SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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DELIVERABLE D2.3

Paper of quantification of new disease biomarkers linked to production. New disease phenotypes for endemic diseases linked to key production traits.

Chapter1. Paper: "Breeding options for nematode resistance in Lacaune dairy sheep" (disease = parasite infestation)

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Chapter2. Paper: "Including genotypic information in genetic evaluations increases the accuracy of sheep breeding **values" (disease = mastitis** and footrot)

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1 Summary

In this deliverable we report papers written/published as part of the wider Deliverable and report in detail new work from two new papers on quantification (genetic and phenotypic parameters) of new disease biomarkers linked to endemic disease in the framework of SMARTER WP2 Task 2.1. The objective was to address the main endemic diseases (footrot, mastitis, gastro intestinal parasites) and link biomarkers to key production traits.

The first chapter reports a paper on quantification of biomarkers linked to parasite infestations, namely faecal egg counts (FEC), FAMACHA© (a colour classification of the eyelid) and packed cell volume. The case study was developed by FIBL in a swiss Lacaune dairy sheep population. New disease biomarkers were linked to milk production, the main production trait in this population. The paper has since been published in the journal ANIMAL. Werne S, Schwarz K, Tuer S and Bapst B 2023 Breeding options for nematode resistance in Lacaune dairy sheep. Animal 2023 May; 15(5):100772 https://doi.org/10.1016/j.animal.2023.100772

The second chapter reports a paper for health traits measured in adult ewes, namely footrot (FRT) and California Mastitis Test score (CMT) as a poxy for mastitis [SRUC and TEXEL]. The paper more widely addresses the impact of inclusion of genome-wide genotypes into breeding value predictions for UK Texel sheep. New genetic parameters for a range of lamb growth, carcass composition and health traits are described and applied in the estimation of conventional breeding values (EBVs) for almost 822 000 animals as well as genomic breeding values (gEBVs) after adding 10 143 genotypes. The paper has since been published in 2023 (see below) in the journal ANIMAL. Kaseja K, Mucha, S, Yates J, Smith E Banos, G and Conington J. 2023. Including genotypic information in genetic evaluations increases the accuracy of sheep breeding values. J.Anim.Breed.Genet. 140: 4: 462-471 https://onlinelibrary.wiley.com/doi/full/10.1111/jbg.12771

Both papers show substantial genetic variation for biomarkers related to endemic disease in sheep, i.e. heritabilities ranging from 0.07 for mastitis (CMT) to 0.12 for footrot and up to 0.30-0.36 for parasite phenotypes (FEC, FAMACHA and PCV).

In response to evaluators' comments regarding D2.3 initial submission, the following additional information is relevant to this Deliverable. Specifically, two other papers have been written that refer to 'quantification (genetic and phenotypic parameters) of new disease biomarkers linked to production' which also address '…a proxy trait for parasites' were written / submitted /published in the Animal journal. Three additional papers are published/in press where proxy traits for mastitis and footrot are reported along with their heritabilities and correlations with performance.

Internal parasites & their proxies

1.Pacheco A, Conington J, Corripio-Miyar Y, Frew D, Banos G and McNeilly T N 2023. Genetic profile of adaptive immune traits and relationships with parasite resistance and productivity in meat sheep. Submitted to Animal 2023, under review.

In brief: Significant genetic variation was observed in immune response traits (interferon-gamma (IFN-γ), interleukin (IL)-4, and IL-10 and immunoglobulin A (IgA). Heritabilities of cytokine production varied from low (0.14±0.06) to very high (0.77±0.09) and were always significantly greater than zero (P<0.05). IgA heritability was found to be moderate (0.41±0.09). Live weight was negatively genetically correlated with IFN-γ responses.

2.Pacheco A , Banos G., McNeilly, T and Conington J. 2021. Genetic parameters of animal traits associated with coccidian and nematode parasite load in Scottish Blackface sheep. Animal 15:4: 100185 January 2021. https://doi.org/10.1016/j.animal.2021.100185

In brief: Heritability estimates (±SE) were 0.16 ± 0.03, 0.17 ± 0.03, 0.09 ± 0.03, 0.09 ± 0.03 and 0.33 ± 0.04 for FECS, FECN, FOC, DAG and LWT, respectively. Strongyles faecal egg count had a strong and positive genetic correlation with FECN (0.74 ± 0.09) and a moderate positive correlation with FOC (0.39 ± 0.15) while DAG was negatively genetically correlated with LWT (−0.33 ± 0.15).

Mastitis and Footrot

3. McLaren, A., Kaseja, K., Yates, J., Mucha, S., Lambe, N and Conington J. 2018. New mastitis phenotypes suitable for genomic selection in meat sheep and their genetic relationships with udder conformation and lamb live weights. Animal. 12:1-10
DOI: https://doi.org/10.1017/S1751731118000393

In brief: Heritability estimates for traits relating to mastitis (somatic cell score and the California Mastitis Test), ranged from 0.08 to 0.11 and 0.07 to 0.11, respectively. High genetic correlations were observed between somatic cell score and the California Mastitis Test (0.76 to 0.98), indicating the California Mastitis Test to be worthwhile for assessing infection levels, particularly at mid-lactation. The strongest correlations observed between the mastitis traits and the udder conformation traits were associated with udder depth (0.61 to 0.75) also at mid-lactation. Negative phenotypic correlations were estimated between mastitis and the weight of lamb reared by the ewe (−0.15 to −0.23), suggesting that lamb weights fell as infection levels rose. Genetic correlations were not significantly different from zero.

Also, additional information that supports outputs for D2.5, D3.5, D7.3 and D7.4 are in the following paper:-

4. Kaseja K, Mucha S, Yates J, Smith E, Banos G and Conington J. 2023. Genome-wide association study of health and production traits in meat sheep. In Press (Pre-proof https://doi.org/10.1016/j.animal.2023.100968)

5. Sotiria Vouraki, Athanasios I. Gelasakis, Vasileia Fotiadou, Georgios Banos, Georgios Arsenos. *Vet. Sci.* **2022**, *9*(6), 289 . Repeatability of health and welfare traits and correlation with performance traits in dairy goats reared under low-input farming systems.

https://doi.org/10.3390/vetsci9060289

The objectives of the study were to estimate the repeatability of health and welfare traits and investigate their association with performance in three breeds of dairy goats reared under low-input farming systems in Greece. A total of 1210 goats of Eghoria (n = 418), Skopelos (n = 429), and Damascus (n = 363) breeds were assessed. Udder health, parasitic resistance, welfare, milk yield and quality, and body condition score were recorded monthly for two milking periods. Udder health records included somatic cell count (SCC) and total viable count (TVC). Based on combinations of SCC and TVC and thresholds set at >106 cells/mL and >2 × 104 cfu/mL, respectively, additional udder health phenotypes were defined. Parasitism included myiasis, tick infestation, gastrointestinal nematode (GIN) and cestode faecal egg count (FEC), and lungworm faecal larval count (FLC). Infection with each of the endoparasites was defined based on FEC/FLC. Welfare assessment parameters included the presence of ear and horn injuries, ocular and nasal discharge, body and udder abscesses, injury and lesions on the skin of different regions, diarrhoea, hernias, overgrown hooves, arthritis, lameness, and udder asymmetry. Trait repeatability and animal correlations were estimated. Significant ($p < 0.05$) repeatability was reported for all udder health and most welfare traits in all breeds, GIN and cestode FEC, and GIN and lungworm infection in Eghoria, and myiasis in Skopelos. Correlations of health and

most of welfare traits with performance were non-significant or favourable. Overall, results demonstrate potential to improve health and welfare of the studied breeds without compromising performance.

Also, in Ireland, genetic parameters using 39,315 animal records from industry flocks (multibreed) were estimated and used to include lameness, mastitis and dag score into the national sheep evaluations. This means that the impact of collecting and analysing the data in SMARTER has immediately been taken up by the industry as rams can be searched according to their breeding values for these (and other) traits.

The results from the published Kaseja et al., 2023 paper (Including genotypic information in genetic evaluations increases the accuracy of sheep breeding values) were used to **generate breeding values** for the Texel Sheep breed in the UK. Regarding WP7 specifically, the T7.3 (creation of **balanced breeding goals**) and assessing **the impact of new breeding goals** were tested to see the long-term impact of breeding on sheep and goat populations. The same paper tests how new genomic data and tools can improve breeding programs and populations faster. The work also contributed to the modelling work using selection index theory model to show how a broader balance of efficiency and resilience traits (including genomic prediction) will increase the efficacy of genetic improvement in small ruminant breeding programs. The index work used existing desired gains indexes and built in some desired gains weights for functional longevity and feed efficiency to determine the % emphasis for each trait, and then sensitivity- tested for different weights (to reflect different farmer and breeders' preferences for improved economic, social or environmental performance), correlation with production traits, and adding genomics. There was very little resemblance between outcomes of 7.1 and 7.3 and the "weight inputs" in 7.4. We couldn't calculate profitability gains over 20-years because there were no economic indexes. **In WP7.1, mastitis and parasites were modelled at the farm system level** and showed that there was value to be gained, mostly through improvements in performance for production traits. More detailed information on the link between WP7 and WP2 outputs are reported in D7.4 - Report on recommendations for breeding: Summary of whole work package including recommendations for breeders for how to use balanced breeding goals.

CHAPTER 1. Paper "Breeding options for nematode resistance in Lacaune dairy sheep"

1.1.1 Summary

Due to progressing anthelmintic resistance of gastrointestinal nematodes (GIN), supportive measures are needed to control these parasites. In sheep it has been shown that selection towards an increased nematode resistance is feasible and that Faecal egg count (FEC) is the generally acknowledged trait for selection. However, a selection based on FEC would come with certain costs, therefore auxiliary, cheaper resistance-traits would be most welcome. FAMACHA©, a colour classification of the eyelid, usually used to determine the manifestation of an infection with Haemonchus contortus, could serve as such. Therefore, we collected FAMACHA©, packed cell volume (PVC) and FEC phenotypes of nearly 1200 naturally infected Lacaune ewes on 15 commercial farms in Switzerland. The Haemonchus-

proportion was determined on farm level. Phenotypic correlations of FEC and FAMACHA© as well as FAMACHA© and PCV were 0.25 (SE 0.03) and -0.35 (SE 0.08), respectively and correspond well with results of other studies. A multi-trait animal model was applied to estimate genetic parameters with FEC, FAMACHA©, PVC and milk yield as dependent variables. The heritabilities of FEC, FAMACHA©, PCV and milk yield were estimated to be moderate with values of 0.33 (SE 0.08), 0.30 (SE 0.08), 0.36 (SE 0.08) and 0.34 (SE 0.08) respectively. The genetic correlations between FEC and FAMACHA© and between FEC and PCV were estimated to be close to zero with values of 0.03 (SE 0.22) and 0.01 (SE 0.21) respectively. The average Haemonchus-proportion compared to other GIN was found to be 43%. The FAMACHA© classification of the Lacaune ewes seems to indicate a rather high worm challenge, with 38%, 14% and 2% of observations classified to score 3, 4 and 5, respectively. However, the worm challenge according to FEC was moderate. It has been suggested that the genetic correlation of FAMACHA© and FEC is more pronounced when FEC was high. It could therefore be that the lack of genetic correlation was due to an insufficient worm challenge, even though the Lacaune were grazing at least 70 days before phenotyping. The genetic correlation of FEC and milk yield was estimated to be 0.07 (SE 0.22, slightly unfavourable). We conclude that if FEC is used as trait, the Lacaune could be selected for lower susceptibility towards nematode infection. The use of FAMACHA© as auxiliary trait for FEC is not feasible, due to an inexistent genetic correlation of these two traits.

1.1.2 Introduction

The control of infections with gastrointestinal nematodes (GIN) in pasture-based sheep production systems is crucial due to associated high production losses (Morgan et al., 2013) and animal welfare issues. Gastrointestinal nematodes have been mainly controlled by the use of anthelmintics for the last decades. However, the available agents are losing efficiency and resistant populations of GIN are now widespread in Europe (Ploeger and Everts, 2018; Rose Vineer et al., 2020; Untersweg et al., 2021). This development will make it difficult for small ruminant farmers to safely control GIN by the use of anthelmintics. Beside the loss of effectiveness, the widely used anthelmintic family of the 'macrocyclic lactones' is assumed to be associated with long-lasting negative effects on invertebrates after deposition in the environment (Finch et al., 2020; Sands and Noll, 2022). This is another reason why the reduced use of anthelmintics is appreciated.

One of the possible ways to reduce the dependence on anthelmintics could be the selection of sheep with lower susceptibility to nematode infection (Torres-Acosta and Hoste, 2008; Gilleard et al., 2021), as the mechanisms for resistance towards GIN are genetically determined (Karlsson and Greeff, 2012). In sheep, the number of nematode eggs per gram faeces (FEC) is widely acknowledged as resistance trait. In two recent meta-analyses, the global heritability for FEC was estimated to be 0.17 (Medrado et al., 2021) and 0.22 (Hayward, 2022). It has been shown that meat sheep genotypes that were selected for 15 years for low FEC had a significantly lower number of adult nematodes at necropsy and a FEC of only 18% compared to the unselected control (Kemper et al., 2010). This proves that selection for a significantly lower susceptibility to GIN-infection is feasible when using FEC as trait. However, little information exists on the nature of genetic correlations of FEC and milk yield (MY) in dairy sheep.

The routine use of FEC in a breeding programme would have the disadvantage of a relatively labour and costs intensive approach (animals sampling and coprological procession). Therefore, cheaper auxiliary traits for parasite resistance would be highly appreciated. The FAMACHA© system has been developed to assign a score to the colouration of the conjunctiva of small ruminants, as a tool to identify animals impacted by Haemonchus contortus infection (Wyk and Bath, 2002). Haemonchus contortus is a blood sucking abomasal nematode and infection can cause anaemia which is reflected in the bleaching of the conjunctiva. The soring is considered cheap and relatively easy to carry out. Decent phenotypic correlations between FAMACHA©, packed cell volume (PCV) and FEC have been

reported (Kaplan et al., 2004; Notter et al., 2017), improving with increasing H. contortus proportions (Schwarz et al., 2020). Although reports on phenotypic correlations of FAMACHA© or packed cell volume (PCV) and FEC are somewhat inconsistent, some authors have reported favourable genetic correlation and a moderate heritability of FAMACHA© (Cloete et al., 2016; Balconi Marques et al., 2020), suggesting that FAMACHA© might be used as auxiliary trait for the selection of sheep with lower susceptibility towards GIN infection.

Therefore, the objectives of this study were to get information on the heritability of FEC and FAMACHA© as well as on genetic correlations of FEC, FAMACHA©, PCV and MY in a Swiss Lacaune subpopulation.

1.1.3 Methods

Study design, farm and animal requirements

Data collection took place from end August to mid December 2019 on 15 commercial Swiss Lacaune dairy sheep farms, of which 14 were certified organic. In order to be considered for the study, the potential animals and farms had to fulfil a number of conditions: (i) pure bred Lacaune animals only, defined as animals with ≥87.5% Lacaune blood), (ii) at least 30 lactating animals per farm, (iii) daily pasture access per farm for all animals for at least 70 days before sampling date to allow natural infection with gastrointestinal nematodes, (iv) availability of milk performance data, (v) no applied anthelmintic treatment during lactation and grazing period 2019 and (vi) the respective dairy sheep farm had to be a member of the Swiss dairy sheep herdbook, which guarantees known pedigrees of each phenotyped animal. Farm visits were timed so that they were no more than three days away from an official milk recording date.

Faecal egg count, coproculture and H. contortus identification

Procedures for FEC, coprocultures and H. contortus identification were done as described in Schwarz et al. (2020). In brief, animals were sampled individually and faecal samples were taken directly from the rectum and stored at 6°C until processing them until no later than four days with a modified McMaster technique. At each farm visit, 10 to 25 random animals, depending on farm size (approx. 10% of total stock), were additionally sampled and pooled in two to five jars with a volume of 250 ml each, to obtain third stage larvae from coproculture after incubation at 25°C and 80% humidity for 10-14 days. From each jar, 100 third stage larvae were differentiated according to keys provides by Deplazes et al. (2013) and van Wyk et al. (2004) to determine the proportion of H. contortus compared to all other third stage GIN-larvae.

Packed cell volume and FAMACHA© score

Blood samples were taken by jugular vein puncture in 2 ml EDTA vacutainer tubes and stored cool at 5°C until processing within 24 hours, using a microhematocrit method. To do so, samples were allowed to adjust to room temperature for one hour, then the blood was filled into microhematocrit tubes and centrifuged at 9600g for five min (Heraeus Pico 17). The FAMACHA© score was obtained by using the FAMACHA© card to classify the animals to a score from one to five as described by van Wyk and Bath (2002).

Statistical analysis

Descriptive statistics and data preparation for variance component estimation were performed using R (R Core Team, 2022). A total of 1208 animals with phenotypic data were available on the 15 farms. Of these, 21 were rams. Although the rams were phenotyped, they were excluded from the estimation of genetic parameters due to different management compared to females and small numbers. Variance components and breeding value (EBV) estimations as well as the preceding pedigree preparation and renumbering were performed with programs from the BLUPF90 package (Misztal et al., 2018). A multi-trait animal model with fixed and random effects was applied. The model for the analysis was built following Heckendorn et al. (2017):

yijklmno = herdi + monthj + lack +dimcll + heamclm + an + eijklmno (1)

where yijklmno is the trait of interest of animal n in herd i, with phenotyping month j, in lac k, in dimcl l and with haemcl m. Herdi is the fixed effect of herd, monthj the fixed effect of the phenotyping month, lack the fixed effect of the lactation, dimcll the fixed effect of the days in milk class, heamclm the fixed effect of the average H. contortus class of the herd, an the random animal effect and eijklmno the random residual effect. All traits of interest, namely FEC, FAMACHA©, PCV and MY were evaluated with the same fixed and random effects.

In order to achieve an approximation of a normal distribution for FEC the untransformed trait was converted with a Box Cox transformation (Box and Cox, 1964) applying the following formulas and a prior computed $\lambda = -0.464$.

FEC100 = FEC + 100 (2)

FEC100_trans = (FEC100 λ - 1) / λ (3)

Prior to the transformation, FEC phenotypes >20000 were set to 20000. All values of the categorial trait FAMACHA© which were not 1, 2, 3, 4 or 5 were set to missing. The PCV values had to be in the range of 15 to 45, otherwise the outlier is replaced by a missing value code. In the plausibility check for MY (result for the test day closest to the day of worm phenotyping), the lower and upper limits were set at 0.1 kg/d and 4.5 kg/day, respectively.

All fixed and random effects had to be present and they were checked or categorised as follows: Each phenotypic record had to be assignable to a herd number ranging from one to 15. The phenotyping period has taken place from August to December. Samples taken from August to October were given a value of one, and samples taken later than October were given a value of two. Days in milk (DIM) was categorised as follows: DIM ≤ 100, class one; DIM>100 and DIM ≤ 150, class two; DIM>150 and DIM ≤ 200, class three; DIM > 200, class four. The lactation numbers 1, 2 and 3 were handled separately as three groups, and from fourth lactation onwards all were assigned to group four. In addition, the herds were divided into three groups according to average H. contortus infestation: Haemonchus-infestation ≤ 30, class one; Haemonchus-infestation > 30 and Haemonchus-infestation ≤ 60, class two; Haemonchus infestation > 60, class three. It was verified that each animal ID was registered in the official pedigree of the breeding organisation and that each phenotype sample had a complete set of effects. After applying all pre-conditions, 1109 ewes with phenotypic records were available for genetic analysis. These ewes descended from 89 different sires and 809 different dams. The size of the pedigree was in total 2712 animals.

In order to avoid numerical problems in the variance component estimation (VCE) FEC100_trans, FAMACHA© and MY were multiplied by 1000, PCV by 100. The variance component estimation was conducted with AIREMLF90 (Misztal et al., 2018) after passing 100 rounds in REMLF90 (Misztal et al., 2018). Heritabilities (h2) and genetic correlations (rg) between the traits of interest were computed

with airemlf90 (Misztal et al., 2018) applying the appropriate options. Subsequently, EBV were estimated with BLUPF458990+ from the software package mentioned above.

1.1.4 Results

Phenotypic key figures

The total number of alive Lacaune ewes in lactation registered in the Swiss herdbook is 4589 (database query December 2022). Of these, 1187 animals with phenotypic data were available on 15 farms. Additionally, 21 rams were phenotyped. Mean, median and SD of the traits of interest are shown in Table 1. Not all animals had measurements for all phenotypes, therefore the number of observations per herd is partly different. Mean value of FEC over all animals was 875±2347; rams were much higher with 1748±3206 than ewes with 858±2327. Faecal egg count median for female and male animals was 150 and 450, respectively. The mean FAMACHA© score was 2.67±0.89 and differed between ewes (2.68±0.89) and rams (2.33±0.90). There was also a difference in PCV between ewes (31.11±3.99) and rams (33.88±2.80). Milk yield for the test day closest to the day of worm phenotyping was 1.4±0.7 kg milk/d. Thereby the ewes were on average 191±74 DIM. At the time of phenotyping, 26.6% of the ewes were in their first lactation, 17.2% in their second, 19.5% in their third, and the remaining ewes (36.7%) in their fourth or higher lactation.

The comparisons between the phenotyped herds can be found in Table 1. The mean FEC varied between herds (123-4851). With the exception of herd 1 with a mean FEC of 4851, all herds were in a FEC range between 123 and 719. The medians were lower for all herds, which is an indicator of a skewed distributions. The mean FAMACHA© score per herd ranged from 2 to 3.2, and the medians were also in the same range. The herd averages of PCV were found between 29.4 and 35.7. Except herd 7 with a mean PCV of 35.7, all other herds were close together. The herd average of daily MY scattered more. The lowest mean was 0.9 kg/day (herd 9) and the highest was 2.4 kg/d (herd 15).

Phenotypic correlations (rp) between the traits of interest can be found in Table 2. All are in a very low to moderate positive or negative range between -0.36 and 0.25. The phenotypic, as well as the genetic correlation between FEC/FEC100_trans and FAMACHA© are of particular interest. We computed rp=0.25 between these two traits and more detail, especially the distribution of the number of observations on the individual scores can be seen in Figure 1.

Variance components and genetic parameters

The estimated variance components as well as the h2 can be found in Table 3. All h2 are in a favorable medium range indicating that breeding efforts are possible. Genetic correlations between the traits of interest (Table 2) are between -0.47 (PCV, FAMACHA©) and 0.23 (MY, FAMACHA©). Genetic correlation (FAMACHA/ FEC100_trans), rg (PCV/ FEC100_trans) and rg (MY, FEC100_trans) are almost 0. Genetic correlation between our main trait (FEC100_trans) and the targeted auxiliary trait FAMACHA© is 0.03. Unfortunately, we found a weak rg between FEC100_trans and MY. However, it is evident from Figure 3 that there are animals in our phenotyped subpopulation that have favorable EBV at FEC100_trans as well as at MY.

1.1.5 Discussion and Conclusion

Nearly 1200 Lacaune ewes were assessed for possible selection towards improved resistance to GIN. The traits of interest were FEC100_trans as main trait and FAMACHA© as auxiliary traits as well as genetic correlations between these traits and with MY.

Heritabilities

The estimated heritability of FEC100_trans in our study was at the upper end of the usually reported scale and exceeded the global estimates pointed out in the recent meta-analyses being 0.17 (Medrado et al., 2021) and 0.22 (Hayward, 2022). However, recent studies on the heritability of FEC in dairy sheep did report also heritabilities above 0.3 (Aguerre et al., 2018; 2022). The rather high heritability of FEC100_trans in our study could be partly due to the rather small subpopulation of nearly 1200 animals only. This may contribute to slight deviations from the estimates reported in the two recent meta-analyses. It also seems that the sex of the phenotyped animals can have an effect on the estimated heritability, with observations concerning females only, as is the case our study, yielding higher heritabilities (Hayward, 2022). Even though the heritability of FEC100_trans would be slightly overestimated in our work, it would in any case allow a selection of the Lacaune for a lower susceptibility towards GIN infection. The implementation of a breeding strategy based on FEC100_trans would be feasible but would come with a certain amount of costs for sampling and coproculture analysis. Therefore, we also recorded the FAMACHA© score and heritability was estimated to be 0.30. This estimate is at the upper end, but within the confidence intervals estimated by the two recent meta-analyses on genetic parameters of sheep (Medrado et al., 2021; Hayward, 2022).

FAMACHA© and its correlation to Faecal egg count

Our observed phenotypic correlations of FAMACHA© and PCV are within the usually reported range (Burke et al., 2007; Kaplan et al., 2004; Moors and Gauly, 2009). As four of the 15 farms had a Haemonchus-proportion below 20%, we decided to include this information in the model for the estimation of genetic parameters, since the sensitivity of FAMACHA© depends on the presence of this hematophagous nematode. Nevertheless, the rg of FEC100_trans and FAMACHA© was estimated to be close to zero in our study. A low rg (0.17) of FEC and FAMACHA© was also estimated by Rodrigues et al. (2021) in a herd of Santa Inês sheep. In contrast, Balconi Marques et al. (2020) have found a moderate to high rg (0.55) of FAMACHA© and FEC in Corriedale meat lambs. Cloete et al. (2016) found contradictory results when estimating the rg of FAMACHA© and FEC in two farm populations (Dormer x Merino lambs and Merino hoggets): a high positive correlation (0.66) on one farm but a moderate negative rg (-0.29) on the other.

It seems that rg of FAMACHA© and FEC does not only depend on the Haemonchus-proportion, but also on the intensity on the worm challenge. Riley and Van Wyk (2009) found a higher rg between FAMACHA© and FEC when worm challenge peaked (0.32) but no linkage when worm challenge was low (0.01). These authors defined a period with high worm challenge as a period when mass treatments were necessary, e.g. all animals judged to the FAMACHA© categories three to five were drenched. According to this, 53% of the Lacaune ewes in this study would have been classified as animals with high worm challenge. In the work of Balconi-Marques et al. (2020), in which a moderate-to high rg of FEC and FAMACHA© was estimated, only 29% of the observations were classified FAMACHA© three or higher. The comparison of the FAMACHA© classifications in our work with the two beforementioned studies does not suggest that the worm challenge was particularly low in our observed population. When comparing the FEC-level however, the lambs in both aforementioned studies showed a higher egg excretion. The observations in our study took place late in lactation and lactation peak was passed, suggesting that immune functions were prioritised over milk production again (Houdijk et al., 2003). It could be that this improved immune response against GIN resulted in moderate FEC-levels. Eventually, the worm challenge was not high enough to yield a significant genetic correlation of FEC100_trans and FAMACHA©, analogous to the group of lambs with low worm challenge in the work of Riley and Van Wyk (2009). On the other hand, FEC was not particularly low either, with a mean FEC of 745, 1957 and 4294 in animals scored FAMACHA© three, four and five,

respectively. The decision to phenotype only animals after lactation day 70 has been set with the intention to allow a sufficient contact with GIN on pasture, after drenching of the ewes in the dry period. This period considers also the use of products with longer lasting impact as well as the subsequent prepatency period. Sampling earlier in lactation might have resulted in more animals with higher worm challenge. But the risk of false-negative animal assessments due to the lasting impact of anthelmintic use would have increased.

Genetic correlation of Faecal egg count and milk yield

The estimate for the heritability of MY in our study was moderate and slightly higher than usually reported (Carta et al., 2009). The genetic correlation of MY and FEC100_trans was positive (e.g. unfavourable), but low. Aguerre et al. (2022) even found moderate positive correlations of FEC and MY, supporting our estimates that selection for a low FEC might at the same time select for lower a MY. On the other hand, Hayward (2022) concluded that a selection for improved resistance towards GIN, contrary to popular belief, is not necessarily unfavorably correlated with performance traits. In fact, he estimated a low but favourable correlation between FEC and performance traits. However, few dairy sheep data were included in that meta-analysis. Generally, the mean day of lactation being day 191 was late in our study. Beyond the possible impact on the relationship between FAMACHA© and FEC100_trans, this may also have had an impact on the genetic correlation between FEC100_trans and MY. Phenotyping in an earlier stage might have yielded different genetic correlations, which has to be considered when interpreting our data.

1.1.6 Conclusion

We conclude that a selection for lower susceptibility towards GIN-infection in the Swiss Lacaune population would be possible when using FEC as a trait. Even though there was an unfavourable but low genetic correlation of FEC and MY, a selection should be possible due to a nevertheless considerable share of animals with low EBV of FEC100_trans and above average MY at the same time. A non-existent genetic correlation of FAMACHA© and FEC100_trans suggests that the use of FAMACHA© as auxiliary trait will not be feasible in Swiss Lacaune.

1.1.7 Acknowledgements

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1.1.8 References

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1.1.9 Tables and figures

Table 1: Descriptive characterisation SD of Faecal egg count (FEC), FAMACHA©, Packed cell volume (PCV) and milk yield for each herd contributing phenotypes.

Herd	Sex	Trait															
		FEC				FAMACHA©				PCV				Milk yield			
		n	mean	median	SD	n	mean	median	SD	n	mean	median	SD	n	mean	median	SD
1	f	134	485.1	350	49.62	13	3.1	3.0	1.0	13	30.1	30	5.8	14	1.6	1.6	0.6
2	f	72	123	50	19.3	72	2.9	3.0	1.0	73	33.1	33	2.7	73	1.1	1.0	0.3
3	f	85	163	100	23.9	84	3.0	3.0	0.7	85	31.0	31	3.2	85	1.1	1.0	0.3
4	f	16	197	25	28.1	17	3.2	3.0	1.1	17	26.3	26	2.2	17	1.2	1.2	0.3
5	f	208	208	50	65.3	21	2.6	3.0	0.7	21	29.1	29	2.9	21	1.1	1.0	0.4
6	f	52	150	75	19.7	54	2.8	3.0	0.8	54	31.7	32	4.1	54	1.6	1.6	0.5
7	f	72	427	0	17.55	75	2.1	3.0	0.5	74	35.7	36	3.9	75	1.2	1.2	0.5
8	f	33	233	100	45.0	35	2.8	3.0	0.9	35	31.8	32	2.3	35	1.0	1.0	0.3
9	f	30	472	425	37.0	33	2.9	3.0	0.6	33	30.9	32	2.2	33	0.9	1.0	0.3
10	f	64	315	200	48.5	66	3.0	3.0	0.7	66	33.2	33	2.6	66	1.0	1.0	0.3
11	f	64	144	50	30.6	69	3.0	3.0	0.9	69	30.5	30	3.4	69	1.3	1.2	0.5
12	f	58	719	550	74.2	61	2.6	3.0	0.6	61	29.4	29	3.1	61	1.2	1.0	0.6
13	f	177	476	150	79.5	17	2.0	2.0	0.8	17	32.4	32	3.3	17	1.5	1.2	1.0
14	f	41	602	550	35.3	42	2.8	3.0	0.9	42	30.7	31	3.0	42	2.7	2.5	0.7
15	f	46	642	475	55.0	46	2.9	3.0	0.8	46	30.6	30	3.4	46	2.4	2.5	0.5
all	m/f	1173	875	150	23.47	11	2.7	3.0	0.9	11	31.2	31	4.0	11	1.4	1.2	0.7
all	m	21	1747	450	32.06	15	2.3	2.0	0.9	17	33.9	34	2.8	-	-	-	-
all	f	1152	858	150	23.27	11	2.7	3.0	0.9	11	31.1	31	4.0	11	1.4	1.2	0.7
Genetic analysis	f	1109	876	150	23.65	11	2.7	3.0	0.9	11	31.1	31	4.0	11	1.4	1.2	0.7

Table 2: Phenotypic (lower triangular) and genetic correlations (upper triangular) between Faecal egg count (FEC), FAMACHA©, Packed cell volume (PCV) and milk yield. Heritabilities are on the diagonal, SE are in brackets. Phenotypic correlations were calculated with untransformed FEC, genotypic correlations are based on transformed data (FEC_{100_trans}).

	FEC	FAMACHA	PCV	milk yield
FEC	*0.33 (0.08)*	0.03 (0.22)	0.01 (0.21)	0.07 (0.22)
FAMACHA	0.25 (0.03)	*0.30 (0.08)*	-0.47 (0.19)	0.23 (0.21)
PCV	-0.36 (0.03)	-0.35 (0.08)	*0.36 (0.08)*	-0.11 (0.20)
milk yield	0.16 (0.03)	0.07 (0.03)	-0.20 (0.03)	*0.34 (0.08)*

Table 3: Estimated variance components and heritabilities (SE in brackets).

	σ^2_a [1]	σ^2_r [2]	σ^2_p [3]	h^2 [4]
Faecal egg $count_{100\_trans}$	1055 (286)	2133 (225)	3188	0.33 (0.08)
FAMACHA	192060 (56056)	456480 (45496)	648540	0.30 (0.08)
Packed cell volume	42439 (10796)	74808 (8345)	117247	0.36 (0.08)
Milk yield	70210 (18551)	137670 (14584)	207880	0.34 (0.08)

[1] σ^2_a: additive genetic variance; [2] σ^2_r: residual variance; [3] σ^2_p: phenotypic variance; [4] h^2: heritability

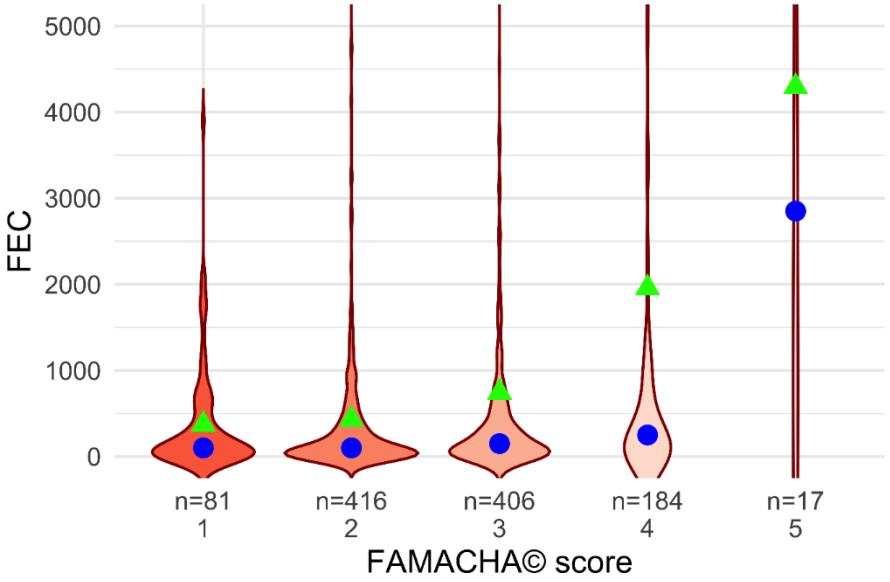

Figure 1. Violin plot of Faecal egg count (FEC) and FAMACHA© including the number of observations for each score. The median and the mean are indicated by a blue dot and a green triangle, respectively.

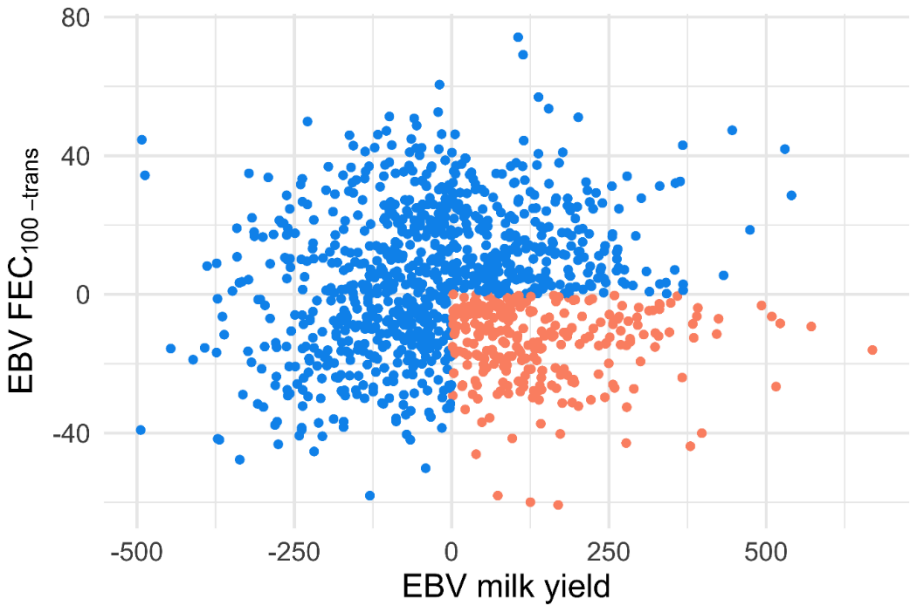

Figure2. Scatter plot of estimated breeding values of transformed Faecal egg count (FEC100_trans) and milk yield. Animals with estimated breeding values above average and FEC100_trans below average (suitable for selection) are indicated by red dots (quarter down right).

2 CHAPTER2. Paper "Including genotypic information in genetic evaluations increases the accuracy of sheep breeding values"

2.1.1 Implications

The use of animal genotypes from genome-wide DNA arrays in the genetic evaluation process is becoming a new standard for many livestock species. Improving the accuracy of breeding value estimates is critical to the success of breeding programmes. Accuracies are often low especially for lowly heritable traits with low numbers of phenotypic measurements. They are also often low when the traits of interest are expressed in female adults, but males are selected as young stock, such as in sheep breeding programmes. This research shows that incorporating genomic information into the genetic evaluation increases the accuracies of breeding values enabling selection especially for animals without phenotypes and for low to moderate heritability traits. It allows for more accurate selection of males and female replacements to be made at an earlier stage in life without having to wait for phenotypes from adult females to be collected.

2.1.2 Introduction

Genomic evaluation is now widely used as a breeding tool for genetic selection in several species of farm animals across the world but is less well developed for ovine (Hayes et al., 2012; Berry et al., 2016, Rupp et al., 2016, Fitzmaurice et al., 2021, Berry et al., 2022). In the UK, estimation of breeding values in sheep is based only on the conventional Best Linear Unbiased Prediction (BLUP, Henderson. 1949) method of analysis of animal phenotypic and pedigree data provided by the breeders and Breed Societies. This approach works well, especially for animal traits with moderate to high heritability and/or sufficient amounts of phenotypic data available. Availability of informative pedigree linking animals from different flocks is also a prerequisite (Simm, 1998). These conditions are met for multiple growth and carcass traits; however, this method has a limitation to the maximum accuracy level of the estimated breeding values (EBV) that can be achieved by young animals which have not yet had the chance to be phenotyped. Furthermore, for traits that are hard to record, measured on one sex only or with low heritability, such as reproduction and health traits, the accuracy of EBV may be low, even for animals with measured phenotypes. This means that selection decisions based on such EBVs may slow down the achievement of genetic goal set by the breeders. The alternative approach, and one which simultaneously combines animal genotypes with phenotypes and pedigree is Single-Step BLUP (SS-BLUP) (Legarra et al., 2009; Misztal et al., 2009; Christensen and Lund, 2010). This approach may lead to more accurate EBVs and reduce the generation interval by enabling an early selection, especially for traits that can be measured late in life or on adult progeny only, such as mastitis.

Genomic selection is already used in small ruminant breeding in many countries, such as Australia (https://www.sheepgenetics.org.au), New Zealand (Auvray et al., 2014), Ireland (https://www.sheep.ie/), France (Palhière et al., 2022), or internationally (Teissier et al., 2022) mostly addressing production traits. Furthermore, incorporating health traits such as mastitis or parasite resistance to the breeding programmes might affect positively the overall animal welfare, as well as the economic gain (Pacheco et al., 2021, Walkom S.F. et al., 2022) and this will be possible only if the accuracy of animal EBVs are satisfactorily high and above a certain threshold, that would allow publication of EBVs and reduce risks associated with making selection decisions. Minimum accuracy thresholds are extensively used across variety of traits in many species in the UK (www.fas.scot),

Australia (https://breedplan.une.edu.au/general/understanding-ebv-accuracy/), and Ireland (Sheep Ireland Guide & Directory of Breeders, 2020).

The objective of the present study was to assess the impact of incorporating genomic information in the EBV estimation on the accuracy of genetic evaluation for health (footrot and mastitis) and production (birth weight, weaning weight, scan weight and fat and muscle depth) traits in UK Texel sheep.

2.1.3 Material and Methods

2.1.3.1 Phenotypes

Two sets of traits were examined in this research. Firstly, these included growth and carcass composition traits measured in lambs, which were: birth weight (BWT), eight-week weight (EWW, growth rate to eight weeks of age), scan weight (SWT, growth rate to finishing), muscle depth (MD, loin muscularity) and fat depth (FD, potential to produce lean/fat carcasses). Secondly, these included health traits measured in adult ewes, namely footrot (FRT) and California Mastitis Test score (CMT). The CMT was used instead of the conventional somatic cell count in milk as a mastitis indicator because it was found to be highly (up to 0.98) correlated with somatic cell count (McLaren et al., 2018), and can be measured on-farm without the need for laboratory analyses. For health traits (FRT and CMT), the data were collected between 2015 and 2019 on 32 farms across the UK on 3 434 milking females. Trained technicians visited the farms at least once per year to score animals using five-point scale, from 0 – not infected, to 4 – severe infection (Conington et al., 2008; McLaren et al., 2018) for both health traits. Animals were scored between one and five times over the course of five years in 2015-2019. Health data are summarised in Table 1.

Growth and carcass measurements of sheep were taken from the iTexel database, where data for these phenotypes are routinely reported by the breeders. This dataset contained phenotypes for 645 840 animals born between 1970 - 2021. Further edits on phenotypes were performed, removing values that were out of biologically expected ranges, as summarised in Table 1.

2.1.3.2 Genotypes

The data used in this research contains 10 193 Texel sheep genotypes, collected between January 2015 and March 2019 on participating partner farms in the UK from male and female animals that were part of a wider study investigating novel traits for sheep meat production. Animals were genotyped with four SNP arrays, including 1 180 genotypes on the Illumina OvineHD BeadChip with 606 006 SNPs (HD), 2 894 genotypes on Illumina OvineSNP50 with 54 241 SNPs (50K), 2 463 genotypes on Illumina OvineLD BeadChip with 15 000 SNPs (LDv1) and 3 606 genotypes on Illumina OvineLD BeadChip with 16 560 SNPs (LDv2).

The preparation of genotypic data that were sent from the processing laboratory were subject to standard quality control procedures. These included the rejection of genotypes that did not meet the call rate threshold of 89.4% (which is used in the UK national genomic evaluations for cattle). Subsequently, a parentage check was undertaken to discard genotypes for which the parentage was not confirmed, which were removed from the dataset. As the samples were collected on four different SNP arrays, a subset of 8 119 SNPs common for all arrays were selected as described in Kaseja et al (2022), and then checked using the opposing homozygotes method (Hayes 2011). Hence, if an animal failed on the genomic parentage verification (over 1% of conflicting SNPs), the unverified parent was set to being 'unknown'. Additionally, when there was more than one sample per animal and only one passed parentage verification, then that sample was kept. If more than one sample confirmed the parentage, then the genotypes were compared to each other to confirm they were identical and if so, one genotype was chosen by looking at the density of the SNP array used in the following order: 50K, HD, LDv2, LDv1.

The final dataset contained 9 391 genotypes (971 HD, 2 709 50K, 2 350 LDv1 and 3 361 LDv2). The next stage was the standard checks at the SNP level, which involved removing SNPs with call rate under 89.4%, minor allele frequency below 0.05 (p-value at 0.05) and not being in Hardy-Weinberg equilibrium, producing subsets of 45 686, 36 654, 12 427 and 10 725 SNPs for HD, 50K, LDv2 and LDv1 SNP arrays, respectively. All genotypes were then imputed to the subset of most informative SNPs from the 50K array (n=45 686 SNPs) using Findhap V3 software (VanRaden et al., 2011).

The population structure to elucidate breed composition was determined using Principal Component Analysis (PCA) (Macciotta et al., 2010; S Mucha et al., 2015) in R software (R Core Team, 2021).

2.1.3.3 Pedigree

A pedigree file including all phenotyped animals and their parents (n = 821 692) was built using information provided by the breeders on the iTexel database and altered accordingly based on the information from genomic parentage verification and discovery as described above (where possible).

2.1.4 Data analysis

The following mixed effect model was used in all data analyses:

$$y = Xb + Za + Wp + e \quad (1)$$

where y is vector of observations, X is design matrix of order, relating records to b – vector of fixed effects, Z is design matrix of order, relating records to a – vector of random additive genetic effects, W is designed matrix for random permanent environment effect, p is vector for random permanent environment effect and e is a vector of random residual effects. Random effects were assumed to be normally distributed with the mean of zero. A summary of the fixed and random effects is shown in Table 2. As the data were collected across many years and in many flocks, contemporary grouping (CG) was used to compare animals more directly. CG were defined as flock-season of birth-sex for production traits or month-year and farm-year for CMT.

Both FRT and CMT were analysed as the natural logarithm of the sum of scores for all hooves and both udder halves, respectively, plus one (to avoid sum of zero) as described in McLaren et al. (2018).

Variance components were first estimated for each trait with Model (1) using the ASReml software (Gilmour et al. 2015), with the use of an informative subset of data containing only animals with at least one valid phenotype, born between 2011-2021. Additional data edits in this step excluded lambs that had been fostered, were born as a result of embryo transfer, or born within a litter of over four lambs. The contemporary group had to have a minimum of five individuals. The data used for parameter estimations are summarised in Table 1. In this analysis, the random additive genetic effects were assumed to be normally distributed ~ (0, 〖Aσ〗 _a^2) where a is vector of for all animals, σ_a^2 is the additive genetic variance and A is the pedigree relationship matrix. A separate series of bivariate analyses based on Model (1) derived estimates of the genetic and phenotypic correlations among the studied traits.

The estimated variance components were then used to derive animal EBVs for each trait with Model (1) and the MiX99 software (Lidauer et al., 2015).

Conventional BLUP estimates were derived first with the same distribution assumptions for the random effects as the variance component estimation step. Subsequently, the random genetic effect variance structure was modified to accommodate inclusion information from two sources: G-1-A-1gg where G (obtained using first method from VanRaden 2008) is a genomic relationship matrix and Agg is pedigree-based relationship matrix for genotyped animals, replacing in the model the A matrix with

H – combined relationship matrix (Christensen et al. 2012). The key difference between these two analyses was the addition of information from animals' genotypes to SS-BLUP, while pedigree and phenotypes remained the same in both.

Breeding values were estimated for the full available dataset (n=821 692 animals). Reliabilities of the estimated breeding values were estimated using Apax99 software (Lidauer et al., 2015), using a two-step method which, in the first instance, calculates information due to observations coming from the above model, and secondly uses Misztal and Wiggans (1988) method to add the relationship information. The reliabilities produced were subsequently converted to accuracy values by using their square root value.

2.1.5 Results and discussion

The results from the PCA to determine population structure are shown in Figure 1. Clustering based on the principal components of the genotype matrix did not reveal any major outliers, indicating that the population is mostly homogenous. The first two principal components explained 14.8% and 4.7% of variation, respectively. The obtained structure of this population is showing a small cluster of 80 animals being somewhat separated from the main cluster. Further investigation has indicated that these animals were imported into the UK from New Zealand, hence their genetic background differs from the rest of the main population which is UK Texel sheep.

A summary of variance components and genetic parameters by trait is shown in Table 3. The trait heritabilities range from 0.07 (low, for CMT) to 0.33 (moderate, for SWT) and are in line with the heritabilities obtained from similar research for growth and health traits in sheep (McLaren et al. 2018; Mucha et al. 2015; Safari et al. 2005). All correlations between traits estimated using the bivariate models are summarised in Table 4. The genetic correlation between FRT and CMT was 0.28 (0.11), indicating likely pleiotropic effects on these two health traits. To the authors' knowledge, these are the first estimates of mastitis and lameness correlation for meat sheep. The genetic correlations between the health traits and growth or body composition traits were not significantly different from zero. However, the correlations estimated amongst lamb growth and body composition were significantly different from zero and within the range of values expected and previously reported for example by Fitzmaurice et al. (2021), Lambe et al. (2008) or Mortimer et al. (2018).

When comparing accuracy values generated from SS-BLUP to conventional BLUP, there was almost no change in mean accuracy values for the whole population (n=821 692). For BWT, EWW, SWT, MD and FD the average difference in accuracy was 0, for FRT and CMT, the change was 0.02 and 0.03, respectively. This is due to very high volume of animals included in the prediction, where some of them are not that very well connected with the genotyped population, hence do not benefit from the inclusion of the genotypes in the evaluation. The results also showed that there are some animals whose EBV accuracy may decrease after the inclusion of genotypes although this was only observed for production traits. The maximum reduction was 0.03 for BWT, EWW and SWT and 0.04 for MD and FD. There was no observed reduction in accuracy value for FTR and CMT. Further analysis revealed that animals which had lower accuracy values following the inclusion of genotypic information were not themselves genotyped or phenotyped and had no close relatives that were phenotyped either. The accuracy for the conventional BLUP EBVs of these animals was less than 0.15 meaning that these animals were not likely to be serious candidates for selection. There were no reductions in accuracy values for any traits for any of the animals that had been genotyped.

The accuracy of EBVs increased for the majority of genotyped animals. The maximum increase in accuracy values were 0.40 for BWT, 0.32 for FD, 0.31 for MD, 0.25 for EWW and 0.22 for SWT. For

health traits these were 0.47 for FRT and 0.52 for CMT. These high increases were observed for animals that were genotyped, but not phenotyped.

Changes in the accuracy of estimated breeding values from SS-BLUP and BLUP for genotyped animals are summarised in Table 5 which shows there are no genotyped animals with reduced accuracy values following the inclusion of their genotypes in the genetic evaluation. On average, the biggest change in accuracy values is observed for traits with the lowest heritability which are the health traits (CMT and FRT) and eight-week weight. Changes in accuracy values were greater for animals with no phenotypic information available, meaning that the inclusion of genotypic information is critical to increase the precision of estimating breeding values especially for young animals or for males in terms of measuring the CMT. The average changes in accuracy values for un-phenotyped animals were 170% higher than those from the reference population (animals which are both genotyped and phenotyped). The accuracy values for all traits obtained with conventional BLUP vs SS-BLUP for both phenotyped and non-phenotyped animals that were genotyped are shown on Figure 2, illustrating the potential of genomic information to enhance the accuracy values, especially for hard to measure health traits with low heritability (FRT and CMT), where the maximum accuracy increased from 0.18 to 0.47 for FRT and 0.30 to 0.52 for CMT. For traits that are more easily recorded, have more records available, and which are moderately heritable (SWT, MD and FD), the increase of accuracy for genotyped animals is still clear but substantially lower than for FRT or CMT. For all traits of this study, phenotyped animals had more accurate EBVs regardless of the evaluation method, which is in accordance with the theoretical expectations (Simm G., 1998).

These findings are in line with results from previous studies, demonstrating increased accuracy when information from genotypes is included, such as for Manech Tête Rousse dairy sheep (Macedo et al., 2020), small population of (Dorper sheep) (Moghaddar N. et al., 2021) or chicken mortality (Bermann et al., 2020).

2.1.6 Conclusion

This study has combined production and health traits recorded in a well-phenotyped population of UK Texel sheep. This was the first study to estimate the potential gain in prediction accuracy of adding genomic data into the estimation of breeding values for UK sheep. It has showed that the structure of the data used for the evaluations affects the changes seen in accuracy values, that also differ according to the traits analysed. In all scenarios, adding animal genotypes in a single step BLUP evaluation increased the accuracy of prediction comparing to conventional BLUP. Therefore, increased animal genotyping is recommended in a breeding programme in order to improve the accuracy of estimated breeding values and reduce the risks associated with making selection decisions. It also will achieve accelerated rates of genetic gain, enhanced efficiency of production and lead to enhanced animal welfare when health traits are included in the breeding programme.

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2.1.8 Tables and figures

Table 1: Data description by trait

Trait (unit of measurement)	**Range of biologically accepted values**	**No. animals with records used for breeding value estimation**	**No. animals with records used for parameter estimation**
Birth weight (kg)	2-10	188,606	33,857
Eight-week weight (kg)	5-50	402,787	72,845
Scan weight (kg)	10-150	296,239	70,492
Muscle depth (mm)	5-55	284,317	67,865
Fat depth (mm)	0.1-20	283,644	67,867
Footrot (0-4 scale; presence/absence of infection)	0 (no infection) – 4 (infected)	6,216	6,216
California Mastitis Test (0-4 scale; presence/absence of infection))	0 (no infection) – 4 (infected)	3,346	3,346

Table 2: Fixed and random effects considered in parameter and breeding value estimation

Trait	Fixed effects	Random effects
Birth weight	LSB DamAge DamBreed ET CG	Animal Dam PE
Eight-week weight	LSB DamAge DamBreed Foster CG	Animal Dam PE
Scan weight	LSR DamAge DamBreed CG Adjustement: age at scan	Animal
Muscle depth	LSR DamAge DamBreed CG Adjustement: age at scan	Animal
Fat depth	LSR DamAge DamBreed CG Adjustement: age at scan	Animal
Footrot	DamAge Scorer Vax Flock	Animal
California Mastitis Test	Lambing LSB Scorer CG2	Animal PE

LSB – litter size born; ET – embryo transfer status; Foster – foster code status; Vax – vaccination status for footrot; CG – contemporary group as flock-season-sex; CG2 – contemporary group as month-year and farm-year

Table 3: Estimated variance components and parameters, followed by standard errors

Trait \ Variance	**Direct genetic variance**	**Permanent Environment variance**	**Maternal variance**	**Residual variance**	**Phenotypic variance**	**Heritability**
Birth weight	0.05 (0.01)	0.07 (0.01)	0.12 (0.01)	0.21 (0.01)	0.45 (0.01)	0.10 (0.01)
Eight-week weight	1.09 (0.11)	1.25 (0.08)	3.78 (0.09)	6.33 (0.09)	12.44 (0.08)	0.09 (0.01)
Scan weight	8.97 (0.33)			18.58 (0.24)	27.55 (0.19)	0.33 (0.01)
Muscle depth	1.96 (0.07)			4.59 (0.06)	6.54 (0.05)	0.30 (0.01)
Fat depth	0.28 (0.01)			0.62 (0.01)	0.90 (0.01)	0.31 (0.01)
Footrot	0.04 (0.01)			0.28 (0.01)	0.32 (0.01)	0.12 (0.02)
California Mastitis Test	0.04 (0.02)	0.07 (0.02)		0.40 (0.02)	0.51 (0.01)	0.07 (0.03)

Table 4: Estimates for genetic (below diagonal) and phenotypic (above diagonal) correlations among animal traits; estimate followed by standard error in brackets

Trait	BWT	EWW	SWT	MD	FD	FRT	CMT
Birth weight (BWT)		0.34 (0.010)	0.31 (0.007)	0.13 (0.007)	0.04 (0.007)	$^{N}/_{E}$	$^{N}/_{E}$
Eight-week weight (EWW)	0.53 (0.079)		0.76 (0.002)	0.42 (0.004)	0.36 (0.004)	$^{N}/_{E}$	0.01 $^{N}/_{S}$ (0.024)
Scan weight (SWT)	0.60 (0.045)	0.95 (0.007)		0.60 (0.003)	0.54 (0.003)	-0.01 $^{N}/_{S}$ (0.020)	-0.01 $^{N}/_{S}$ (0.024)
Muscle depth (MD)	0.19 (0.061)	0.61 (0.031)	0.51 (0.019)		0.42 (0.004)	-0.02 $^{N}/_{S}$ (0.020)	0.02 $^{N}/_{S}$ (0.025)
Fat depth (FD)	-0.01 $^{N}/_{S}$ (0.063)	0.52 (0.035)	0.48 (0.019)	0.37 (0.023)		-0.03 $^{N}/_{S}$ (0.020)	-0.02 $^{N}/_{S}$ (0.025)
Footrot (FRT)	$^{N}/_{E}$	$^{N}/_{E}$	0.07 $^{N}/_{S}$ (0.096)	-0.05 $^{N}/_{S}$ (0.094)	-0.15 $^{N}/_{S}$ (0.096)		0.04 (0.019)
California Mastitis Test (CMT)	$^{N}/_{E}$	0.12 $^{N}/_{S}$ (0.249)	0.10 $^{N}/_{S}$ (0.149)	-0.06 $^{N}/_{S}$ (0.324)	-0.68 $^{N}/_{S}$ (0.368)	0.28 (0.111)	

$^{N}/_{E}$ Correlation could not be estimated due to Negative Sum of Squares
$^{N}/_{S}$ not significant

Table 5: Summary of changes* in accuracy of estimated breeding values (EBV) for genotyped animals with and without phenotypic records per trait

		Birth Weight	Eight-week weight	Scan weight	Muscle depth	Fat depth	Footrot	California Mastitis Test
No. animals without phenotype		7 223	4 305	3 784	3 878	3 887	5 612	6 482
EBV accuracy change	avg	0.09	0.09	0.07	0.07	0.07	0.19	0.21
	min	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	max	0.40	0.30	0.22	0.22	0.22	0.47	0.52
	sd	0.06	0.05	0.04	0.04	0.04	0.09	0.09
No. animals with phenotype		2 158	5 086	5 607	5 513	5 504	3 779	2 909
EBV accuracy change	avg	0.05	0.04	0.02	0.02	0.02	0.06	0.11
	min	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	max	0.27	0.18	0.10	0.10	0.10	0.18	0.30
	sd	0.03	0.03	0.01	0.01	0.01	0.03	0.05

avg – average, min – minimum, max – maximum, sd – standard deviation
* Calculated as the SS-BLUP accuracy minus the conventional BLUP accuracy.

Figure 1: Plot of first (Comp.1) and second (Comp.2) principal component of the genomic relationship matrix for all genotyped animals

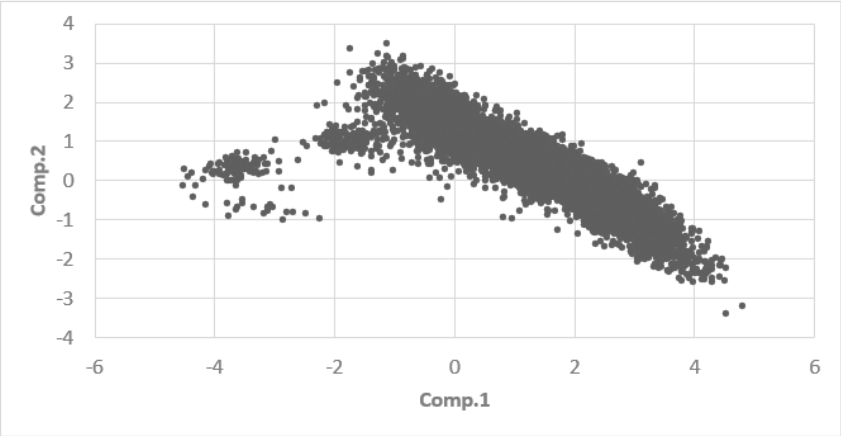
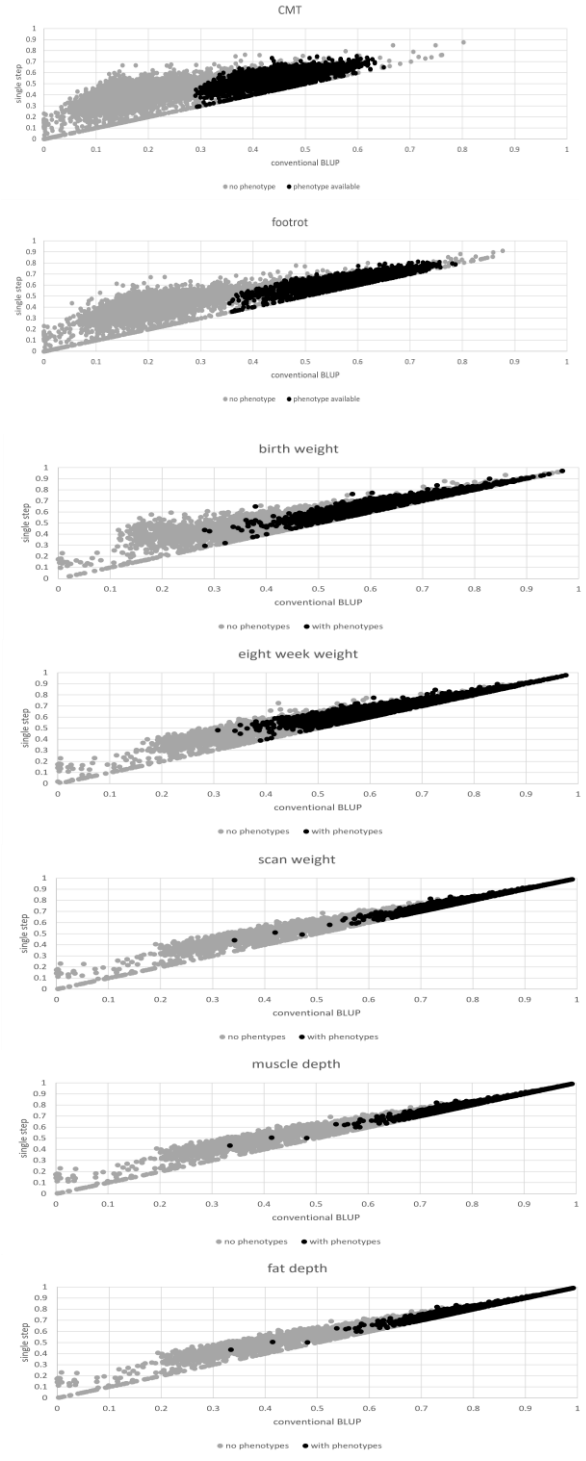

4
3
2
1
0
-1
-2
-3
-4
Comp.2
-6
-4
-2
0
2
4
6
Comp.1

Figure 2: Regression of the accuracy of estimated breeding values derived from single step BLUP on conventional BLUP for genotyped animals with and without phenotypes by trait



Grey dots represent genotyped animals without phenotypes and black dots represent animals with both genotypes and phenotypes available.

3 Deviations or delays

Deliverable due M48 was first submitted M50 with a 2-month delay due to smarter internal reviewing process.

The two included manuscripts on parasites (chapter1) and on footrot and mastitis (chapter2) have since been published in 2023 in the journal ANIMAL.

- Werne S, Schwarz K, Tuer S and Bapst B 2023 Breeding options for nematode resistance in Lacaune dairy sheep. Animal 2023 May; 15(5):100772 https://doi.org/10.1016/j.animal.2023.100772
- Kaseja K, Mucha, S, Yates J, Smith E Banos, G and Conington J. 2023. Including genotypic information in genetic evaluations increases the accuracy of sheep breeding values. J.Anim.Breed.Genet. 140: 4: 462-471 https://onlinelibrary.wiley.com/doi/full/10.1111/jbg.12771

In this second submission with the final report, the deliverable has added a long summary that that includes 5 additional papers (on top of the 2 originally reported for parasites, footrot and mastitis linked to key production parameters e.g. milk yield and lamb growth). These additional papers were submitted/published on new disease biomarkers and genetic parameters incorporating proxy measurements and including the impact of selection for these within breeding programmes.