Jutland cattle (*Heidekoe*) of the Stroomdal herd

Evaluation of pedigree information and genetic comparison with the Dutch native dual-purpose cattle breeds

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Summary - The population Jutland or Heath cattle (‘*Heidekoe*’ in Dutch) in the Netherlands contains less than 100 breeding females (status 2021). Complete and reliable pedigree information is essential in order to minimize inbreeding rates in this small population. Centre for Genetic Resources, the Netherlands (CGN) of Wageningen University & Research (WUR) performed several analyses of the Jutland cattle populations in 2021/2022 for ‘*Stichting Schaapskudde Het Stroomdal’*. The results showed higher mean kinships for the younger generations than for the older animals. The Jutland cattle can be genetically distinguished from the Dutch native (dual purpose) cattle breeds. Though with just hundred breeding females registered in the Netherlands, it is a challenge to maintain the Jutland cattle as a separate population on its own. The advice is therefore to set up a sustainable breeding programme for the long term, working together with all Dutch Jutland cattle farmers or shepherds and explore possible collaborations and exchange of genetic material with Danish organisations involved with the conservation and breeding programme for Jutland cattle in Denmark.

Samenvatting - Gezien de kleine populatie Heidekoe in Nederland, minder dan 100 volwassen vrouwelijke fokdieren (status 2021), is het belangrijk om te sterke inteelttoename te voorkomen, en zijn complete en betrouwbare afstammingsgegevens essentieel. Centrum voor Genetische bronnen Nederland (CGN), van Wageningen University & Research (WUR) heeft in 2021/2022 meerdere analyses van de populatie Heidekoe uitgevoerd voor Stichting Schaapskudde Het Stroomdal. Jongere generaties lieten veelal een hogere mean kinship (gemiddelde verwantschap) zien dan de groep oudere dieren. Door de mean kinship van de populatie te monitoren kunnen op tijd maatregelen worden genomen om inteelt te beperken. De Heidekoe in deze dataset zijn als populatie genetisch goed te onderscheiden van de erkende Nederlandse dubbeldoel runderrassen. Maar dit maakt de Heidekoe nog niet een stabiel ras met een eigen fokpopulatie. Het dringende advies luidt om gezamenlijk, met alle veehouders en herders met Heidekoe, een duurzaam fokprogramma op te stellen voor de lange termijn. Een tweede advies is om contact op te nemen met Deense organisaties die betrokken zijn bij het beheer van de levende populaties en de genenbank van het vergelijkbare ras in Denemarken (Jutland vee).

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Foreword

Centre for Genetic Resources, the Netherlands (CGN) offers technical and strategic support in the development of sustainable breeding programmes and the conservation of genetic diversity within the Dutch livestock breeds. Apart from the Dutch livestock breeds officially recognized by the Dutch government, CGN (at request) offers advice to other organisations involved in other (native) livestock breeds as well. With a focus on the conservation of genetic diversity and sustainable use of available breeding animals.

Jutland cattle (Heidekoe in Dutch) is a cattle breed that originally lived in the Netherlands and was kept for a specific purpose, namely grazing the heath. After all the animals disappeared from the Netherlands, a reintroduction of the Jutland cattle breed in the Netherlands was initiated at the start of this century. At this moment (2021) there are approximately one hundred animals living in several herds on the heath where they are deployed for grazing and to complement the sheep herds. Given the limited number of animals, proper registration and a well-thought-out breeding programme are essential to secure the breed's future health.

Thanks to the hair samples and the genotypes provided by 'Stichting Schaapskudde Het Stroomdal', CGN was able to perform the analyses in this report. CGN offers her knowledge and support for the follow-up of the recommendations described in this report in order to maintain the Jutland cattle population in the Netherlands and to expand the population into a healthy breeding population.

The report was initially written and available in Dutch. Due to the transboundary status of Jutland cattle and the collaboration of some Dutch breeders with Jutland cattle breeders in Denmark, we decided to translate the report to English as well. We hope to stimulate a transboundary cooperation and possibly exchange of more breeding animals in the future. Hereby I would like to thank my colleagues Fenna van der Poel en Noelle Hoorneman for the support in translating this report.

Summary

Given the small population of Jutland cattle in the Netherlands - less than one hundred adult female breeding animals (status 2021) - complete and reliable genealogical records are essential. The board of 'Stichting Schaapskudde Het Stroomdal' suspected that not all the genealogical records were complete and correct. Apart from verification of ancestry, they also requested advice on how to make the best possible use of the available genetic diversity for the long term. Centre for Genetic Resources (CGN) of Wageningen University & Research (WUR) has carried out multiple analyses for 'Stichting Schaapskudde Het Stroomdal' in 2021/2022. It was assessed whether the genotype data matched the expectations based on the genealogical records. Also, it was assessed if the Jutland cattle breed can be recognised as a distinctive breed based on unique genetic diversity from the recognised Dutch dual-purpose cattle breeds.

The results of the analyses can be used for the substantiation of the available genealogical records. The kinships between individuals and their dams were almost always the highest, confirming the maternal parent of these animals. The same is true for the different (half)siblings and cousins. Also, a possible dam was found for the animal with missing records on the maternal side. One of the registered sires of six daughters is, based on the results of the analyses, probably not the actual sire. However, based on the available data, no definitive conclusion can be drawn yet and no other potential sires can be supplied. Hair samples from other herds could contribute to this issue.

The mean kinships of the genotyped animals vary. There are mostly low kinships between older animals, and higher mean kinships in the younger generations. It is important to note that a lot more animals from the Stroomdal herd were recorded in this dataset than from the second, smaller herd. Thus, it is very likely that the Mean kinships from the Stroomdal animals are (on average) a lot higher than the mean kinships of the other animals, and that the results do not provide an actual representation of the total population, but rather solely for this herd. Here as well, hair samples from other herds could contribute. The mean kinships are a valuable method to limit the rate of inbreeding. The 'self-repairing' ability following the use of the same breeding animals makes it the most sustainable system in the long run. However, a very reliable animal registration is essential for this system, especially of all the breeding animals in the total population.

The Jutland cattle breed can be recognised as a distinctive 'population' compared to the native Dutch dual purpose cattle breeds with breeding programmes in line with the EU-legislation for animal breeding (recognized by and with an approved breeding programme of the Dutch government). Compared to the Dutch dual-purpose cattle breeds, the highest proportion of overlapping SNP's corresponded with the Dutch Friesian (black-and-white) population. Though with an average of less than 25% by far not enough to identify them as the same breed. The proportions of overlapping SNP's with the different breeds was relatively uniform for the tested Jutland animals. When no breed of origin was taken in account, the Jutland animals were assigned all to one group based on all SNP's. Both results suggest the Jutland cattle of the 'Stroomdal herd can be distinguished as a separate population from the other 'official' Dutch dual-purpose cattle breeds.

However, it is important to note the small number of Jutland animals in the Netherlands at the moment (approximately 100 in 2021) are by far not enough breeding animals to maintain a healthy population on its own. To be recognized as a breed with their own distinct breeding population, a sustainable breeding programme should be set up. The urgent advice is therefor to set up a joint, sustainable and long-term breeding programme with the 'Stroomdal herd' and (as many as possible) other Jutland cattle breeders. To make arrangements about exchange of breeding animals and ways to limit the rate of inbreeding for the total Dutch population. CGN is able to contribute with advice and ideas to provide support for the short and long term conservation of Dutch Jutland cattle breed.

1 Jutland cattle in the Netherlands

The Jutland cattle breed ('Heidekoe' in Dutch) is a breed that existed on the Dutch heath for a long time. In the last century the Jutland cattle disappeared from the Netherlands. The specific qualities of the Jutland cattle and its value for cattle grazing on the heath were not taken into account. In 2006 Jutland cows were imported from Denmark to the Netherlands by 'Geldersch Landschap en Kasteelen'. These cows were the original type of Jutland cattle that we knew in the Netherlands. On the first of January 2021 there were ninety-five purebred Jutland cows and twenty-five purebred Jutland bulls registered in the Netherlands. The animals are divided over several large herds and there are some small groups spread across private parties and different nature reserves in the Netherlands.

'Stichting Schaapskudde Het Stroomdal' (Stroomdal herd) owns one of the largest herds, with twenty breeding females (mature cows) and three breeding males (mature bulls), of which two can be used for breeding. Furthermore there were two heifers, two young bulls and two heifer calves (status end 2021).

In 2020 the board of the Stroomdal herd contacted the Centre for Genetic Resources, the Netherlands (CGN) of Wageningen University & Research (WUR). Given the small population Jutland cattle in the Netherlands, less than one hundred breeding female (status 2021), complete and reliable genealogy records are essential. The board of the Stroomdal herd suspects that not all genealogical records were complete and correct. In addition, there were several animals where either one or both parents were unknown. Apart from a verification of ancestry, the board also requested advice on how to make the best possible use of the available genetic diversity for the long term.

The limited number of Jutland breeding animals in the Netherlands means that this population is considered as a breed with a 'rare breed status'. Because of its rare breed status, the Jutland cattle breed is eligible for exceptions when setting up an EU-approved breeding programme[1]. When applying for EU-approval for a breeding programme, it is not only essential to have a reliable registration of purebred animals, but also to make sure there are enough purebred breeding animals to maintain a healthy population. The advantage of an EU-approved breeding programme would be that purebred Jutland cattle from Denmark could be registered here as purebred animals, which would enable a significant expansion of the breeding population. Another advantage of an EU-approved breeding programme is that purebred Jutland cattle may be eligible for protection through the so-called '*Paraplubestand*'[2]. For both advantages it is important that the Jutland cattle breed in the Netherlands functions as a distinctive breed (which means that there needs to be sufficient uniformity and it has to be a distinctive, unique population of animals). In the second part of this report this latter question will be answered with an analyses to determine how unique the Jutland animals as a population are compared to Dutch dual-purpose cattle breeds with an EU-approved breeding programme. To see whether the Jutland population can also be seen as a genetically distinct population.

Research questions (by '*Stichting Schaapskudde Het Stroomdal*'):

1. Are the available genealogical records in agreement with what can be expected based on the genotype data? And is it possible to identify potential parents for animals with missing parental information using the genotypes?
2. Which animals are best suited to as breeding animals, and how can the genetic diversity be conserved in the long term?
3. Can the Jutland cattle breed be seen as a genetically distinctive populations compared to the native Dutch dual-purpose cattle breeds?

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[1] EU-approved breeding programme: Official breeding organization and approved breeding programmeme by Dutch government and according to the EU legislation of animal breeding.

[2] The Paraplubestand was set up at the request of the Ministry of Agriculture, Nature and Food Safety (LNV). It maps animals that belong to one of the Dutch rare farm animal breeds (at the moment; cattle, goats and sheep). The rare status of an animal is indicated in the Identification & Registration system (I&R) with an individual animal flag. In the event of an outbreak of an infectious animal disease, possible exceptions will be considered for these animals. www.paraplubestand.nl

2 Material and methods

Based on advice from the Centre for Genetic Resources, the Netherlands (CGN), hair samples from all the adult, and several young, animals from the Stroomdal herd were collected and genotyped. Several hair samples from a second cattle breeder were also genotyped and included in the research. The available pedigree information and genotyped DNA information were used to check (and, where possible, to supplement) the genealogical records. The DNA information was also used to genetically compare the Jutland cattle of the Stroomdal herd with the native Dutch dual-purpose cattle breeds with EU-approved breeding programmes. This was done to gain insight into the uniqueness of the Jutland cattle breed in relation to the other Dutch cattle breeds, and to see if there is sufficient genetic uniformity within the Jutland cattle breed to be stated as a distinctive population.

2.1 Materials

In total 34 hair samples were genotyped by the laboratory, corresponding to 31 unique animals. Of three animals double hair samples were genotypes, one from each herd (the animals were sold in between the collection of the hair samples in both herds). After an initial check whether the samples represented the same individual, the genotype with the least missing values was used for further analysis. The final dataset consisted of 31 animals (27 cows and 4 bulls). 28 animals were from the Stroomdal herd and 6 animals from the EigenErf herd. The eldest animals were born in 2008 and the youngest in 2020. Full information can be found in table 1.

The complete pedigree file was received as a dump-file from the online registration program ZooEasy. These records were complemented with separated pedigree information from the Stroomdal herd.

Table 1 *Animal- and genealogical information from the Jutland cattle dataset.*

M/F	Herd	Animal number	DOB	Name	Sire	Dam
1	**SD**	NL489979228	10-04-2008	H Hilda	KK Amdi	W Mille
2	**SD**	NL945990228	01-04-2019	Bente	K Audhildson	
3	**SD**	NL329364023	14-01-2019	K Anniken 06	K Audhildson	K Anniken
4	**SD**	NL945990211	04-02-2019	HO Heide 03	K Audhildson	HO Heide 02
5	**SD**	NL549883159	26-10-2011	H Heide 01	K Arne	H Heide
6	**SD**	NL329363981	15-06-2017	O Ragna 04	K Audhildson	O Ragna 02
7	**SD**	NL916480264	09-03-2009	H Henrike	KK Amdi	W AnnMarie
8	**SD**	NL329363897	26-04-2015	O Ragna 02	O Stervig Eskild OM	K Ragna
9	**SD**	NL522479568	15-06-2008	K Alfhildr 1	KK Amdi	K Alfhildr
10	**SD**	NL569258632	05-09-2020	SD Sonam	O Ragnason 01	H SD Froukje
11	**SD**	NL569258618	10-02-2020	KO SD Ciara	K Audhildson	O Ragna 06
12	**SD**	NL871746254	22-04-2016	H SD Knelsina	K Randers	H Henrike
13	**SD/AS**	NL866958503	05-05-2018	M SD Zwaantje	M Rambo	M Marlene 02
14	**SD**	NL871746247	13-04-2016	K SD Lammechien	K Audhildson	K Raghild
15	**SD**	NL866958495	14-11-2017	H SD Froukje	K Randers	H Heide 01
16	**SD**	NL871746076	17-04-2015	O SD Aaltje	O Stervig Eskild OM	K Runa
17	**SD**	NL866958488	25-09-2017	H SD Derkje	K Randers	H Henrike
18	**SD**	NL871746069	14-04-2015	O SD Grietje	O Stervig Eskild OM	K Raghild
19	**SD**	NL866958471	23-09-2017	K SD Harmen	K Randers	K Runa
20	**SD**	NL712109569	23-08-2014	HO Heide 02	O Stervig Eskild OM	H Heide
21	**SD**	NL871746285	27-04-2016	HO SD Hillechien	O Annikenson 04	H Heide 01
22	**SD**	NL712109552	23-08-2014	H Henrike 1	K Ragnar	H Henrike
23	**SD/AS**	DK8746800696	26-07-2012	K Runa	K GRU Ras	K 00601 RR Catla S
24	**AS**	NL719149788	08-04-2014	M Marlene 02	H Dany_Holger	W Malene 1
25	**SD**	DK8746800695	24-07-2012	K Raghild	K 00039 Engdals 39	DK Eddadotter
26	**AS**	NL934431110	09-07-2020	Roelfina v EigenErf	O Ragnason 01	M Marlene 02
27	**SD/AS**	NL567700294	10-05-2018	K Ragna 05	K Audhildson 01	K Ragna
28	**SD**	NL567700287	28-04-2018	O Ragnason 01	K Audhildson 01	O Ragna 01
29	**SD**	NL567700270	09-07-2017	O Ragna 03	K Audhildson 01	O Ragna 01
30	**SD**	NL878900073	06-07-2013	HO Hanna 01	O Stervig Eskild OM	H Hanna (Dena 1)
31	**AS**	NL875043584	01-12-2013	K Audhildson	K Ragnar	K Audhild 01

Coloured cells are animals present in the genotype dataset. Sires or dams that occurred more than once, but without genotypes are shown in the same font colours, light gray is a single occurrence. M/F shows the cows (F) in orange and the bulls (M) in blue. Animal number, date of birth, name (abbreviated) and parents taken from the available pedigree data.

2.1.1 DNA-information

All animals are genotyped with the BovineSNP50 v3 DNA Analysis BeadChip by Illumina (53,218 SNPs). The majority of the dataset (28 animals) had less than 200 missing SNPs per animal (table 2). Three animals had more than 1,000 missing SNPs (1,029, 2,277, 5,192). In total there were 7,067 unique SNPs with a missing SNP for at least one animal. These were all removed from the dataset and more than 45,000 SNPs (46,141) remained. There were also 7,153 SNPs without variation which were the same for all the animals. These SNPs cannot show any differences between animals and were removed from the dataset. The final dataset consisted of 38,998 SNPs for 31 individual animals.

Table 2 *Number of homozygous (0 and 2) and heterozygous (1) SNP combinations per animal (-9 are missing SNPs.*

	Number of SNP combinations (-9 = missing)			
Animal	**0**	**1**	**2**	**-9**
H Hilda	16936	16205	19999	72
Bente	17825	14327	20895	165
K Anniken 06	19305	11053	22756	98
HO Heide 03	17301	15307	20547	57
H Heide 01	17719	14175	20290	1029
O Ragna 04	17274	15364	20493	81
H Henrike	16776	16435	19944	57
O Ragna 02	17154	15590	20404	64
K Alfhildr 1	18365	13042	21724	81
SD Sonam	18097	13856	21193	66
KO SD Ciara	17843	14055	21217	97
H SD Knelsina	17171	15592	20387	62
M SD Zwaantje	19177	11560	22408	67
K SD Lammechien	17954	13850	21338	70
H SD Froukje	17763	14593	20764	92
O SD Aaltje	18109	13604	21410	89
H SD Derkje	16278	15205	16539	5192
O SD Grietje	18359	13157	21586	110
K SD Harmen	18091	13601	21441	79
HO Heide 02	17329	14605	19003	2277
HO SD Hillechien	18722	12621	21806	63
H Henrike 1	16921	15947	20264	80
K Runa	17166	15675	20286	85
M Marlene 02	19101	14173	19873	65
K Raghild	19059	14425	19663	65
Roelfina v EigenErf	18097	16424	18636	55
K Ragna 05	18022	14191	20919	80
O Ragna 03	17632	15066	20456	58
O Ragnason 01	17575	15266	20325	46
HO Hanna 01	17340	15432	20360	80
K Audhildson	17999	14078	21086	49

2.2 Methods

Prior to the analysis of the genealogical data, the relatedness between the available animals was calculated. The genotypes were coded as 0, 1 and 2 (where 1 is the heterozygote and 0 and 2 the opposite homozygotes). By subtracting 1 the numbers become -1, 0 and 1. The relatedness is calculated by multiplying the genotypes of two individuals and taking the average. The results were displayed in a matrix together with the mean kinship.

> ***Relatedness:*** *relatedness can be viewed as the percentage of DNA that two individuals possess which originates from one communal ancestor. Two animals are related if they have one (or more) common ancestor(s). For example, cow Bertha is related to her cousin Bertus, because they have the same grandparents, the grandparents are their common ancestors.*
>
> ***Mean kinship:*** *average kinship of a breeding animal in relation to all the breeding animals (male and female) in the population. The mean kinships in relation to all the breeding animals is calculated for each breeding animal individually. This average provides information on how many (closely) related animals with the same ancestors there are, compared to all the animals in the population. Animals with a low average kinship are important/valuable for animal breeding because they have more genetic diversity compared to the average breeding animal.*

We first looked at each animal individually and made a top 3 for each animal based on the highest relatedness in order to confirm the potential parents. Secondly, all the available animals were ranked based on the average relatedness to find the animals most suitable as breeding animal.

An additional check was carried out based on the basic principle of inheritance. Inheritance means that offspring always receives 50% of the father's DNA and 50% of the mother's DNA (Figure 1). If the mother is homozygote for an allele, which means she has two of the same alleles for a particular SNP, the principle of inheritance is that the offspring will have at least one of these alleles as well, and cannot be 'opposite' homozygote (i.e. have two of the same alleles which the mother does not have) because that would mean that the offspring did not receive any of the mother's alleles. Exceptions that are caused by (spontaneous) mutations are possible, but these should not occur on a regular basis. The results were compared to the available genealogical records.

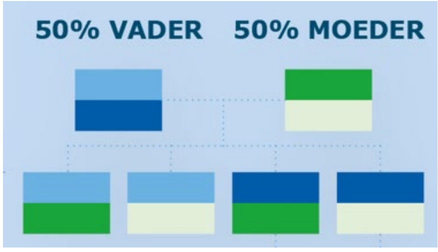

Figure 1 *The basic rule of DNA: 50% of the DNA comes from the sire (blue blocks) and 50% of the DNA comes from the dam (green blocks).*

In order to investigate whether Jutland cattle could be assigned to one of the EU-approved Dutch dual-purpose cattle breeds (see research question 3), first a DNA analysis was performed to identify overlapping SNPs for each of the Dutch dual-purpose cattle breeds and the Jutland cattle. Consequently, the software program STRUCTURE (Pritchard et al., 2000) was used to check if all the Jutland cattle would be assigned to one single separated group, or the variation within the group would be too high to be seen as a distinctive population.

3 Results

Chapter 3.1 discusses the results regarding the genealogical records, the mean kinship and the familial relationships between the genotyped animals. It starts with a matrix with an overview of all the kinships between the genotyped animals, followed by a table that summarizes the highest kinships in combination with the available genealogical records. Finally, a ranking based on the Mean kinship is provided with advice and explanations on how to use this information.

Chapter 3.2 focuses on the Jutland cattle as a population in relation to the EU-approved Dutch dual-purpose cattle breeds. First, the results of comparison between the Jutland cattle and Dutch dual-purpose cattle breeds are discussed. Secondly the results are shown whether or not the Jutland cattle are identified as a distinct population compared to the Dutch dual-purpose cattle breeds.

3.1 Relatedness within the Jutland dataset (Stroomdal herd)

The relations are presented in a matrix (Table 3), where the diagonal line represents the kinship of the animals with themselves. The results above and below the diagonal line are mirrored. For each row the four highest kinships (including with themselves) are shown in green, and the lowest kinships are orange. The green cells show the animals that, based on their DNA, should be the most closely related. These can be parent – daughter relations, but also (half)siblings or cousins.

Looking at the columns, a few animals stand out because they have a lot of orange cells. This means that these animals are in the top 3 of the lowest kinships for several other animals, and that they have the lowest degree of kinship to the animals in this analysis. The animals concerned are M Marlene 2, Raghild, Roelfina v EigenErf and M SD Zwaantje. In the next section, we will further discuss what this means in relation to the Mean kinship.

Table 3 *Relatedness between all animals within the analysis.*

Name	H Hild	Bente	K Anni	HO He	H Heid	O Ragn	H Hen	O Ragn	K Alfh	SD Son	KO SD	H SD K	M SD Z	K SD La	H SD F	O SD A	H SD D	O SD G	K SD H	HO He	HO SD	H Hen	K Runa	M Mar	K Ragh	Roelfi	K Ragn	O Ragn	O Ragn	HO Ha	K Audh
H Hilda	0.635	0.329	0.310	0.332	0.410	0.326	0.377	0.306	0.359	0.345	0.321	0.340	0.421	0.321	0.361	0.320	0.337	0.319	0.320	0.347	0.383	0.346	0.294	0.357	0.273	0.331	0.328	0.306	0.317	0.328	0.305
Bente	0.329	0.678	0.363	0.355	0.346	0.503	0.305	0.401	0.337	0.372	0.399	0.338	0.297	0.368	0.359	0.356	0.329	0.360	0.349	0.347	0.345	0.359	0.317	0.258	0.298	0.303	0.402	0.385	0.382	0.366	0.376
K Anniken 06	0.310	0.363	0.752	0.448	0.311	0.395	0.346	0.312	0.365	0.346	0.414	0.348	0.300	0.360	0.336	0.358	0.341	0.368	0.356	0.291	0.317	0.336	0.322	0.262	0.317	0.298	0.413	0.369	0.370	0.320	0.345
HO Heide 03	0.332	0.355	0.448	0.658	0.366	0.383	0.341	0.355	0.389	0.364	0.378	0.348	0.323	0.352	0.371	0.360	0.333	0.355	0.357	0.489	0.367	0.337	0.328	0.281	0.324	0.306	0.357	0.367	0.357	0.301	0.336
H Heide 01	0.410	0.346	0.311	0.366	0.680	0.328	0.351	0.300	0.326	0.412	0.335	0.341	0.381	0.345	0.502	0.327	0.330	0.318	0.322	0.397	0.546	0.340	0.300	0.337	0.283	0.320	0.333	0.310	0.309	0.353	0.341
O Ragna 04	0.326	0.503	0.395	0.383	0.328	0.654	0.307	0.494	0.378	0.398	0.421	0.339	0.298	0.362	0.354	0.364	0.334	0.363	0.357	0.374	0.361	0.334	0.328	0.251	0.312	0.331	0.459	0.444	0.439	0.334	0.358
H Henrike	0.377	0.305	0.346	0.341	0.351	0.307	0.630	0.280	0.379	0.328	0.329	0.472	0.402	0.310	0.343	0.316	0.460	0.326	0.322	0.309	0.324	0.463	0.301	0.345	0.286	0.315	0.319	0.301	0.299	0.322	0.295
O Ragna 02	0.306	0.401	0.312	0.355	0.300	0.494	0.280	0.650	0.336	0.365	0.415	0.325	0.279	0.359	0.335	0.365	0.312	0.359	0.339	0.405	0.352	0.313	0.328	0.234	0.320	0.289	0.396	0.385	0.384	0.320	0.331
K Alfhildr 1	0.359	0.337	0.365	0.389	0.326	0.378	0.379	0.336	0.707	0.379	0.379	0.375	0.368	0.377	0.376	0.373	0.371	0.386	0.389	0.352	0.347	0.357	0.322	0.304	0.343	0.329	0.364	0.361	0.361	0.304	0.338
SD Sonam	0.345	0.372	0.346	0.364	0.412	0.398	0.328	0.365	0.379	0.688	0.397	0.390	0.321	0.393	0.519	0.398	0.395	0.407	0.392	0.359	0.400	0.353	0.326	0.272	0.320	0.375	0.410	0.418	0.492	0.343	0.381
KO SD Ciara	0.321	0.399	0.414	0.378	0.335	0.421	0.329	0.415	0.379	0.397	0.682	0.360	0.307	0.453	0.379	0.372	0.360	0.405	0.367	0.343	0.349	0.377	0.344	0.254	0.340	0.309	0.424	0.395	0.394	0.369	0.518
H SD Knelsina	0.340	0.338	0.348	0.348	0.341	0.339	0.472	0.325	0.375	0.390	0.360	0.649	0.347	0.363	0.424	0.424	0.489	0.435	0.431	0.325	0.339	0.424	0.330	0.293	0.331	0.304	0.358	0.336	0.334	0.343	0.346
M SD Zwaantje	0.421	0.297	0.300	0.323	0.381	0.298	0.402	0.279	0.368	0.321	0.307	0.347	0.742	0.294	0.343	0.289	0.337	0.291	0.292	0.324	0.345	0.367	0.270	0.530	0.251	0.393	0.296	0.275	0.270	0.319	0.285
K SD Lammechien	0.321	0.368	0.360	0.352	0.345	0.362	0.310	0.359	0.377	0.393	0.453	0.363	0.294	0.687	0.390	0.405	0.358	0.465	0.401	0.326	0.345	0.381	0.354	0.244	0.475	0.291	0.376	0.361	0.363	0.371	0.523
H SD Froukje	0.361	0.359	0.336	0.371	0.502	0.354	0.343	0.335	0.376	0.519	0.379	0.424	0.343	0.390	0.673	0.443	0.434	0.442	0.424	0.387	0.438	0.366	0.331	0.307	0.327	0.322	0.365	0.346	0.344	0.363	0.384
O SD Aaltje	0.320	0.356	0.358	0.360	0.327	0.364	0.316	0.365	0.373	0.398	0.372	0.424	0.289	0.405	0.443	0.695	0.415	0.479	0.519	0.341	0.346	0.350	0.497	0.241	0.363	0.284	0.379	0.356	0.365	0.340	0.376
H SD Derkje	0.337	0.329	0.341	0.333	0.330	0.334	0.460	0.312	0.371	0.395	0.360	0.489	0.337	0.358	0.434	0.415	0.631	0.422	0.403	0.307	0.327	0.405	0.318	0.291	0.307	0.300	0.344	0.329	0.326	0.336	0.344
O SD Grietje	0.319	0.360	0.368	0.355	0.318	0.363	0.326	0.359	0.386	0.407	0.405	0.435	0.291	0.465	0.442	0.479	0.422	0.705	0.464	0.319	0.328	0.365	0.362	0.242	0.502	0.277	0.390	0.375	0.363	0.337	0.383
K SD Harmen	0.320	0.349	0.356	0.357	0.322	0.357	0.322	0.339	0.389	0.392	0.367	0.431	0.292	0.401	0.424	0.519	0.403	0.464	0.694	0.326	0.338	0.347	0.504	0.255	0.353	0.286	0.371	0.352	0.350	0.337	0.373
HO Heide 02	0.347	0.347	0.291	0.489	0.397	0.374	0.309	0.405	0.352	0.359	0.343	0.325	0.324	0.326	0.387	0.341	0.307	0.319	0.326	0.661	0.408	0.321	0.303	0.279	0.299	0.305	0.314	0.337	0.339	0.290	0.307
HO SD Hillechien	0.383	0.345	0.317	0.367	0.546	0.361	0.324	0.352	0.347	0.400	0.349	0.339	0.345	0.345	0.438	0.346	0.327	0.328	0.338	0.408	0.715	0.328	0.306	0.300	0.288	0.315	0.331	0.332	0.339	0.335	0.343
H Henrike 1	0.346	0.359	0.336	0.337	0.340	0.334	0.463	0.313	0.357	0.353	0.377	0.424	0.367	0.381	0.366	0.350	0.405	0.365	0.347	0.321	0.328	0.641	0.322	0.301	0.319	0.304	0.351	0.322	0.324	0.389	0.396
K Runa	0.294	0.317	0.322	0.328	0.300	0.328	0.301	0.328	0.322	0.326	0.344	0.330	0.270	0.354	0.331	0.497	0.318	0.362	0.504	0.303	0.306	0.322	0.648	0.246	0.320	0.275	0.359	0.336	0.336	0.336	0.360
M Marlene 02	0.357	0.258	0.262	0.281	0.337	0.251	0.345	0.234	0.304	0.272	0.254	0.293	0.530	0.244	0.307	0.241	0.291	0.242	0.255	0.279	0.300	0.301	0.246	0.681	0.295	0.477	0.250	0.246	0.229	0.285	0.245
K Raghild	0.273	0.298	0.317	0.324	0.283	0.312	0.286	0.320	0.343	0.320	0.340	0.331	0.251	0.475	0.327	0.363	0.307	0.502	0.353	0.299	0.288	0.319	0.320	0.295	0.676	0.325	0.335	0.329	0.313	0.296	0.338
Roelfina v EigenErf	0.331	0.303	0.298	0.306	0.320	0.331	0.315	0.289	0.329	0.375	0.309	0.304	0.393	0.291	0.322	0.284	0.300	0.277	0.286	0.305	0.315	0.304	0.275	0.477	0.325	0.630	0.332	0.340	0.418	0.297	0.299
K Ragna 05	0.328	0.402	0.413	0.357	0.333	0.459	0.319	0.396	0.364	0.410	0.424	0.358	0.296	0.376	0.365	0.379	0.344	0.390	0.371	0.314	0.331	0.351	0.359	0.250	0.335	0.332	0.680	0.448	0.475	0.375	0.404
O Ragnason 01	0.306	0.385	0.369	0.367	0.310	0.444	0.301	0.385	0.361	0.418	0.395	0.336	0.275	0.361	0.346	0.356	0.329	0.375	0.352	0.337	0.332	0.322	0.336	0.246	0.329	0.340	0.448	0.660	0.496	0.336	0.374
O Ragna 03	0.317	0.382	0.370	0.357	0.309	0.439	0.299	0.384	0.361	0.492	0.394	0.334	0.270	0.363	0.344	0.365	0.326	0.363	0.350	0.339	0.339	0.324	0.336	0.229	0.313	0.418	0.475	0.496	0.658	0.343	0.373
HO Hanna 01	0.328	0.366	0.320	0.301	0.353	0.334	0.322	0.320	0.304	0.343	0.369	0.343	0.319	0.371	0.363	0.340	0.336	0.337	0.337	0.290	0.335	0.389	0.336	0.285	0.296	0.297	0.375	0.336	0.343	0.653	0.421
K Audhildson	0.305	0.376	0.345	0.336	0.341	0.358	0.295	0.331	0.338	0.381	0.518	0.346	0.285	0.523	0.384	0.376	0.344	0.383	0.373	0.307	0.343	0.396	0.360	0.245	0.338	0.299	0.404	0.374	0.373	0.421	0.683
MK	**0.345**	**0.364**	**0.358**	**0.365**	**0.361**	**0.377**	**0.349**	**0.353**	**0.369**	**0.389**	**0.384**	**0.374**	**0.341**	**0.380**	**0.390**	**0.381**	**0.365**	**0.384**	**0.377**	**0.349**	**0.362**	**0.363**	**0.343**	**0.303**	**0.337**	**0.332**	**0.379**	**0.365**	**0.370**	**0.347**	**0.370**

The diagonal shows the relatedness of the animals with themselves. The results above and below the diagonal are mirrored. For each row the four highest relatedness (including the relatedness with itself) are shown in green, the three lowest in orange.

3.2 Top 3 based on relatedness

For all the animals the available information from the genealogical records was combined with the three animals with which the highest degrees of kinship were found (Table 4). The results of the genotype analysis are largely consistent with the available genealogical records. For all genotyped animals, of which the dam was genotyped as well, the dam found based on genotype was consistently in the first or second place as well. Furthermore, cows from the same lineage are often included in the top 3 of the related individual.

Bente

In this dataset, Bente is the only cow with missing dam record. Based on the degree of kinship and the accompanying top 3, it seems that Bente is most closely related to the Ragna lines, with O Ragna 04 as the most likely dam for Bente. After a check of the UBN location of O Ragna 04 and the UBN location on the date of Bente’s birth, this would be possible. All the available SNPs of Bente and Ragna 04 were checked on ‘opposite’ homozygotes, and out of the total set of over 50,000 SNPs this only occurred 14 times. Based on these results and findings, it is likely that Bente is the offspring of Ragna 04. This would also mean that Bente is reasonably inbred. According to the records, K Audhildson would be both her sire and grandsire (although later in this report it will become clear that the sire in question is probably not her actual sire).

HO Hanna 01

A remarkable result is the high degree of kinship between K Audhildson and HO Hanna 01. No descendants of HO Hanna 01 were genotyped, and this cow does not feature in any of the top 3’s. Whereas K Audhildson is not featured in the top 3 of several of his direct descendants, he is number 1 in HO Hanna 01’s top 3. If we compare these results to the genealogical records, a communal grandparent becomes apparent, which, according to the records, is KK Amdi. Another remarkable result is that none of HO Hanna 01’s halfsisters, four other direct descendants of O Stervig Eskild OM, are featured in her top 3. Nor vice versa. It does feature H Henrike 1 and K Ragna 05, first and second generation descendants of K Ragnar, as well as K Audhildson. An additional finding is that the female animals H Heide and H Hanna have the same ancestry on paper (KK Amdi x W Maria), but that HO Hanna 01 as a daughter of H Hanna has the second to lowest kinship of all the animals in the list of HO Heide 02, the daughter of H Heide. These results indicate that it is unlikely that O Stervig Eskild OM is the father of HO Hanna 01. Based on the genotypes in this dataset it is more likely that K Ragnar (or a directly related bull) is the sire of HO Hanna 01.

Table 4 *Pedigree data per animal and top three relations based on relatedness analysis.*

M/V	Kudde	Diernummer	gebdat	naam	vader	moeder	Top 1	Top 2	Top 3
1	SD	NL489979228	10-04-2008	H Hilda	KK Amdi	W Mille	M SD Zwaantje	H Heide 01	HO SD Hillechien
2	SD	NL945990228	01-04-2019	Bente	K Audhildson		O Ragna 04	K Ragna 05	O Ragna 02
3	SD	NL329364023	14-01-2019	K Anniken 06	K Audhildson	K Anniken	HO Heide 03	KO SD Ciara	K Ragna 05
4	SD	NL945990211	04-02-2019	HO Heide 03	K Audhildson	HO Heide 02	HO Heide 02	K Anniken 06	K Alfhildr 1
5	SD	NL549883159	26-10-2011	H Heide 01	K Arne	H Heide	HO SD Hillechien	H SD Froukje	SD Sonam
6	SD	NL329363981	15-06-2017	O Ragna 04	K Audhildson	O Ragna 02	Bente	O Ragna 02	K Ragna 05
7	SD	NL916480264	09-03-2009	H Henrike	KK Amdi	W AnnMarie	H SD Knelsina	H Henrike 1	H SD Derkje
8	SD	NL329363897	26-04-2015	O Ragna 02	O Stervig Eskild O	K Ragna	O Ragna 04	KO SD Ciara	HO Heide 02
9	SD	NL522479568	15-06-2008	K Alfhildr 1	KK Amdi	K Alfhildr	HO Heide 03	K SD Harmen	O SD Grietje
10	SD	NL569258632	05-09-2020	SD Sonam	O Ragnason 01	H SD Froukje	H SD Froukje	O Ragna 03	O Ragnason 01
11	SD	NL569258618	10-02-2020	KO SD Ciara	K Audhildson	O Ragna 06	K Audhildson	K SD Lammechien	K Ragna 05
12	SD	NL871746254	22-04-2016	H SD Knelsina	K Randers	H Henrike	H SD Derkje	H Henrike	O SD Grietje
13	SD/AS	NL866958503	05-05-2018	M SD Zwaantje	M Rambo	M Marlene 02	M Marlene 02	H Hilda	H Henrike
14	SD	NL871746247	13-04-2016	K SD Lammechien	K Audhildson	K Raghild	K Audhildson	K Raghild	O SD Grietje
15	SD	NL866958495	14-11-2017	H SD Froukje	K Randers	H Heide 01	SD Sonam	H Heide 01	O SD Aaltje
16	SD	NL871746076	17-04-2015	O SD Aaltje	O Stervig Eskild O	K Runa	K SD Harmen	K Runa	O SD Grietje
17	SD	NL866958488	25-09-2017	H SD Derkje	K Randers	H Henrike	H SD Knelsina	H Henrike	H SD Froukje
18	SD	NL871746069	14-04-2015	O SD Grietje	O Stervig Eskild O	K Raghild	K Raghild	O SD Aaltje	K SD Lammechien
19	SD	NL866958471	23-09-2017	K SD Harmen	K Randers	K Runa	O SD Aaltje	K Runa	O SD Grietje
20	SD	NL712109569	23-08-2014	HO Heide 02	O Stervig Eskild O	H Heide	HO Heide 03	HO SD Hillechien	O Ragna 02
21	SD	NL871746285	27-04-2016	HO SD Hillechien	O Annikenson 04	H Heide 01	H Heide 01	H SD Froukje	HO Heide 02
22	SD	NL712109552	23-08-2014	H Henrike 1	K Ragnar	H Henrike	H Henrike	H SD Knelsina	H SD Derkje
23	SD/AS	DK8746800696	26-07-2012	K Runa	K GRU Ras	K 00601 RR Catla S	K SD Harmen	O SD Aaltje	O SD Grietje
24	AS	NL719149788	08-04-2014	M Marlene 02	H Dany_Holger	W Malene 1	M SD Zwaantje	Roelfina v EigenErf	H Hilda
25	SD	DK8746800695	24-07-2012	K Raghild	K 00039 Engdals 3	DK Eddadotter	O SD Grietje	K SD Lammechien	O SD Aaltje
26	AS	NL934431110	09-07-2020	Roelfina v Eigen Er	O Ragnason 01	M Marlene 02	M Marlene 02	O Ragna 03	M SD Zwaantje
27	SD/AS	NL567700294	10-05-2018	K Ragna 05	K Audhildson 01	K Ragna	O Ragna 03	O Ragna 04	O Ragnason 01
28	SD	NL567700287	28-04-2018	O Ragnason 01	K Audhildson 01	O Ragna 01	O Ragna 03	K Ragna 05	O Ragna 04
29	SD	NL567700270	09-07-2017	O Ragna 03	K Audhildson 01	O Ragna 01	O Ragnason 01	SD Sonam	K Ragna 05
30	SD	NL878900073	06-07-2013	HO Hanna 01	O Stervig Eskild O	H Hanna (Dena 1)	K Audhildson	H Henrike 1	K Ragna 05
31	AS	NL875043584	01-12-2013	K Audhildson	K Ragnar	K Audhild 01	K SD Lammechien	KO SD Ciara	HO Hanna 01

The coloured cells are animals that were genotyped. The animals with matching coloured letters occur multiple times in this table, but were not genotyped. The animals shown in light grey font colour only occurred once as a parent in this overview and no genotypes were available. M/V: M is female (orange) and V is male (blue). Kudde: SD is Stroomdal herd and AS is the second smaller farmer. Diernummer: Unique identification number of animal. Gebdat: date of birth. Naam: (abbreviated) name of the animal. Vader: sire as stated in the pedigree file of breeding organisation. Moeder: dam as stated in file of breeding organisation. Top1,2,3: three most related animals based on the available genotypes.

Table 5 *Number of different SNPs (of the 50,000) and number of opposite homozygotes.*

Ouder <-> nakomeling		Verschillend	# 2	# -2	totaal #
H Heide 01	HO SD Hillechien	12192	0	6	6
H Heide 01	H SD Froukje	13861	4	3	7
M Marlene 02	Roelfina v EigenErf	13548	4	3	7
HO Heide 03	HO Heide 02	14390	5	4	9
H Henrike	H Henrike 1	13193	6	3	9
H Henrike	H SD Knelsina	12681	3	7	10
H Henrike	H SD Derkje	16531	1	10	11
SD Sonam	H SD Froukje	12385	4	8	12
Bente	**O Ragna 04**	12527	8	6	14
O Ragna 04	O Ragna 02	12013	19	16	35
O SD Aaltje	K Runa	12673	77	197	274
K SD Harmen	K Runa	12191	79	198	277
K Audhildson	K SD Lammechien	11830	196	82	278
K Audhildson	KO SD Ciara	12079	203	81	284
SD Sonam	O Ragnason 01	12861	158	275	433
O Ragnason 01	Roelfina v EigenErf	15006	27	1028	1055
M Marlene 02	M SD Zwaantje	11205	1129	9	1138
K Raghild	K SD Lammechien	13132	1138	8	1146
K Raghild	O SD Grietje	11872	1141	13	1154
K Audhildson	O Ragna 04	17077	1182	1105	2287
Bente	K Audhildson	16655	1145	1206	2351
K Audhildson	HO Heide 03	17950	1365	1214	2579
K Audhildson	K Anniken 06	17685	1874	1767	3641

Only when there were genotypes available for both parent and offspring, their information is shown in this table. Ouder <-> nakomeling: parent – offspring based on pedigree file except for Ragna 04 has been added as a potential dam for Bente (based on previous results). Verschillend: number of different genotypes for all available SNPs. #2 and -2: number of SNPs only one of the animals is homozygous for. Total: number of SNPs with opposite homozygous SNPs

K Audhildson

According to the genealogical records, K Audhildson is the sire of six cows in the dataset, and for two out of the six cows he also features in the top 3 of the closest relations (Table 4), namely SD Ciara and SD Lammechien. He did not feature in the top 3 of the other four cows, Bente, K Anniken 06, HO Heide 03 and O Ragna 04, but ranked at number 7, 16, 22 and 26 (Table 6). Normally parent-offspring relations are clearly visible in the analyses with the highest degrees of kinship, as is the case for (almost) all the mother-daughter relations and the two father-daughter relations between SD Ciara and SD Lammechien.

A second verification was the calculation of the number of ‘opposite’ homozygotes (Table 5). The results clearly show that for the four cows Bente, K Anniken 06, HO Heide 03 and O Ragna 04 the largest number of ‘opposite’ homozygotes was found out of all the parent-offspring relations for which genotype records were available. This can occur in very small amounts, but for all four animals this was found for more than 2,000 SNPs. Based on the results it is very unlikely that the registration of K Audhildson as a father of Bente, K Anniken 06, HO Heide 03 and O Ragna 04 is correct. The available genotypes cannot be used to pinpoint the correct sires from the population .

Table 6 *Registered daughters of K Audhildson, who did not have him in their top three of most related animals. Relatedness per animal ranked from high to low.*

Bente		K Anniken 06		HO Heide 03		O Ragna 04		K Audhildson	
Bente	0.678	K Anniken 06	0.752	HO Heide 03	0.658	O Ragna 04	0.654	K Audhildson	0.683
O Ragna 04	0.503	HO Heide 03	0.448	HO Heide 02	0.489	Bente	0.503	K SD Lammechien	0.523
K Ragna 05	0.402	KO SD Ciara	0.414	K Anniken 06	0.448	O Ragna 02	0.494	KO SD Ciara	0.518
O Ragna 02	0.401	K Ragna 05	0.413	K Alfhildr 1	0.389	K Ragna 05	0.459	HO Hanna 01	0.421
KO SD Ciara	0.399	O Ragna 04	0.395	O Ragna 04	0.383	O Ragnason 01	0.444	K Ragna 05	0.404
O Ragnason 01	0.385	O Ragna 03	0.370	KO SD Ciara	0.378	O Ragna 03	0.439	H Henrike 1	0.396
O Ragna 03	0.382	O Ragnason 01	0.369	H SD Froukje	0.371	KO SD Ciara	0.421	H SD Froukje	0.384
K Audhildson	0.376	O SD Grietje	0.368	O Ragnason 01	0.367	SD Sonam	0.398	O SD Grietje	0.383
SD Sonam	0.372	K Alfhildr 1	0.365	HO SD Hillechien	0.367	K Anniken 06	0.395	SD Sonam	0.381
K SD Lammechien	0.368	Bente	0.363	H Heide 01	0.366	HO Heide 03	0.383	Bente	0.376
HO Hanna 01	0.366	K SD Lammechien	0.360	SD Sonam	0.364	K Alfhildr 1	0.378	O SD Aaltje	0.376
K Anniken 06	0.363	O SD Aaltje	0.358	O SD Aaltje	0.360	HO Heide 02	0.374	O Ragnason 01	0.374
O SD Grietje	0.360	K SD Harmen	0.356	O Ragna 03	0.357	O SD Aaltje	0.364	K SD Harmen	0.373
H SD Froukje	0.359	H SD Knelsina	0.348	K SD Harmen	0.357	O SD Grietje	0.363	O Ragna 03	0.373
H Henrike 1	0.359	H Henrike	0.346	K Ragna 05	0.357	K SD Lammechien	0.362	K Runa	0.360
O SD Aaltje	0.356	SD Sonam	0.346	O Ragna 02	0.355	HO SD Hillechien	0.361	O Ragna 04	0.358
HO Heide 03	0.355	K Audhildson	0.345	O SD Grietje	0.355	K Audhildson	0.358	H SD Knelsina	0.346
K SD Harmen	0.349	H SD Derkje	0.341	Bente	0.355	K SD Harmen	0.357	K Anniken 06	0.345
HO Heide 02	0.347	H Henrike 1	0.336	K SD Lammechien	0.352	H SD Froukje	0.354	H SD Derkje	0.344
H Heide 01	0.346	H SD Froukje	0.336	H SD Knelsina	0.348	H SD Knelsina	0.339	HO SD Hillechien	0.343
HO SD Hillechien	0.345	K Runa	0.322	H Henrike	0.341	H SD Derkje	0.334	H Heide 01	0.341
H SD Knelsina	0.338	HO Hanna 01	0.320	H Henrike 1	0.337	HO Hanna 01	0.334	K Raghild	0.338
K Alfhildr 1	0.337	HO SD Hillechien	0.317	K Audhildson	0.336	H Henrike 1	0.334	K Alfhildr 1	0.338
H Hilda	0.329	K Raghild	0.317	H SD Derkje	0.333	Roelfina v EigenErf	0.331	HO Heide 03	0.336
H SD Derkje	0.329	O Ragna 02	0.312	H Hilda	0.332	K Runa	0.328	O Ragna 02	0.331
K Runa	0.317	H Heide 01	0.311	K Runa	0.328	H Heide 01	0.328	HO Heide 02	0.307
H Henrike	0.305	H Hilda	0.310	K Raghild	0.324	H Hilda	0.326	H Hilda	0.305
Roelfina v EigenErf	0.303	M SD Zwaantje	0.300	M SD Zwaantje	0.323	K Raghild	0.312	Roelfina v EigenErf	0.299
K Raghild	0.298	Roelfina v EigenErf	0.298	Roelfina v EigenErf	0.306	H Henrike	0.307	H Henrike	0.295
M SD Zwaantje	0.297	HO Heide 02	0.291	HO Hanna 01	0.301	M SD Zwaantje	0.298	M SD Zwaantje	0.285
M Marlene 02	0.258	M Marlene 02	0.262	M Marlene 02	0.281	M Marlene 02	0.251	M Marlene 02	0.245

3.3 Ranking based on mean kinship

In the previous part of this chapter we mentioned kinships. With those kinships, the mean kinship was calculated for all animals and a ranking was made (from lowest to highest mean kinship) (Table 7). The mean kinship is the average kinship of a breeding animal in relation to all the breeding animals (both male and female) in a population, or, as is the case in this report, in relation to all the other genotyped animals. The higher the mean kinship, the more closely related the animal is to the other animals in the dataset. A lower mean kinship indicates that the animal is less related to the other animals and has more unique diversity than the other animals with more relatives in the dataset.

M Marlene 02 is in the top position with the lowest mean kinship. This makes her a valuable breeding animal within the group of animals in this dataset. This animal is from the AS herd, and the majority of the animals in this dataset are from the Stroomdal herd. Thus, it is important to state that the mean kinships do not count for the total Dutch population of Jutland cattle, but only for the group of animals in this particular dataset. It might be the case that M Marlene 02 already has several offspring on different locations, which might mean she has a higher mean kinship than what we found in this analysis.

Looking at the Stroomdal herd, K Raghild appears to be the most valuable breeding animal based on genetic diversity. O SD Grietje and H SD Froukje are ranked lowest because they have the highest mean kinship out of all the animals in this group. From a genetic diversity point of view, these animals are less suited for breeding purposes.

Off the bulls, O Ragnason 01 is in top position of the mean kinships ranking, which means that he is the most valuable breeding bull of the group. SD Sonam occupies the bottom position of the ranking with the second -highest Mean kinship, which means that he is less suited for breeding purposes within this group of animals.

Because there are also several older animals included in the dataset, we also looked at animals who were born after 2015. Roelfina of EigenErf, M SD Zwaantje and K Anniken 06 are the animals with the lowest mean kinship, which means that they are important breeding animals to limit the rate of inbreeding in this population Jutland cattle.

Table 7 *Mean kinship of the genotyped animals, ranked from low to high mean kinship.*

herd	m/f	Mean kinship	Animal ID	Date of birth	Name
AS	cow	0.303	NL719149788	08-04-2014	M Marlene 02
AS	cow	0.332	NL934431110	07-09-2020	Roelfina v EigenErf
SD	cow	0.337	DK8746800695	24-07-2012	K Raghild
SD/AS	cow	0.341	NL866958503	05-05-2018	M SD Zwaantje
SD/AS	cow	0.343	DK8746800696	26-07-2012	K Runa
SD	cow	0.345	NL489979228	10-04-2008	H Hilda
SD	cow	0.347	NL878900073	06-07-2013	HO Hanna 01
SD	cow	0.349	NL916480264	09-03-2009	H Henrike
SD	cow	0.349	NL712109569	23-08-2014	HO Heide 02
SD	cow	0.353	NL329363897	26-04-2015	O Ragna 02
SD	cow	0.358	NL329364023	14-01-2019	K Anniken 06
SD	cow	0.361	NL549883159	26-10-2011	H Heide 01
SD	cow	0.362	NL871746285	27-04-2016	HO SD Hillechien
SD	cow	0.363	NL712109552	23-08-2014	H Henrike 1
SD	cow	0.364	NL945990228	01-04-2019	Bente
SD	cow	0.365	NL945990211	04-02-2019	HO Heide 03
SD	cow	0.365	NL866958488	25-09-2017	H SD Derkje
SD	bull	0.365	NL567700287	28-04-2018	O Ragnason 01
SD	cow	0.369	NL522479568	15-06-2008	K Alfhildr 1
SD	cow	0.370	NL567700270	09-07-2017	O Ragna 03
AS	bull	0.370	NL875043584	01-12-2013	K Audhildson
SD	cow	0.374	NL871746254	22-04-2016	H SD Knelsina
SD	cow	0.377	NL329363981	15-06-2017	O Ragna 04
SD	bull	0.377	NL866958471	23-09-2017	K SD Harmen
SD/AS	cow	0.379	NL567700294	10-05-2018	K Ragna 05
SD	cow	0.380	NL871746247	13-04-2016	K SD Lammechien
SD	cow	0.381	NL871746076	17-04-2015	O SD Aaltje
SD	cow	0.384	NL569258618	10-02-2020	KO SD Ciara
SD	cow	0.384	NL871746069	14-04-2015	O SD Grietje
SD	bull	0.389	NL569258632	05-09-2020	SD Sonam
SD	cow	0.390	NL866958495	14-11-2017	H SD Froukje

Herd: SD represents animals from Stroomdal herd while AS represent animals from the second smaller farmer. m/f: cows are represented in the orange cells and bulls in blue. Mean kinship is ranked from low (green) to high (red).

4 Results Jutland vs. Dutch native dual-purpose cattle breeds

The results of the first analysis (*principal component analysis*) show the distribution of the EU-approved Dutch dual-purpose breeds along with the genotyped Jutland cattle (Figure 2). Important to take into account is that this analysis is based on a pre-selected set of SNPs that were selected specifically for distinguishing between the Dutch (rare) dual-purpose cattle breeds.

The three Dutch breeds that have been registered in separate studbooks for the longest period of time are most clearly separated (Figure 2a). At the top left in pink is the Dutch Friesian (dark blue is Dutch Red and White Friesian), at the top right in light blue is Meuse-Rhine-Yssel cattle (and Deep Red cattle in purple), and at the bottom in the middle is the Groningen White Headed (green), which is clearly separated from the other breeds. If we look at figure 2c and even more at 2d, these breeds are separated to a somewhat lesser degree, but the Jutland cattle (black), Dutch Belted (red) and Holstein Friesian, which was added as a reference population (yellow), stand out more as separate groups, although not sufficiently to draw any conclusions.

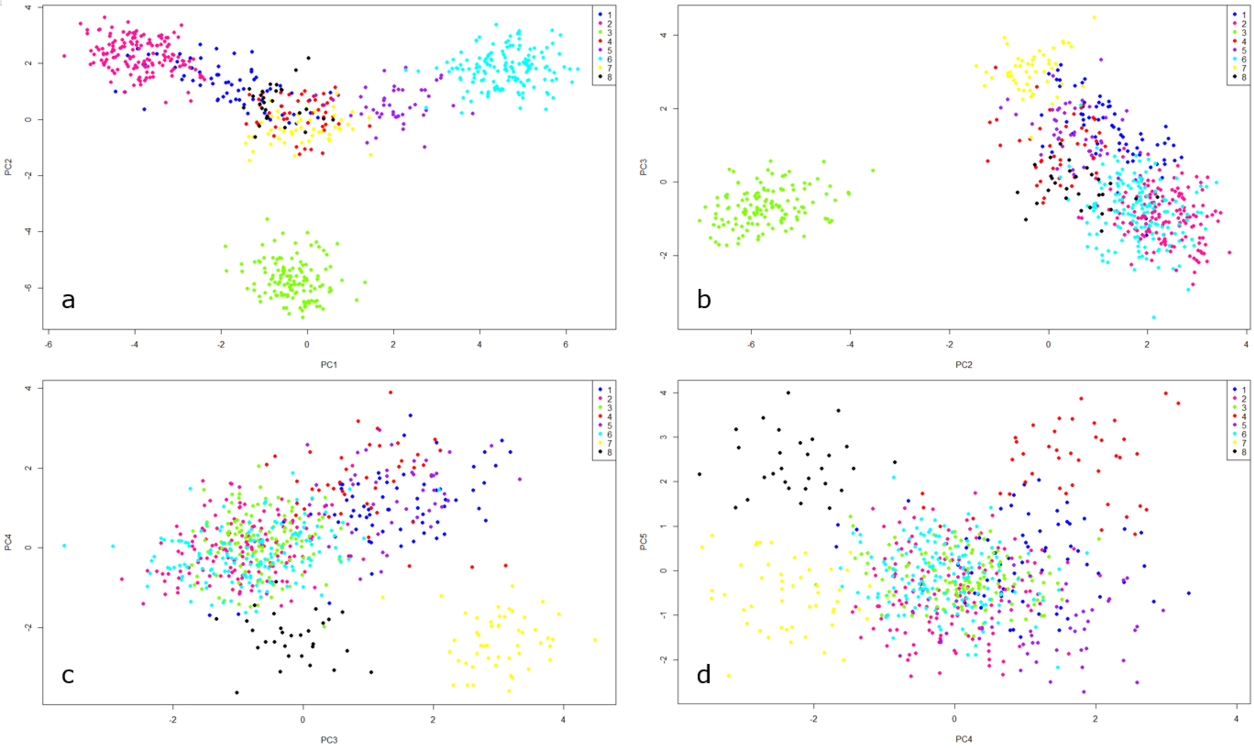

Figure 2 *Distribution of the native Dutch dual-purpose cattle breeds and the Jutland cattle based on a pre-selected SNP set to distinguish the Dutch dual-purpose cattle breeds.*

Pink = Dutch Friesian (black and white) / Dark blue = Dutch Red and White Friesian / Green = Groningen White Headed / Red = Dutch Belted / Purple = Deep Red / Light blue = Meuse-Rhine-Yssel (MRY) / Yellow = Holstein Friesian / Black = Jutland cattle.

4.1 STRUCTURE results DNA-test for breed identification

The Jutland cattle from the dataset were analyzed using a DNA-test for breed identification of the Dutch rare dual-purpose breeds. Based on 133 selected SNPs and reference populations of the Dutch rare dual-purpose breeds, the Jutland cattle are categorized according to similarities per breed. The majority of all the Jutland cattle had the highest similarities with Dutch Friesian (black and white). The average proportion for Dutch Friesian lays around 0.200 (at max). For the DNA-test for breed identification to identify an animal as a pure bred individual the proportion should be at least 0.775. Therefor no conclusions should be made that the Jutland cattle is in fact the same breed as the Dutch Friesians. Second highest proportion of overlapping SNPs were found for Dutch Red and White Friesian and/or Holstein Friesians. A few animals shared more SNPs with Meuse-Rhine-Yssel cattle, or the Dutch Belted. Groningen White Headed and Deep Red had the lowest similarities with this set of selected SNPs.

Interesting that, even though the proportions differ a little between the animals, on average the proportions overlapping SNPs per breed for the Jutland individuals are kind of similar.

Table 8 *Proportion of overlapping SNPs between Jutland cattle and the reference populations of the Dutch dual-purpose breeds (plus Holstein Friesian as outlier) based on 133 pre-selected SNPs.*

	RWF	**DF**	**GWH**	**DB**	**DR**	**MRY**	**HOL**
H Hilda	0.172	0.174	0.090	0.153	0.138	0.117	0.156
Bente	0.143	0.185	0.147	0.145	0.109	0.122	0.149
K Anniken 06	0.142	0.175	0.096	0.161	0.129	0.128	0.169
HO Heide 03	0.139	0.186	0.096	0.157	0.112	0.159	0.150
H Heide 01	0.186	0.193	0.085	0.165	0.098	0.149	0.124
O Ragna 04	0.116	0.158	0.133	0.138	0.114	0.170	0.170
H Henrike	0.149	0.199	0.106	0.143	0.126	0.151	0.126
O Ragna 02	0.133	0.147	0.107	0.112	0.128	0.159	0.215
K Alfhildr 1	0.152	0.223	0.102	0.136	0.104	0.144	0.139
SD Sonam	0.167	0.191	0.131	0.129	0.130	0.118	0.135
KO SD Ciara	0.138	0.199	0.109	0.139	0.137	0.137	0.141
H SD Knelsina	0.160	0.216	0.113	0.158	0.101	0.124	0.127
M SD Zwaantje	0.174	0.189	0.112	0.143	0.117	0.135	0.130
K SD Lammechien	0.131	0.197	0.141	0.127	0.130	0.137	0.137
H SD Froukje	0.148	0.173	0.132	0.163	0.117	0.149	0.118
O SD Aaltje	0.134	0.177	0.113	0.169	0.114	0.166	0.128
H SD Derkje	0.200	0.165	0.115	0.153	0.127	0.122	0.117
O SD Grietje	0.151	0.165	0.124	0.131	0.132	0.146	0.153
K SD Harmen	0.150	0.155	0.109	0.150	0.116	0.163	0.156
HO Heide 02	0.128	0.207	0.114	0.146	0.113	0.146	0.146
HO SD Hillechien	0.171	0.204	0.084	0.128	0.113	0.178	0.122
H Henrike 1	0.149	0.196	0.119	0.149	0.111	0.152	0.125
K Runa	0.162	0.173	0.111	0.118	0.116	0.129	0.190
M Marlene 02	0.180	0.184	0.119	0.158	0.105	0.120	0.135
K Raghild	0.142	0.192	0.107	0.119	0.122	0.155	0.164
Roelfina v EigenErf	0.164	0.187	0.119	0.158	0.106	0.128	0.139
K Ragna 05	0.124	0.185	0.141	0.144	0.128	0.131	0.147
O Ragnason 01	0.160	0.184	0.125	0.134	0.133	0.124	0.139
O Ragna 03	0.124	0.186	0.140	0.143	0.128	0.131	0.148
HO Hanna 01	0.117	0.158	0.122	0.147	0.115	0.200	0.142
K Audhildson	0.170	0.233	0.117	0.124	0.095	0.139	0.122

DF = Dutch Friesian (black and white) / RWF = Dutch Red and White Friesian / GWH = Groningen White Headed / DB = Dutch Belted / DR = Deep Red / MRY = Meuse-Rhine-Yssel / HOL = Holstein Friesian

4.2 STRUCTURE results clustering

When the number of predefined clusters is set to 7 or more, the software program STRUCTURE assigned the Jutland cattle as a distinct group (based on the 133 pre-selected SNPs). Figures 3 to 6 show the classification per animal, each vertical line is 1 animal. The results of the analyses for 6, 7, 8 and 9 clusters are shown in Figures 3, 4, 5 and 6 resp., of which 8 is the actual number of breeds (Figure 5). The order of the breeds is: Dutch Red and White Friesian, Dutch Friesian, Groningen White Headed, Dutch Belted, Deep Red, Meuse-Rhine-Yssel (MRY), Holstein Friesian and Jutland Cattle.

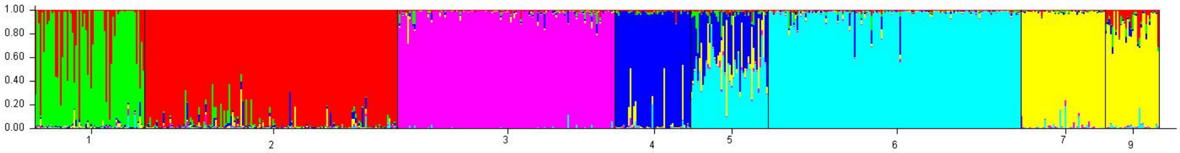

Figure 3 *Distribution over 6 clusters (2 clusters less than the number of breeds): Jutland (second half of yellow) and Holstein are clustered together. This could be the result of the SNP selection, these are specifically selected to distinguish between the dual-purpose breeds. Deep Red is not recognised either as a distinct cluster and is divided over the Dutch Belted and the MRY.*

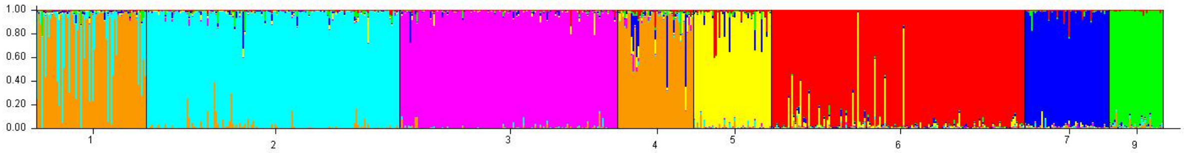

Figure 4 *Distribution over 7 clusters (one cluster less than the number of breeds): the Jutland (green) is assigned its own cluster. The software hasn't recognised Dutch Red and White Friesian as a separate cluster yet, but has assigned these animals partly to the Dutch Belted and partly to the Dutch Friesian.*

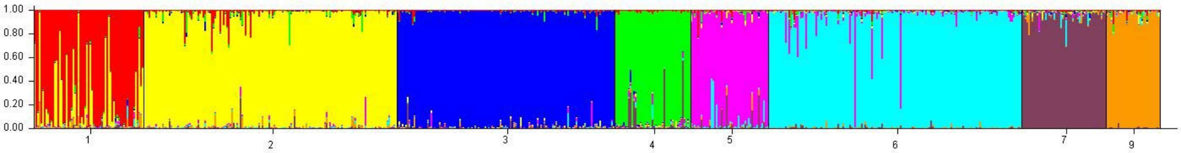

Figure 5 *Distribution over 8 clusters (actual number of breeds): Jutland (orange) is assigned to its own cluster and all breeds are classified as expected.*

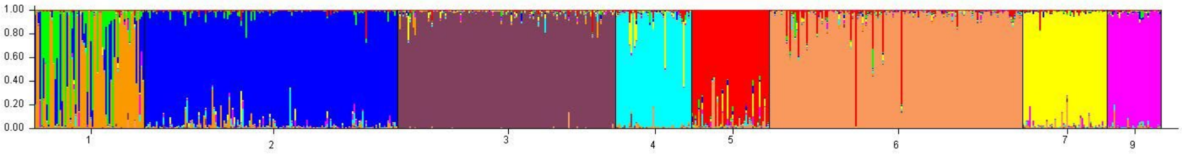

Figure 6 *Distribution over 9 clusters (one more than the number of breeds): the Jutland (pink) is still fully assigned to its own cluster. The extra cluster causes a split within the Dutch Red and White Friesian – this might be due to the distribution of 'original' old red Friesian lines vs. red and white Friesians from black ancestors.*

5 Conclusions and recommendations

The available genealogical records were verified with the help of DNA analyses. The kinships between individuals based on genotypes were in generally highest for the dams registered in the pedigree files of the breeding organisation. This confirmed the maternal parent of these animals. The same was true for the (half)siblings and cousins within this dataset. For Bente, the only animal in the dataset without a registered dam, O Ragna 04 was found as a potential dam, which completed her pedigree.

K Audhildson is probably not the actual sire to four (out of six) of his registered daughters, based on the analyses of the available genotypes. However, no definitive conclusion could be drawn yet and no suggestions for other potential sires could be supplied due to limitations in available genotypes. Hair samples from other herds, as there are many other Jutland individuals throughout the Netherlands, may help to identify potential sires for these four cows. Centre for Genetic Resources, the Netherlands (CGN) of Wageningen University & Research (WUR) can advise on the process and support with the necessary analysis.

The mean kinships of the genotyped animals varied, from low kinships between old animals to younger generations with higher mean kinships. It is important to realize that more animals from the Stroomdal herd were included in this dataset. Consequently, the mean kinships of these animals probably have to be (usually) higher than kinships of animals from the second farmer, and results do not provide a true representation of the total population throughout the Netherlands, but rather for the Stroomdal herd only. There are several possibilities to get a more definite representation, but this will require more material and hair samples from other Dutch Jutland individuals.

The Jutland cattle breed can be identified as a distinctive ‘population’, compared to the EU-approved Dutch dual-purpose cattle breeds. The highest proportion of genetic overlap was with the Friesian Dutch black-and-white population, but not nearly enough for the Jutland cattle breed to be placed within this breed. Therefore, the conclusion is that the Jutland cattle is not the same breed as the Dutch Friesian cattle. Interestingly, the proportions of overlapping SNPs for the Jutland individuals with the Dutch dual-purpose cattle breeds are on average pretty similar.

With approximately one hundred registered breeding animals in the Netherlands, it will be a major challenge to maintain the Jutland cattle as a distinctive, closed, population, with sufficient genetic diversity. Therefore, the urgent advice is to set up a joint, sustainable and long-term breeding programme with as many Jutland cattle breeders as possible in the Netherlands. All parties will need to make arrangements about the exchange of breeding animals and ways to limit the rate of inbreeding for the whole population. Also, potential collaboration with Danish organisations involved in the conservation of living populations or management of the Danish gene bank could offer possibilities for the exchange of animals or of genetic material. The CGN is happy to contribute ideas and provide support and advice for the short and long term.

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