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**Feed restriction effect on progeny of mice selected for birth weight environmental variability***N. Formoso-Rafferty<sup>1</sup>, I. Cervantes<sup>1</sup>, J.P. Gutiérrez<sup>1</sup> and L. Bodin<sup>2</sup>*<sup>1</sup>*Universidad Complutense de Madrid. Facultad de Veterinaria, Avda. Puerta de Hierro s/n, 28040, Madrid, Spain,*<sup>2</sup>*INRA – GenPhySe, CS 52627, 31326, Castanet-Tolosan, France; n.formosorafferty@ucm.es*

In line with aspects of the H2020 Feed-a-Gene project (grant agreement no. 633531) aiming to understand the genetic relationship between feed efficiency and robustness, we analysed the influence of mice feeding restriction on their offspring birth weights (BW) in two lines divergently selected for birth weight environmental variability. A total of 120 females (four full-sib females from 10 random different litters of the 12, 13 and 14 generations of selection) were chosen within high and low selected lines and split in four groups of feeding type combining restriction or not in two periods: from weaning at 21 to 77 days, and one week before mating to the 2<sup>nd</sup> parturition. Restriction consisted of feeding with 75, 90 and 85% of *ad libitum* consumed feed in the respective three studied generations. The data included 158 litters with 1,275 BW and 4,093 animals in the pedigree. A heteroscedastic model (using ASReml Release 4.1 software) was fitted to ascertain the genetic and environmental factors affecting the BW mean and its residual variance. The model included the diet type of the dam (restricted or not during the growing period and during the reproductive period), its line, generation, litter size where it was born and its parity, as well as the litter size of the progeny and its sex; including also all diet, line and generation interactions. The line (lower BW for the low variability line), and the generation effect for the progeny of dams restricted both during the growing and the reproductive period had significant effects on the progeny BW. Whereas the sex, the interaction diet-line (in dam pregnancy period) and the dam genetic effect have had effect on the BW variability. The interaction diet-line produced a decrease in environmental variability of 5 and 18% in low and high variability lines respectively. It seems that selection for BW variability has conferred a lower sensitivity of the dams to the environmental conditions, which could be interpreted as higher robustness.

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**Session 24****Theatre 10****Using metafounders to model purebred relationships in genomic prediction for crossbreeding***E.M. Van Grevenhof, J. Vandenplas and M.P.L. Calus**Wageningen University and Research, Animal Breeding and Genomics, P.O. Box 338, 6700 AH Wageningen, the Netherlands; mario.calus@wur.nl*

Selection for feed efficiency in purebred pig and poultry breeding animals should ideally account for the performance of crossbred animals. As part of the Horizon2020 Feed-a-Gene project (grant agreement no. 633531), methodologies to account for crossbred data are being developed and optimized using simulated data. The advantage of using crossbred data instead of purebred data in genomic evaluations for feed efficiency will be evaluated to propose new selection schemes for feed efficiency in monogastric animals. Simulations were set up using a three-way crossbred breeding program, with 10 generations of purebreds (PB), and 5 generations of two-way and three-way crossbred animals. The last generation of PB are validation animals. True breeding values are simulated for each line/cross (5 traits). Genetic correlations between all PB lines were randomly sampled in the range 0.2-0.8. Heritabilities were randomly sampled in the range of 0.2-0.4. Each PB generation exists of 2,000 phenotyped individuals, and all genotyped animals were also phenotyped. Three scenarios will be tested with varying amounts of data available. In the first scenario 2,000 phenotypes and no genotypes will be available, in the second 2,000 phenotypes and 1000 genotypes, and in the third 2,000 phenotypes and 2,000 genotypes. The simulated genotypes follow the size and number of chromosomes of the pig genome (18 chromosomes). The number of SNP simulated is ~60k, with 4,500 QTL in total. Each simulation is replicated ten times. Breeding values of validation animals are predicted using pedigree-based BLUP, or single step GBLUP (SS-GBLUP) that either uses metafounders or not. Metafounders enable to estimate parental relationships between purebred lines using the genotypic information of different lines in the G-matrix (usually no relationship is assumed between PB lines). Results will contain estimated variance components and accuracies of breeding values of purebred selection candidates for crossbred performance. We hypothesize that the use of metafounders will lead to improved accuracies and more unbiased estimated variance components for SS-GBLUP.