**The use of novel phenotyping technologies in animal breeding**
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In the coming decades livestock production faces tremendous challenges to produce high quality animal products in a sustainable and animal friendly way. In order to meet future market needs breeding goals need to be adjusted and extended with new traits. Automation and technological innovations can contribute to recording new phenotypes that provide information on both existing and new breeding goal traits. In addition, this information can be used by farmers to better manage animals according to their individual needs, i.e. precision livestock farming. However, criteria for management indicators and breeding indicators (selection index traits) are not the same. Whereas for management indicators false-negative (e.g. missing a disease occurrence) as well as false-positive alerts (e.g. an alert but no disease) are highly undesirable, this might be less relevant for selective breeding purposes. Even if an indicator is strongly affected by random measurement errors, collecting repeated observations on multiple animals might be used to reduce effects of random errors and result in accurate estimates of breeding values. However, if indicator phenotypes are subjected to systematic errors, the issue is more serious as these cannot be accounted for in statistical analyses and they might be relevant for selective breeding in case these systematic errors are partly genetic. Even in this case the indicator phenotype might provide valuable information about breeding goal traits, depending upon the genetic correlation between the indicator phenotypes and the breeding goal trait.

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**Precision phenotyping using Fourier-transform infrared spectroscopy for expensive-to-measure traits**
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Large-scale phenotyping is rapidly becoming the major operational bottleneck in precision farming and animal breeding. The Fourier-transformed infrared spectroscopy (FTIR) technique has been proven to be a powerful tool for high-throughput milk quality assessment. The objective of this study was to evaluate the ability of FTIR-derived phenotyping in the prediction of protein composition for Brown Swiss cows, as opposed to different genotyping strategies. Data were from 1,011 cows, phenotyped using the High Performance Liquid Chromatography method. These records will be considered as LAB in the present study, and include fractions of αS1-casein (CN), αS2-CN, β-CN, κ-CN, β-lactoglobulin (LG), and α-lactalbumin (LA). FTIR calibration equations were developed. At the end, it was possible to obtain ~600,000 FTIR predictions from the test-day records for ~30,000 cows. This dataset will be considered as FIELD in this study. Genotyped individuals consisted of: 1,011 LAB cows, 1,493 of the FIELD cows, the 181 sires with both LAB and FIELD daughters and 540 sires with FIELD daughters only. Individuals were genotyped with different SNP panels and imputed to 50k. A 4-fold cross-validation was used to assess the predictive ability of models, meant as the ability to predict masked LAB records from daughters of progeny testing bulls, the correlation between observed and predicted LAB measures in validation was averaged over the 4 training-validation sets. Predictions were obtained using the Single-Step GBLUP method. Different sets of phenotypic information were defined, including sequentially LAB cows from the training set; FIELD cows from the training set; FIELD cows from the validation set. Results show that the use of genomic information does not provide any advantage in predictive ability, but prediction models that included FIELD records showed an advantage for most of the traits.

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**Towards a genomic evaluation of cheese-making traits including candidate SNP in Montbéliarde cows**
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In the FROM'MIR project, milk cheese-making and composition traits were predicted from 6.6 million mid-infrared (MIR) spectra in 410,622 Montbéliarde cows (19,862 with genotypes). In this study, we assess the reliability of single step GBLUP breeding values (ssEBV) for 11 traits (cheese yields, coagulation, casein and calcium contents). The dataset was split in two independent training and validation (VAL) sets that respectively contained cows with the oldest and the most recent lactations. The training set, including 155,961 cows (12,850 with genotypes), was used to predict ssEBV of 2,125 VAL genotyped cows. For each trait, the reliability of ssEBV (ratio of squared correlation between ssEBV and adjusted phenotypes of VAL cows to the heritability) was estimated. We first tested 4 models including lactation (LACT) or test-day (TD) records from the first (1) or the first three (3) lactations, giving the 50K SNP effects equal variances. Mean reliabilities were 56, 57, 64 and 65% for the LACT1, LACT3, TD1 and TD3 models, respectively. Keeping the most accurate model (TD3), we then added to the 50K SNP, the research SNP of the EuroG10K chip that included candidate SNP for cheese-making traits detected from GWAS on imputed whole genome sequences. SNP effect variances were either equal (50K+) or increased for 5 to 14 candidate SNP, depending on the trait (CAND). The 50K+ and CAND scenarios led to similar mean reliabilities (67%) and both outperformed the 50K scenario (65%). The CAND scenario gave the less biased ssEBV. These results were implemented in a genomic evaluation for cheese-making traits predicted from MIR spectra in Montbéliarde cows. This study was funded by the French Ministry of Agriculture, Agro-food

and Forest (CASDAR), the French Dairy Interbranch Organization (CNIEL), the Regional Union of Protected Designation cheeses of Franche-Comté (URFAC) and the Regional Council of Bourgogne-Franche-Comté, under the project FROM'MIR.

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**Feed efficiency: the next step in animal breeding**
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After years of breeding for production and health, we are now able to breed for improved feed efficiency. Although the CO2 emission per animal has increased over the past years, the CO2 emission per kg of milk produced has decreased. Breeding for an animal that converts feed in an efficient way into milk (or meat) is key to enlarge environmental sustainability. Besides the long-term advantage of a smaller carbon footprint the direct benefit is a reduction of feed costs for the farmer. The heritability of dry matter intake (DMI) is around 28% (overall trait), with a genetic standard deviation of 1.4 kg/day. The breeding value for DMI is available in the Netherlands since 2014. More recently a breeding value saved feed costs for body maintenance is added. EBVs are estimated based on more than 130,000 weekly DMI records, measured on more than 5,500 Holstein-Friesian cows. In July 2017 CRV started with data collection on feed intake in a commercial dairy farm with 260 cows. The coming years more commercial dairy farms will be equipped with roughage intake bins and concentrate feeders to increase the number of animals with DMI measurements. Based on these data we found large differences in feed efficiency between farms. Farm averages vary between 1.2 and 1.6 kg milk / kg DMI. Differences between animals are even larger (between 1.1 and 1.8 kg milk / kg DMI). These results show that there are considerable differences in efficiency of dairy production and in profit per cow. The use of breeding value is a way to improve the feed efficiency of the herd. The goal is not to reduce the amount of DMI, but to increase kg milk per kg dry matter. The 25% best cows for feed efficiency produce 9 kg milk per day compared to the 25% worst animals, on the same amount of feed. Animals with a higher feed efficiency provide more profit for the farmer and have a lower carbon footprint per kg milk.

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**Genetic parameters for environmental traits in Australian dairy cattle**
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As enteric methane accounts for 57% of the Australian dairy industry's environmental impact, mitigating emissions is key to improve efficiency and sustainability. Genetic selection is a cummulatve, permanent reduction option with minimal labor or cost. However, measuring methane is difficult and expensive, resulting in a small sample size to use as a reference population for genomic prediction equations. Therefore, alternative options for obtaining methane phenotypes should be explored. Methane predicted using mid-infrared spectroscopy (MIR predicted methane) offers and inexpensive and relatively simple method of obtaining may methane phenotyes. In this study, we estimated the genetic parameters for methane, dry matter intake (DMI), and MIR predicted methane. Methane and DMI records were obtained from 327 cows over a 5-day period at the Ellinbank Dairy Research Institute using the $SF_6$ method and an electronic feed recording system, respectively. MIR predicted phenotyes were from a mid-infrared prediction equation applied to 3425 commercial cows from 18 herds across Australia. All animals were genotyped and imputed to 633,3374 SNP genotypes with Beagle3 software. Heritabilities were estimated using univariate models, correcting for fixed effects and fitting a genomic relationship matrix, for DMI (0.27), methane (0.11), and MIR predicted methane (0.34). The genetic correation estimated using bivariate models between methane and MIR predited methane was 0.93 (0.34) while methane and DMI was 0.53 (0.04). Accuracies of gEBV were validated using a 6-fold cross validation, as r(gEBV,methane) where $SF_6$ methane phenotypes were corrected for fixed effect. Obtained accuracies were low (0.01 - 0.16). Our results indicate that the improvement in accuracy gained by using MIR predicted methane is low and more data is required to determine the effect of MIR predicted methane on gEBV accuracies.

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**Development of a NIRS method to assess the digestive ability in growing pigs**
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In growing animals, feed efficiency is determined by the digestive and metabolic efficiency. The digestive efficiency is difficult to assess in a large number of animals. In pigs, its measurement requires to house animals in a digestibility cage during a prolonged period to measure feed intake and totally collect the feces that should be analyzed for the nutrient contents. The objective of this study is to identify an alternative methodology to characterize the digestive ability in pigs. For this purpose, 63 pigs from Large White, Pietrain, and Duroc breeds were fed alternatively two diets differing in crude fiber content (3.1 and 8.5% of dry matter) during four periods of three weeks each. The diets were supplemented with three molecules that may be used as indigestible marker: silicone oil, the plastic resin Kynar®, and polyethylene glycol. At each period, digestibility was measured using the gold standard as previously described. At the end of each period, a sample of feces was also collected directly from the rectum of the pigs. All samples were also analyzed by Near InfraRed Spectroscopy (NIRS). The digestive ability was variable among pigs during the growing period, especially when the diet contained a high level of fiber. The digestibility of this

type of diet increased when body weight increased. The utilization of indigestible markers did not give satisfying results, because of low recovery in the feces (plastic resin or polyethylene glycol) or because of large variability in the recovery (silicone oil). The NIRS prediction of digestibility coefficients from a sample collected directly in the feces was adequate (bias of digestibility coefficients for dry matter, organic matter, energy, and N did not differ from 0%) when pigs were heavier than 60 kg and when they are fed a diet with a high fiber content. The method of collecting a single sample of feces directly from the rectum of the pig and analyzed by NIRS can be used in selection farms of breeders to give information on the digestive ability of individual pigs in a population. The Feed-a-Gene Project has received funding from the European Union's H2020 Programme under grant agreement no 633531.

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**Keeping up with a healthy milk fatty acid profile require selection**
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The effect of various fatty acids and fatty acid groups on human health is under discussion, and results are not unambiguously. However, current knowledge shows that a health-promoting milk fat profile is likely to be obtained by increasing the content of unsaturated fatty acids and reducing the proportion of palmitic acid. From a milk product point of view this would contribute to butter with a softer texture which is easier to spread. The objective of this study was to investigate the genetic impact on the milk fatty acid profile measured as g/100 g total fat for 7 FA fractions and 4 individual FA. Milk samples from all cows in the Danish herd testing scheme were collected from May 2015 to December 2017 and analyzed at a certified laboratory using MilkScanTM FT+/FT600 equipped with special software for predicting 7 FA fractions: saturated FA (SFA), Mono-unsaturated FA (MUFA), Poly-unsaturated FA (PUFA), short chain FA (SCFA), medium chain FA (MCFA), long chain FA (LCFA), and transFA; and 4 individual FA: C14:0, C16:0, C18:0, and C18:1. Heritabilities for test day measurement of the different fractions and individual FA were at the same level (0.08 to 0.16) as heritability for overall fat yield for both Danish Holstein and Danish Jersey. Genetic correlations between the fraction of unsaturated FA and total fat yield were however unfavorable indicating an unfavorable trend for the healthy FA contents unless selected for. Correlations between breeding values for FA (groups and individuals) and the different traits in the Nordic Total merit index were in general below 0.15 for both Holstein and Jersey. This suggest that selection for FA (groups and individual FA) can be carried out without harming other traits in the breeding goal. It is therefore proposed to substitute the present Fat index in the total merit index with and index composed of the FA's weighed together based on their health promoting values and their values in relation to product quality.

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**New phenotypes from milk MIR spectra: challenges to obtain reliable predictions**
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In the recent years, the research aiming to predict new phenotypes from the FT-MIR analysis of milk was very active. Models were developed to predict phenotypes such as fine milk composition, cow health and environmental impact or technological properties of milk. Those models could be of great interest in order to perform genetic studies as they could allow generating large amount of data at large scale and with reasonable cost. To achieve this, it is nonetheless necessary to insure that the models provide reliable predictions when applied on the large diversity of spectral data met on real field conditions. The robustness of models -its capacity to be "all terrain" and provide good results in various conditions- is therefore essential to ensure reliability of predictions. Robustness could be estimated by evaluating the error in external validation (RMSEP), the reproducibility of predictions between instruments and the ability of the calibration dataset to cover the variability of routine field data. However, in current literature, the model robustness is often omitted. Models are frequently developed on reduced dataset, with limited number of herds, breeds and diets. Additionally, models are evaluated by looking to the statistical performances, through the R² and the standard error (RMSE or SEC), while the robustness is rarely assessed. Finally, only a limited number of models is used in routine and faces the large variability of real field conditions to provide phenotypes for management of cows or genetic studies. The objective of this work is consequently to evaluate the impact of different factors influencing robustness on prediction quality. The impact of sampling scheme (oriented vs. random), and model development are investigated. Effect of inclusion of variability in the model by adding countries, breeds, MIR instruments and days in milk are also investigated. The obtained results encourage for international collaborations in order to constitute large and robust datasets and enable the use of models in routine conditions.

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**Zootechnical parameters added to the milk MIR spectra as predictive value to estimate CH4 emissions**
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Breeding needs tools to quantify at large scale greenhouse gases emissions in order to develop levers to reduce them. Milk mid-infrared (MIR) spectrum is a promising proxy to estimate daily methane ($CH_4$) emissions of individual dairy cows. A model has been developed based on 1,089 reference measurements combining milk MIR spectra and $CH_4$ records, collected using the $SF_6$ tracer technique (n=513) and respiration chambers (n=576). These data came from 7 countries (BE, IRL, CH, UK, FR, DK and D) and from cows of 5 major breeds: Holstein (74%), Brown Swiss (13%), Jersey (3%), Red Holstein (3%) and Sweedish Red Crossed (2.5%). Using a 5 groups cross-validation (CV), statistics reached an $R^2$ of 0.64 with a SE of 61 g of $CH_4$/day. A cow and country dependent external validation (CCDEV) has been performed: all the data from 20% of the cows per country are removed, calibration was then done on the 80% remaining cows from all countries and validated on the 20% removed. After 500 repetitions, the $R^2$ and the RMSEP of CCDEV were 0.55 ± 0.07 and 70 ± 4.5 g of $CH_4$/day respectively. To asses improving these results, parity, milk yield and breed information have been added individually and by combination to the MIR spectra. This led to 7 new calibration models. Statistics were improved with the parameters included, with an optimum found for the version combining milk MIR spectra, milk yield, parity and breed as predictors. The statistics reached a $R^2cv$ of 0.68, a SECV of 57 g of $CH_4$/day, and $R^2$ and RMSEP of CCDEV of 0.6 ± 0.06 and 65 ± 4.1 respectively. Including these routinely available cow parameters improves the model prediction performance. Practical applications are stil required to observe and confirm the relevance of these new predictions.

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Abstract number: 31997 / accepted / order: 10 / pres.means: Theatre / time: 15
**Potential use of MIR spectra in the prediction of hoof disorders in Holstein Friesians**

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The prediction of hoof disorders using MIR (mid-infrared) could be a promising approach for genomic selection of locomotion in dairy cattle and management of hoof problems in herds. Previously, we studied the temporal relationship between locomotion scores and MIR based biomarkers. This time we focussed on hoof disorder scores and MIR spectra directly instead of the biomarker concentrations derived from the spectra. The data provided by CRV through the ClawMIR project, consisted of 638,904 hoof disorder records and 5,708,128 MIR records, coming from 261,647 Holstein Friesian cows in 1,983 herds between 2013 and 2018. Each lactation was subdivided into 30-day month classes. Pre-processing of the spectral data consisted of the first derivative, applied with a window size of 5 wavenumbers. The MIR data and hoof disorder scores were corrected for animal-lactation, herd-testday and lactation group (1, 2 or 3+) with a fixed effect model. The spectral data and hoof disorder severity scores were then averaged over animals and month classes. Only the first five months of lactation were investigated as that is the period when the cow is most at risk of developing a metabolism related locomotion disorder. The first step of this research was to establish correlations between the hoof disorders at a specific month and each of the 212 wavenumbers during the 1,2 ,3 or 4 months before the hoof disorders. Looking at the results, certain patterns appeared in these correlations. White Line disorders have the highest correlations with absorbance values taken the last month before their occurrence (r between 0.06 and 0.08). Sole Hemorrhage and Sole Ulcer scores did not make a distinction between the months preceding their occurrence, but inside each month, they have the highest correlations with the same groups of wavenumbers (r between 0.03 and 0.05 for certain wavenumbers for Sole Hemorrhage and r between 0.06 and 0.09 for similar wavenumbers for Sole Ulcer). These patterns showed time-dependent but also intra-waveband patterns that are potentially very useful in the establishment of early warning equations for diseases.

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Abstract number: 31347 / accepted / order: 11 / pres.means: Theatre / time: 15
**Validation of the prediction of body weight from dairy cow characteristics and milk MIR spectra**

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Body weight (BW) recording is of interest to optimize herd management and environmental fingerprint. Due to its cost, a weighing system is not installed in many farms. Linear type traits are mostly available only once in the lifetime of the cow. So, an interest exists to develop a method to predict routinely BW with traits easily recorded and cheap. First investigation was conducted one year ago to build a prediction equation of BW from parity, test month, milk yield, days in milk and milk MIR spectrum. This study based on 717 records obtained a herd validation root mean square error (RMSEv) ranged from 37 to 64 kg. Cross-validation (cv) $R^2$ was equal to 0.51 with RMSE of 50 kg. This equation was applied on 1,161 milk MIR spectra collected in the GplusE project from Holstein cows. Validation $R^2$ was 0.51 with RMSEv of 65 kg. A total of 109 spectra had a global H distance higher than 3 suggesting spectral outliers. After their removal, $R^2v$ increased slightly (0.54). Difference of RMSEv can be explained by a lack of spectral variability in the calibration set. So, the 2 datasets were merged to build a PLS regression including the same predictive traits as the first study. After a spectral cleaning based on GH and residual analysis, the best equation used 1,837 records and gave a 10 fold $R^2cv$ of 0.64 ± 0.02 with a RMSEcv of 46 ± 2 kg. The ability to predict BW was improved by adding this new data. Lowest errors were observed for BW ranged from 500 to 750 kg which represents 94% of the set. So, low and high BW lack in the calibration set. This study confirms the preliminary results and the potentiality to predict an indicator of body weight. This alternative BW prediction could explain a part of the BW variability not already covered by other BW predictors as those based on linear scores. Moreover, this method allows to consider the past information if the spectral data is available. This approach should help research on BW changes and selection for this trait in the future.

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Abstract number: 31413 / accepted / order: 12 / pres.means: Theatre / time: 15
**Chromosome regions affecting MIR spectra indirect predictors of cheese-making properties in cattle**

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The current study aimed to identify single nucleotide polymorphism (SNP) markers and candidate genes associated with titratable acidity (TA), total caseins (TC) and dry cheese yield (DC) predicted from MIR spectra as indirect predictors of milk cheese-making properties in early lactation cows. These predicted MIR novel phenotypes were obtained by using equations developed through GplusE and former EU projects. Only autosomes SNPs (n=29) with call rates >0.95, minor allele frequencies (MAF) >0.05 and significant deviations from Hardy–Weinberg equilibrium ($P > 10^{-7}$) were used for the genome-wide association study. After quality control edits, 32,687 SNPs remained for further analysis. The detection of SNPs affecting TA, TC and DC were obtained based on the proportion of variation explained by each SNP. The SNPs were considered as outliers if the proportion of variance explained was higher than 5*IQR+Q3, where IQR is the interquartile range and Q3 is the third quartile of the distribution. The putative genes located within or close to an outlier SNP were further identified. A total of 1,109 SNPs were considered as outliers with 8, 13, and 4% in common to all, between TC and DC, and between TC and TA traits, respectively. The remaining 833 were trait specific SNPs, with 18, 28, and 29% affecting TC, TA and DC, respectively. The 84 common SNPs to all traits were identified on BTA14 (75%), 1 (19%), 19 (5%) and 6 (1%). The trait specific markers were located on 26 out of 29 chromosomes. For TA, 86% of SNPs were located on chromosomes 1, 20, 7, and 14. On the other hand, TC showed the majority of SNPs on BTA6, BTA20 and BTA10 whereas for DC, SNPs were mainly on BTA5, BTA14 and BTA27. The top 5% outlier SNPs were located on BTA14, BTA1 and BTA20 with 20 (RPL8; FOXH1; CYHR1; OPLAH; HSF1; CPSF1; DGAT1; CYC1; GRINA; PARP10; NRBP2; PUF60; RNF19A; RRM2B; C8orf33; FBXO43; LY6H; ANKRD46; NAPRT; LY6E), 11 (FAM3B; MX1; HSF2BP; RRP1B; CSTB; C21orf2; LRRC3; DSCAM; ADARB1; ITGB2; MX2) and 3 (ANKH; TRIO; OTULIN) potential candidate genes affecting MIR indirect predictors (TA, TC and DC) of cheese-making properties in early lactation, respectively.

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**Using milk MIR spectra to identify candidate genes associated with climate-smart traits in cattle**
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Enhancing the resilience to extreme climate events and reducing greenhouse gases (mitigation), while improving productivity are of large importance in future breeding objectives. However, gaps to get large-scale phenotyping as well as limited knowledge about the biological basis are still challenges. This study tried to exploit the milk MIR spectra jointly with genomics to identify potential candidate genes affecting mitigation and resilience abilities. For mitigation, methane emissions (CH4) and Phosphorus (P) could be viewed as major sources of environmental pollution. Biomarkers reflecting the equilibrium between mobilisation and intake and body ketones associated with energy status are potential indicator traits for resilience to thermal stress. Predicted phenotypes form MIR data, CH4 and P (mitigation), and C18:1cis-9, Acetone, BHB in addition to milk yield (resilience) were used in this study. The proportion of variance explained by SNPs was evaluated for all studied traits. The putative genes located within or close to outliers SNPs were further identified. Concerning CH4 and P, 31; 28 and 7% of the what we called outliers SNPs were located at BTA14; BTA1 and BTA15, respectively. The markers in the most informative windows on BTA1 were close or within several genes such as RIPK4, PRDM15, ABCG1, SLC37A1, UBASH3A and FAM3B. On BTA14, the top outlier SNPs were located in LD block containing 3 genes (DGAT1, CYHR1, and PLEC). For resilience traits, the two outlier markers associated with acetone slope were located on BTA7 at approximately 45.5-45.7 Mb. Possible candidate genes located within this interval are UQC411 and ATP5F1D. The SNPs ARS-BFGL-NGS-4939 and ARS-BFGL-NGS-34135, located on BTA14 were top SNPs and were also detected to affect milk, C18:1cis9, acetone, and BHB slopes. Interesting candidate genes such as DGAT1, HSP1 and SLC52A2 were identified surrounding those two markers. In conclusion, markers identified for resilience and mitigation traits could prove useful in genomic selection for climate-smart breeding programs.

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**Using of spectral global H distance improves the accuracy of milk MIR based predictions**
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Milk MIR spectrometry predicts traits related to quality, health and environment. Standardizing MIR data enables to share prediction equations. The prediction accuracy depends partly on the calibration spectral variability. So, the calculation of spectral global H (GH) distance is of interest. The effect of GH on the accuracy of MIR predictions were studied using 198,394 milk samples collected from Chinese cows and analyzed on 3 Bentley FTS machines. The content of fat, protein, monounsaturated fatty acid (MFA), unsaturated FA (UFA), saturated FA (SFA), polyunsaturated FA (PFA) predicted by manufacturer's models were the reference values. Fat, protein, MFA, PFA, SFA and UFA averages were 3.97, 3.43, 0.86, 0.07, 2.62 and 0.93 g/dL of milk. Bentley MIR spectra were standardized to master MIR spectra according to the method developed by the European Milk Recording network. Then the studied traits were predicted on those spectra using published MIR equations. The averaged predicted content of fat, protein, MFA, PFA, SFA, and UFA were 3.99, 3.53, 1.15, 0.15, 2.64, 1.29 g/dL of milk. GH ranged from 0 to 475. Correlation values between predicted and reference contents ranged from 0.92 to 0.98, except for PFA (0.59). Root mean square errors (RMSE) were 0.19, 0.18, 0.32, 0.09, 0.21, and 0.39 g/dL for fat, protein, MFA, PFA, SFA, and UFA. Correlation values between the squared residuals and GH were positive (0.17-0.42). This suggests a positive effect of GH on the prediction accuracy. When a threshold of GH≤5 was applied, the data loss ranged from 3.83% to

9.27%. Correlation values between predicted and reference contents increased (0.94 to 0.98, 0.64 for PFA). RMSE decreased from 1.26% to 7.37%. Considering GH limits spectral extrapolation. To improve the accuracy, samples with GH>5 must be included in the calibration set to cover the spectral variability. Moreover, the spectral standardization must be performed on a regular basis in order to check the potential spectral deviation of an instrument. In this study, the standardization was performed once.

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**Including the scapula width from CT-scans improves selection accuracy for sow longevity**

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The longevity of sows is a key economical trait for pig breeders. In the breeding nucleus, sows are mainly selected based on their breeding values. Longevity traits are therefore rather collected in multipliers or in commercial crossbreed herds, on animals with long genetic distance from selection candidates. To improve selection accuracy for longevity traits, it is useful to find indicator traits which could be measured closer to the nucleus. In this study we utilize the width of scapula measured in CT-scanned purebred Norwegian Landrace (NL) boars as such an indicator trait. We estimate the genetic correlations against two sow longevity traits in addition to shoulder lesions (SL) and body condition score (BCS) of sows at weaning of the first litter. The longevity traits, LGY12, which is a binary trait indicating whether the sow was inseminated after the first weaning, and LGY15, which is the number of litters achieved within 570 days after first farrowing, were measured on purebred NL sows in multipliers outside of Norway. BCS and SL were measured on purebred NL sows both in the nucleus and in multipliers. We found that the scapula width had high heritability (0.72 ± 0.06) and genetic correlations with BCS (-0.27 ± 0.08), SL (0.27 ± 0.08), LGY12 (-0.18 ± 0.15) and LGY15 (-0.37 ± 0.15). Through a cross validation study, we also measure how including the scapula width on a selection candidate improves the accuracy of sow traits. This was done by removing data for all daughters of 151 genotyped boars with the scapula width phenotype. Then we predicted genomic breeding values for the sow traits from one model where scapula width was included as a correlated trait and one where it was excluded. The breeding values was then compared with daughter yield deviations for the 151 boars. By including scapula width as a correlated trait in a single step genomic prediction, the accuracy of sow traits was increased from 0.32 to 0.55 for LGY15, from 0.63 to 0.64 for SL, and 0.57 to 0.59 for BCS, while for LGY12, the accuracy was not affected. As all NL nucleus boars are being CT-scanned, this study quantifies the potential for improvement of sow longevity traits by including novel precision phenotypes from CT-scan before selection