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Final report

Genomic selection for more efficient beef breeding

Genomisk selektion för effektivare avel i nötköttsraserna

Project number: O-18-20-175

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Part 1.1: Summary/Abstract

Summary/Abstract

This project aimed to enable introduction of genomic selection in Swedish beef breeding. Reference populations were established for Swedish Charolais and Hereford. Access to data from the recently introduced Nordic beef genetic evaluation enabled upgrading to Nordic (Sweden, Finland and Denmark) level. More than 40,000 SNP markers for 4,321 Charolais and 4,532 Hereford were included, together with phenotype records for growth and carcass traits, in single-step genomic prediction (ssGBLUP) using BLUPF90 family software. A multi-trait animal model with unknown parent groups was used for breeding value estimation. Cross-validation was applied by truncating phenotypes after 2018. Using ssGBLUP instead of pedigree based BLUP improved accuracy and reduced bias for breeding values of genotyped animals. Relative accuracy improvements of 3% to 71% were seen for different traits in genotyped females. Implementing ssGBLUP would benefit Swedish, and Nordic, beef cattle breeding.

Sammanfattning

Projektet syftade till att möjliggöra genomisk selektion i svensk nötköttsavel. Referenspopulationer skapades för svenska Charolais och Hereford. Data från den nyligen

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införda nordiska avelsvärderingen möjliggjorde uppgradering till nordisk (Sverige, Finland och Danmark) nivå. Mer än 40 000 SNP-markörer för 4 321 Charolais och 4 532 Hereford inkluderades, tillsammans med registreringar för tillväxt- och slaktkroppsegenskaper, i single-step genomisk avelsvärdering (ssGBLUP) med hjälp av BLUPF90-familjens programvara. En djurmodell med flera egenskaper och genetiska grupper användes för skattning av avelsvärden. Korsvalidering tillämpades genom trunkering av fenotyper efter 2018. Användning av ssGBLUP istället för härstamningsbaserad BLUP förbättrade säkerheten och minskade bias för genotypade djurs avelsvärden. Relativa förbättringar av säkerheten på mellan 3 % och 71 % sågs för olika egenskaper hos genotypade hondjur. Att införa ssGBLUP skulle gynna svensk och nordisk nötköttsavel.

Part 1.2: Main report

Introduction

Background

The importance of specialized beef breeds for Swedish beef production has increased as the number of dairy cows has decreased, and the use of beef semen in dairy herds is also expected to increase further in the future. Attention has been brought to the climate impact of beef production, and thereby highlighted the importance of increased efficiency also for other than the obvious economic reasons. A more accurate genetic selection of the animal material for both functional and production traits would enable higher production efficiency. This could be achieved by utilizing genomic information and base the selection of breeding animals on genomic-enhanced breeding values.

In dairy cattle, the implementation of genomic selection around 2010 (Meuwissen et al. 2016) resulted in shortened generation intervals and up to doubled genetic gain (Garcia-Ruiz et al. 2016). It has been shown to be successful also in the Nordic populations (Bengtsson et al. 2021). Genomic selection was not as early adopted in beef as in dairy breeding, but it has been implemented in some countries such as the U.S., Ireland, France (Gunia et al., 2014; Lourenco et al., 2015; Kearney et al., 2018;), and is under development in several others. For beef breeds, the single-step genomic BLUP (ssGBLUP) that allows simultaneous use of all pedigree, phenotype and genotype information (Legarra et al., 2009; Aguilar et al., 2010) has become the method of choise for implementing genomic breeding values.

In 2019 a planned transfer from the use of microsattelite markers to SNP genotyping for parentage verification of beef cattle was initiated in Sweden, and from 2020 this has been in use. This provided a good opportunity to lay a foundation for future genomic selection in the populations. At the same time, genomic beef projects had started in both Finland and Denmark, and in 2021 a joint pedigree-based BLUP evaluation of beef breeds in the three countries was established (Nordic Cattle Genetic Evaluation, 2022). To increase the reference population size for genomic prediction, across country breed reference populations can be used for genomic prediction. The level of genetic relationships between animals in different populations is important to consider as it influences the value of including foreign animals in the reference population (Saatchi et al., 2013).

Aim and objectives

The overall aim of the project was to lay the foundation for genomic selection in Swedish beef cattle populations. The long-term goal was that, after implementation, genomic-enhanced breeding values will be available for selection in beef breeds. Ultimately, this was expected to improve the competitiveness and profitability for Swedish beef producers. The project was also expected to give a basis for future international collaborations both in research and for genetic evaluations. More specifically, the objectives were to 1) establish Swedish reference populations for the two most common beef breeds in Sweden: Charolais and Hereford; 2) develop the estimation of genomic-enhanced breeding values based on these reference populations and single-step methods, using already recorded phenotypes; 3) survey known genes of importance for qualitative traits.

Materials and methods

Simulation study

During the collection of DNA-samples we performed a simulation study, mimicking the structure of the most common beef breeds in Sweden to compare breeding value accuracies using pedigree-based BLUP (PBLUP) and ssGBLUP in different scenarios. We studied traits with two or four categories, similar to calving ease, with and without normal score transformation and with different information sources. The QMSim software (Sargolzaei et al., 2009) was used, and 750 QTL and 40K SNP were simulated across 29 autosomal chromosomes. A historical population was created, followed by a period of fewer animals. Finally, 86,000 individuals were used for further analyses. Quantitative traits with heritability of 0.3 and 0.05 were studied and compared with binary traits with different thresholds to mimic e.g. calving ease, with and without the use of normal score transformation. Breeding values were estimated with linear and threshold models using the BLUPF90 family programs (Aguilar et al., 2018) in scenarios with different information sources, with five replicates for each simulation. In all cases, phenotypes were removed for animals in the last two generations (for further details see Nazari-Ghadikolaei et al., 2022).

Data collection and genotyping

An important early part of the project was to collect DNA-samples for genotyping. The first steps were to apply for an ethical permit to collect samples, and to inform about the project. GDPR regulations limited our ability to reach individual breeders, but with the help of our reference group and articles, we instead got contacted by in total 53 interested beef breeders. For these herds we extracted information from the beef recording scheme with information about number of offspring, age and pedigree of animals. We suggested animals to be genotyped and the animal owner made the final decision about which animals to sample and which type of samples to collect (predominantly hair samples and to some extent tissue sampling ear tags). We prioritized animals old enough to have multiple trait records, animals with offspring, and animals with different pedigrees, including those from AI-sires. The majority of animals sampled in the farms were cows with offspring, but also some young bulls and heifers, as well as breeding bulls were included. The samples were sent through the established routine used by Växa Sverige for genotyping by Eurofins DNK using the Eurogenomics bovine MD SNP array, and the resulting data was processed and stored in the Nordic Cattle Genetic Evaluation (NAV) database in the same way as for all other samples analyzed for parentage verification.

In addition to samples from farms we genotyped stored frozen blood samples from station performance tested bulls. We chose samples from the most recent years and added older samples from AI-bulls and other breeding bulls with many offspring. For a few bulls for which blood samples were lacking we used stored hair samples for genotyping. In total 227 stored Hereford samples and 571 Charolais samples were sent for genotyping. Also, we genotyped sperm samples from a few AI-bulls of importance for breeding. Together with the samples from breeding farms, genotyping was ordered for more than 2300 Charolais and more than 1800 Hereford. Since then, more animals have been genotyped by farmers.

When requesting the SNP-marker information for genotyped animals from NAV in 2021, we were asked to include also Hereford and Charolais from Finland and Denmark to make the study more relevant for the industry since the introduction of a joint Nordic genetic evaluation. We thereby obtained SNP array information for in total over 9700 animals, whereof 9269 were genotyped on a medium density SNP array. After the quality control, a total of 40988 autosomal SNPs for 4532 Hereford, and 43141 SNPs for 4231 Charolais were kept for further analysis (Figure 1).

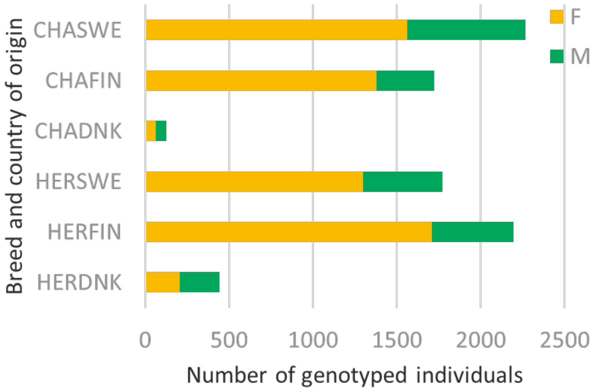

Figure 1. Distribution of genotyped animals per sex (female or male), breed, and country.

Pedigree and pre-edited phenotype data for the growth and carcass traits including birth weight (BW, kg), weaning weight gain (WWG, kg), post weaning weight gain (PWG, kg), yearling weight (YW, kg), slaughter daily gain (SDG, kg), EUROP conformation class (SCONF. points 1-15), and EUROP fat class (SFAT, points 1-5), were provided for Hereford and Charolais from the joint NAV evaluation through Växa Sverige. In total the data included more than 560,000 unique individuals (52% Charolais and 48% Hereford) had records on birth weight in the data, which was the trait with the most complete recording. More than 80% of the genotyped animals had at least three own trait records in the data. Genotyped bulls had 1-357 offspring with trait records, with an average of 52 offspring for Charolais and 32 for Hereford bulls.

Data analysis and estimation of breeding values

Linkage disequilibrium (LD) decay patterns and principal component analysis (PCA) were studied and compared across the breeds and countries to give a basic understanding of how similar the populations were. For these analyses PLINK v 1.07 (Purcell et al., 2007) was used.

A multiple trait linear animal model was used including in total 10 traits: BW (maternal (m) and direct (d)), WWG (maternal and direct), PWG (Swedish and Finnish animals), YWG (maternal and direct, only for Danish animals), SDG, SCONF and SFAT. The same statistical model and genetic parameters (Table 1) that are currently used in the NAV beef evaluation were used when estimating breeding values in this project. The included fixed effects were country-sex, country-twin (only carcass), country-year-month, country-dam age-time, and herd-birth year contemporary group, and adjustment for age at weighing (only carcass). Random effects were animal, maternal genetic and permanent environmental effect of dam (for some traits, see above), residual, and genetic group based on year of birth in 10-year groups and country of origin (Danish, Finnish, Swedish, European, American, Canadian and Other).

Table 1. Genetic correlations for Hereford (above diagonal) and Charolais (below diagonal), and heritability on the diagonal (Charolais\Hereford) used in the breeding value estimations

	BWm	BWd	WWGm	WWGd	YWm	YWd	PWG	SDG	CCO	CFA
BWm	**0.10\0.11**	-0.21	0.23	0.12	0.35	0.12	0.16	0.24	-0.08	0.01
BWd	0.02	**0.38\0.47**	-0.14	0.43	-0.18	0.53	0.34	0.18	0.01	-0.29
WWGm	0.12	-0.11	**0.13\0.16**	-0.16	0.95	-0.07	-0.02	0.61	0.16	0.29
WWGd	0.21	0.35	-0.16	**0.17\0.15**	-0.13	0.84	0.49	0.50	0.10	-0.12
Ywm	0.27	-0.17	0.90	-0.09	**0.10\0.10**	-0.15	-0.05	0.60	0.19	0.27
YWd	0.20	0.48	-0.08	0.83	-0.15	**0.31\0.29**	0.71	0.58	0.07	-0.11
PWG	0.19	0.31	-0.17	0.38	-0.25	0.71	**0.20\0.20**	0.50	0.03	-0.06
SDG	0.19	0.17	0.54	0.52	0.54	0.61	0.40	**0.36\0.46**	0.38	0.16
SCOND	0.01	0.08	0.12	0.07	0.14	0.16	0.15	0.42	**0.31\0.28**	0.11
SFAT	-0.07	-0.23	0.23	0.00	0.24	-0.05	-0.02	0.13	-0.10	**0.34\0.30**

Breeding values were estimated using both PBLUP and ssGBLUP using the BLUPiod2f90 program for large data included in the BLUPF90 software family (Aguilar et al., 2018). Genetic groups were included as UPGs with a QP transformation. We tried partial transformation but that did not work properly, however genetic trends were essentially the same as in current NAV evaluation. We also tried different weights (alpha value) on genomic information in building of H matrix 0.95 and 0.70.

We compared genetic trends when using ssGBLUP and PBLUP. We also used a cross-validation method by truncating phenotypes for animals born after 2018 in a reduced data set and comparing with results from analysis of the full data. This was done in different scenarios within and across countries. We calculated accuracy ratio and bias based on linear regression method (Legarra & Reverter, 2018) for genotyped and non-genotyped groups of animals. The improvement of accuracy by using ssGBLUP compared with pedigree BLUP (PBLUP) was estimated for different traits. Additional validations using adjusted phenotypes are ongoing.

Literature study

A survey of published literature on known monogenic traits of importance for beef cattle was conducted, with focus on beef breeds that are common in Sweden.

Results

Simulation study

Using ssGBLUP instead of PBLUP improved accuracies with 14% to 30% in the simulated data. The accuracy improvement was generally higher when the animals with phenotypes (females) were genotyped than when males without phenotypes were genotyped. For more details about the simulation study see Nazari-Ghadikolaei et al. (2022).

Data analysis and estimation of breeding values

We found very small differences in LD decay pattern between populations of the same breed in the different studied Nordic countries. The PCA analysis (Figure 2) showed that the populations were well mixed across countries (within breed).

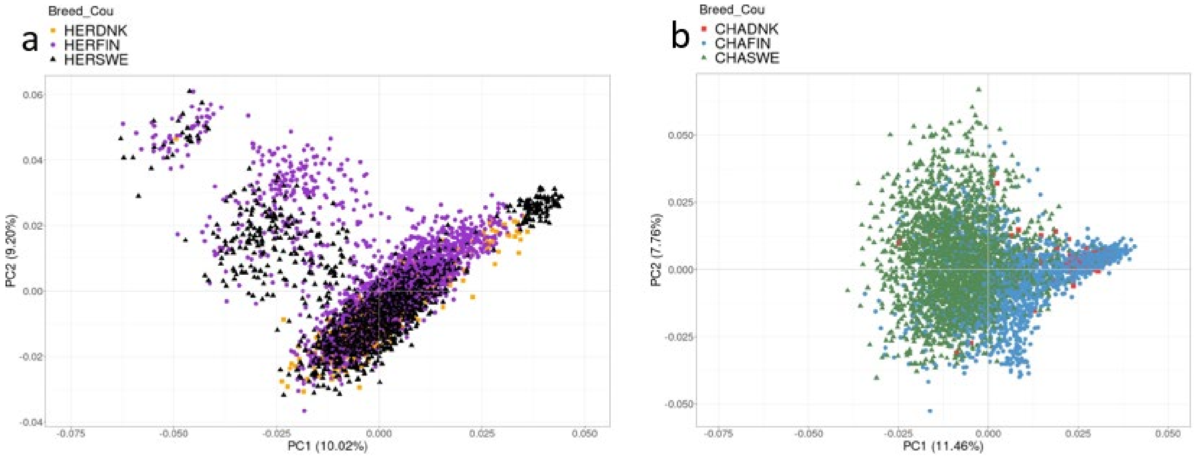

Figure 2. Genomic relatedness between animals of the same breed, born in Denmark, Finland or Sweden from principal component analysis, Hereford is shown in a) and Charolais in b).

The estimated genetic trends were as expected very similar between PBLUP and ssGBLUP and between ssGBLUP using full and reduced data sets (examples shown in Figures 4 and 5). However, somewhat more variation between the trends were seen for maternal traits than for direct traits, and in general larger deviations between trends were seen for Danish animals (that were relatively few) compared with the Finnish and Swedish.

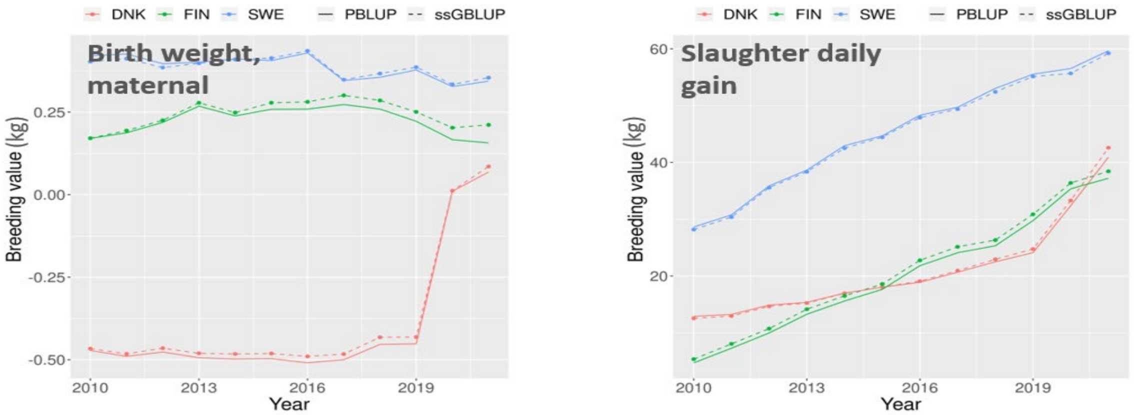

Figure 4. Genetic trend from Pedigree BLUP (solid lines) and single-step GBLUP (dotted lines), for the traits birth weight maternal and slaughter daily gain in Hereford.

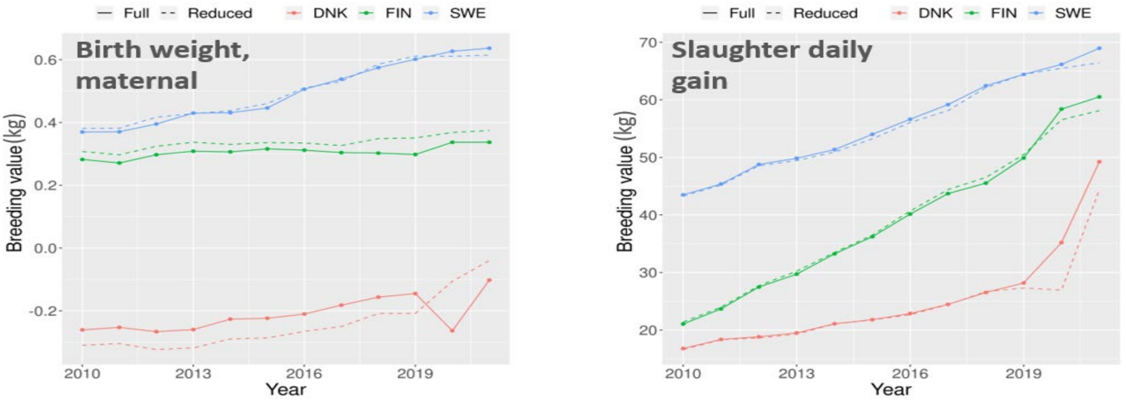

Figure 5. Genetic trend from full (solid lines) and reduced (dotted lines) data using ssGBLUP, for the traits birth weight maternal and slaughter daily gain in Charolais.

Results of linear regression (LR) cross-validation showed that using ssGBLUP gave higher accuracy ratio and in the majority of cases less bias for genotyped animals compared to using PBLUP. Relative accuracy improvements of 3% to 71% were seen for the different traits in genotyped females in Sweden, with somewhat larger improvements in Hereford than in Charolais and for Swedish animals compared with Finnish (Table 2).

Table 2. Relative increase in accuracy of estimated breeding values for genotyped female animals in the test data set, when using ssGBLUP instead of PBLUP, for different weights (0.95 and 0.70) on genomic information when building the relationship matrix

	Charolais				Hereford			
	weight 0.95		weight 0.70		weight 0.95		weight 0.70	
Trait	FIN	SWE	FIN	SWE	FIN	SWE	FIN	SWE
BWm	18%	16%	10%	10%	31%	38%	21%	26%
BWd	20%	22%	14%	15%	35%	57%	28%	44%
WWGm	19%	34%	12%	21%	24%	40%	13%	22%
WWGd	26%	42%	18%	30%	64%	51%	48%	38%
PWG	11%	26%	7%	18%	33%	71%	23%	49%
SDG	22%	40%	16%	26%	38%	66%	26%	43%
SCONF	5%	16%	3%	9%	26%	32%	19%	22%
SFAT	9%	23%	6%	15%	37%	43%	24%	29%

Discussion

The results from this study showed that it would be possible to introduce prediction of genomic-enhanced breeding values for Swedish beef breeds. The Hereford and Charolais populations in Sweden, Finland and Denmark showed enough genetic similarities to make a joint Nordic genomic prediction meaningful. The reference population was more than doubled when adding Finnish and Danish data to the Swedish in this study, which is important for the accuracy of estimations. The level of relative improvement of accuracy in our study was dependent on several factors, including the group of animals studied (e.g. genotyped or not), type of validation used, the weight put on genomic information, and the type of trait and amount of information available (number of genotyped and phenotyped animals).

As expected, we saw considerable improvements for most traits in young genotyped females in this study. In a simulation of a beef cattle population, Lourenco et al. (2013) found the largest benefits of using ssGBLUP instead of PBLUP in young genotyped animals without phenotype information. The results from our initial simulation study showed that although the response to selection for low heritability categorical traits such as calving ease is not as fast as for e.g. growth rate, adding genotype data could improve accuracy estimations. In our project, we prioritized moving to a joint Nordic level and did not have time to study the effect of genomic selection in calving ease field data, and this remains to be done in Swedish or Nordic beef cattle. In real Angus data, Lourenco et al. (2015) estimated considerable improvement in predictive ability for birth weight, weaning weight and post weaning gain, and some improvement also for calving ease. Saatchi et al. (2013) reported 55%-66% higher average accuracy of genomic predictions using compared to those obtained from traditional PBLUP method in American Holstein animals. Van Eenennaam et al. (2011) predicted that genomic selection had the potential to increase genetic and economic gain with between 29% and 158% in beef cattle.

To be able to complete this study on time, we extracted genotype data in mid-2021 from the Nordic database. Since then more animals, also from other breeds, have been genotyped, and genotyping of breeding animals will continue now that the pedigree verification is based on SNP array information. The availability of information on certain monogenic traits related to genetic diseases and to polledness in beef cattle has also proven to be an important motivation for beef breeders to genotype animals. Our literature study showed that there are several monogenic traits of potential interest for Swedish beef breeders. Validation of markers for such traits are needed in the Nordic populations before implementation, but we foresee that more information on monogenic traits will be available in the future. In our study we focused on the two most common beef breeds in Sweden, to enable inclusion of a sufficient number of animals per breed in spite of a limited budget for genotyping. In Finland, more animals of different beef breeds, as well as crossbreds, have been genotyped. Joining information across countries will be very useful for future implementation of genomic-enhanced breeding values in the Swedish, and Nordic, beef breeding programs. The recently introduced joint Nordic PBLUP evaluation gives a good basis for adding on genomic information on Nordic level.

Conclusions

Introduction of single-step genomic best linear unbiased prediction (ssGBLUP), would improve the accuracy and reduce the bias of breeding values for growth and carcass traits in Swedish beef breeds. It is feasible to do this on a joint Nordic level and that would give a considerably increased reference population and thus more accurate predictions.

Relevance and recommendations

We recommend introduction of genomic predictions for beef breeds on Nordic level, as this would improve the accuracy of estimated breeding values especially in young genotyped animals. This has the potential to increase the genetic gain in several important traits and thereby lead to more efficient beef breeding. Discussions have already started between relevant parties such researchers, NAV with owner organizations, and breed associations about the future implementation of results from this project as well as results from the other Nordic, especially the Finnish, beef genomic projects. From the discussions we have taken part in, it appears that the intention is to continue development toward implementation of genomic prediction for beef breeds on a Nordic level.

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Result dissemination:

Scientific publications, *manuscript*	Nazari-Ghadikolaei, A., Fikse, W.F., Eriksson, S. Single-step GBLUP evaluations for growth and carcass traits in Nordic Charolais and Hereford cattle.
Conference publications/ presentations	Nazari-Ghadikolaei, A., Eriksson, S., Fikse, W.F. 2022. Single-step GBLUP evaluation for categorical traits for beef cattle. Proc. 12th WCGALP, 3-8 July 2022, Rotterdam, the Netherlands, 47-018, 4 pp. https://www.researchgate.net/publication/361984114_Single-step_GBLUP_evaluation_for_categorical_traits_for_beef_cattle
	Nazari-Ghadikolaei, A., Fikse, W.F., Eriksson, S. 2022. Single-step GBLUP for growth and carcass traits in Swedish beef cattle. Annual Report 2021/2022 of Dept. Animal Breeding and Genetics, Swedish University of Agricultural Sciences. Report no. 154., p30.
Other publications, *media etc.*	Eriksson, S. 2021. Forskningsprojektet om genomisk selektion går in i ny fas. Hereford. Medlemstidning för svenska Herefordföreningen. Nr 4, December 2021. P 17.
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	Persson, S. 2020. Framtidens avelsverktyg inom räckhåll. Charolais. Nr 1 2020. p 29.
	Persson, S. 2020. Genomisk selektion för effektivare köttrasavel. Charolais. Nr 2 2019. p 30.
Oral communi-cation, ***to sector, students etc.***	Presentation by F. Fikse about single-step genomic predictions for Växa's Avelsråd, 7 Dec. 2022.
	Seminar about the project and results by A. Nazari-Ghadikolaei at the Dept. seminar series at SLU: "ssGBLUP for growth and carcass traits in Swedish beef cattle", Uppsala 17 Nov. 2022.
	Presentation by S. Eriksson: "Genomic prediction of (Swedish) Hereford and Charolais" for NAV representative and the Finnish and Swedish beef genomic project groups online meeting "Single step beef - results from Swedish and Finnish project" 7 Nov. 2022.
	Presentation by M. Johansson at international Hereford meeting in France in Oct. 2022.
	Presentation by F. Fikse: "Genomic prediction of (Swedish) Hereford and Charolais" at NAV beef cattle workshop for Nordic beef breeders and breeding associations, Copenhagen 22 Sept. 2022.
	Presentation by S. Eriksson about genomic selection at online meeting arranged by the Swedish Hereford Association 29 Jan. 2021.
	Presentation by S. Eriksson about the project and genomic selection at online NAB-meeting (beef breed associations) 17 Nov. 2020.
	Presentation by F. Fikse at seminar about beef breeding arranged by Växa Sverige, 3 Nov. 2020.
	Presentations by S. Eriksson at online meeting between project groups in Finland, Denmark and Sweden working with beef genomics 18 Aug. 2020 and 15 Dec. 2020.
	Presentation by S. Eriksson online reference group meeting 6 Oct. 2020.
	Presentation by S. Eriksson at online meeting with VikingGenetics 3 March 2020.
	Presentation by S. Eriksson at workshop between SLU and VikingGenetics in Uppsala 20 Jan. 2020.
	Presentation by S. Eriksson online for reference group 26 Sep. 2019.
	Presentation by S. Eriksson at online meeting with the board for Svensk Köttrasprövning AB, 19 April 2019.
	Presentation by O. Thomsson for slaughter industry Dec. 2019.
	Project used as example in discussions with students in the course "Designing Breeding Programmes" at SLU 2019 and 2021.
Other	Literature report about monogenic traits by S. Duchemin, 2020, for internal use in discussion with breed organizations.