due to many herds with few offspring per year. The differences of including herd x year as a random or a fixed effect, were small and not significant. By excluding the crossbred dams the residual variance was reduced. Therefore, the model with herd x year as a

random effect and no crossbred dams (3), will be used to calculate heritabilities and correlations between the traits of interest.

Table 12 - Heritability estimates for young stock survival 31-200 days after birth for each dam breed, number of calves (N), with the corresponding heritabilities (h^2), standard error (SE) of the heritability and the additive genetic (σ_A), environmental (σ_E) and phenotypic (σ_P) standard deviations.

Dam breed	N	h^2 - observed	SE	h^2 - underlying	σ_A	σ_E	σ_P
HOL	61,441	0.0193	0.0041	0.0832	0.0287	0.2051	0.2071
JER	17,200	0.0342	0.0116	0.1361	0.0397	0.2109	0.2146
RDC	6,869	-	-	-	-	-	-
XXX	11,385	0.0189	0.0108	0.0793	0.0287	0.2069	0.2089

The heritabilities were also estimated for each dam breed using model 3 to investigate potential breed differences, the results are presented in table 12. The heritability on the underlying scale was highest for JER and lowest for XXX. JER also had the highest σ_A , which shows that the genetic variation between animals is larger than for the other dam breeds. It was not possible to calculate any estimates for RDC as there were too few offspring with a RDC dam. The heritability is higher for all dam breeds when estimated separately as the animals are more uniform, so the fixed effects can be estimated more accurately. However, the reliability of the estimates is lower due to fewer animals.

Table 13 – Heritability estimates for young stock survival 1-30, 31-200 and 1-200 days after birth, with the corresponding heritabilities (h^2), standard error (SE) of the heritability and the additive genetic (σ_A), environmental (σ_E) and phenotypic (σ_P) standard deviations.

Young stock survival	h^2 – observed	SE	h^2 - underlying	σ_A	σ_E	σ_P
1-30 days	0.0103	0.0026	0.0449	0.0215	0.2109	0.2120
31-200 days	0.0177	0.0034	0.0745	0.0280	0.2085	0.2104
1-200 days	0.0122	0.0027	0.0350	0.0278	0.2501	0.2516

In Table 13 the estimates of the genetic parameters for all 3 traits are shown. All the heritability estimates are significant. The heritability on the underlying scale is highest for survival from 31-200 and lowest for 1-200 days. On the observed scale it is 1-30 days that has the lowest heritability. The reason that the rankings change is that the heritability on the underlying scale has been transformed according to the frequency. Double the amount of calves died from 1-200 days compared to 1-30 days, which is why the heritability is lower on the underlying scale. There are also large differences in the residual standard deviation, which is much greater for 1-200 days compared to the other two traits. The amount of genetic standard deviation is greatest for 31-200 days, and the residual standard deviation is also the lowest. This indicates that most genetic variation is captured for this trait, with the least noise from the model.

4.2.2 Genetic correlations

A multi trait model in DMU was used to estimate the genetic correlations between all three survival traits using model 3. Due to the data structure it was not possible to calculate phenotypic and genetic correlations between all of the traits. The genetic correlation between survival from 31-200 days and 1-200 days did not converge. This is probably due to the data structure, as there are only common observations on live calves the first 30 days, all dead calves from 1-30 days have a missing value for survival from 31-200 days. In order to take this into account, a sire model was used instead of an animal model. By using a sire model it is presumed that each sire will have calves that are both dead and alive in the first period. However, many of the sires have few offspring in the dataset and it was not possible to obtain an estimate with either an animal or a sire model.

For young stock survival from 1-30 and 31-200 days after birth a genetic correlation of -0.15 (SE 0.15) was estimated. As the standard error was as large as the estimate, the result is not significant and the estimate is very unreliable. This was probably due to the data structure as explained previously.

The only genetic correlation that yielded a plausible result was the correlation between survival from 1-30 and 1-200 days 0.51 (SE 0.11). There was a significant genetic correlation between the two traits, but they were only moderately correlated. This confirms that survival from 1-30 and 1-200 days are two different traits. Survival in the first month of life is not the same trait as survival to 200 days after birth.

The genetic correlation between calving ease and young stock survival from 1-30 and 31-200 days was also estimated. The results showed an insignificant correlation between survival from 31-200 days and calving ease, but a significant negative correlation of -0.47 (0.12) between calving ease and survival from 1-30 days after birth. This indicates that calving ease has a large impact on the survival in the first month, but an insignificant impact later in life. With decreasing calving ease the survival of the calf also decreases in the first month after birth.

4.3 Breeding values for young stock survival

All sires with less than 100 offspring in the data set have been disregarded for the following analysis. Breeding values were calculated using model 3. In Table 14 the number of offspring, sires and sires with >100 offspring are shown for young stock survival 31-200 days. BLK has the highest amount of offspring followed by LIM. Surprisingly SIM has the greatest number of sires, but only 28 have more than 100 offspring. This indicates that many different SIM sires have been used on a small number of cows. The average absolute breeding value (EBVab) and the corresponding standard deviations are visualized in Figure 9.

Table 14 – The number of offspring, sires, sires with <100 offspring, the average absolute breeding value (EBVab) and standard deviation for the 5 sire breeds for young stock survival 31-200 days

Sire breed	Number of offspring	Number of sires	Number of sires with >100 offspring	Average EBVab	Standard deviation
SIM	9,027	126	28	0.6%	0.9%
BAQ	3,170	40	8	0.2%	1.7%
CHA	2,888	42	8	0.6%	1.2%
LIM	16,392	69	34	-1.5%	1.6%
BLK	54,476	113	58	2.6%	1.3%

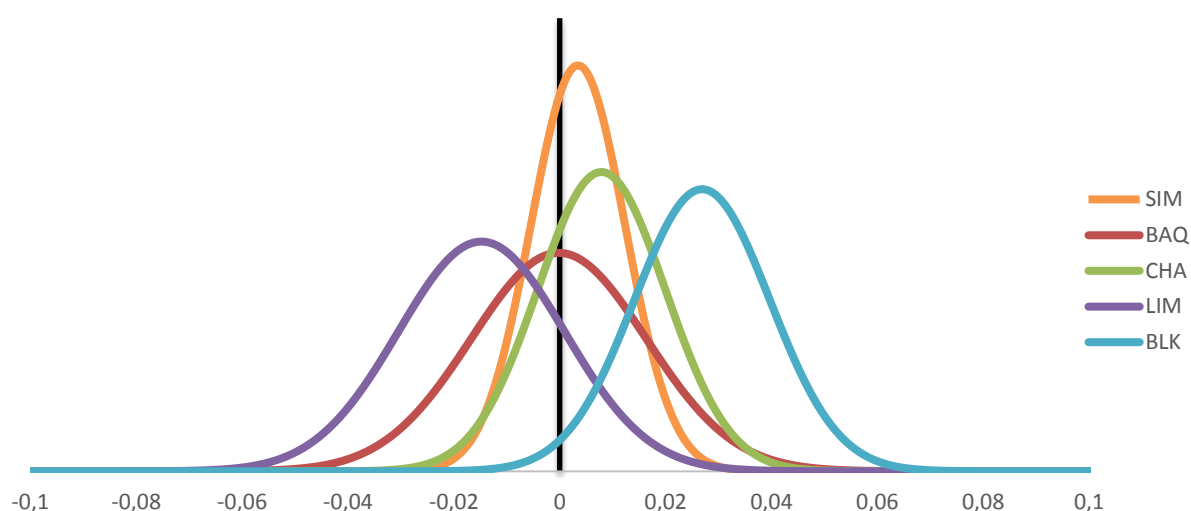


Figure 9 - Normal distribution of sire breeding values for young stock survival 31-200 days

Figure 9 shows the normal distribution curves for the average breeding values of the sires with >100 offspring for the 5 sire breeds. It should be noted that for BAQ and CHA there are only 8 sires in the group, so the results will be uncertain. The average breeding values are highest for BLK and lowest for LIM, whilst CHA, BAQ and SIM are slightly positive. BAQ has the largest variation, whilst SIM has the smallest. It is interesting to note that only the very best LIM can compete with the worst BLK.

In table 15, the results regarding young stock survival from 1-30 days are shown. The sire breeds are more equal compared to survival from 31-200 days and the standard deviations are slightly lower. LIM sires have the lowest average breeding value for survival from 1-30 days, whilst BAQ and CHA have the highest, but they also have the smallest number of sires, so the most unreliable results.

Table 15- The number of offspring, sires, sires with <100 offspring, the average absolute breeding value (EBVab) and standard deviation for the 5 sire breeds young stock survival 1-30 days.

Sire breed	Number of offspring	Number of sires	Number of sires with >100 offspring	Average EBVab	Standard deviation
SIM	9,027	126	28	0.4 %	0.9 %
BAQ	3,170	40	8	0.9 %	1.0 %
CHA	2,888	42	8	0.6 %	1.0 %
LIM	16,392	69	34	-0.6 %	0.8 %
BLK	54,476	113	58	0.4 %	1.0 %

4.3.1 Comparison of the best and worst sires

The five best and worst sires were ranked based on the average EBVab of their offspring for survival from 1-30 days (Table 16). SIM, BAQ and BLK are represented in the top five, whilst LIM and BLK are represented in the five worst sires. The sire with the lowest EBVab had a survival rate from day 1-30 that was 2.5 % lower than the average, whilst the best sire had a survival rate that was 3.5 % higher.

Table 16 – The five sires with the highest and lowest average absolute breeding value (EBVab) for young stock survival 1-30 days

The five best sires			The five worst sires		
Sire breed	Number of offspring	EBVab	Sire breed	Number of offspring	EBVab
SIM	137	3.5 %	LIM	718	-2.5 %
BAQ	597	2.5 %	LIM	359	-2.2 %
BLK	887	2.3 %	LIM	481	-1.8 %
BLK	456	2.0 %	BLK	227	-1.6 %
SIM	124	2.0 %	BLK	754	-1.4 %

For young stock survival from 31-200 days, the ranking of the bulls was quite different see Table 17. The best sire had a 4.7 % higher survival rate than the average, whilst the worst had a 5.4 % lower survival rate. All the five best bulls were BLK; indeed the 35 best bulls were all BLK. With regards to the five worst bulls, LIM are heavily represented, with only one BAQ among the worst five sires.

Table 17 - The five sires with the highest and lowest average absolute breeding value (EBVab) for young stock survival 31-200 days

The five best sires			The five worst sires		
Sire breed	Number of offspring	EBVab	Sire breed	Number of offspring	EBVab
BLK	955	4.7 %	LIM	1468	-5.4 %
BLK	167	4.6 %	LIM	124	-4.3 %
BLK	440	4.5 %	LIM	205	-4.2 %
BLK	1438	4.5 %	LIM	140	-3.3 %
BLK	596	4.5 %	BAQ	200	-3.2 %

4.3.2 Breed comparison

To investigate if the bulls ranked differently between the breeds, sires used on JER and HOL dams were compared for young stock survival from 31-200 days. The results are displayed in table 18. Some re-ranking is expected as the survival rate is lower for JER compared to HOL and the genetic variation is larger.

Table 18 - The number of (No.) offspring, sires, sires with <100 offspring, the average absolute breeding value (EBVab) and standard deviation for the five sire breeds, for offspring with either a Holstein or Jersey dam.

Sire breed	No. offspring	No. sires	No. sires >100 offspring	Mean EBVab	Std. dev. EBVab
Holstein					
SIM	7.141	120	25	0.3 %	0.7 %
BAQ	2.569	39	6	-0.2 %	1.0 %
CHA	1.796	36	5	0.9 %	0.8 %
LIM	10.497	66	25	-1.7 %	1.1 %
BLK	39.439	107	57	1.8 %	1.0 %
Total	61.442	368	118		
Jersey					
SIM	936	77	-	-1.9 %	0.8 %
BAQ	264	26	-	-0.8 %	0.8 %
CHA	829	31	2	-0.1 %	0.9 %
LIM	4.105	59	12	-1.8 %	1.3 %
BLK	11.066	79	33	2.6 %	0.8 %
Total	17.200	272	47		

An actual comparison between the ranking of the bulls proved to be problematic as many bulls had less than 100 offspring, especially for JER. For HOL 118 bulls had more than 100 offspring in the data set compared to only 47 for JER. No SIM and BAQ bulls had more than 100 JER offspring. Therefore, the averages and standard deviation for these two breeds were calculated based on the whole population and not only the bulls that had >100 offspring as for the other three breeds.

With regards to the mean EBVab all breeds except BLK had a lower survival rate for JER. The standard deviations of the estimates were similar. For both HOL and JER dams, BLK sires ranked the highest and LIM the lowest. CHA and SIM changed from having a positive EBVab on average for offspring with HOL dams to having a negative EBVab for JER.

Genetic trend

The genetic trend reflects the historical progress achieved. Average breeding values of individuals by birth year is a common measure of genetic trend. The genetic trend in young stock survival from 31-200 days for sires born from 1996-2012, that have more than 100 offspring in the data is shown figure 10. Due to a small amount of sires that fulfilled this requirement, there were few sires per birth year, which resulted in large variation and low reliability.

The red line illustrates the standard deviation of the mean which is the blue line. A linear trend line has been plotted using the Excel function. There is a slight positive genetic trend ($P>0.06$) with an annual increase of 0.09 % in survival rate from 31-200 days. The standard deviation varies greatly as does the mean. In 2008 the average EBVab is much lower compared to all other years, but it can also be seen that the standard deviation is much higher. As there are only 4 bulls from 2008 the result is quite uncertain, and a single sire could strongly bias the results. For young stock survival from 1-30 days there was no significant genetic trend.

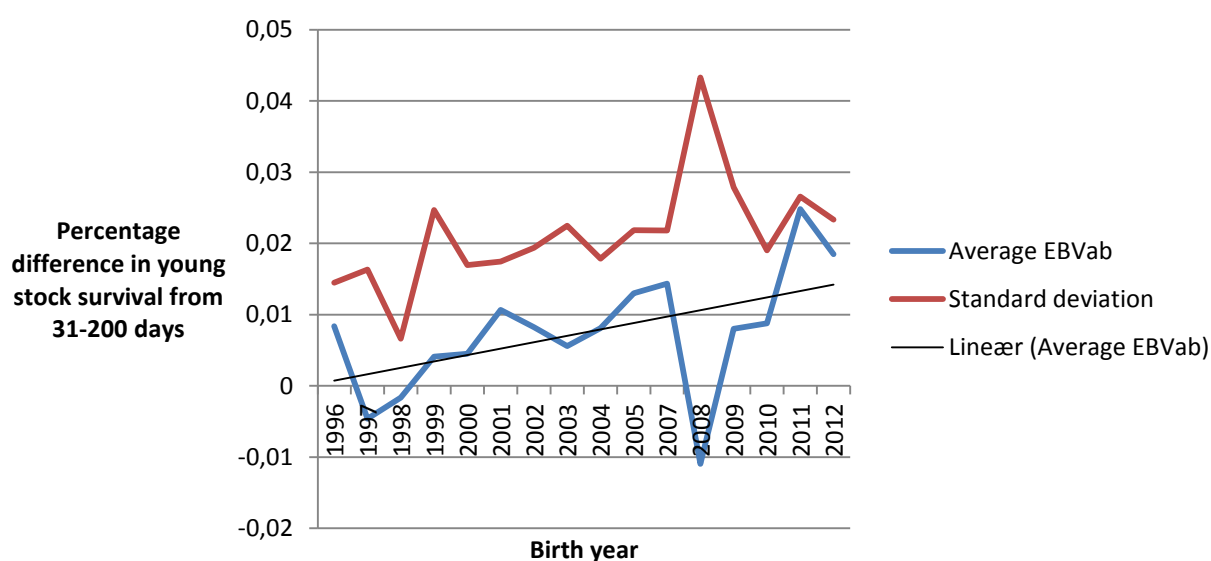


Figure 10 - Genetic trend for young stock survival 31-200 days

The genetic trend for offspring with HOL and JER dams is shown in Figure 11. There was, especially for JER few sires per birth year, which resulted in large variation and low reliability. For both HOL and JER there is a slightly positive trend in concordance with the overall genetic trend for survival from 31-200 days, however none of the trends are significant.

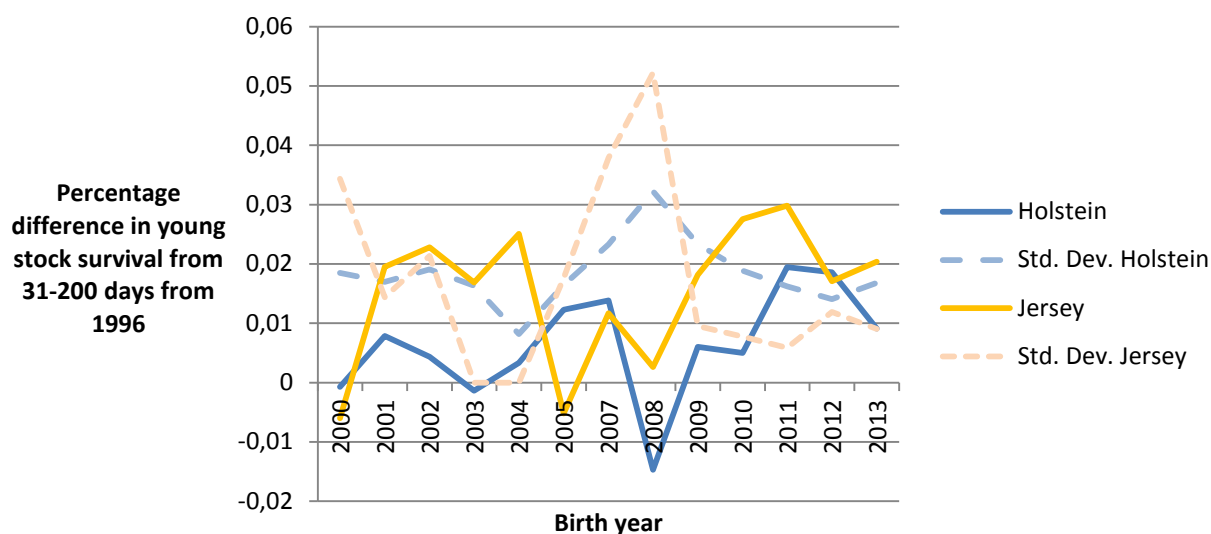


Figure 11 - Genetic trend for young stock survival 31-200 days for offspring with Holstein or Jersey dams. The solid line shows the average EBVab for each year and the dashed line shows the coherent standard deviation.

5 Discussion

The discussion is split up in two parts, the first part discusses the final model and the variables used to determine the genetic parameters. The second part, discusses the main findings of the thesis.

5.1 Final model

Young stock survival is a binary trait: The calf can either be dead or alive. When modelling a binary trait several problems have to be addressed. As a binary trait only has two options, it cannot be normally distributed. Therefore, the phenotypic expression of a binary trait is usually attributed to an underlying continuous unobservable trait that is normally distributed; this is referred to as the liability (Falconer et al., 1996). Both linear and non-linear models can be applied for the genetic analysis of binary traits, with the assumption that the underlying liability is normally distributed. The advantage of a linear model compared to a non-linear model is the ease of implementation. Non-linear models are often more complex and have higher computational requirements. For binary traits a non-linear model such as a threshold model could be relevant, the lower the heritability and frequency, the larger advantage is gained by using a threshold model compared to a linear model (Mrode 2014). Both the heritability and the frequency of young stock survival were low and therefore it could have been an advantage to use a threshold model instead of a linear model. However, when the amount of information from fixed effects is small, as in the present study, threshold models have problems estimating variance components and may cause unreliable results (Altarriba et al., 1998).

Many studies have addressed this issue, (McGuirk et al., 1998b) remarked that whereas threshold models may be useful in more unbalanced data sets with widely different incidences across fixed

effects (e.g. contemporary groups), they may offer small advantages in well-designed progeny testing programs with large numbers of records per sire. Weller et al. (1988) concluded that the advantages of a threshold over a linear model when evaluating calf mortality were slight, and rank changes were small in most cases. Furthermore, Fuerst-Waltl and Sørensen (2010) showed that for stillbirth and prepubertal mortality, rank correlations between breeding values estimated with a linear model and a threshold model were very high.

Carlen et al. (2016) studied the implementation of young stock survival in the Nordic routine genetic evaluation. They found that when using a linear model, the predicted breeding values were highly correlated to those estimated using a binary model. In the Dutch routine evaluation for young stock survival a linear model is also used (van Pelt et al., 2012). Furthermore, all the models in the Nordic breeding value estimation are linear models. As the model developed in this study in the future may be implemented in the Nordic breeding value estimation and there is evidence that prediction by a linear model is highly correlated to estimates from a threshold model, it seems that a linear model is sufficient to estimate genetic parameters for young stock survival.

5.1.1 Definition of young stock survival

In this study two traits were defined: Young stock survival from 1-30 (period 1) and 31-200 days (period 2) after birth. The survival rates in the two periods were similar, despite period 2 being longer which indicates that calf mortality was highest during the first weeks in concordance to Agerholm et al. (1993). In the literature other time periods have been defined, many studies have used 1-14 days as the first period and the second period went to 180 and not 200 days. Another difference in this study was that bull and heifer calves were evaluated together, only corrected for by a fixed effect.

By setting the period to 1-30 days and not 1-14 days, more variation is captured as less calves survive. This enables the genetic parameter for 1-30 days to be estimated more precisely. Retrospectively, it may have been better to set the first time period from day 3-30, as van Pelt et al. (2012) or 2-30 as Buch (2012). This would avoid including calves that were not registered correctly as stillborn or dead within the first 24 hours. Death within the first 24 hours is included in the index for calf vitality and therefore, it should not be included in an index for young stock survival.

Another difference from other studies is that the second period runs to 200 days from birth and not 180. The time of slaughter was investigated, and it was concluded that an insignificant amount of calves was slaughtered before 200 days. All calves slaughtered in period 2 were excluded from the data set. The calves were not slaughtered before they were at least 8 months old and the majority were slaughtered just before 10, 12 or 16 months of age. By limiting period 2 to 200 days and not 180 days a slightly larger frequency of calves die within the period. The two traits defined

in this thesis seem to be in concordance with other studies on young stock survival, despite slight differences. This makes the obtained results comparable to similar studies.

5.1.2 Model

The final model for estimating the genetic parameters was chosen to be a linear animal model with herd x year as a random effect. The following section will discuss the model and some the effects that were included.

Fixed effects

Herd

The herd effect can be considered as an effect that takes management practices and other environmental conditions that are likely to vary from herd to herd into account (Van Bebber et al., 1997). For the Nordic young stock survival in dairy cattle, the effect of the herd that the calf was born in was used in the first period, and for the second period it was the herd that the calf was registered in at day 30. Hansen et al. (2003) did not account for the effect of the second herd if the calf had been transferred, and stated that in retrospect including this effect would have presumably improved the model for survival from d 61-180 days.

In this paper, it was also the birth herd that was used in the first period, but in the second period the effect from the herd the calf had been in for the longest period of time was used. If the herd in which the calf was at day 30 is used, there is a possibility that it is still in the birth herd, or it is in a transition facility. Therefore, the actual herd the calf was reared in would not be accounted for. This is avoided by using the approach in this thesis. Similarly to our approach the Dutch routine genetic evaluation also uses the herd that the calf has stayed in the longest in the given time period to account most correctly for the herd effect (van Pelt et al., 2012).

Gender

In the Nordic young stock survival index for dairy cattle the sub-indexes are split up separately for heifer and bull calves (Carlen et al., 2016). For dairy cows one of the reasons is that heifer calves are raised to be replacement animals, whilst bull calves are raised for meat production in a fattening unit. This means that the calves are raised in different production systems, and for different periods of time depending on the gender. However, the majority of both sexes in beef x dairy calves are sent to a fattening unit and therefore the environmental effect is the same for bull and heifer calves. There is however differences in survival rate between heifer and bull calves and it is therefore necessary to correct for this difference. Indeed, a significant effect of including sex in the model was confirmed: The bull calves had a significantly lower survival rate. If the indexes were split up according to sex in this study, it would halve the amount of data for each index. This would decrease the accuracy of the model substantially, and might make it difficult to calculate breeding values, especially for breeds with few offspring.

Parity of dam

In both the Danish and Dutch routine evaluation for young stock survival a fixed effect of the parity of the dam was included (van Pelt et al., 2012b, Carlen et al., 2016). Also Henderson et al. (2011) and Weller et al. (1988) included this effect in their evaluations. There was no significant effect of including parity in the model in this study. The main reason for including parity in the model is that the use of sire breeds varies between first and later parities. It can be discussed whether to pool all parities except first parity, into one group as the use of sire breeds is very similar and there are no significant differences between the later parities. There were only few first parity cows as it is not common to inseminate dairy heifers with beef semen, so another option is to exclude the first parity cows.

Transfer

From 1-200 days after birth, 67.1 % of the calves were transferred at least once. This is in concordance with Pedersen et al. (2008) that stated that 70 % of the dairy bull calves are raised in specialized units. In the Nordic routine genetic evaluation transfer was defined only for the late period (2-7 months) and only if the transfer occurred within 60 days from offset of the time period (Carlen et al., 2016). In this paper, transfer has been defined in a different way. It was the transfer from the dairy herd to the fattening unit that was of interest, and therefore only these transfers were included in the model despite the time of transfer. As the time of transfer varies greatly, and 50 % of the transferred calves were moved before day 31, it is important to include transfers from the first period in the second period.

Other studies assume that calves that are transferred have a higher mortality rate (Hansen et al., 2003, Norberg et al., 2013), but the opposite was found in this study. However, the higher mortality rate in the non-transferred calves is partly due to the fact that an animal has to be alive to be transferred (Carlen et al., 2016). Hansen et al. (2003) found that there was significantly higher calf mortality in transferred calves, compared to non-transferred calves. Their model included an effect of transfer during the period of risk in their initial study, but this effect was confounded with the fact that the animals had survived until they had been transferred. Therefore, they only chose to account for transfers before the period of risk. However, their study was conducted on Holstein calves, of which only 14 % of the calves (mainly bull calves (98 %)) were transferred. In this paper the majority of calves were transferred which makes it difficult to compare the two papers.

Norberg et al. (2013) also included a transfer variable in their study on Jersey heifers in a similar way to this study. Calves that were not moved in the first 180 days were assigned to one group, calves that were transferred from d 14 to 30 were assigned to a second group and calves transferred from d 31 to 180 were assigned to a third group. Only few animals were transferred (<1 %), however mortality rates were higher for the transferred calves: 16.5 % and 44.4 % for calves transferred between d 14 and 30 and between d 31 and 180, respectively (Norberg et al.,

2013). In contrast to the Nordic studies van Pelt et al. (2012) did not account for transfer in their estimation of genetic parameters for young stock survival, neither did Weller et al. (1988).

Buch (2012) included the month of transfer in their model to account for interactions between transfer and month. Furthermore, they defined if the animal had been moved or not in the first period, moved in the first period and not the second, or moved in the second period regardless if it had been moved in the first period or not. This approach could also have been used in this paper in order to account for the transfer in the period that the animal actually was transferred. Using this approach would possibly assign the effects more correctly to the period of risk. Accounting for the interaction between month of transfer and transfer might also have improved the model. Clear seasonal variation in calf mortality was seen for birth month of the calf, so it could be expected that it was also the case for transfer month. Hansen et al. (2003) also found seasonal variations in their study; calves transferred during the autumn had a higher mortality compared to all other seasons.

Random effects

Herd x year

All herds with less than 5 calves in the dataset were deleted, but there were still many herd x year groups that had less than 5 calves, or had no observations. Due to high young stock survival rates and few observations in the first years included in the data set, there are many herd x year levels where all the animals either survive or die, leaving no variation in the trait. Data from these herds is therefore non-informative from a statistical point of view in the linear model, as there is no variation (Pedersen et al., 2014).

If the contemporary group sizes are small, such as small herd sizes, or if seasons are defined as short time periods, then the effective number of offspring per sire (n_e) is decreased and the prediction error variance (PEV) is increased (Van Vleck 1987). If some or all of the contemporary groups are fitted as random effects within herd-year blocks, n_e is increased and PEV is decreased. However, this may result in biased genetic evaluations (Van Vleck 1987). Van Vleck (1987) found that if herd x year x season (HYS) was treated as a fixed effect, the information from one sire was lost if there were no daughters of other sires in that group. If in contrast HYS is treated as a random effect, the number of daughters of other sires serves to increase the weighting, but their absence will not yield an effective number of zero for the sire in question.

Dempfle (1982) suggested replacing HYS with herd x class x year x season (HYCS) in situations with small herd levels. The herds can be grouped based on their production results, into comparable classes. They found that the residual error variance was only slightly increased whilst the effective number of daughters was increased considerably. However, grouping of herds is not quite as simple for young stock survival, as the variation between herds is not as great as for example milk production. But it could have been considered in order to avoid bias and decrease the PEV.

However Preisinger et al. (1986) stated that certain fixed effects will be ignored by setting up HYCS instead of HYS, which could lead to biased estimates. Chauhan et al. (1990) also investigated HYCS and found that indeed estimates were biased, probably because herds with good management and poor sires were pooled in the same group as herds with poor management and good sires. Therefore it was concluded that to classify herds by production level the genetic merit of the herd should be taken into account (Chauhan et al., 1990).

In most NAV evaluation models herd x year is included as a random effect, with a fixed herd x 5 year effect to ensure that groups are large enough. In the Dutch statistical model for young stock survival the herd x year effect is included as a fixed effect (van Pelt et al., 2012). In a study in Israeli Holstein herd x year x season was included as a random effect (Weller et al., 1988). In this study both herd x year as a fixed and a random effect was tested. The results showed that the differences were small, but the model that included herd x year as fixed effect, resulted in a slightly higher heritability, less residual variance but a slightly higher standard error compared to the model that included herd x year as a random effect. Based on the results it seems that when herd x year is included as a fixed effect, slightly more variance is accounted for, but the models are not significantly different. From a theoretical point of view it was therefore decided to include herd x year as a random effect due to the many small groups.

In the future it is expected that the number of beef x dairy crossbred calves will increase greatly, this will presumably lead to larger herd x year levels. This would make it feasible to include the herd x year effect as a fixed effect instead of a random.

Alternative variables

Other studies on young stock survival have included additional variables in their models that have not been included in the present study. The alternative variables are calf size, calving ease, maternal additive genetic effect and heterosis and will be described briefly in the following.

Calf size and calving ease

Some studies have included an effect of calf size and calving ease in their model for estimation of genetic parameters for young stock survival. This omits these effects in the variance components (Fuerst-Waltl and Sørensen 2010). By doing this double counting from the calving traits can be avoided. Fuerst-Waltl and Sørensen (2010) found a significant effect of calf size and calving ease on survival from d 1-30, d 181 to 365 and d 1 until first calving. Henderson et al. (2011) also included an effect of calving ease in their study on young stock survival in Holstein heifers. However, the effect of calving ease on calf mortality has generally been documented within the first 24 or 48 hours after birth only. Several studies have provided evidence that the effect of calving difficulty influences survival beyond the first 30 days of life through to heifer maturity (Henderson et al., 2011). In this thesis a significant negative correlation between calving ease and survival from 1-30 days was found, but no significant effect was found from 31-200 days. This confirms that calving ease has an impact on survival in the first period after birth, but no effect

after this period was found. The results regarding calf size are more ambiguous, as some studies find the larger the size the greater the survival rate (Sieber et al., 1989, McCorquodale et al., 2013), whilst others state that both calves that are under or above average size have an increased risk (Henderson et al., 2011). Weller et al. (1988) did not include any of the effects in their study in Israeli Holstein. If calving ease and calf size were included in the model, the calculated estimates for young stock survival would be corrected for these effects. As the traits are correlated the estimates would be a corrected phenotype and not the true phenotype.

Maternal additive genetic effect

A maternal additive genetic effect could have been included in the model as a random effect in order to model the effect of the dam's phenotype on her calf's phenotype. This is especially relevant if the calf is raised with its dam, as in extensive production forms. However, this is rarely the case in modern dairy production system. Therefore, the maternal effect is minimal, because calf and dam are usually separated within 12-24 hours. The maternal effect on young stock survival has been investigated by several studies and none of them found it to be significant (Norberg et al., (2013); Hansen et al., (2003)). Norberg et al. (2013) found that maternal heritabilities of mortality in Jersey cattle were very small and not significant, implying that the dam's role in calf mortality was genetically less important than the direct effect. This is consistent with early mortality in beef cattle reported by Goyache et al. (2003). Therefore, this effect has not been addressed, and the focus has solely been on the direct effect in this study.

Heterosis

It was not possible to estimate heterosis effects as groups of purebred individuals were unavailable. Furthermore, as the beef x dairy calves are predominantly terminal crosses, it is not necessary to correct for the heterosis effect, because genes will not be passed on. However, the farmer is interested in maximum heterosis in the crossbred calves, so it could have been interesting to investigate if some breed combinations result in more heterosis compared to others. It was not possible to find any estimates from other studies. Ultimately, the sires are compared to each other based on their performance, so those sires that produce the best calves, regardless of if it is due to genetics or heterosis should be used, and therefore the heterosis effect should not be corrected for in the model.

5.2 Main findings

From 2000-2011 only few beef x dairy calves were born each year, this makes any results based on the first years quite unreliable, especially for the small breeds. From 2012 and onwards the number of calves increased greatly. It is expected that the number of beef x dairy calves will continue to increase during the next decade; this will make it possible to gain more reliable results and capture more genetic variation.

When beef semen was first used on dairy cows the selection of sires was not as focused as it is now. Some bulls only sired few offspring, whilst others sired many. In this study it was clear that BLK has been used quite intensively; they have by far the greatest average number of offspring per sire, whilst SIM have used many sires but each has only few offspring. For SIM, BAQ and CHA which all have an average of less than 100 offspring per sire, the estimation is more unreliable than for BLK and LIM that on average have a larger amount of offspring per sire. Especially BAQ and CHA have low reliabilities as they only had 40 and 43 different sires in the data set respectively.

In addition to different use of the sires, the use of sires within dam breed also varies. Only 5 % of the JER dams were inseminated with SIM compared to 14, 11 and 19 % for RDC, HOL and XXX respectively. The amount of BLK also varied greatly, JER and HOL dams most frequently had offspring with BLK sires (67 % and 65 % respectively) compared to 55 % for RDC and 45 % for XXX. This could impact the calculated survival rates; if the sire breeds are not used similarly across dam breeds it could cause bias in the results. If a sire breed is used primarily for a specific dam breed that has a lower survival rate, this will impact the sire breeds average survival rate. The herd effect could also possibly confound with the breed effects, as many herds only have dams of the same breed, and use the same sire breed. This makes it difficult to estimate the breed effects correctly.

No significant phenotypic trend was found despite negative tendencies. Large fluctuations between year, especially from 2000-2011 were apparent. In the future, as the amount of calves per year increases, it will be possible to more accurately predict the phenotypic trend. If the trend is predicted for young stock survival 1-30 days for 2011-2015 instead, the phenotypic trend is almost completely insignificant with a P-value of 0.99. For survival from 31-200 days in the same time period the trend is also insignificant, but the variation between years is greater. The Danish average for calf mortality from 1-30 days in dairy herds showed no significant trend from 2014-2016 either.

5.2.1 Mortality rates

Mortality rates may commonly be underestimated, as twin and multiple births or animals with incomplete information are mostly excluded from analysis. This is also the case in the present study. Average survival rates from 1-30 days after birth ranged from 92.0 % (JER) to 95.6 % (HOL and XXX) in this study. The average calf mortality from 1-30 days after birth in Danish dairy herds was found to be approximately 8 % (including death within the first 24 hours) (Raundal 2017). The results from this study are in concordance with the national average, if the first 24 hours are disregarded.

Hansen et al. (2003) found mortality rates of 2.4 and 3.1 % for HOL heifer and bull calves respectively for the period 1-14 days from birth. Fuerst-Waltl and Sørensen (2010) found mortality rates of 3.2 % for the period 1-30 days for HOL heifer calves. The estimated survival rates in this study are slightly lower than Fuerst-Waltl and Sørensen (2010) and in the same range as those

obtained by Hansen et al. (2003). The reason that survival rates are lower in this study is that heifer and bull calves are evaluated together, whilst Fuerst-Waltl and Sørensen (2010) only estimated mortality rates in heifer calves that have a higher survival compared to bull calves.

For young stock survival from 31-200 days, average survival rates ranged from 94.0 % (RDC) to 94.7 % (HOL). Fuerst-Waltl and Sørensen (2010) estimated the mortality rate from day 31-180 to be 2.66 % for HOL heifers. van Pelt et al. (2012) reported a survival rate of 97.5 % from 15-180 days in dairy calves raised in veal production. Again survival rates in this study are slightly lower, probably due to the inclusion of both heifer and bull calves and different production systems.

For survival of the whole period (1-200 days) survival rates were estimated to be from 89.3 % (JER) to 91.0 % (HOL) for both sexes. Norberg et al. (2013) stated that calf mortality is a larger problem in JER calves than for HOL and RDC. Mortality of Danish JER heifers has been reported to be 12-13 % compared to 5-6 % and 6-7 % Danish Holstein and RDC respectively (Norberg et al., 2013). Hansen et al. (2003) found a mortality rate of 6.6 % for HOL from 1-180 days. The Danish average mortality from 1-180 days after birth reflected similar, but slightly lower mortality rates than this study. It seems that the beef x dairy crossbred calves in this study have lower survival rates than purebred dairy calves, except for calves with JER dams who have a slightly higher survival rate compared to the national average for purebred calves.

Other studies have stated that dairy crossbred calves have higher survival rates (Sørensen et al., 2008; van Pelt et al., 2012), however Pardon et al. (2012), found a higher survival rate for beef x dairy crossbred calves in a white veal production system compared to purebred dairy calves. Mortality rates for beef cattle are ambiguous, some state higher mortality rates (Pardon et al., 2012), whilst others found similar mortality rates (Cundiff et al., 1986) to the mortality rates in this study. It is difficult to compare studies on beef cattle, as there are many different production systems, some are very intensive and others are extensive. For beef cattle, the Danish average mortality rate from 1-180 days after birth is lower than that for all dairy breeds. However, beef cattle in Denmark are often raised under conditions that are less extensive than dairy cattle, so comparisons are problematic.

The differences between dam breeds are quite clear; offspring with JER dams have the lowest survival from 1-200 days, whilst HOL and XXX have the highest survival rates. Interestingly it is RDC offspring that have the lowest survival rate from 31-200 days, but have the highest from 1-30 days. It should be noted that the results regarding RDC are more uncertain than for the other dam breeds due to a small amount of offspring in the data set. JER offspring have a low survival rate from 1-30 days, but are similar to the other dam breeds from 31-200 days. It would be natural to assume that this could be an effect of a difficult calving, but the average calving ease score for JER dams is actually the lowest compared to all other dam breeds. HOL have the highest average calving ease score which means they on average have the most difficult calvings, but the impact on the survival rate does not seem to have a large effect. Mccorquodale et al. (2013) similarly

found no significant effect of calving difficulty on the risk of mortality, but both Gulliksen et al. (2009) and Henderson et al. (2011) observed significant associations between calving difficult and calf mortality.

For the sire breeds, there are also distinct differences. In the first period (1-30 days) SIM and BLK have the highest survival rates of 95.6 and 95.5 % respectively, whilst BAQ have the lowest (93.9 %). According to the Danish average for pure bred beef cattle, it is LIM that has the highest survival rate from 1-30 days and CHA has the lowest. There are no average survival rates for purebred BLK, as there are very few individuals. From 31-200 days it is BAQ that has the lowest survival rate (91.4 %) and BLK has the highest (95.4 %). For the whole period 1-200 days BAQ and LIM with survival rates of 86.7 % and 87.7 % respectively are clearly the worst, and BLK and SIM are the best with 91.8 % and 91.1 % respectively. This could be due to the fact that SIM are not used to the same extent on JER dams as the other dam breeds.

All results regarding BAQ and CHA in this study are not as reliable as for the other breeds, as there are few offspring and only few sires. If there are too few sires, a single sire can have a large impact on the survival rates. This may be the case for the low survival rates in BAQ sired offspring. The results are in concordance with those found for beef sires used on dairy cows (McGuirk et al., 1998a). They also found that SIM and BLK had the lowest mortality rate and BAQ the highest. However, the mortality rates were only calculated for the first 48 hours after birth. The differences in the use of BAQ and CHA are small, but it seems they are used to a lesser extent on first parity cows. The low survival rates of BAQ can therefore not be explained by the distribution of the dam's parity.

Large differences between the use of sire breeds in first and later parities were found. LIM and SIM were used to a much greater extent on first parity cows, and BLK was used much less. This could bias the calculated mortality rates. Heifers have more difficult calvings and calf mortality is usually higher compared to older cows. Therefore, SIM and LIM could have been slightly negatively biased, whilst BLK is slightly positively biased as they are mostly used for older cows that have easier calvings and lower calf mortality.

As stated earlier there is a significant difference in survival rate between heifer and bull calves. The mortality rates in this study are higher than those found by van Pelt et al. (2012), but in concordance with those found by Hansen et al. (2003), who found a 2 % difference in survival rate between heifer and bull calves from 1-180 days. This could explain why some studies that are based only on heifers calves, find higher survival rates than in this study.

5.2.2 Heritabilities

The estimated genetic parameters found for young stock survival in this thesis, are low but similar to what other studies have previously found. The low heritabilities are due to low frequencies within the two traits, large environmental variation, and the fact that multiple factors affect calf mortality. Heritabilities were calculated on the underlying scale to take account for the binary

nature of the traits. Transformation to the underlying scale works well, but tends to overestimate heritabilities when the frequency of the trait and the observed heritability is high (Van Vleck 1972). This is because heritabilities of binary traits are dependent of the frequency (Norberg et al., 2013). As both the frequency and heritability estimates are low, the problem with overestimation should not be as large for young stock survival, and the approximation by Dempster and Lerner (1959) should be appropriate.

On the observed scale, the heritability for survival from 1-200 days was higher than survival from 1-30 days however; on the underlying scale it was opposite. This is due to a lower survival rate, and thereby a higher frequency in the whole period compared to 1-30 days. Even though, σ_A was lowest for 1-30 days, σ_E was also the lowest. This means that there is little genetic variation, but the amount of residual variation is also low, so the model fits the data well. For 31-200 days both σ_A and σ_E were higher, but σ_P was nearly the same as for 1-30 days. This indicates that more genetic variation is captured, despite having slightly more noise in the model. The σ_E was highest for 1-200 days, which indicates that there was more noise, and the model did not fit the data as well, which led to a lower heritability. This is presumably due to the herd effects being insufficient, as only the slaughter herd is accounted for in the model and information regarding the birth herd is disregarded.

The heritability estimate for survival from day 1-30 after birth was in line with Erf et al. (1990) , but double that found by Fuerst-Waltl and Sørensen (2010), Hansen et al. (2003) and van Pelt et al. (2012) in purebred HOL. Norberg et al. (2013) found a higher heritability in JER heifers, but estimates for JER are generally higher than for all other breeds. The estimates in this study were much larger for all traits except for the total period. For the total period the heritability was in line with Fuerst-Waltl and Sørensen (2010), Hansen et al. (2003) and van Pelt et al. (2012), but lower than that found by Norberg et al. (2013) in Jersey.

It seems that the heritabilities estimated in this study are in line with previous research, but are slightly higher than results obtained on HOL and lower than JER. The traits 1-30 and 31-200 days have the highest estimated heritabilities on the underlying scale. It therefore seems feasible to include them in the breeding value estimation for beef x dairy crossbred calves.

5.2.3 Breed differences

In the initial data set, crossbred cows with less than 12.5 % beef breed were included. The dam breed effects were accounted for in the model, but the breed composition in crossbred cows varies much more than for the three purebred dam breeds. This could give some bias in the data, as crossbred cows express heterosis that has not been accounted for in the model. Therefore, it was tested if more accurate estimates of the genetic parameters could be obtained by excluding the crossbred cows from the data. The heritability obtained was slightly larger than the estimate where crossbred cows were included. The additive genetic standard deviation was larger in the model without crossbred cows, but the residual standard deviation was almost the same, which

indicates that more genetic variation between the animals is accounted for when crossbred cows are not included.

It was attempted to estimate the genetic parameters for RDC alone, but this was not possible due to a small number of observations. It is expected that the number of beef x dairy calves will increase, which would increase the validity of RDC data. The heritability of young stock survival for calves with a Jersey dam is much larger than for the other breeds. This is due to higher calf mortality for Jersey and more genetic variation. It could be an advantage to split the evaluation into two separate evaluations, one for Jersey and one for Holstein. However, when the confidence intervals were investigated, it showed that there was no significant difference between dam breeds within sire breed. Norberg et al. (2013) found in their study on Danish Jersey heifer calves, higher heritabilities compared to studies on Holstein calves for the same time periods. The same was the case in this study. This indicates that heritabilities of young stock survival seem to be higher in Jersey than in other dairy breeds.

5.2.4 Genetic correlation

It was not possible to calculate significant genetic correlations between the two traits survival from 1-30 (period 1) and 31-200 (period 2) days after birth, or between the whole period and the second period. This is probably due to the data structure and a small amount of observations. Fuerst-Waltl and Sørensen (2010) were not able to estimate the genetic correlation between survival from day 1- 30 and day 365 until the day of calving as it would not converge. The majority of the studies that have presented genetic correlations have high standard errors (SE) of the estimates (Henderson et al., 2011; Hansen et al., 2012) and some did not present SEs (van Pelt et al., 2012). This indicates that calculation of genetic correlation for young stock survival is challenging, and if possible the estimates often have a high standard error.

It could be expected that the genetic correlation between the first and second period was moderate as the time periods do not overlap, and several studies have found the periods to be different traits as stated previously. Buch (2012) estimated a moderate genetic correlation of 0.51 for Holstein bull calves between the periods 1-30 and 31-183 days after birth. Similar results would be expected for this study.

A significant genetic correlation between the first period and the whole period was estimated to be 0.51 which is lower than previous studies. This could be due to small amount of observations and the construction of the model. The correlation between the second period and the whole period is expected to be high, as many of the observations are the same. This was also found by Norberg et al. (2013). The calculated estimate was not significant in this study, possibly because the traits were too similar, or that the data structure made it hard for the model to converge. Perhaps it will be possible in the future to predict more reliable results if more data becomes available.

It was attempted to use a sire model to calculate the genetic correlation in order to take the data structure into account. When using an animal model, all individuals would only have one observation for young stock survival in each time period. If the individual died during the first period, it does not have an observation in the following time period. This is problematic as all individuals in the second time period will have survived the first period. When using a sire model, all the offspring of the sire are included, and therefore all combinations are accounted for. However, as there are relatively few observations in the data set, not many bulls have enough offspring to predict a reliable result. This is why the predicted correlations have a high standard error, and some cannot be calculated.

5.2.5 Breeding values

All bulls with more than 100 offspring were selected for the comparison of the best and worst sires. As the frequency of calf mortality was low, small differences in the number of dead calves have a large impact on the individual sire. Therefore, it could have been beneficial and more accurate to evaluate sires with over 500 offspring instead. However, only very few sires could fulfill that requirement at present. In the future, as more offspring are born every year, it would presumably be possible, but for now a level of above 100 offspring was chosen.

van Pelt et al. (2012) found for Holstein bulls born between 1985-2009 that around 14 % of the bulls had favorable breeding values for survival from day 3-365 of plus one standard deviation or higher. They found a genetic standard deviation of 2.49 % and therefore concluded that it was possible to distinguish good and bad bulls from each other with regards to calf survival and therefore breed for a higher calf survival rate.

Norberg et al. (2013) found a difference of 8 % in breeding value for calf mortality between 1 and 180 days for the BV of the best and worst sires. For young stock survival from 1-30 and 31-200 days the average standard deviation was 1.0 and 2.1 % respectively. The breeding values for survival from 1-30 days and 31-200 days had a difference of 6 and 10 % respectively. This is in concordance with previous studies, and shows that there is large variation between bulls. The best bulls ensure that the survival rate is over 4 % higher than the average, whilst the worst bulls have a survival rate that is more than 3 % lower than the average for survival from 31-200 days. By using the best bulls more calves will survive, ensuring increased welfare and profit.

The differences in breeding value for offspring with JER or HOL dams are hard to compare, as not all bulls have a sufficient amount of offspring for both breeds. Therefore rank correlations have not been calculated. For all sires with more than 100 offspring, the standard deviation for offspring with JER dams was 2.3 % and 1.8 % for HOL dams. It is expected that the standard deviation is higher for JER as the frequency and genetic variation is higher.

Also, the sire breeds had different mean breeding values depending on the dam breed. In the future, when more data is available, it could be interesting to calculate rank correlations between sire breeding values for offspring with JER and HOL dams. This would unveil whether the bulls rank

in the same way between dam breeds, or if it is necessary to calculate sire breeding values independently for each dam breed.

Genetic trend

Both Carlen et al. (2016) and Norberg et al. (2013) found no genetic trend for in calf mortality and Fuerst-Waltl and Sørensen (2010) found a very small positive trend for survival from d 1-30 after birth, but none from d 1 until first calving. These slightly ambiguous results indicate that the genetic trend is very small, but is possibly slightly positive. This is in concordance with the results from the present study, that also indicate no or a slightly positive genetic trend for young stock survival from day 1-30 and day 31-200 respectively. This indicates that the trait has neither been deteriorating nor improving during recent years. By including young stock survival in the breeding goal for beef x dairy crossbred calves, both the genetic and phenotypic trend should hopefully begin to show an increase in survival rates.

6 Conclusion

Young stock survival is a large problem for farmers in the form of economic loss and reduced animal welfare. Both the phenotypic and genetic trends indicate that there has been little or no development in survival rate during the last years. In order to improve survival rates it is therefore necessary to include the trait in the routine genetic evaluation. For dairy and beef cattle this has already been instated, but not for beef x dairy crossbred calves.

Low, but significant heritabilities (0.045-0.075) for both survival traits in beef x dairy crossbred calves were found. Estimates were in line with or slightly higher than previous studies have found. It was not possible to calculate reliable estimates of phenotypic or genetic correlations between the traits, except for survival from 1-30 and 1-200 days after birth. Breed combinations with Danish Blue cattle sires outperformed all other sire breeds. The lowest survival rates were found for breed combinations with Jersey dams or Blonde d'Aquitaine sires. Breeding values ranged from -2.5 to 3.5 % and -5.4 to 4.7 % for survival from 1-30 days and 31-200 respectively. It seems feasible to breed for an increased young stock survival from day 1-30 and 31-200, as they are both significantly heritable and genetic variation for both traits exists. This will increase the survival rate of the calves and hereby increase animal welfare and decrease economic loss for the veal producers.

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