

## **P94 Marker-assisted introgression of blue eggshell color into a white egg layer line.**

C. Dierks\*<sup>1</sup>, N. T. Ha<sup>2</sup>, D. Cavero<sup>3</sup>, H. Simianer<sup>2</sup>, R. Preisinger<sup>4</sup>, and S. Weigend<sup>1,2</sup>, <sup>1</sup> Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt, Germany, <sup>2</sup> University of Goettingen, Department of Animal Sciences, Goettingen, Germany, <sup>3</sup> H&N International, Cuxhaven, Germany, <sup>4</sup> EW GROUP GmbH, Visbek, Germany.

As part of the EU project IMAGE (Innovative Management of Genetic Resources) under the umbrella of Horizon 2020 the aim of this study is the demonstration of the efficient transfer of a specific trait maintained in gene bank, here blue eggshell color, into a contemporary high performing white egg layer chicken line. Monogenic dominant inherited blue eggshell color is caused by a large retroviral insertion on chromosome 1 at 65.2 Mb upstream of *SLCO1B3* (Wang et al., 2013, Wragg et al., 2013). For the initial F1, 6 Araucana cocks, homozygous for blue eggshell color, were mated with 10 White Leghorn (WL) hens. Based on 2 marker-assisted backcrosses (BC1 and 2) followed by an intercross (IC) a high performing blue layer WL-like line will be developed. Whole genome sequence data of the Araucana cocks and 580K SNP Axiom Genome-Wide Chicken Array data of the WL hens were used in search of breed/line specific markers. We identified 37 highly informative SNPs from 60.1 to 71.7 Mb on chromosome 1 surrounding the insertion. Thirteen of them were included in a customized 52K Genotyping Array which was used to genotype candidate birds. The additional 24 SNPs, the trait genotype and sex were determined by KASP technology. Criteria to select animals for the next generation were distinct breed/line specific haplotypes including the 37 markers surrounding the introgressed locus, the overall similarity to recipient white egg layer line as well as maximum diversity expected in future generations analyzed using the R package MoBPS. Introgression haplotypes were constructed with Merlin and we observed 30 paternal recombinants out of 137 male carriers. Out of them, 14 cocks with high proportion of recipient genome and highest degree of diversity were selected for the BC2 production. The proportion of the WL genome of the introgressed haplotype ranged from 56.9 to 76.5% in these 14 males. Out of 550 BC2 animals, 291 carriers were detected. From BC1 to BC2 the WL genome content increased in 37 animals by additional recombination up to 93.2% in the introgressed region.

**Key Words:** poultry and related species, genetic introgression, haplotype, breed/population identification