

Indtryk fra verdenskongres i genetic (WCGALP)

Der er deltaget i kongressen for at indhente ny viden, der kan bruges i forbindelse med udviklingsarbejdet i FutureBeefCross projektet. Det vil sige inspiration fra indlæg der omhandler fodereffektivitet, udledning af metan og spisekvalitet hos drøvtyggere. Desuden ny viden om metoder og modeller til beregning af genomiske avlsværdital.

Estimates of genetic parameters for feeding behavior traits and its association with feed efficiency in Holstein cows

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Abstract

The objective of this study was to estimate genetic parameters for feeding behavior and the genetic correlations with feed efficiency traits in Holstein cows. Data consisted of 75,877 daily feeding behavior records of 1,328 Holstein cows in 31 different experiments conducted from 2009 to 2020. The statistical model included lactation and days in milk as fixed effects, and experiment-treatment, animal, and permanent environment as random effects. Estimates of heritability ranged from 0.09 to 0.23 and repeatability from 0.23 to 0.52 for feeding behavior, with strong genetic correlations between traits. Feeding rate and intake per visit or meal showed positive and strong genetic correlations with residual feed intake, dry matter intake, and metabolic body weight. We conclude that cows that eat at a slower rate may be more feed efficient. Measures of feeding behavior could be useful indicators of dairy cow feed efficiency.

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Kommentar: muligheder for at inkludere andre indikatoregenskaber for at styre avlsværdiurderingen for fodereffektivitet

A hypomorphic mutation in the *ATP2A1* gene increases muscle mass yet compromises meat quality of Belgian Blue cattle

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Abstract

We herein describe a novel phenotype related to meat quality in Belgian blue cattle breed, named 'tough and dry meat syndrome'. A genome-wide association study pinpointed a single significantly associated locus on chromosome 25, encompassing the *ATP2A1* gene coding for the SERCA1 protein. A previous reverse genetic screen identified a breed-private missense mutation (*R143W*) in this gene. It segregates at high frequency (0.15) without deviation from expected genotypic proportions and was proven to be causative for this syndrome. The prevalence of the condition is estimated at 12.5% and its severity correlates with *W143* allelic dosage. The mutation is partially dominant with a penetrance of 43% and 100% in *R/W* and *W/W* animals respectively. Retrospective examination of *W143* frequency revealed a clear linear upward trend, likely due to the fact that the *W143* variant has a positive effect on muscle mass. Direct selection against the mutation is underway.

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Kommentar: et enkelt gen der påvirker spisekvaliteten negativt. Kødet bliver hårdt og tørt. Findes i 15% af blåkvægs populationen i Belgien. Forårsager stort økonomisk tab – også på heterozygote dyr

Genetic parameters for fatty acid traits of beef in Australian Angus

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Abstract

Preliminary genetic and phenotypic parameters were estimated for fatty acid traits in feedlot finished Australian Angus cattle. This included the relationships between saturated fatty acids (SAT), monounsaturated fatty acids (MONO) and polyunsaturated fatty acids (PUFA), with carcass weight (CWT), carcass rump fat (CP8) and carcass intramuscular fat (CIMF). All fatty acid traits showed phenotypic variation, with a considerable portion attributed to genetics as shown by heritabilities for SAT, MONO and PUFA of 0.64 ± 0.11 , 0.67 ± 0.12 and 0.25 ± 0.09 respectively. SAT had moderate negative genetic correlation with CWT, CP8 and CIMF (-0.30 ± 0.16 , -0.21 ± 0.17 and -0.38 ± 0.14 respectively), while MONO and PUFA have moderate positive genetic correlation with CWT, CP8 and CIMF ranging from 0.14 ± 0.17 to 0.46 ± 0.22 . The results show that the proportion of MONO and PUFA can be increased, and SAT decreased, in intramuscular fat through selection. Importantly, this can be achieved without being detrimental to carcass weight, carcass rump fat or total intramuscular fat.

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Kommentar: Sundere fedtsyreprofil i kød uden at det samtidig påvæcker vækst og intramuskulært fedt

Heritability and genetic correlations of enteric methane emissions of dairy cows measured by sniffers and GreenFeed

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Abstract

Before methane (CH₄) emission can be mitigated with animal breeding, breath measurements have to be recorded on a large number of cows. Our aim was to estimate heritabilities for, and a genetic correlation between, CH₄ recorded by GreenFeed and sniffers. Repeated records were available for CH₄ production (g/cow/day) by GreenFeed and for CH₄ concentration (ppm) by sniffers. The data included 24,284 GreenFeed daily means from 822 cows, 172,948 sniffer daily means from 1,800 cows, and 1,787 daily means from both devices on the same day from 75 cows. Additionally, records were averaged per week. The datasets were analyzed using bivariate animal models. The results show that CH₄ emissions recorded by either device has a moderate heritability (0.18-0.37). Furthermore, the genetic correlation between weekly mean CH₄ recorded by GreenFeed or by sniffers was high (0.77). This suggest that the measurements can be used in the same genetic evaluations.

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Kommentar: Sammenligning af metanmåling med sniffer og Greenfeed. Opløftende at korrelationen mellem de to metoder er meget høj (0,77). Antyder at den metode vi bruger i FutureBeefCross har potentiale

Prediction of breeding values for feed intake in pigs using individual versus group records along with correlated traits

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Abstract

Individual average daily feed intake (ADFI), age at 120kg (AGE), backfat (FAT), loin muscle depth (LMD), and group feed intake (sumFI) were used to investigate estimated breeding values (EBV) for feed intake (FI) using individual versus group FI data, along with individual data on AGE, FAT, and LMD, which had moderate to high genetic correlations with ADFI. The correlation of FI EBV using only ADFI versus sumFI was <0.25, which increased to 0.78-0.93 when adding data of the correlated traits in 4-trait models. The correlation between FI EBV from the 4-trait model with/without sumFI data was 0.99. The correlation between EBV from the 4-trait model with/without ADFI ranged from 0.79-0.94. Thus, group FI has negligible value when using correlated traits in pedigree-based analyses, while individual ADFI provides benefit, especially for young selection candidates.

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Kommentar: Foderregistreringer på enkelt dyr kan suppleres med data fra grupper af dyr hos grise. Det kunne være relevant for at forbedre datamængden hos krydsningskalve

Genetic parameters for growth, feed intake and greenhouse gasses emissions in Italian Holstein-Friesian bulls.

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Abstract

The objective of this study was to estimate genetic parameters for growth, feed intake and greenhouse gasses emission traits in Italian Holstein, using data collected on young bulls undergoing performance test.

The phenotypic information was recorded on 189 bulls, for which genomic information was obtained using SNP chips. Data were analysed using a linear mixed model, which included an additive genetic effect using a genomic relationship matrix.

Results show high heritability estimates for growth traits, moderate to high estimates for emission and feed intake traits. Selection for reduced emissions appears possible and reducing methane will also reduce carbon dioxide emissions (genetic correlation of 0.96). Feed intake traits could serve as indicators, because the genetic correlations range between 0.58 and 0.85. Growth traits showed strong positive correlations with emission traits (0.66 to 0.81), selection indices built at reducing emissions should carefully consider these traits as well.

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Kommentar: Heritabiliteter for foderoptagelse og metanudledning som giver grundlag for at vurdere de estimater vi får i FutureBeefcross