Udvikling af Singlestep model for fodereffektivitet

Aktiviteter i 2021

Udviklingen sker i samarbejde med AU. I den indledende fase har vi færdiggjort de datasæt som anvendes i opsætningen af en singlestep model, samt lavet de første indledende analyser/fejlfinding på de grundlæggende data.

Udtræk af data

Der er lavet programmer til dataudtræk, samt opdateret eksisterende udtræk. Det drejer sig om:
• Afstamningsfil med information om krydsningskalvene og deres afstamning 4 generationer tilbage
• Genotyper på krydsningskalvene og dyrene i deres afstamning
• Vægte på krydsningskalvene ved indgang og udgang af sti med foderautomater
• Opdatering af editerede foderdata
• Basale data på krydsningskalvene (fødselsdato, flytninger mm.)

Analyser og fejlfinding af data

I forbindelse med grundlæggende analyser er der fundet udfordringer som er blevet rettet. Det er eksempelvis:
• Tilretning af udtræksprogrammer for genotyper og vejninger
• Retning af krydsningsdyr i mismatch
• Kontakt til avlsselskaber omkring manglende genotyper på kødkvægstyre
• Kontakt til landmænd omkring manglende vægte

Det formodes at vi i den indledende fase har fået tilrettet de største udfordringer i forhold til opsætning af genomisk model

Vægte på krydsningskalvene ved indgang og udgang af sti med foderautomater

Aktiviteter i 2022

Editing of phenotype data

To use information more effectively, it was allowed for a 14-day gap between entrance weighing day and first day of feed registration and between exit weighing day and last day of feed registration. The average daily gain (ADG; kg/d) of each animal within the period was calculated as the increase in body weight divided by the number of days of growth. Daily dry matter intake (DMI; kg/d) of each animal was calculated as daily feed intake (DFI) multiplied with dry matter content (%). The feed conversion ratio (FCR; kg/kg), as a measure of feed efficiency, was then calculated as DMI/ADG.

Editing of genotype data

For all genotyped animals, the procedure of filling in missing genotypes and imputation from EuroG 10K Bead Chip to Eurogenomics 75K custom SNP Chip was done with FImpute v2.2. Quality controls of genomic data was done with software Plink.

Preparation and discussion of models

A simple single-step model was implemented by combining phenotypes of crossbred animals and all available genotypic and pedigree information, allowing for the estimation of breeding values of all the genotyped and un-genotyped beef sires and crossbreds. The variance components were estimated, and heritability was calculated (Table 1). The bias was calculated as difference in estimated breeding values (EBVs) of focal individuals based on a partial and the whole dataset ($\hat{u}_p - \hat{u}_w$), respectively. Focal individuals of partial dataset were defined as the set of crossbreed animals which were born after November 1, 2021. Prediction accuracy was calculated as the correlation between corrected phenotype and EBVs of focal individuals divided by square root of heritability.

Table 1. The estimated additive genetic variance (σ^2_a), random residual variance (σ^2_e), heritability (h^2), bias and prediction accuracy for average daily gain (ADG), dry matter intake (DMI) and feed conversion ratio (FCR) using the single-step model.

Trait	σ^2_a(SE)	σ^2_e(SE)	h^2(SE)	Bias	Prediction accuracy
ADG	0.011(0.004)	0.092(0.004)	0.100(0.037)	0.005	0.32
DMI	0.164(0.045)	0.994(0.043)	0.141(0.037)	-0.006	0.41
FCR	0.171(0.057)	1.235(0.056)	0.121(0.039)	-0.04	0.37

The next step is to set up a more complicated single-step model such as a breed-specific single step model by tracing the breed-of-origin. This type of model requires phasing of genotypes and takes account that genetic effect is different across breeds. Compared to the simple single-step model, the breed-specific single-step model is expected to increase the predictive ability for crossbred performance and reduce the bias.

Der har derfor været diskussioner af fordele og ulemper ved forskellige typer modeller. Dette sker i et tæt samarbejde mellem AU og SEGES. Dette er nødvendigt og omfattende, da der skal bruges en ny type modeller der tager højde for at det er kødkvægtyren der skal avlsværdivurderes, men at fænotypen måles på et dyr som er en krydsning.