## Unravelling the genetic basis of founder phenotypes shared among traditional chicken breeds of divergent demographic history

Chiara Bortoluzzi<sup>1\*</sup>, Richard PMA Crooijmans<sup>1</sup>, Martien AM Groenen<sup>1</sup>, Hendrik-Jan Megens<sup>1</sup>

- <sup>1</sup> Animal Breeding and Genetics Group, Wageningen University & Research, Droevendaalsesteeg 1, 6708PB, Wageningen, The Netherlands
- \* Corresponding author. E-mail: chiara.bortoluzzi@wur.nl

## **Oral presentation**

Phenotypes shared between domesticated populations often have the same underlying genetic mechanism(s) that got fixed as a result of selective breeding. Of all morphological traits shared among traditional Dutch chicken breeds, rose comb (R) and feathered leg (Pti) are of great interest, as they yield important insights into the phenotypic consequences of selection. Such "founder phenotypes" are observed in breeds of divergent demographic and management history and are not found in any of the wild jungle fowl species. Here, we perform an across-breed association mapping analysis of SNPs using non-pedigree traditional Dutch heritage breeds to characterise the genetic diversity underlying rose comb and feathered leg. We refined the mapping interval of the rose comb phenotype (Gga7: 16.8-21.3 Mb) and that of the feathered leg phenotype at position 10.8-12.6 Mb on Gga15. We propose that strong artificial selection for rose comb has also occurred in breeds lacking phenotypic descriptions. This is the case for neo-bantams, the result of a cross between large fowl and true bantam breeds, which display most of the large fowl phenotypes. We found evidence of common genomic mechanisms underlying the feathered leg phenotype, as shown by the Tbx3 gene responsible of foot feathers development also in pigeons. The conservation of Tbx genes could indicate parallel evolution of a trait independently cultivated by breeders for fancy purposes since the early stages of domestication. Our study confirms the power of the across-breed mapping approach to characterise the genetic diversity underlying shared phenotypes among divergent domesticated populations.