

Modelling intensity of interaction to estimate direct and indirect genetic effects*Juan P. Steibel¹, Rodolfo J.C. Cantet² and Janice M. Siegford¹**¹Michigan State University, USA, ²University of Buenos Aires, Argentina; steibelj@msu.edu*

Selecting for social genetic effects has been proposed for improving welfare of group-housed livestock. In classical social genetic effects, the social effects are modelled assuming uniform intensity of social interaction among all group members. Such models may lead to confounding of the social effect incidence matrix with the pen or group incidence matrix. The confounding is generally avoided by using multiple mixings, where each animal is grouped with different animals in each mixing. But even if re-mixing is performed, the underlying assumption is that intensity of interaction within group is uniform among all possible pairs of individuals. Exploiting estimates of intensity of competition between all pairs of individuals has been proposed in the context of forest tree breeding, but it has not been attempted with animals. In this work, we show how dyadic social interactions estimated from decoded video observations of group-housed pigs could be used to parameterize social genetic effects models. We show that this approach allows estimation of social genetic effects separately from other group-specific effects without having to re-mix animals. We also illustrate how to build social interaction matrices to obtain variance estimates that are comparable to estimates of direct genetic variance and environmental variance components. Furthermore, we propose alternative metrics for the incidence matrix of social interactions by using frequency or duration of different types of interactions and suggest a framework for model comparison, including cross validation in the presence of successive mixings. Finally, we present equations to use the proposed models to perform genome-wide association of indirect genetic effects in addition to predicting animal-specific indirect breeding values. We conclude that in the presence of pairwise-behaviour observations, indirect genetic effects models could be parametrized to account for such information, and they could lead to an increased amount of phenotypic variance that is explained by genetic effects.