

# Shrinking domestic chickens leads to increased genomic diversity

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**Abstract**—Since domestication, chickens (*Gallus gallus domesticus*) have experienced intensive anthropomorphic evolution and selection. In The Netherlands, bantamized variants have, over the past few decades, become popular alternatives to large fowls of traditional breeds, because they are easily housed in a hobby setting. Making these new bantam breeds is done by crossing a large breed with a small chicken breed, with subsequent selection to retain the exterior phenotype of the large donor breed and the small size of the bantam donor breed. However, while backcrossing for phenotype selection is threatening the long-term existence and genetic makeup of most neo-bantams, genetic exchange between breeders may also generate genetic diversity in these new breeds.

In this study, high-density single nucleotide polymorphism (SNP) arrays were used to characterize the genetic diversity and demographic history of 37 traditional Dutch chicken breeds, comprising large fowls ( $n=17$  breeds), true bantams ( $n=4$ ), and neo-bantams ( $n=16$ ). In particular, genetic relationship, admixture patterns, and level of inbreeding of neo-bantams were investigated to assess their contribution to the national chicken genetic diversity.

Large fowls and neo-bantams showed slightly similar polymorphism, though neo-bantams were the most inbred of the traditional breeds. Principal component analysis (PCA) and distance-based neighbor joining (NJ) tree revealed high genotypic similarities between large fowls and neo-bantams, while identifying signatures of recent genetic introgression during neo-bantams development. Population admixture analysis supported these findings, along with revealing on going changes in the bantamising trend of most neo-bantams. Traditional breeds showed remarkable variation in the run of homozygosity (ROH) profile, which was characterized by a low number of long homozygous segments. Despite that, long ROHs covered a significant proportion of the genome, particularly of neo-bantams.

The genetic variation we observed within breeds is explained by the metapopulation structure comprising small farmer-based breeding units, whose genetic diversity is strongly influenced by breeding practices and selection preferences of individual breeders and breed associations. Results show that a small flock size and gene flow of varying extent have divergent consequences on the genetic diversity of large fowls and neo-bantams. We observed that the bantamising trend has changed over time towards an increased development of new phenotypes or breeder's decision to establish new small size varieties. We showed that extensive gene flow contributes to the neo-bantams genetic diversity. However, sequential backcrossing derived from the lack of information of the degree of recent inbreeding. Hence, rapid

genetic changes are expected to particularly affect neo-bantams, due to their smaller founder size and unstructured selection for morphological standards.

The present study confirms the importance of using genotype data to inform genetic management and conservation priority of traditional breeds to preserve genetic diversity. We conclude that neo-bantams are reservoirs of emerging quantitative traits and phenotypes, suggesting that the bantamising breeding strategy can generate and maintain genetic diversity. However, such exceptional diversity can be preserved in the near future only with proper genetic information and structured breeding programmes.

**Keywords**—Bantam, chicken, molecular characterization, traditional breeds

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