Natural 15N abundance of animal proteins: a promising biomarker of feed efficiency in beef cattle

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Phenotyping animal feed efficiency, the animal's ability to transform feed into food, is challenging because it is time and labor consuming and not always feasible in livestock systems based on pasture. Thus, biomarkers should be developed and validated for a high-throughput phenotyping of feed efficiency in practical conditions. The natural ^{15}N enrichment of animal proteins over the consumed diet ($\Delta^{15}N = \delta^{15}N_{animal} - \delta^{15}N_{diet}$) has recently been proposed as a biomarker of animal feed efficiency. This study aimed to confirm by meta-analysis the potential of $\Delta^{15}N$ to capture the between-animal variation in feed conversion efficiency (FCE; body weight gain/ dry matter intake) in young beef cattle reared in different European conditions. For this, individual data of $\Delta^{15}N$ measured in plasma and FCE of 468 growing-fattening bulls of different pure and cross continental breeds, from 25 different diets, 8 experiments and 3 countries (France, UK and Switzerland) were evaluated by regression analysis. All animals were tested for at least 60 days for FCE and their blood (7 experiments) or muscle tissue (1 experiment) sampled at the end of the test period. Diets were sampled throughout the feed efficiency test. Diets and animal proteins (plasma or muscle) were analysed for their natural ^{15}N abundance ($\delta^{15}N$) and the $\Delta^{15}N$ was calculated for each animal. Two models were used to assess the relationship between $\Delta^{15}N$ and FCE at the individual level. First, a mixed regression model of FCE on $\Delta^{15}N$ with the experiment and diet as random effects, allowing these two effects to be excluded from the explored relationship. For the second model, residuals were first obtained for FCE and $\Delta^{15}N$ after correcting for the experiment and diet effects and then regressed on each other by simple linear regression. For the first approach, the mixed model confirmed that $\Delta^{15}N$ is significantly ($P<0.001$) and negatively correlated to FCE within each diet and experiment according to the following equation: FCE=0.27 (se 0.025)-0.030 (se 0.0056) × $\Delta^{15}N$ (RSE=0.017). For the second approach, the significant ($P<0.001$) correlation between both residuals confirmed the results obtained with the first approach with a similar slope: FCE=-0.031(se 0.0027) × $\Delta^{15}N$ (RSE=0.017). Present data confirm that $\Delta^{15}N$ can be used in future to predict between-animal variation in feed efficiency in beef cattle.

Managing genetic diversity to ensure resilience using the IMAGE multi-species SNP arrays

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Monitoring genetic variation of animal collections of ex-situ as well as in-situ collections is important to make decisions on which breeds and animals may need to be stored for the future in genebanks. Inbreeding in every species is of major concern but for small populations it is even more critical. Precision mating to ensure optimal use of the genetic diversity will diminish the chance that deleterious alleles are transmitted which will contribute to ensure resilience. At present, gene banks have few molecular data to characterise their collections and compare them with in-situ populations. Different tools are available according to species. Within the IMAGE project (a European H2020-project) we made two multi species SNP arrays for the major farm animal species represented in gene banks, which include cattle, pig, chicken, horse, goat, sheep for the IMAGE001 array and water buffalo, duck, quail, rabbit, bee, and pigeon for the IMAGE002 array. For each species, on average 10K SNPs were selected for the array. Both arrays can capture biodiversity of traditional breeds for each species on the autosomes and sex chromosomes but also harbour ancestral SNPs, mtDNA SNPs, trait related variation and variation in genes detected in QTL regions. For IMAGE001 we included MHC variation for each species. The Affymetrix IMAGE arrays are worldwide available without restriction at a low cost ($19.50 including genotyping) at the major genotype providers which enhance routine use of these arrays. We validated and tested both arrays with 1,920 and 1,152 DNA samples covering over 300 breeds for IMAGE001 and IMAGE002 respectively. The IMAGE portal has been opened to facilitate exploration of gene bank data (https://www.image2020genebank.eu). The MoBPS software (https://github.com/tpook92/MoBPS) has been developed to facilitate the introduction into breeding programs of genetic diversity from gene banks, using pedigree as well as molecular data.