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## Accounting for variation among individual pigs in deterministic growth models

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**Does lameness in the sow influence her reproduction?***H.T. Le<sup>1</sup>, N. Lundeheim<sup>1</sup> and E. Norberg<sup>2</sup>**<sup>1</sup>Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Gerda Nilssons väg 2, Ultuna, Box 7023, 75007 Uppsala, Sweden, <sup>2</sup>Aarhus University, Department of Molecular Biology and Genetics, Blichers Allé 20, P.O. Box 50, 8830 Tjele, Denmark; [thu.le.hong@slu.se](mailto:thu.le.hong@slu.se)*

Lameness is not only a welfare issue but also a major source of economic loss in pig production. Lameness is assumed to suffer from pain and stress which might cause negative effects on her reproduction. Our aim was to estimate the genetic association between leg scoring (performed at performance testing, at approx. 100 kg live weight) and reproductive performance of the sows. Data analyzed consists of records on purebred Swedish Yorkshire pigs born and raised in nucleus herds. In total 119,345 pigs were tested for two lameness traits: movement score (MOV) and overall leg score (LEG). Both scores of MOV and LEG ranged from 1 (worst) to 3 (best) and were transformed using normal score transformation to obtain normality. Information on fertility in first parity (in total 13048 sows) included gestation length, number of total and alive born piglets, weaning to service interval (within 7 days after weaning; WS17), and litter weight at 3 weeks of age. The DMU package using bi-variate and multitrait animal models was used to perform the genetic analyses. As expected, the two lameness traits (MOV and LEG) were highly correlated with a genetic correlation of  $0.88 \pm 0.02$ . Due to relatively high standard error, correlation between lameness traits and reproductive traits in the first parity were not significantly different from 0. Lameness traits and WS17 seem negatively correlated ( $r_g = -0.33 \pm 0.21$ ), meaning that sows with worse score of lameness tend to have longer weaning to service interval. In order to have a better conclusion about genetic association between lameness of the sow and her reproduction performance, further studies, including information on later parities will be performed.

**Accounting for variation among individual pigs in deterministic growth models***B. Vautier<sup>1,2</sup>, N. Quiniou<sup>1</sup>, J. Van Milgen<sup>2</sup> and L. Brossard<sup>2</sup>**<sup>1</sup>IFIP, BP 35104, 35651 Le Rheu cedex, France, <sup>2</sup>INRA-Agrocampus Ouest, UMRI1348 PEGASE, 35590 Saint-Gilles, France; [ludovic.brossard@rennes.inra.fr](mailto:ludovic.brossard@rennes.inra.fr)*

Accounting for variation among pigs in deterministic growth models can be performed by repeating simulations using different realistic sets of parameters. However, model parameters are not independent and variation among them is therefore not random. The structure of relationships among parameters describing individuals has been considered only to a limited extent. In this study, the mean and covariance structure of model parameters describing daily feed intake (DFI) and growth were analyzed on data obtained from ten batches of growing pigs from different crossbreeds (dam: Large White  $\times$  Landrace, sire: 10 different lines). Performance of group-housed crossbred gilts and barrows was tested from 70 days of age to approximately 110 kg body weight (BW). The DFI was recorded continuously and BW was measured at least every 3 weeks. Based on the observed DFI and BW, the InraPorc model was used to characterize each pig through a set of five model parameters, three of which described growth and two described *ad libitum* DFI. The data set included parameters for 1,288 pigs. Almost all parameters were affected by sex and batch, but not by crossbreed within batch. Covariance matrices computed according to batch, sex, crossbreed, or their combinations were all different as evaluated using the Flury hierarchy. The unit of covariance corresponded to the combination of batch, sex and crossbreed. As the variance structure is affected by batch, sex, and crossbreed, this information would be required for each situation, which is impossible from a practical point of view. The next-best solution is to use a generic covariance matrix structure based on the median matrix accounting for the size of subpopulations. This covariance matrix can be used, in combination with average parameters obtained on-farm to generate virtual populations of pigs and to evaluate different nutritional and management strategies on performance and variability of groups of pigs.