



Re-Livestock
RESILIENT FARMING SYSTEMS

75th EAAP Annual Meeting 2024

01-04 September 2024, Florence, Italy

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RESILIENT FARMING SYSTEMS

Global Methane Genetics: a global program to accelerate genetic progress for reduced methane emission in ruminants

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Abstract

Methane (CH₄) emissions have been identified as major contributor to global warming. In livestock, various CH₄ mitigation strategies are heavily researched, such as management and feeding strategies or genetic selection. Genetic selection is a reliable, cost-effective, cumulative and permanent mitigation tool. Despite several countries having started to record individual CH₄ emission of cattle and small ruminants, it is still far from routine implementation, given the currently small number of phenotypes. The Global Methane Genetics (GMG) program aims to accelerate genetic progress towards low-CH₄ emitting ruminants in the Global North and South by (1) enhancing harmonisation of recording and trait definition by shared protocols, SOP and existing data in the public domain (2) expanding methane recording and phenotype collection globally (3) developing efficient breeding programs for CH₄ reduction, and (4) implementation of routine genetic evaluations. The GMG program and global activities are centred around seven working groups, database development, new research and recording of methane emission in cattle and small ruminants and involves key livestock industry segments. The working groups are assigned to identify gaps and needs and develop research proposals for global dairy and beef cattle, small ruminants and buffalos. Specific working groups for Africa, Asia and South America address regional peculiarities in recording of CH₄ emission. The program conducts impact analysis across all working groups to show the potential of animal breeding as CH₄ emission mitigation tool.



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RESILIENT FARMING SYSTEMS

Exploring different definitions of methane concentration phenotypes in dairy cattle

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Abstract

Due to the 2030 climate targets, where the EU aims for a 55% reduction in greenhouse gas emissions, several countries are monitoring enteric methane (CH₄) from livestock. One of the mitigation options is to identify and selectively breed low-emission animals. A widely employed phenotyping method involves breath sampling, by a device commonly referred to as a “sniffer.” This device samples breath during milking, reporting CH₄ concentration in parts per million. While CH₄ concentration (MC) has been proposed as an indicator for CH₄ emissions (CH₄ g/d) due to its high correlation, there’s a lack of consensus on which phenotype should be used for estimating the breeding value. This study aims to 1) investigate 3 distinct phenotypes across three countries: a) average MC during lactation (MC_{avg}), b) sum of the average of the 2 top values within each peak (MC_{sa2p}), c) number of peaks (MC_{nop}), 2) Estimate genetic parameters for these 3 phenotypes, including genetic correlations. The dataset consist as follow 132,961 records from 7,669 cows (Netherlands), 16,924 records from 3,426 cows (Spain), and 34,359 from 483 cows Poland. This work has received funding from the European Union’s Horizon Europe research and innovation programme under the grant agreement No 01059609 (Re-Livestock project) and BO-43.10-002 B1 Klimaat: Emissie reductie methaan veehouderij.



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Are the most productive, the less thermotolerant animals in low input beef cattle populations? The case of the Avileña-Negra Ibérica beef cattle breed

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Abstract

Climate change is imposing many distresses in livestock populations. Many studies have been performed on dairy species where trade-offs are described between production level and the susceptibility to heat stress. On the contrary, little attention has been paid to low input beef cattle populations under extensive systems. Our objective was to characterize the effect of heat stress on weaning weight (WWT) of calves and age at first calving (AFC) of cows of ANI breed, as well as to estimate trade-offs. WWT and AFC records of 55,248 and 22,779 calves and cows were used for the analysis, respectively. Average (Tave), maximum and minimum daily temperatures (°C) collected from weather stations were used as measures of heat load (HL). For WWT, lags were HL at day of weighing and average HL up to 30 d prior to weaning. For AFC, HLs were studied around conception (± 30 days), assuming a gestation length of 285 days. Reaction norm models under the so called “broken-line” model were applied. Thus, we first estimated the temperature change points at which the animals began to show some response to thermal stress. The best models were those including Tave for a period of 30 d (Tave30) for WWT and 7 d post-conception (Tave7post) for AFC. Change points were 22°C for WWT and 25°C for AFC. Slopes were negative for WWT. and positive for AFC but, as modeled, the impact of heat stress on AFC was negligible. Genetic correlation between the intercept and slope of change in WWT with HL was high and positive, indicating that animals that weigh more are those coping better with heat stress. This work is funded by the EU’s Horizon Europe research and innovation programme under the grant agreement No 01059609 (Re-Livestock).



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Estimation of heritability and genetic correlation of methane phenotypes and yield traits in the Spanish Holstein population

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Abstract

Methane from livestock accounts for 6.3% of anthropogenic greenhouse gas emissions. One strategy to mitigate its effects is the genetic selection of animals with low methane emissions. Sniffer device is becoming popular in this effort because it is an accurate non-invasive method, and allows large-scale recording of individual methane emission. In dairy farms, it is usually attached to the milking robots and collect the gases released during the eructation. In this study, different phenotypes of methane were compared, obtaining heritability values and genetic correlations among them and with yield traits (milk, protein and fat). Data obtained from 3426 dairy cows in 34 spanish commercial farms were analyzed to calculate meanCH₄, ratio of mean CH₄/CO₂, sum of peaks CH₄, mean of peaks CH₄, sum of max peaks and area under the curve. Further, meanCH₄ and sum of peaks CH₄ were also calculated using one measurement every 5 seconds for comparison. Methane traits showed h² ranging from 0.01 to 0.15. Genetic correlations among methane traits showed wide variability, but it was low to moderate with yield traits (-0.05 to 0.16). Definition of suitable methane phenotypes with moderate h² allows implementation of genetic selection to mitigate the methane emission in cattle. Acknowledgment: Horizon-Europe Re-Livestock project (101059609) XXXX



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On the use of mid-infrared spectra and physiological measures for the characterization of dairy cattle thermotolerance

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Abstract

In livestock farming, efforts to combat the consequences of climate change (CC) focus mainly on mitigating the impact of livestock on climate and reducing the impact of CC on animals. For the latter, breeding tools are presented as a promising strategy. One of the main challenges is the need to define selection criteria that allows us to characterize individual thermotolerance, thus allowing us to select for more thermotolerant animals. The present study explored the use of mid-infrared (MIR) spectra from routine milk recording schemes to discriminate heat stress vs. thermoneutral samples and to classify heat tolerant vs. heat susceptible cows. MIR data from monthly milk recordings was available for 620 dairy cows. In addition, respiration rate (RR) was measured during a heat wave on a sample of 230 cows with MIR data available. Those cows were categorized as heat tolerant or heat susceptible based on RR. A PLS-DA model was used to predict group membership using the MIR data. The prediction of the heat load group of the individuals based on MIR data resulted in relatively good accuracy when considering the average daily temperature as a measure of heat load. However, the prediction accuracy was low when attempting to characterize the thermotolerance group based on RR. To address the identification of patterns of response to heat stress in individuals according to their degree of thermotolerance, more data (MIR data and RR evaluations) are needed to characterize the degree of individual thermotolerance in a more precise way. This work has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No 01059609 (Re-Livestock project).



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RESILIENT FARMING SYSTEMS

Characterization of a new heat tolerance phenotype in dairy cattle based on automatic milking systems and mid-infrared spectra

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Abstract

In recent years, breeding for heat tolerance in dairy cattle has become increasingly important to ensure good animal welfare and to reduce milk yield losses in stressful conditions such as heat waves. We here propose novel phenotypes for heat tolerance that utilize routinely generated data including automatic milking systems with daily measurements of milk yield and body weight, and monthly generated mid-infrared spectra. Within the Horizon Europe project Re-Livestock (GA No. 01059609), data from 1,478 farms including 677,318 cows from 2013 to 2021 across the Netherlands was used to estimate the effects of THI on various traits. For this, a kernel regression-based framework was developed to allow for a less rigid modelling than traditional reaction norm models including interaction effects to days-in-lactation, season, and parity. Individual heat tolerance was subsequently characterized as the relative impact of heat stress on a specific animal compared to estimated population-wide parameters, with the resulting heat resilience traits for F% and P% having an estimated heritability of 0.25 & 0.16. This subsequently results in an animal that is showing average performance at THI 50, yielding 0.36% above average F% and 0.19% above average P% at THI 70 in case it is one genetic standard deviation about population average for the respective heat resilience trait.



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RESILIENT FARMING SYSTEMS

Effects of goat willow's tannin profile on in vitro methane production and rumen fermentation

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Abstract

This study assessed the effect of high-procyanidin (HPC) and high-prodelphinidin (HPD) goat willow (GW) on in vitro gas, methane (CH₄) and volatile fatty acid (VFA) production when included at 20% DM basis. Diets included grass silage (GS), HPC (96% PC in tannins), HPD (73% PD in tannins); with the addition of polyethylene glycol (+PEG; 1.7:1 tannin:PEG) or without. Diets were incubated for 72h at rumen fluid:medium at 1:9 v/v in triplicate. Gas pressure (psi transducer) and CH₄ concentration of gas (gas chromatography) were measured throughout. DM degradability (DMD) and VFA concentrations were assessed at 72h. Data were analysed by linear mixed models using treatment as fixed factor and batch run (1-3) as random factor. HPC, HPD, HPC+PEG, HPD+PEG diets had lower ($P<0.001$) DMD (697, 683, 677, 680, g/kg DM), and 72h production of cumulative gas (120, 113, 144, 133 ml) and CH₄ (9.1, 9.1, 10.6, 11.0 ml), than GS (754 g/kg DM, 163.7, 15.7 ml). GS produced more ($P<0.001$) VFA and acetic acid (70.0, 42.2 mM) than the four GW diets (60.4-67.8, 35.2-39.7 mM respectively), and less ($P<0.001$) butyric acid (4.5 mM) than HPD (7.7 mM). Adding GW reduced in vitro CH₄ production, partly due to tannins.



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Heat stress effects on the gut microbiome profile of Iberian purebred and Duroc x Iberian crossbred weaned piglets

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Abstract

Heat stress (HS) can adversely affect swine gut health by altering the microbiota profile, influencing the host's stress response, which can be different according to distinct genetic backgrounds. We investigated the impact of HS on the gut microbiome of weaned piglets from two distinct genotypes: Iberian purebred (IB) and Duroc x Iberian crossbred (DUIB). Forty pigs (20 per genotype) were individually housed in 20 pens and exposed to thermoneutral conditions (22°C) for one week, followed by a week under HS conditions (30°C), in two consecutive batches. Fecal samples were collected before HS (T0), two days after (T2), and seven days after HS (T7). Sequencing of the 16S rRNA gene and subsequent bioinformatic analyses showed significant differences in alpha and beta diversity across different time points and genotypes. Differential abundance analyses revealed one genus differentially abundant between T0 vs T2, 14 genera between T0 vs T7 and 17 genera between genetic backgrounds. Particularly, DUIB pigs exhibited a higher abundance of *Clostridium_sensu_stricto_1* compared to IB, only under HS, indicating a distinct HS response. The findings suggest a potential higher resilience to HS of the gut microbiome in IB compared to DUIB pigs. This work has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No 01059609 (Re-Livestock project).



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Heat stress effects on the growth and metabolism profile of Iberian purebred and Duroc x Iberian crossbred weaned piglets

A. Heras-Molina¹, J. García-Casco^{2,3}, E. Gómez-Izquierdo⁴, J. Gómez-Fernández⁴, H. Laviano¹, C. López-Bote¹, S. Astiz², C. Óvilo², M. Muñoz²

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Abstract

Heat stress (HS) is a major concern in pig industry. Rustic breeds like the Iberian pig are more resilient to HS than commercial breeds. We investigated the impact of HS on the metabolic profile and enzyme concentration in Iberian purebred (IB) and Duroc x Iberian crossbred (DUIB). Forty pigs (20 per each genotype) were individually housed in 20 pens and exposed to thermoneutral conditions (22°C; TN) for one week, followed by a week under HS (30°C), in two consecutive batches. Weight was measured at the beginning and ending of the TN period and at the end of HS period to calculate average daily weight gain (ADWG), fractional growth rate (FGR) and feed conversion ratio (FCR). Blood samples were collected before HS (T0 and two days (T2), and seven days (T7) after the start of HS in the morning and the afternoon. FGR was higher during HS than TN, but increased more in IB than DUIB pigs. Glucose metabolism decreased in T2, while lipidic metabolism in IB pigs and protein metabolism in DUIB pigs were increased in T7. Enzymes related to tissue damaging increased more with HS in IB than DUIB pigs possibly related to the higher oxidative stress status previously studied in the IB pig. Thus, HS stress affected both IB and DUIB animals' metabolism and stress but differently between breeds. This work has received funding from the European Union's Horizon Europe research and innovation program under the grant agreement N°01059609 (Re-Livestock project).



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Heat tolerance in Polish local pigs: preliminary results of metabolomics analysis of blood

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Abstract

The heat tolerance becomes an urgent issue in livestock farming. It is assumed that the local breeds have a higher resilience to the rapid changes in the temperature, especially the heat waves. Here we evaluate the blood parameters (standard and metabolomic) in Polish local pig breed. In total 23 sows and boars were used: 11 females from Złotnicka White breed with body weight ~140kg, 6 females from Złotnicka White x Złotnicka Spotted cross (body weight ~150kg), and 6 males came from Złotnicka White x Złotnicka Spotted cross (body weight ~150kg). The pigs were kept on a small farm in Poland (52°36'50"N 17°20'30"E) and fed standard commercial diet for fatteners with unlimited access to water. The barn did not have controlled environment. The blood was collected by the veterinarian on the evening of 19th June and morning of 20th June 2023. Frozen plasma was sent to Metabolom USA for metabolomic analysis (data to be obtained). The statistical analysis of the blood parameters was done in R statistical package. The significant differences between morning and evening samples were observed only for free fatty acids and eosinophils levels. Between breeds the differences were significant for alanine aminotransferase, aspartate aminotransferase, magnesium, percentage of lymphocytes, erythrocytes, hematocrit, hemoglobin, hemoglobin concentration. In case of sexes the differences were between aspartate aminotransferase, alkaline phosphatase erythrocytes, hematocrit, hemoglobin, hemoglobin concentration. Further investigation is needed to evaluate those results and correlate them with matobolomics. This project was financed by the European Union grant no. 101059609.



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Molecular phenotyping through metabolomic analyses in pig breeds

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Abstract

The animal phenome can be defined as the ensemble of the physical and molecular traits of an animal. The molecular traits can be further dissected into different layers of internal phenotypes, also including many metabolites. Here we analysed ~800 metabolites detected from an untargeted metabolomic platforms on plasma of ~700 Italian Large White and ~300 Italian Duroc pigs to identify metabolites that could be useful to characterize the two breeds. Animals were sib-tested pigs, included in the selection programmes of Italian heavy pigs run by the Italian Pig Breeders Association (ANAS), raised in the same genetic station, and slaughtered at nine months of age when they reached about 160 kg live weight. After quality control, univariate, multivariate and machine learning analyses were used to identify metabolites that could discriminate the two breeds. Combining information from these approaches, a total of ~100 metabolites were identified (including ~1/3 amino acids and ~1/3 lipids among others). The selected metabolites clearly separated the two pig breeds. The observed differences for these molecular phenotypes can describe genetic differences between Italian Large White and Italian Duroc pigs. Acknowledgments: This study has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No. 01059609 (Re-Livestock project). X



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Re-Livestock
RESILIENT FARMING SYSTEMS

Integrating genomic information in metabolomic networks to dissect molecular phenotypes in pigs

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Abstract

The complexity of an organism arises from the interplay of different molecular layers (e.g. the genome, transcriptome, proteome, and metabolome) that generate biological processes and pathways that, in turn, define the animal phenome. In this study, we combined metabolomics and genomics to explore and gain knowledge on the interplay between these two layers using systems biology approaches. For these aims, we used both genome (~60,000 SNPs) and plasma metabolome information (~1,000 metabolites obtained from targeted and untargeted platforms) from ~1,000 Italian Large White and Italian Duroc pigs. Metabolomics data were used to reconstruct pathways through two network generation approaches, i.e. correlation networks and Gaussian graphical models. Then, genome-wide association studies were carried out to identify genetic loci influencing metabolites (mQTL). A first comprehensive catalog of mQTL was obtained, including a few hundreds of putative causative genes. These loci were subsequently studied and used to inform metabolite networks. The inclusion of mQTL in the metabolic pathways improved the estimation and generation of simple correlation networks and revealed relationships between known and unknown metabolic features. These results provided a first picture of genetic factors and metabolic interactions affecting the pig metabolism. Acknowledgements: This study has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No. 01059609 (Re-Livestock project).



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How to reduce enteric methane from dairy cows

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Abstract

Enteric methane constitutes a predominant part of the carbon footprint of milk and the use of feed additives and manipulation of the nutrient composition of the diet are ways to reduce the emission of methane. The use of feed additives such as 3-nitrooxypropanol, nitrate and different types of seaweed have been shown to reduce enteric methane emission from dairy cows, but the concurrent effects on feed intake and milk production have in some cases been negative. Increased inclusion of fat in the diet reduces enteric methane emission primarily due to the dilution of the content of fermentable organic matter in the diet. Also increased inclusion of concentrate at the expense of forages high in fibre is a way to reduce the emission of enteric methane. Strategies related to changes in diet composition should always be accompanied by an evaluation of the effect on the carbon footprint of the diet.



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Describing feed efficiency using metabolomic data in pigs

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Abstract

Feed conversion ratio (FCR) is commonly used to determine production efficiency in pigs. However, the basic biological mechanisms of this complex trait are still largely unexplored. In this study, we aimed to describe FCR in Italian Large White pigs using metabolomic data. For 691 pigs, FCR random residuals (FCR-RR), untargeted plasma metabolomic data (constituted by about 1000 metabolites) and high-density single nucleotide polymorphisms were available. We first identified two extreme groups of pigs (100 with the lowest and 100 the highest FCR-RR) and compared their metabolomic data using Sparse Partial Least Squares Discriminant Analysis and Boruta algorithm. With the combination of these two approaches, we identified 12 metabolites that could discriminate the two extreme groups of pigs. These metabolites were involved in a few metabolomic pathways, including fatty acid oxidation, carnitine, alanine, and histidine metabolism. Genomic heritability of the selected metabolites ranged from 0.11 to 0.35. The obtained results can contribute to identify molecular proxies useful to describe feed efficiency and develop new breeding strategies in pigs. Acknowledgments: This study has received funding from the European Union – NextGenerationEU under the National Recovery and Resilience Plan (PNRR) – FEEDTHEPIG, proposal code P2022FZMJ9 – CUP J53D23018310001 and from the European Union’s Horizon Europe research and innovation programme under the grant agreement No. 01059609 (Re-Livestock).



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Re-Livestock
RESILIENT FARMING SYSTEMS

Methane emissions from beef fed different protein sources and a forage-based diet

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Abstract

This study assessed the effect of different dietary protein sources (soyabean, SB; brewers' spent grains, BSG; local field beans, BNS) on methane (CH₄) emissions of beef cattle fed a 70:30 forage:concentrate basal diet, and also compared with a 100% pasture-fed beef system (PAS). 16 Holstein × Angus growing steers were allocated to four experimental diets (SB, BSG, BNS, PAS; four animals each) for 16 weeks. Every 4 weeks animals were transferred in digestibility stalls (for nutrient balance measurements) within respiration chambers (for CH₄ emission measurements) for 4 days. During the chamber measurement periods, dry matter intake (DMI, kg/day) and gross energy intake (GEI, MJ/day) did not differ between groups ($P > 0.05$). PAS steers had lower CH₄ production (g/day; $P < 0.001$) and CH₄ yield (g/kg DMI, $P = 0.001$; MJ/MJ GEI, $P = 0.005$) compared with the three concentrate-fed groups. Faeces and urine energy outputs (expressed as % GEI) were higher ($P < 0.001$) in PAS steers compared to the concentrate-fed beef. There were no significant differences ($P > 0.05$) in the studied parameters between the three concentrate-fed groups. The lower CH₄ production and yield in pasture-fed steers could indicate potential environmental benefits associated with pasture-based beef systems, but the higher energy loss in faeces and urine demonstrates potential inefficiencies in energy utilisation.



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Re-Livestock
RESILIENT FARMING SYSTEMS

Dissecting production traits using metabolomics in pigs

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Abstract

Italian heavy pigs are mainly raised to produce Protected Designation of Origin (PDO) dry-cured hams. To breed pigs with the characteristics of the meat and legs needed for this purpose, specific selection programmes have been developed, using traits related to the overall fat/lean meat content of the animals, to growth and efficiency of the animals and to ham quality (e.g. intermuscular fat and weight loss at first salting). Metabolites represent simple molecular phenotypes that can be used to deconstruct complex phenotypes in their single biological components. We analysed targeted and untargeted metabolomic profiles (up to 1000 molecules) from plasma of Italian Large White and Italian Duroc pigs for which production traits and their estimated breeding values were available. We studied the relationship between all these simple and complex traits via correlation analyses and multivariate modelling. In general, metabolite abundances poorly correlated genetically with production traits (up to $|r_G| < 0.15$), except for a few metabolites (up to $|r_G| \sim 0.4-0.5$). Overall, we obtained a first picture of the correlation between molecular phenotypes and economically relevant traits that could be useful to further exploit their usefulness in designing selection programmes in Italian heavy pig breeds. Acknowledgements: This study has received funding from the European Union's Horizon Europe research and innovation programme under the grant agreement No. 01059609 (Re-Livestock project).



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Re-Livestock
RESILIENT FARMING SYSTEMS

Nitrogen use efficiency from beef fed different protein sources and a forage-based diet

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Abstract

This study evaluated the effect of three different protein sources (soyabean, SB; brewers' spent grains, BSG; local field beans, BNS) on digestion and nitrogen (N) balance from beef cattle consuming a 70:30 forage to concentrate basal diet, also compared with a 100% pasture-fed beef system (PAS). 16 Holstein × Angus growing steers were divided into four groups, each assigned to one of the experimental diets (SB, BSG, BNS, PAS) with four animals in each group. Every 4 weeks, the animals were moved to digestibility stalls for 4 days for N balance measurements. Dry matter (DM) intake (DMI, kg/day), DM digested (kg/d), N intake (NI, g/day), and N digested (g/d and kg/kg) did not differ between groups ($P > 0.05$). PAS steers had higher urinary N output (UNO, $P = 0.011$), manure (faeces and urine) N output (MNO, $P = 0.039$), UNO/NI ($P < 0.001$), and MNO/NI ($P = 0.005$). Also, PAS steers had lower digested DM (kg/kg) ($P = 0.005$) and N balance ($P = 0.025$) than concentrate-fed steers. When concentrate-fed groups were tested alone, SB and BSG had higher N digested ($P < 0.001$) and lower faecal N output/NI ($P < 0.001$) than BNS. BSG had higher UNO ($P = 0.030$) and MNO ($P = 0.049$) than BNS and lower ($P = 0.002$) DM digested (kg/kg) than SB. Overall, N use efficiency was lower in PAS, likely due to rapid degradation of forage protein in the rumen, and this may have implications to growth rates of PAS steers.



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Re-Livestock
RESILIENT FARMING SYSTEMS

Large scale analysis of the cattle rumen microbiome in relation to methane emissions

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Abstract

Methane emissions of dairy cattle are associated with the rumen microbiome. To predict or mitigate cattle methane emissions, detailed knowledge of the rumen microbiome is of advantage. So far, few studies have investigated methane emissions and its relationship to the rumen microbiome using modern long-read metagenomic (LRM) methodology. In this study the microbiome of 955 Dutch Holstein dairy cows from 12 different farms were sequenced using LRM while recording methane emissions with sniffers in automated milking systems. Also related metadata (genotype, diet, milk records, etc.) was gathered. The LRM data was analysed using SqueezeMeta software and >3500 species of microbes were found across all animals. This study aims to use the dataset to provide new insights into the rumen microbial abundance and diversity to a great level of detail. Moreover, to analyse the heritability of species, and to identify which species are associated with methane emissions. This will identify microbial species relevant for breeding for reduced methane emission. This study is part of the Re-Livestock EU Horizon project and the Knowledge and Innovation Agenda of the Dutch Ministry of Agriculture, Nature, and Food Quality.



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Re-Livestock
RESILIENT FARMING SYSTEMS

Impact of microbiome on genomic predictions for methane emissions in Holstein cows

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Abstract

The rumen microbial composition is partly determined by host genetics, and its variation has been associated with variation in methane emission, offering a potential tool to mitigate indirectly greenhouse gasses via animal breeding. So far, breeding approaches that include microbial information are hindered by low sample sizes. In this study, we collected rumen fluid samples from 955 Holstein cows from 12 commercial farms in the Netherlands and analysed them via long-read metagenomic sequencing. To the best of our knowledge, this is the biggest dataset of rumen microbial samples collected in one country worldwide. Individual daily methane concentration, pedigree, genotypes, and milk records for the cows are also available. This study aims to investigate the impact of microbial composition on genomic predictions for methane emissions. Thus, we will use a previously developed pipeline and implement three genomic prediction scenarios for methane emissions: 1) a model using only genomic data (benchmark); 2) a model using only microbial data (microbiability); 3) a model jointly using both genomic and microbial data. Each scenario will be validated to estimate the accuracy and bias of genomic predictions. This study is part of the Re-Livestock EU Horizon project and the Knowledge and Innovation Agenda of the Dutch Ministry of Agriculture, Nature, and Food Quality.



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Re-Livestock
RESILIENT FARMING SYSTEMS

Evaluation of the soybean replacement as protein source with Mediterranean legumes in the performance of growing pigs

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Abstract

The aim of this study was to evaluate the effect of soybean replacement as protein source by local legumes in terms of performance of growing pigs. Pea, lentil and chickpea were selected to replace 50 or 100% of protein from soybean in the diet, making up six groups (pea100, pea50, lentil100, lentil50, chickpea100, chickpea50) that were compared with a negative control (NC, soybean as main protein source). A total of 252 pigs (20.3±1.34 kg) were allocated to 7 experimental treatments (6 replicates/treatment; 6 pigs/replicate). Diets were formulated to be isonutritive (13.1 MJ/kg ME and 16.2% CP). Pigs were weighed on day 0 and 28 of trial. Average daily gain (ADG), average daily feed intake (ADFI) and gain feed ratio (GFR) were calculated. Fecal samples were taken directly from the rectum on days 24-28 to determine apparent fecal digestibility of dry matter, organic matter and protein. Statistical analysis was conducted by ANOVA. Contrast analyses were conducted between NC and each legume. The highest ADG and ADFI were obtained in pigs fed the pea and NC diets. Pigs fed the lentil diets had the lowest ADG and pigs fed chickpea were intermediate ($P<0.05$). Pigs fed pea diets showed the highest feed efficiency ($P<0.05$) and pigs fed the lentil diets had the lowest GFR. Pigs fed the pea100 diet showed the highest nutrient digestibility values, while pigs fed the chickpea diets showed the lowest ones. To sum up, peas seem to be the best alternative to replace soybean as protein source in terms of performance and nutrient digestibility. Funded by European Union's Horizon Europe Research and Innovation Program, Grant agreement No. 01059609 (Re-Livestock).



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Re-Livestock
RESILIENT FARMING SYSTEMS

Coupling precision livestock farming technologies with artificial intelligence for mitigating heat stress in Mediterranean dairy cattle systems

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Abstract

Rising temperatures in Mediterranean regions represent not only the risk of heat stress and deterioration of animal welfare but also cause a negative impact on the productivity of dairy production systems (DPS). In this context, facilitating the adoption and evaluation of context-specific strategies to alleviate heat stress, particularly in areas such as the Mediterranean that suffer the most from rising temperatures, is paramount. To this end, this study proposes two integrative strategies combining precision livestock farming (PLF) technologies and artificial intelligence (AI) to mitigate heat stress. The first approach focuses on shading in outdoor feedlots as a strategy to mitigate heat stress. The temperature-humidity threshold (THI) at which animals seek shaded areas was identified using PLF tools, such as cameras and machine learning algorithms. Preliminary results allow us to indicate which is the combination of day/night THI values above which animals come to the shade, thus allowing optimisation of shade management to improve animal welfare. The second approach identified the optimal showering regimes in DPS by combining AI and collars for behavioural monitoring. The results show that increased daily showers can significantly mitigate heat stress in dry and lactating cows, reducing panting by up to 36%. In all, these approaches offer knowledge-based solutions for farmers, allowing the optimisation of their management practices and ensuring animal welfare and the long-term sustainability of the DPS across Mediterranean environments.



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Re-Livestock
RESILIENT FARMING SYSTEMS

Effect of replacement of soybean by Mediterranean legumes on intestinal health of growing pigs

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Abstract

The effect of soybean protein replacement by local legumes in diets for growing pigs was evaluated for intestinal health. Calprotectin, an indicator of inflammation, and cecal volatile fatty acids (VFA) were analyzed. Local peas, lentils and chickpeas replaced 50 or 100% of dietary protein from soybean (pea100, pea50, lentil100, lentil50, chickpea100, chickpea50) and they were compared with a soybean control. A total of 252 pigs (20.3 ± 1.34 kg) were allocated in 7 experimental treatments (6 replicates/treatment; 6 pigs/replicate). Diets were isonutritive (13.1 MJ/kg ME and 16.2% CP). Fecal samples (1 sample/replicate) were obtained on days 0, 14 and 28 to determine calprotectin. Cecum content was sampled on day 28 (4 samples/treatment) to determine VFA. For statistical analysis, contrasts were conducted between control and each legume. Calprotectin values were not different from control for any legume ($P > 0.05$) at any time. However, chickpeas increased total VFA, acetate, propionate, butyrate, and decreased ($P < 0.05$) the sum of isoacids (isobutyrate and isovalerate, plus valerate) and branched chain ratio (ratio of isoacids to straight-chain VFA; BCR). BCR indicates the fraction of VFA, related to protein fermentation. Peas tended to increase total VFA, acetate and propionate, tended to decrease BCR and decreased isobutyrate and isovalerate. Lentil tended to increase butyrate and decreased BCR, isobutyrate and isovalerate ($P < 0.05$). Increased butyrate and straight chain VFA and decreased BCR indicated enhanced intestinal health of local legumes compared to soybean. Funded by European Union's Horizon Europe Research and Innovation Program, Grant agreement No. 01059609 (Re-Livestock).



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Re-Livestock
RESILIENT FARMING SYSTEMS

Insights and experiences of two Living Labs in Tuscany (Italy)

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Abstract

Living Lab (LL) is an innovative tool constituted by a multi-actor working group that develops, tests, and evaluates innovative solutions to solve specific problems of an agricultural sector. The LL Consorzio Tutela Pecorino Toscano DOP (LL1) and Granducato (LL2) are part of Codecs (No. 101060179) and Re-Livestock (No. 101059609) Horizon 2020 projects. The LL1 is located in the South of Tuscany region (Italy) and deals with the sheep milk devoted to the production of Pecorino Toscano DOP cheese. The LL2 is located in the North of Tuscany and deals with the dairy cattle farms for fresh milk production belonging to the Granducato farmers' cooperative. The aim of LL1 was to analyze the best digital innovations to be implemented in the dairy sheep sector and to assess costs and benefits of farm digitization. The LL2 aimed to evaluate dairy farmers' knowledge and perception for innovative practices to reduce the environmental impact and to increase the resilience to climate change. In both LLs, local farmers, consultants, the cheese factory technicians (for LL1), Farmers' cooperative (for LL2), policymakers, researchers, and retailers were included. In both cases, the participatory approach allowed to identify the main issues of the sectors and the innovative solutions able to help the farmers to overcome the problems. Decision support systems implemented in mobile app, sensors for monitoring animal behavior and health status and other innovations related to animal feeding and management were discussed and classified for the level of interest by all the actors of LLs. In any case, technical assistance and economic support have been identified as limiting factors for the application of innovations.



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