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POSTER PRESENTATIONS

Estimation of additive and dominant variance of egg quality traits in pure-line layers

David Picard Druet¹, Llibertat Tusell², Frédéric Hérault¹, Florian Herry^{1,3}, Sophie Allais¹, Amandine Varenne³, Thierry Burlot³ & Pascale Le Roy¹

¹PEGASE, INRA, AGROCAMPUS OUEST, 35590, Saint-Gilles, France; ²GenPhySE, Université de Toulouse, INRA, ENVT, 24 chemin de Borde-Rouge – Auzeville Tolosane, 31326 Castanet Tolosan, France; ³NOVOGEN, 5 rue des Compagnons, Secteur du Vau Ballier, 22960 Plédran, France

Corresponding author: david.picard-druet@inra.fr

Improved performances are partly due to heterosis effects. One of the basis of heterosis is dominance, which cannot be inherited. However, it can be exploited to boost the total genetic merit of the animals. This has a special interest in avian selection schemes where commercial animals are crossbred. In this study, we have estimated additive and dominance genetic variances for several egg quality traits in pure-line layers.

Around 10,500 egg quality performances were used, collected from 1,148 female Rhode Island layers, phenotyped at 70 weeks old and genotyped using a 600K high density SNP chip. Five egg quality traits were analysed: egg weight (EW), egg shell color (ESC), egg shell strength (ESS), albumen height (AH) and egg shell shape (ESShape). Additive and dominance genetic variances were estimated via EM-REML with univariate models. That included an inbreeding coefficient and an additive and a dominance random effect. Dominance variance explained a small fraction of the phenotypic variance (between 2 to 4 % across all traits). However, it represented a relevant fraction of the total genetic variance for some of the traits (16%, 10%, 35%, 2.4% and 15% of the total genetic variance for EW, ESC, ESS, AH, ESShape, respectively).

Further research will estimate additive and dominance genetic correlations between the traits to maximize the total genetic gain of these traits simultaneously. In addition, a genomic BLUP with dominance effects is envisaged for the joint analyses of purebred and crossbred performances, to evaluate the potential to generate superior crossbred performances.

Keywords: genomic selection, dominance genetic variance, pure-line layers, egg quality

Interest of Genotyping-by-Sequencing technologies as an alternative to low density SNP chips for genomic selection in layer chicken

Florian Herry^{1,2}, Frédéric Hérault², David Picard-Druet², Philippe Bardou³, Camille Eché⁴, Amandine Varenne¹, Thierry Burlot¹, Pascale Le Roy² and Sophie Allais²

¹NOVOGEN, Plédran, France; ²PEGASE, INRA, Agrocampus Ouest, Saint-Gilles, France; ³SIGENAE, GenPhySE, Université de Toulouse, INRA, ENVT, Castanet Tolosan, France; ⁴GeT-PlaGe, INRA, Castanet Tolosan, France

Corresponding author: florian.herry@inra.fr

To reduce the cost of genomic selection, low density SNP chip can be used in combination with imputation for genotyping the selection candidates instead of using high density (HD) SNP chip. Concurrently, next-generation sequencing (NGS) techniques has been increasingly used in livestock species but remain expensive to be routinely used in selection. An alternative and cost-efficient solution is the Genotyping by Genome Reducing and Sequencing (GGRS) techniques to sequence only a fraction of the genome by using restriction enzymes. This approach was simulated from sequences of 1027 individuals in a pure layer line, using four enzymes (EcoRI, TaqI, Avall and PstI). Imputation accuracy on HD genotypes was assessed as the mean correlation between true and imputed genotypes. Egg weight, egg shell color, egg shell strength and albumen height were evaluated with single-step GBLUP methodology. The impact of imputation errors on the genomic estimated breeding values (GEBV) was also investigated. Avall or PstI led to the detection of more than 10K SNPs in common with the HD SNP chip resulting in imputation accuracy higher than 0.97. The impact of imputation errors on the ranking of the selection candidates was reduced with Spearman correlation (between GEBV calculated on true and imputed genotypes) higher than 0.97 for Avall and PstI. Finally, the GGRS approach can be an interesting alternative to low density SNP chip for genomic selection. However, with real data, heterogeneity between individuals with missing data has to be taken into account.

Keywords: Genomic selection, Low density panel, Imputation accuracy, Genomic evaluation accuracy, Genotyping-by-Sequencing

