Genomic prediction in laying hens

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P-07. Genomic prediction has revolutionized the field of animal breeding. In laying hens, availability of genomic breeding values may allow more accurate selection at an earlier age and better differentiation of full sib males regarding their genetic potential. This study focuses on assessing the accuracy of genomic prediction in a sample of around 850 individuals from a Rhode Island Red line. All individuals were genotyped with the Affymetrix Axiom® Genome-Wide Chicken Genotyping Array which contains ~580,000 SNPs. After quality control (call rate >95%, MAF >0.5%) around 308,000 SNPs were available for further analyses. Conventional breeding values (EBVs) and de-regressed proofs (DRPs) of economically important traits were used as quasi-phenotypes for genomic breeding value prediction. Predictive ability was studied using a genomic BLUP model in a random five-fold cross-validation as well as in a stratified analysis where genomic breeding values of the youngest individuals were predicted. In the five-fold cross-validation, correlations between EBVs (DRPs) and genomic breeding values were 0.58 (0.45) for laying rate in the early stage and 0.70 (0.62) for egg shell strength. When predicting the youngest individuals, accuracies of prediction were 8 to 16% lower than in a comparably unstratified analysis.