



Genetic correlations between performance traits in F2 layer x broiler reciprocal cross developed for QTL mapping in *Gallus gallus*

Ana C. B. Barbosa*¹, Juliana C. Faveri², Victor B. Pedrosa³, Mônica C. Ledur⁴, Luis F. B. Pinto⁵
¹Graduate student in Animal Science - UFBA, Av. Adhemar de Barros, 500, 40170-110, Ondina, Salvador, BA, Brazil; ²Graduate student in Animal Science in the Tropics- UFBA; ³Animal Science Department, UEPG, Ponta Grossa, PR, Brazil, ⁴Embrapa Swine and Poultry, Concórdia, SC, Brazil, ⁵Animal Science Department, UFBA
*luisfbp@gmail.com

Genetic correlation between two traits shows the extent to which a specific set of genes affect the expression of both traits. In populations developed for quantitative trait loci (QTL) mapping, the knowledge of genetic correlations may help to understand differences between genetic linkage and pleiotropic effect. Thus, this study aimed to estimate genetic correlations between performance traits in an F2 broiler x layer reciprocal cross population developed for QTL mapping in *Gallus gallus* by the Embrapa Swine and Poultry National Research Center. The broiler line was selected for six generations to improve body weight, feed conversion, feed intake, carcass parts, viability, fertility, hatchability, and to reduce the occurrence of abdominal fat and metabolic diseases. The layer line was selected for eight generations for egg production, egg weight, feed conversion, sexual maturity, fertility, hatchability, egg quality, and reduced body weight. Reciprocal cross between broiler male x layer female and layer male x broiler female was performed to obtain the F1 generation. Individuals (males and females) from the F1 generation were mated, avoiding related individuals, to produce the F2 generation. The F2 data file included performance records of 3823 animals, with 2063 coming from the mating of broiler males with layer females and 1760 from the reciprocal cross. The body weights at 1, 35 and 42 days of age, and the weight gain, feed intake and feed conversion from 35 to 41 days of age were measured. Genetic correlation coefficients were estimated with animal model, using the REML method, in the VCE program. Fixed effects of sex (male and female), hatch (16 levels) and reciprocal cross (two levels) were included in the model. Variance components were estimated for random effects of dam and animal. Weight gain is genetically correlated with feed intake (0.96), feed conversion (-0.92), and body weights at 35 (0.97) and at 42 (0.98) days of age, but it had low correlation with birth weight (0.15). Feed intake has high genetic correlation with feed conversion (-0.79) and body weight at 35 (0.76) and 42 (0.83) days of age, but no correlation with birth weight (0.02), while feed conversion has high genetic correlation with body weights at 35 (-0.96) and 42 (-0.91) days of age, and moderated correlation with birth weight (-0.40). The genetic correlation between body weights at 35 and 42 days was 0.98, but those traits had low correlation with birth weight, 0.27 and 0.19 respectively. High genetic correlations indicate that a same set of genes are controlling those traits, except for birth weight that seems to have independent genes. Thus, QTL mapped for weights at 35 and 42 days, weight gain, feed intake and feed conversion between 35 and 41 days, may be pleiotropic QTLs if they are located in very similar positions in a chromosome. On the other hand, QTLs for birth weight, even when mapped near QTLs for other traits, might possibly be linked QTLs.

Keywords: animal breeding, association, genomics, performance.

Acknowledgments: the authors thank Embrapa Swine and Poultry for the data set used in this study, and CAPES for the graduate students scholarship.