Norwegian University
of Life Sciences

Comparison of production and health status of purebred Holstein and Norwegian Red x Holstein crosses in the UK

Anne Gladsø Wibe

Animal Science – Breeding and genetics

Preface

'That's just the trouble with me, I give myself very good advice, but I very seldom follow it.'

- Lewis Carroll, "Alice in Wonderland"

Thank you to my friends and advisors for their patience and support.

Abstract

The goal of this thesis was to compare performance of purebred Holstein cows, Holstein crossed with Norwegian Red (NR) and various crossbreed combinations that included NR, by comparing their milk traits (kg. milk, fat yield, protein yield and somatic cell count), health (mastitis and lameness) and fertility (anoestrous and calving problems). A subgoal was to see how well commercial farm data from the UK could be used for statistical analyses.

Data was received from 5 herds in the UK, with records from 2010 to 2021. The data was collected via Uniform, a farm management tool where the farmer inputs their farm data. Cows and heifers were put into different groups based on the breed of their sire, maternal grandsire, and maternal great grandsire. Breed codes consisted of six letters, for example NRFHFH (NR being Norwegian Red and FH being Holstein), with the two first being the breed of the sire, the two next the maternal grandsire, and the two last the maternal great grandsire. Not all animals had data for all three generations of sires, and those that had breed information from one generation or less were removed from the study. Breed groups considered were pure Holstein, NRxFH (NR sire and FH maternal grandsire), FHxNR (FH sire and NR maternal grandsire) and NRX (NR sire and non-FH maternal grandsire, or non-FH sire and NR maternal grandsire).

Milk records were considered for 1 611 and 1 600 cows in total for all five herds for yield traits and somatic cell count (later used as somatic cell score (SCS)), respectively, while 2 510 individual cows and heifers were used when considering incidents of health and fertility problems. For milk related traits, analyses were only done for the breeds Holstein and NRxFH as there was little data for the other two breed groups. This gave a dataset for milk production with 2 976 observations and a dataset for SCS with 1 364 observations. All breed groups were considered for health and fertility problems.

The study found that Holstein had significantly higher milk yield but lower protein yield than the NRxFH, and that there was no significant effect of breed on fat yield or somatic cell score. Trends of Holstein having more cases of mastitis, calving problems and anoestrous than the crossbreeds were found, as well as the percentage of lame NR-crosses being higher than that for Holstein, but lack of data made it impossible to achieve statistically reliable results for health and fertility. It is possible that incentives are needed to have farmers register more data and thus improve the chances of high statistic reliability.

Sammendrag

Målet med oppgaven var å sammenligne ytelse hos renrasede Holsteinkyr, Holstein krysset med Norsk Rødt Fe (NRF) og forskjellige krysningskombinasjoner som inkluderte NRF ved å sammenligne melkeegenskaper (kg melk, fettytelse, proteinytelse og somatisk celletall), helse (mastitt og halthet) og fertilitet (anøstrus og kalvingsproblemer). Et undermål var å se hvor godt kommersielle gårdsdata fra Storbritannia kunne brukes i statistiske analyser.

Det ble mottatt data fra 5 gårder i Storbritannia, med data fra 2010 til 2021. Data ble innhentet via Uniform, et besetningsstyringsverktøy hvor bonden legger inn egne gårdsdata. Kyr og kviger ble puttet inn i forskjellige grupper basert på rasen til sin far, maternale bestefar og maternale oldefar. Rasekoder besto av seks bokstaver, for eksempel NRFHFH (der NR var Norsk Rødt Fe og FH var Holstein), hvor de to første bokstavene var rasen til far, de to neste rasen til maternal bestefar, og de to siste er maternal oldefars rase. Ikke alle dyrene hadde data for alle tre generasjoner med fedre, og de som hadde raseinformasjon for en eller færre generasjoner ble tatt ut av studien. Rase gruppene som ble vurdert var ren Holstein, NRxFH (NR-far og FH maternal bestefar), FHxNR (FH-far og NR maternal bestefar) og NRX (NR-far og ikke-FH maternal bestefar, eller ikke-FH-far og NR maternal bestefar).

Melkedata ble vurdert for 1611 og 1600 kyr totalt for alle besetninger, henholdsvis for ytelsesegenskaper og somatisk celletall (senere brukt som somatisk cellescore (SCS)), mens 2510 kyr og kviger ble brukt under vurdering av tilfeller av helse- og fertilitetsproblemer. For melkerelaterte egenskaper ble analyser kun gjort for rasene Holstein og NRxFH fordi det var lite data for de andre to rasegruppene. Dette ga et datasett for melkeproduksjon med 2976 observasjoner og et datasett for SCS med 1364 observasjoner. Alle rasegrupper ble vurdert for helse- og fertilitetsproblemer.

Studien fant at Holstein hadde signifikant høyere melkeytelse, men lavere proteinytelse enn NRxFH, og at det ikke var noen signifikant effekt av rase på fettytelse eller somatisk cellescore. Tendenser til at Holstein hadde flere tilfeller av mastitt, kalvingsproblem og anøstrus enn krysningene ble funnet, i tillegg til tendenser for høyere prosentandel av halthet hos NRF-krysningene enn for ren Holstein, men mangel på data gjorde det umulig å oppnå statistisk troverdige resultat for helse og fertilitet. Det er mulig at insentiver trengs for å få bønder til å registrere mer data og slik forbedre sjansene for høy statistisk troverdighet.

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1 Introduction

Sørensen et al. (2008) posited in their review that dairy income could be increased substantially by utilizing crossbreeding, in part due to positive effects on health and fertility. The health status of a dairy cow is of both great importance to the animal welfare and the economic result of the farm. It impacts what the cow has the resources to produce on a day to day basis, as well as her ability to get pregnant and bringing a calf to term (Miglior et al., 2017).

There are several studies on the effects on various traits when crossbreeding Holstein (FH) x Norwegian Red (NR), both in warmer climates (Ezra et al., 2016; Rinell & Heringstad, 2018) and those more akin to the temperate home climate of the Norwegian Red (Begley et al., 2009; Bobic et al., 2020; Buckley et al., 2014; Ferris et al., 2014; Heins et al., 2012; Sveberg et al., 2015).

Some studies find that the NR has better udder health and fertility than the HO (Rinell & Heringstad, 2018; Sveberg et al., 2015; Walsh et al., 2007). This has led to interest in crossbreeding the two breeds. Several studies have been done on this topic (Begley et al., 2009; Bobic et al., 2020; Ferris et al., 2014; Rinell & Heringstad, 2018), and while some agree that the introduction of the NR makes for an overall improvement, others pose the question of whether the drop in milk yield is worth the gain in other areas, and whether there actually is a gain at all (Ezra et al., 2016; McClearn et al., 2020).

2 Aim

The goal of this thesis was to compare performance of purebred Holstein cows, Holstein crossed with NR and various crossbreed combinations that included NR, by comparing their milk traits (kg. milk, fat yield, protein yield and somatic cell count), health (mastitis and lameness) and fertility (anoestrous and calving problems). A subgoal was to see how well commercial farm data from the UK could be used for statistical analyses.

3 Methods

Data was received from 5 herds in the UK, with records from 2010 to 2021. The data was collected via Uniform, a farm management tool where the farmer inputs their farm data. The farms were selected because they had relevant crossbreeds and were using Uniform. The farmers signed agreements giving the study access to the data. Data consisted of pedigree information, somatic cell count (SCC) for the latest lactation of each cow, production by lactation, and health and fertility data. The data was cleaned and handled in both Excel and RStudio.

The farms had different calving patterns, with two farms practicing calving all year round and three farms having a concentrated autumn block pattern. The herd sizes ranged from 200-400 milking cows per year (table 1).

Table 1: Herd number, geographical location, calving pattern, and milking herd size.

Herd number	Location	Calving pattern	No. milking cows
1	Devon	All year round	250
2	Devon	Autumn block	400
3	Cornwall	Autumn block	200
4	Shropshire	Autumn block	400
5	Cheshire	All year round	375

3.1 Data handling

To make data more reliable and manageable, individuals without ear tag numbers were removed from both pedigree, fertility, production, SCC, and health records. Lactations were modified for all data to present as '1', '2' and '3+', with '1' meaning cows in first lactation, '2' meaning cows in second lactation and '3+' meaning cows in third lactation or higher.

3.1.1 Pedigree

Pedigree information and fertility information were combined so that only cattle that also had fertility data would be considered later. This reduced the pedigree from 5 853 individuals to 3 953. The initial pedigree information only contained two generations, i.e., an individual's sire and maternal grandsire. To get maternal great grandsire into the dataset, all individuals that were dams of other individuals in the data had their maternal grandsire data duplicated and put in as maternal great grandsire for their daughter(s). When sire data was missing, sires

generally had data for names, but not AI codes (artificial insemination codes) which gave the breed of the sire. Names of the missing sires, grandsires, or great grandsires were looked up in a spreadsheet provided by Ellen Rinell (personal communication, March 25, 2022) with the names and AI codes of bulls used in the UK and manually inserted where possible.

Cows and heifers were put into different groups based on the breed of their sire, maternal grandsire, and maternal great grandsire. Breed codes consisted of six letters, for example NRFHFH (NR being Norwegian Red and FH being Holstein), with the two first being the breed of the sire, the two next the maternal grandsire, and the two last the maternal great grandsire.

Not all animals had data for all three generations of sires, and those that had breed information from one generation or less were removed from the study. Individuals with a breed code of FHFHXX (FH = Holstein, and XX meaning breed code was unknown) were assumed to be FHFHFH, and thus added into the "Holstein" group. Cows with a NR-sire and FH-grandsire were put in the "NRxFH" group, regardless of breed of the great grandsire. Cows with a FH-sire and NR-grandsire were put in the "FHxNR" group, regardless of the breed of the great grandsire. The NRX group consisted of individuals with NR-sires or -grandsires combined with various other breeds. A total of 32 different NR-sires were used across the herds. Other combinations of breeds within the herds were not considered in the study.

This resulted in a pedigree of 2 510 cows and heifers in total for all herds. The spread of breeds within herds and in total after data cleaning can be seen in table 2.

Table 2: Number of cattle (cows and heifers) of each breed in each herd, sum of cattle per herd, sum of cattle per breed in total, and sum of cattle in total in the pedigree.

	FHxNR	Holstein	NRX	NRxFH	Sum herd
Herd 1	56	152	76	106	390
Herd 2	12	15	192	122	341
Herd 3	63	136	24	105	328
Herd 4	30	622	7	206	865
Herd 5	2	452	17	115	586
Sum breed	163	1377	316	654	2 510

3.1.2 Milk, fat and protein

Milk production data had 8 088 records and 3 127 cows for all herds and all breeds. The dataset provided calculations of 305-day yield for kg. milk, and 305-day percentage of fat and protein based on internal calculations from NMR and CIS (the milk recording organizations of the herds), which had also been updated with an internal calculation in the Uniform program (E. Rinell, personal communication, June 7, 2022).

NA-data and cows with less than 60 DIM and longer than 360 DIM were removed from the dataset. It was then combined with the pedigree data, and individuals without production records or pedigree data were disregarded. Unreasonable data was removed from the 305-day calculations for kg. milk. This gave a total of 3 427 milk records for 1 611 cows from all herds (table 3 and 4).

Table 3: Number of cows of each breed in each herd, sum of cows per herd, sum of cows per breed in total, and sum of cows in total in the milk production data.

	FHxNR	Holstein	NRX	NRxFH	Sum herd
Herd 1	37	127	44	95	303
Herd 2	12	12	103	86	213
Herd 3	19	99	9	80	207
Herd 4	0	369	0	66	435
Herd 5	0	361	9	83	453
Sum breed	68	968	165	410	1611

Table 4: Number of data points for each breed in each herd in each lactation, and sums of each lactation in each herd, sums of data for each breed in all lactations in all herds, and total number of datapoints.

	Lactation	FHxNR	Holstein	NRX	NRxFH	Sum lact. herd
Herd 1	Lact 1	36	104	42	85	267
	Lact 2	19	86	24	74	203
	Lact 3	20	181	18	122	341
Herd 2	Lact 1	8	9	76	63	156
	Lact 2	7	7	59	48	121
	Lact 3	12	10	76	105	203
Herd 3	Lact 1	15	72	9	65	161
	Lact 2	6	59	3	49	117
	Lact 3	8	142	3	56	209
Herd 4	Lact 1	0	225	0	49	274
	Lact 2	0	180	0	29	209
	Lact 3	0	226	0	9	235
Herd 5	Lact 1	0	275	9	81	365
	Lact 2	0	232	1	23	256
	Lact 3	0	310	0	0	310
Sum breed		131	2118	320	858	3427

3.1.3 SCC

The initial cell count data showed 118 725 SCC-tests over ten years, as seen in table 5. The data was then checked against ear tags from the cleaned milk production data, and only individuals that were in both data sets were kept for further consideration, resulting in 51 005 SCC-tests. One NRX cow from herd 3 was also removed for having a cell count of 9 999 999 which is the highest cell count Uniform will register and being the only cow in its lactation, making it a notable outlier in the data. Finally, any observations called 0 or NA, and any individuals with less than 3 SCC-tests were taken out, resulting in 50 986 tests and 1 600 cows in total for all herds.

Table 5: Number of SCC-tests to be used in SCC-calculations for all herds before and after data handling, given for each herd and in total, and the number of cows, in each herd and in total, after data handling.

	Herd 1	Herd 2	Herd 3	Herd 4	Herd 5	Sum
Before	18 011	27 460	14 682	27 638	30 934	118 725
After	7 982	7 337	6 535	15 854	13 278	50 986
Final no. cows	299	212	206	433	450	1 600

To prepare data for statistical analysis, the SCC was log transformed to get the somatic cell score (SCS). The mean SCS for each cow was then calculated and will hereby be referred to as SCS.

3.1.4 Health and fertility

For the health data, there were many naming inconsistencies between farms for the same disease. Variations were manually changed to match a list of terms from a menu in the Uniform system, but only if there was no way of misrepresenting the data i.e., changing "aborted" to "Abortion". Observations with unclear descriptions were not changed to match the list for fear of misconstruing data, and therefore disregarded from the statistical analyses.

Health and fertility data were matched to the pedigree, giving 1 611 individuals for mastitis and calving problems, and 2 510 individuals for lameness and anoestrous because heifers were also considered. Table 6 shows number of observations, and number and percentage of cattle affected by the four different health problems.

Table 6: Number of observations of mastitis, lameness, calving problems and anoestrous, number of cattle (cattle defined as both cows and heifers) affected by each problem, and percentage of total cattle affected (total cows for mastitis and calving problems, and total cattle for lameness and anoestrous).

Health problem	No. of observations	No. of cows/cattle affected	% of total cows/ cattle
Mastitis	462	172	10,67%
Lameness	191	71	2,83%
Calving prob.	81	81	5,03%
Anoestrous	23	22	0,88%

3.2   Statistical models

Analyses were made and run with R Statistical Software (RStudio Team, 2021). Generalized linear models were used for assessing milk yield, fat yield, protein yield and SCS using the glm() function in RStudio. Analyses were only done for the breeds Holstein and NRxFH as there was little data for the other two breed groups. This gave a dataset for milk production with 2 976 observations and a dataset for SCS with 1 364 observations.

The same base model was used for milk yield, fat yield, protein yield, and SCS, and was as follows:

$$Y_{ijkl} = Breed_i + Lactation_j + Herd_k + YearMonth_l + e_{ijkl}$$

- Y_{ijkl} was the observed value of the trait
- $Breed_i$ was the fixed effect of breed group i (Holstein or NRxFH)
- $Lactation_j$ was the fixed effect of lactation j (1, 2 or 3+)
- $Herd_k$ was the fixed effect of herd k (1, 2, 3, 4 or 5)
- $YearMonth_l$ was the fixed effect of the year and month l (year: 2012-2021; month: 1-12)* in which a cow calved
    - *from month 3 in 2012, and until month 10 in 2021
- e_{ijkl} was the residual error

Model effects were excluded if they were not significant at $P < 0.1$. The model remained as described for milk and protein yield. For fat yield and SCS, the effect of breed was not significant. Due to this, the results of these traits were excluded from the thesis as the basis for comparing breeds was lost.

Least square means (LSM) were estimated for the breed variables in the models at a 95% confidence level to check if differences between the two breeds were significant for the traits.

While the intent was to run analyses for mastitis, lameness, calving problems and anoestrous, it was impossible to make reliable statistical analyses for the traits due to lack of data. The data available has been presented in more detailed tables and figures in the results to show the apparent trends.

4   Results

4.1   Explanation of boxplots

The black line within the box represents the median, and the whiskers (lines over and under the coloured box) represent the upper and lower 25% of observations. The coloured box (the interquartile range) represents 50% of the observations, with 25 % on either side of the median. Outliers (black dots) in all boxplots were defined as any value that was more than 1,5 times above the interquartile range or 1,5 times below the interquartile range.

4.2   Production

4.2.1   Milk

As seen in figure 1, the Holstein had the highest median milk yield in all herds as well as having the highest registered milk yield for all but one herd. Four of the five herds had similar ranges for milk yield. The exception was herd 2, which had higher median milk yields than the other herds for both breeds. There was a significant effect of breed within herd in favour of the Holstein for all herds but herd 2, in which there was no significance between the two breeds (table 7).
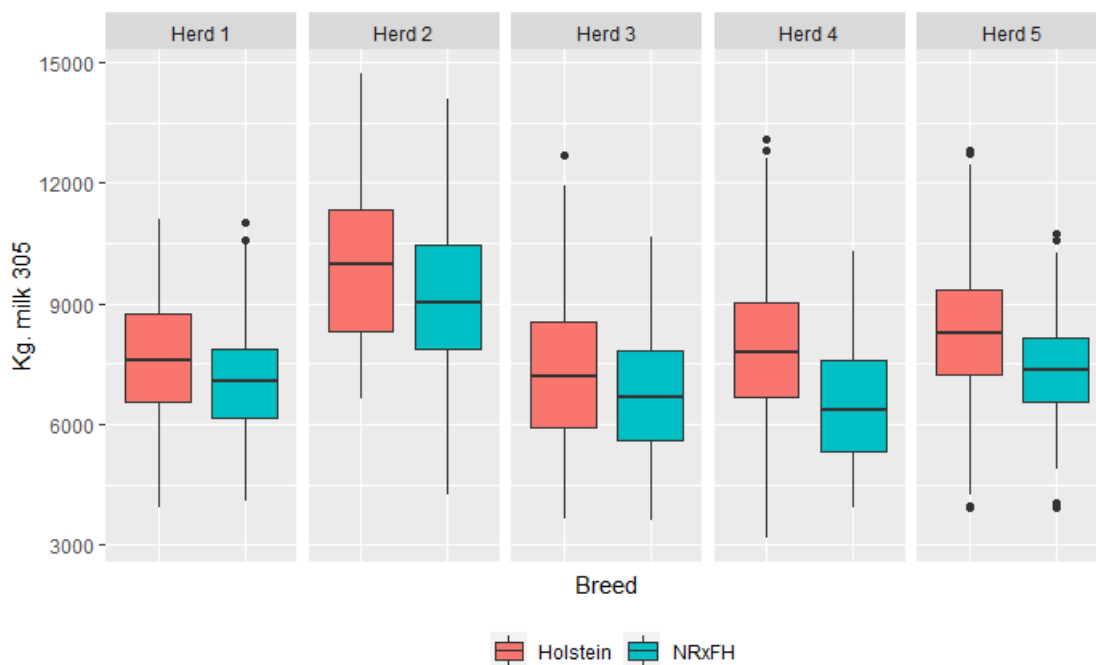

Figure 1: Calculated milk yield at 305 DIM for each breed in each herd.

Table 7: Least square means (LSM), standard error (SE), and lower and upper confidence levels (CL) for milk yield for each breed in each herd.

Milk	Herd	LSM	SE	Lower CL	Upper CL
Holstein	Herd 1	7546	71,0	7406	7685
	Herd 2	9427	118,9	9194	9660
	Herd 3	7176	78,9	7021	7330
	Herd 4	7735	62,6	7612	7857
	Herd 5	8449	58,6	8334	8564
NRxFH	Herd 1	7130	79,3	6974	7285
	Herd 2	9011	100,5	8814	9208
	Herd 3	6760	91,8	6580	6940
	Herd 4	7319	90,8	7141	7497
	Herd 5	8033	100,1	7837	8229

Figure 2 shows an increase in milk yield in later lactations for both breeds, with Holstein staying slightly higher through all lactations. Table 8 shows that there was a significant increase in milk yield within breeds with increase in lactation. The Holstein had a significantly higher yield than the NRxFH within each lactation.
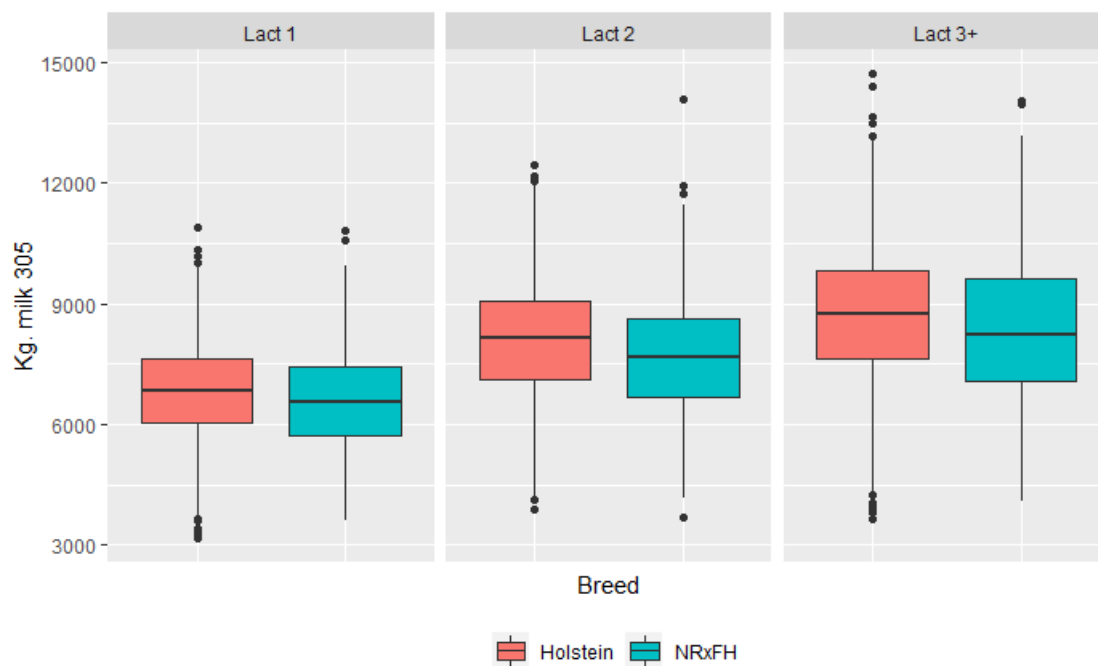

Figure 2: Calculated milk yield at 305 DIM for each breed in each lactation.

Table 8: Least square means (LSM), standard error (SE), and lower and upper confidence levels (CL) for milk yield for each breed in each lactation.

Milk	Lactation	LSM	SE	Lower CL	Upper CL
	1	6982	63,3	6858	7106
Holstein	2	8245	65,0	8118	8373
	3+	8971	55,9	8862	9081
	1	6566	67,2	6435	6698
NRxFH	2	7829	77,4	7678	7981
	3+	8556	84,0	8391	8720

4.2.2   Protein

Results for protein yield can be seen in figure 3 and table 9. While the NRxFH had a slightly higher LSM than Holstein in every herd, there was no significant effect of breed within herd. Between herds, herd 2 and 3 respectively had the lowest and highest protein yielding cows for both breeds. The NRxFH in herd 2 had a significantly lower yield than both breeds in herd 3 and 5, while Holstein in herd 2 had significantly lower yields than NRxFH in all other herds, as well as Holstein in herd 3 and 5. From herd 3, both Holstein and NRxFH had a significantly higher yield than Holstein in all other herds, as well as higher than other NRxFH in all other herds but herd 5.
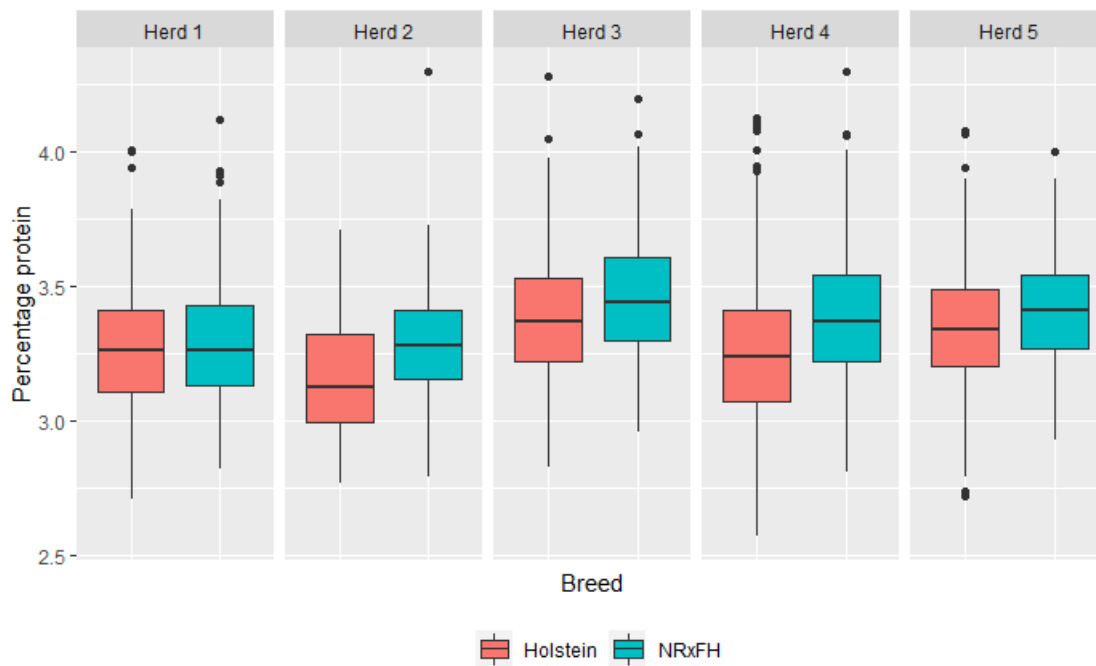
Figure 3: Calculated 305-day protein yield (%) for each cow in each breed in each herd.

Table 9: Least square means (LSM), standard error (SE), and lower and upper confidence levels (CL) for protein yield for each breed in each herd.

Protein	Herd	LSM	SE	Lower CL	Upper CL
	Herd 1	3,26	0,0115	3,23	3,28
	Herd 2	3,21	0,0191	3,17	3,25
Holstein	Herd 3	3,40	0,0127	3,37	3,42
	Herd 4	3,26	0,0101	3,24	3,28
	Herd 5	3,35	0,0095	3,33	3,36
	Herd 1	3,30	0,0128	3,27	3,32
	Herd 2	3,25	0,0162	3,22	3,28
NRxFH	Herd 3	3,43	0,0148	3,41	3,46
	Herd 4	3,29	0,0146	3,27	3,32
	Herd 5	3,38	0,0162	3,35	3,41

The protein yield between lactations was more similar than that between herds (figure 4). There was no significant difference between yields within breeds in lactation 1 and 3 or over

but yield in lactation 2 was significantly higher within both breeds (table 10). The NRxFH maintained a higher mean yield through every lactation, but there was only a significant difference between breeds in the first lactation.
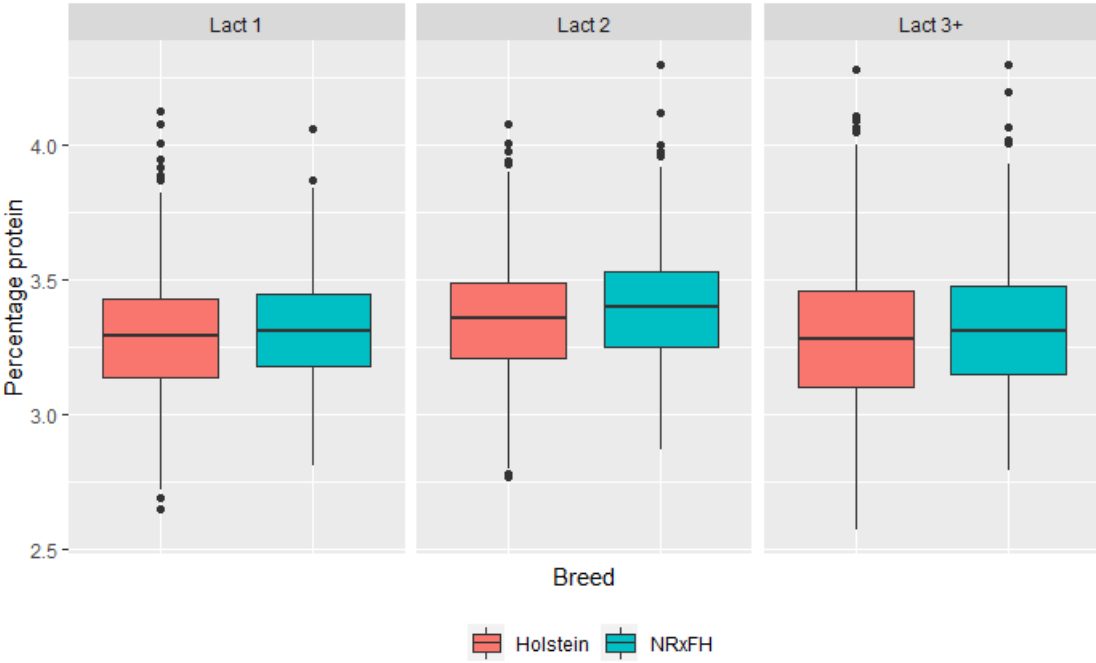

Figure 4: Calculated 305-day protein yield (%) for each cow in each breed in each lactation.

Table 10: Least square means (LSM), standard error (SE), and lower and upper confidence levels (CL) for protein yield for each breed in each lactation.

Protein	Lactation	LSM	SE	Lower CL	Upper CL
	1	3,27	0,0102	3,25	3,29
Holstein	2	3,35	0,0105	3,32	3,37
	3+	3,26	0,0090	3,25	3,28
	1	3,31	0,0108	3,29	3,33
NRxFH	2	3,38	0,0125	3,36	3,41
	3+	3,30	0,0136	3,27	3,33

4.3 Health

In table 11 the number of registered cases of lameness and mastitis per herd can be seen. Most herds have more cases of mastitis than lameness, except for herd 2.

Table 11: Number of cases of lameness and mastitis registered in each herd.

Herd	Mastitis	Lameness
1	81	3
2	5	146
3	46	0
4	222	8
5	108	34
No. of incidents	462	191

For mastitis, 91 out of 263 registrations were individuals that were affected twice or more times (table 12). Of the cows suffering from lameness, 45 of 116 cows were registered as lame twice or more times (table 13). In total, 379 individual cows were affected by mastitis and lameness. For both diseases, most individuals were only affected once.

Table 12: Number of cows registered as having mastitis one or more times.

	Mastitis	
Times registered		**No. of cows**
1		172
2		42
3		31
4		7
5		1
6		1
7		3
8		1
9		5
Total cows		**263**
Cows registered several times		**91**

Table 13: Number of cows registered as lame one or more times.

	Lameness	
Times registered	**No. of cows**	
1		71
2		28

3	12
4	1
6	4
Total cows	**116**
Cows registered several times	**45**

4.3.1 Mastitis

In table 14 the maximum number of times an individual was diagnosed with mastitis, the mean of the breed, the minimum number of times an individual was diagnosed with mastitis and the standard deviation. Sum shows number of individual cows registered with mastitis per breed. The Holstein had the highest maximum number, mean and standard deviation, as well as the highest number of individuals suffering from mastitis. FHxNR had a nearly identical mean, but a much lower maximum number, and a much lower number of individuals affected. The NRX and NRxFH had similar means and standard deviations, but there were nearly four times as many NRxFH individuals with mastitis, and the NRX had a slightly lower maximum number of times an individual was diagnosed with mastitis.

Table 14: Maximum, mean, minimum and standard deviation of registered cases of mastitis per breed, and sum being individuals registered as lame for each breed.

	Mastitis				
Breed	*Max*	*Mean*	*Min*	*SD*	*Sum*
FHxNR	*3*	*1.83*	*1*	*0.98*	*6*
Holstein	*9*	*1.85*	*1*	*1.63*	*210*
NRX	*3*	*1.30*	*1*	*0.67*	*10*
NRxFH	*4*	*1.35*	*1*	*0.75*	*37*

In figure 5 it can be seen that incidents of mastitis seem to increase in later lactations for all breeds.
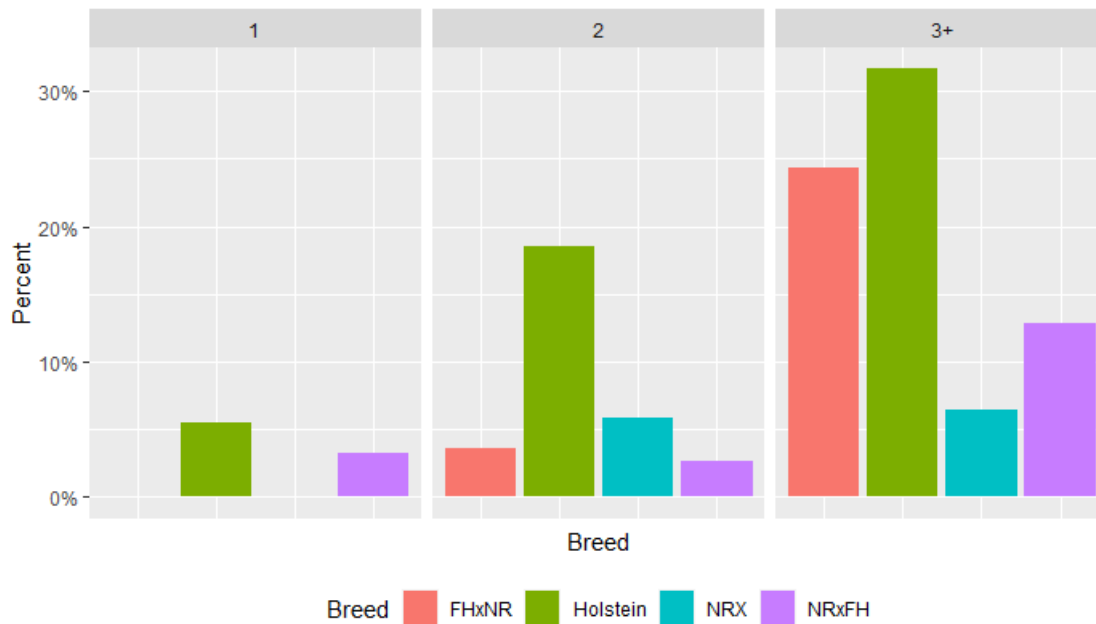
Figure 5: Percentage of mastitis incidents in each breed in each lactation.

4.3.2 Lameness

Table 15 shows the maximum number of times an individual was registered as lame, the mean of the breed, the minimum number of times an individual was registered as lame and the standard deviation. Sum shows number of individual cows registered with lameness per breed. The NRX and the NRxFH breeds have the highest maximum numbers, and the highest standard deviations. The Holstein cows had the lowest mean and fewer number of registrations per individual, but the number of individuals suffering from lameness was nearly the same as for NRX and NRxFH. FHxNR had a low mean, a low maximum number and few individuals suffering from lameness.

Table 15: Maximum, mean, minimum and standard deviation of registered cases of lameness per breed, and sum being individuals registered as lame for each breed.

	Lameness				
Breed	**Max**	**Mean**	**Min**	**SD**	**Sum**
FHxNR	*3*	*1.43*	*1*	*0.78*	*7*
Holstein	*3*	*1.21*	*1*	*0.47*	*38*
NRX	*6*	*1.92*	*1*	*1.44*	*37*
NRxFH	*6*	*1.88*	*1*	*1.07*	*34*

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Like with mastitis, figure 6 shows an increase in lameness incidents in older cows, and especially for non-purebred individuals.
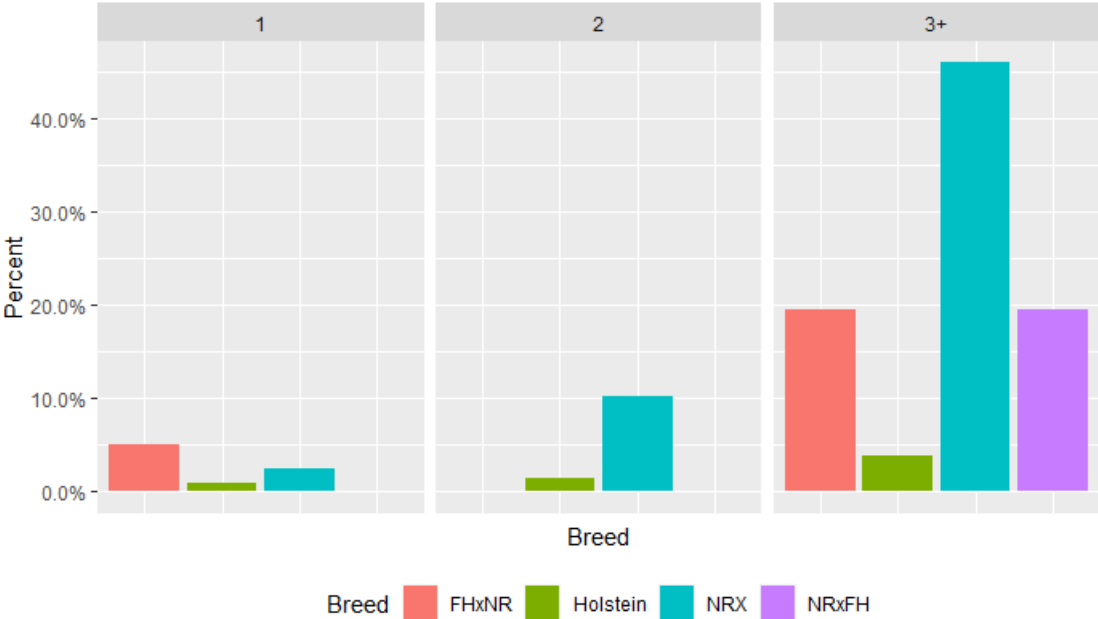

Figure 6: Percentage of lameness incidents in each breed in each lactation.

4.4 Fertility

4.4.1 Anoestrous

Two herds, with different calving systems, had registrations of anoestrous. Table 16 gives an overview of the number of cows affected in each herd. No heifers or first time calvers suffered from anoestrous, while all but two cases were registered in lactation 3 or over. Herd 1 had 20 registered cases in total, while herd 3 had three registered cases in total. Holstein and NRxFH were represented in both herds, while NRX was only affected in herd 1. One of the Holstein cows from herd 1 was treated twice, while all other observations were for different cows.

Table 16: Cows treated for anoestrous shown by herd, breed, and lactation number.

Herd	Breed	Lact. No.	No. of observations
1	Holstein	3+	12
1	NRX	2	1
1	NRxFH	3+	7
3	Holstein	2	1
3	NRxFH	3+	2

4.4.2 Calving problems

There was a total of 81 calving problems registered in the fertility data for all the herds (table 17). The breed with most registered problems was the Holstein with a total of 60 observations, followed by NRxFH with 12 observations, and then FHxNR with 5 and NRX with 4 observations.

Table 17: Number of registered calving problems for each breed in each herd.

Herd	Breed	No. of observations
1	FHxNR	2
1	Holstein	10
1	NRxFH	2
2	NRX	4
2	NRxFH	3
3	FHxNR	3
3	Holstein	6
3	NRxFH	5
4	Holstein	36
5	Holstein	8
5	NRxFH	2

The difference in severity of calving problems can be seen in figure 7. Most of the registrations were of the less severe kind, namely "Assistance needed" and "Slight problem", while the rest were of the more severe kind. The two breeds with the fewest observations were exclusively of the less severe kind except for one observation for first lactation NRX, where there was a case of "Extreme difficulty". The NRxFH required both a caesarean and help with considerable force two times. The Holstein showed the greatest spread in severity of problems, with most observations being of the less severe kind.
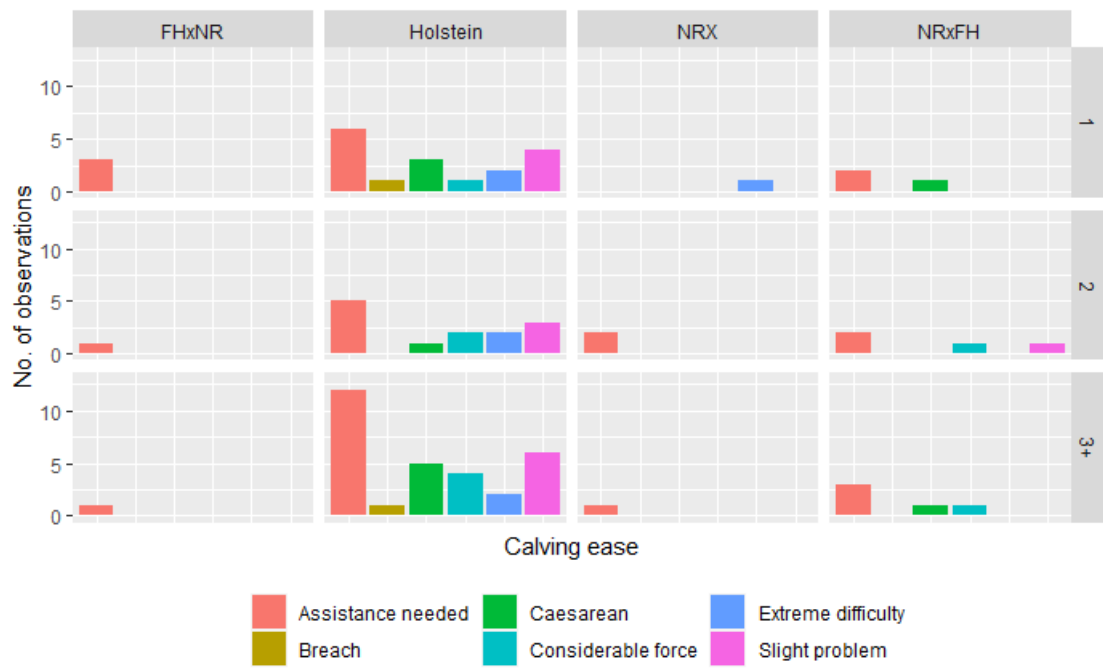
Figure 7: Overview of severity and frequency of calving problems within each breed group and lactation.

5 Discussion

5.1 Production

In this study, it was found that Holstein had significantly higher milk yield but lower protein yield than the NR-crossbreeds, and that there was no significant effect of breed on fat yield or somatic cell score. This was somewhat in line with another study which found that crossbreeds of Israeli Holstein and NR gave slightly higher protein concentration but gave insignificant results for fat concentration and otherwise had lower yields than the purebreds (Ezra et al., 2016).

This differed from the results of Heins et al. (2006) looking at different crosses, amongst them Scandinavian Red (SR), which found that pure Holsteins had both higher milk and protein yields than the crossbreeds. However, they also found fat yield to be lower in Holsteins, and that when testing for fat plus protein production there was no significant difference between purebreds and crosses with SR as opposed to the other crosses which showed lower production than the Holstein. The same was found about fat plus protein production in a follow up study a few years later (Heins et al., 2012).

Yet another study comparing pure Holstein with crosses with Jersey and 3-way crosses with NR found that herds with low fat and protein contents would benefit greatly from crossbreeding, but also concluding that herds with average contents would experience no significant benefits overall (McClearn et al., 2020). A Croatian study looking into differences in production in first lactation of purebred Holstein and crosses with NR found that the crossbreds outperformed the purebreds for both fat and protein in a standard 305 day lactation, as well as having a higher milk yield, though the latter was not significant (Bobic et al., 2020). In other words, the results were both supported and undermined by previous research in equal measure.

5.2 Health and fertility

The Holsteins heavy focus on milk yield over many years has reportedly had a negative impact on the overall fertility and health of the breed (Miglior et al., 2005; Royal et al., 2000; Walsh et al., 2007), though there has been progress in the fertility of the Holstein cow since the focus on fertility gained more weight internationally (Norman et al., 2009; Pryce et al., 2014). Norwegian farmers have been focusing on health and fertility since the 1970s (Heringstad & Østerås, 2013). This has led to Norwegian Red cattle having good results for

both, with an especially positive development since the 1990s (Østerås et al., 2007). The combination of Holstein and NR has therefore been a point of some interest internationally (Buckley et al., 2014). The breeding goal for NR has since 2019 included claws in their total merit index at a weight of 3,8%, but the heritability is quite low with a response of 0,05, while udder health has a weight of 13,4%, with a response of 0,34 (Geno, 2020a). According to Geno's overview, there was a greater weight put on health in and prior to 2010, which is when the first of the cows in the data were born (2020b). A study done with Holstein cows on the relationship between milk yield and clinical mastitis found that a side effect of high milk yield is a tendency for higher incidents of mastitis (Nakov et al., 2012). Bobic et al. (2020) found that the purebred Holstein had more trouble with mastitis, while crossbreds with NR were more prone to hoof problems. With all this in mind, the apparent trends of Holstein having more cases of mastitis, calving problems and anoestrous than the crossbreeds seem to coincide with previous studies, as well as the percentage of lame NR-crosses being higher than that for Holstein.

The results for lameness show more cases in lactation 3+, which coincides with a study on lameness and claw lesions in NR cows in free stalls (Sogstad et al., 2005) that found parity three and over to be one of the risk factors for lameness. Late lactations were also found to be associated with higher incidents of lameness by Alban (1995), when comparing different breeds of Danish dairy cows.

Year-round calving systems tend to struggle more with detection of oestrus and having lower conception rates than seasonal calving systems. Seasonal calving systems have an easier time with detection of oestrus in part due to more cattle being in similar cycles, and therefore often forming sexually active groups that make it easier to spot when animals are ready for insemination, which in turn can lead to higher conception rates. This concentrated form of reproduction does however increase the necessity of making sure the cows are pregnant within a certain time frame, or the farmer may have to cull non-pregnant cows or keep a non-pregnant cow until the beginning of the next breeding season (Buckley et al., 2014; McDougall, 2006). As such, it could have been expected to see more effect of calving system on fertility. This may of course have been the case had there been more data.

Despite the trends found seeming to follow along with previous studies, it is however important to remember that the amount of data for all health and fertility problems was far too low to be able to assert anything about effect of breed.

5.3   Challenges

It is possible that results for production would have been different if the 305-day values were calculated for the thesis, instead of using Uniform's calculations which turned out to be unlikely in at least a handful of cases and therefore removed from the data. This would also make it possible to say how calculations were made, while the formula used by Uniform was unknown to the author. It is always conceivable that using a different statistical model may have been a better fit for the data.

The main challenge was however the quality of data. It became clear that the routines for registering data was quite different from herd to herd. Inconsistencies in input and lacks in data resulted in a lot of data being disregarded from this study. There was a lot of lacking pedigree information, and this made it difficult to ensure that the individuals in each breed group truly consisted of the assumed breeds. While a cow with the breed code NRXXFH could be assumed to have a grandsire that was a Holstein, making the code NRFHFH and as such belong to the NRxFH group, there was also the possibility of XX being an entirely different breed and as such belonging to the NRX group. This could have falsely skewed the performance results of the breed groups both in positive and negative directions.

It was also unfortunate that not all breeds were represented in all herds, and not all breeds that were in the herds were represented in each lactation. More even breed representation would have made herd effect lower and as such made it easier to compare breeds instead.

Out of several thousand cows and heifers across five farms and over the course of 10 years, only 723 individuals were registered as having any form of disease. This was in part due to quite a lot of health data that had been manually put in by farmers instead of checked off in boxes of pre-approved definitions. This led to having to choose between either guessing what the manual input meant or disregarding the data, which naturally lead to a lot of data being disregarded. The subsequent lack of data made for difficulties when attempting to run analyses, as the sample size compared to the total group size was very small.

It is difficult to say whether the lacks in data were due to difficulties with input, lack of interest in the farmers to register data, or simple human error and forgetfulness. It is also possible that since Uniform is a farm management tool, that farmers only register data that they find relevant for themselves and may also have some sort of physical records where they keep information that they might not see the need to put into Uniform. Incentives may be

needed to have farmers register more data and thus improve the chances of high statistic reliability.

5.4   Further studies

While some research supports the findings of this thesis, there are just as many that contradict them. It would therefore be interesting and favourable to look at more data from several herds to see if the results remain the same, or if more data changes the results significantly. It would also be very favourable to have more reliable pedigree data to ensure that breed performance would not be misrepresented. This thesis found large variation in breed performance between herds, but it must be noted that the number of cows in each breed group and lactation varied greatly between herds as well. By comparing herds with more uniform and preferably higher numbers, the effect of herd would be reduced, and it would be easier to compare breeds. In such a case, it would also be increasingly necessary to look at the effect of season in regard to calving pattern and changes in milk yield throughout the year.

6   Conclusion

It was found that Holstein had significantly higher milk yield but lower protein yield than the NRxFH, and that there was no significant effect of breed on fat yield or somatic cell score.
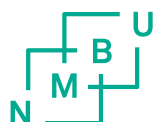
Trends of Holstein having more cases of mastitis, calving problems and anoestrous than the crossbreeds seem to coincide with previous studies, as well as the percentage of lame NR-crosses being higher than that for Holstein were found, but lack of data made it impossible to achieve statistically reliable results. More data for all breed groups would have made for better analyses. Inconsistencies in input and lacking data resulted in a lot of data being disregarded for this study. It is possible that incentives are needed to have farmers register more data and thus improve the chances of high statistic reliability.

This thesis found large variation in breed performance between herds, but it must be noted that the number of cows in each breed group and lactation varied greatly between herds as well. By comparing herds with more uniform and preferably higher numbers, the effect of herd would be reduced, and it may have been easier to compare breeds.

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