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Ingrid David, Juan Pap.Blo Sanchez, Miriam Piles

► **To cite this version:**

Ingrid David, Juan Pap.Blo Sanchez, Miriam Piles. Structured antedependence model for longitudinal analysis of social effects on ADG in rabbits. 69. Annual Meeting of the European Federation of Animal Science (EAAP), Aug 2018, Dubrovnik, Croatia. 705 p. hal-02735651

HAL Id: hal-02735651

<https://hal.inrae.fr/hal-02735651>

Submitted on 2 Jun 2020

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Recursive binomial model to analyse piglet survival in a diallel cross between Iberian pigs

L. Varona¹, J.L. Noguera², J. Casellas³, J.P. Rosas⁴ and N. Ibañez-Escriche⁵

¹Universidad de Zaragoza, Departamento de Anatomía, Embriología y Genética, 50013 Zaragoza, Spain, ²IRTA, Genética i Millora Animal, 25198 Lleida, Spain, ³Universitat Autònoma de Barcelona, Departament de Ciència Animal i dels Aliments, 08193 Bellaterra, Spain, ⁴INGA FOOD S.A., Programa de Mejora Genética CASTUA, 06200 Almendralejo, Spain, ⁵Universitat Politècnica de Valencia, Departamento de Ciencia Animal, 46071 Valencia, Spain; lvarona@unizar.es

Piglet mortality is an important factor in pig production. Nevertheless, its statistical analysis presents serious difficulties because of its categorical nature. In recent studies, it has been suggested that the most appropriate model is a binomial model that modelled the survival of each specific piglet with a logit approach. In this study, we applied a population specific recursive binomial model to obtain estimates of the Dickerson crossbreeding parameters in a diallel cross between three strains of Iberian pigs (Entrepelado; EE, Torbiscal; TT and Retinto; RR). A total of 18,193 records from 3,800 sows distributed as follows: EE (2,843 records, 707 sows), ER (2,336, 527), ET (942, 177), RE (806, 196), RR (4,472, 874), RT (2,450, 488), TE (193, 36), TR (1,993, 359) and TT (2,158, 452). The average litter size (total number born) and stillbirth were 8.292 ± 2.284 and 0.285 ± 0.787 , respectively. In addition, we used a pedigree of 4,609 individuals to analyse these data with a Bayesian approach through a Gibbs Sampler. The recursive relationship between litter size and pig mortality was clearly non-linear for all crosses. The results were examined at 5, 8, 11 and 14 piglets as reference points and they indicate that the direct line effect of the EE population is higher than RR and TT with posterior probabilities over 0.97 at all reference points. Nevertheless, we were not able to detect any relevant differences between maternal effects and only the heterosis effect between TT and RR was clearly positive with posterior probabilities over 0.97 at all reference points. The main advantage of the proposed model is that allows to calculate crossbreeding parameters (line, maternal and heterosis) conditioned to each specific litter size taking into account the population specific non-linear relationships with piglet mortality and litter size.

Structured antedependence model for longitudinal analysis of social effects on ADG in rabbits

I. David¹, J.P. Sanchez² and M. Piles²

¹GenPhySE, Université de Toulouse, INRA, ENVT, Chemin de borde rouge, 31326 Castanet tolosan, France, ²IRTA, Torre Marimon s/n, 08140 Caldes de Montbui, Barcelona, Spain; ingrid.david@inra.fr

Even if there are evidences that the intensity of social interactions between partners vary with time, very few genetic studies have investigated how social genetic effects (SGEs) vary over time. To overcome this issue, the objectives of the present study were to analyse longitudinal records of average daily gain (ADG) in rabbits and to evaluate, by simulation, the response to selection for such longitudinal trait. Five weekly ADG records from 3,096 rabbits under feed restriction after weaning and raised in pen of 8 were used for the analysis. A linear animal mixed model including SGEs with week specific random effects that follow structured antedependence (SAD) functions was fitted to the data using ASReml and the Fortran program that we have developed (freely available on zenodo). The social heritability was higher in week 1 (0.44) than in weeks 2 to 5 (ranging from 0.16 to 0.23). The correlation between the SGEs of different weeks was moderate to high for weeks 2 to 5 (0.62 to 0.91) and weaker between the first week and the other weeks (0.33 to 0.47). The direct-social genetic correlations were negative at any time. Based on the same data design, the same variance components but considering 3 different sets of direct-social genetic antagonism (strong, moderate, weak); we simulated 7 generations of selection using a SAD model including SGEs or not to estimate breeding values. Results obtained showed that the increase in ADG with selection decreased with the direct-social genetic antagonism and was improved (~by 30%) when SGEs were taken into account. In conclusion, results confirmed that SGEs vary over time and do not correspond to the same trait after mixing than later in life, probably as a consequence of social hierarchy establishment observed at that time. Accounting for SGEs in the selection criterion maximizes the genetic progress.