QTL detection and estimation of the epistasis extent for chicken production and resistance to disease traits.

Olivier O. Demeure, Nicola Bacciu, O. Carlborg, Hendrik Bovenhuis, D.J. de Koning, Elisabeth Le Bihan-Duval, Bertrand B. Bed'Hom, Frederique Pitel, F. d'Abbadie, Pascale P. Le Roy, et al.

QTL detection and estimation of the epistasis extent for chicken production and resistance to disease traits

Demeure, O.[1], Bacciu, N.[1], Carlborg, O.[2], Bovenhuis, H.[3], De Koning, D.J.[4], Le Bihan, E.[5], Bed'hom, B.[6], Pitel, F.[7], D'abbadie, F.[8], Le Roy, P.[1] and Pinard, M.H.[6], [1]INRA, UMR598, 65 rue de Saint Brieuc, 35042 Rennes, France, [2]Uppsala University, Linnaeus Center for Bioinformatics, SE-751 24 Uppsala Universit, Sweden, [3]WUR, Animal Sciences, 6700AH Wageningen, Netherlands, [4]Roslin Institute, Roslin, Midlothian, United Kingdom, [5]INRA, UR83, Centre de Tours, 37380 Nouzilly, France, [6]INRA, UMR1313, Domaine de Vilvert, 78352 Jouy-en-Josas, France, [7]INRA, UMR444, Chemin de Borde Rouge BP 27, 31326 Castanet Tolosan, France, [8]SASSO, Route de Solférino, 40630 Sabres, France; olivier.demeure@rennes.inra.fr

Recently, approaches targeting the whole genome (genome wide selection, GWS) have expanded. However, using an additive model without possible interaction (epistasis) between loci, in particular between the few QTLs which explain a large part of the genetic variance of the traits, would be likely to reduce the efficiency of this strategy. In chicken, coccidiosis susceptibility is an economically important trait which could make the most of GWS. Therefore, we proposed to search for QTLs affecting coccidiosis susceptibility, to test if the selection of this trait could have an impact on production traits and to estimate the extent of the epistasis for all these traits. QTL detection and epistasis estimation are performed on two INRA experimental crosses (900 and 1,200 F2 animals phenotyped for coccidiosis susceptbility and composition traits, respectively) genotyped by 1,536 SNPs covering most part of the genome. Our aim is to implement these results for GWS in commercial lines. These lines represent 10 families totalizing 1000 animals which will be genotyped for 384 SNPs targeting the regions identified in the experimental designs. Detecing interacting QTLs is challenging for two reasons: the computation time necessary for testing all the possible interactions and the genetic model used for the detection itself. Especially, one of the most challanging part of the project is to develop a model for outbreed crosses.

The potential of egg shell crystal size and cuticle coverage for genetic selection in laying hens

Bain, M.M.[1], Rodriguez-Navarro, A.[2], Mcdade, K.[1], Schmutz, M.[3], Preisinger, R.[3], Waddington, D.[4] and Dunn, I.C.[4], [1]University of Glasgow, Faculty of Veterinary Medicine, Glasgow, G61 1QH, United Kingdom, [2]Universidad de Granada, Departamento de Mineralogia y Petrologia, Granada, 18002, Spain, [3]Lohmann Tierzucht, P.O. Box 4602, 7454 Cuxhaven, Germany, [4]Roslin Institute, Roslin, EH25 9PS, United Kingdom; ian.dunn@roslin.ed.ac.uk

In an attempt to improve selection for egg shell quality traits linked to prevention of bacterial ingress, we wished to better define aspects of egg quality. Two new measurements were evaluated, cuticle coverage and crystal size. The cuticle is a protein layer deposited on the surface of the eggshell which prevents bacterial ingress. Although stains are available to detect the cuticle it has never been quantified before. In the case of crystal size it is generally believed that smaller crystal size is associated with stronger material properties. Methods to determine the coverage of cuticle and crystal size were developed and their potential for genetic selection evaluated. A Rhode Island Red pedigree line was used in this study. The study population comprised between 32 and 38 sire families and around 880 female offspring. The % reflectance at 650 nm of cuticle stained eggs was measured using a spectrophotometer. For crystal size the total average intensity (TA) of diffracted X-rays which is related to calcite crystal size was measured. Heritability and genetic correlations were estimated for both traits The estimates of heritability for the cuticle were moderate (0.27±0.13) and for TA high (0.61±0.18). There was some evidence that there was genetic correlation between cuticle coverage and shell colour (0.31±0.29) but with high error. TA was genetically correlated with thickness of the palisade layer (0.51±0.20) and breaking strength (0.45±0.25). We conclude that measurement of cuticle quality and crystal size show considerable promise for use in genetic selection programs aimed at improving egg safety and quality. These results are obtained through the EC-funded FP6 Project 'SABRE'.