

Case study 9

Analysis of genetic diversity within and between Dutch heritage chicken breeds to inform gene bank decision-making

Leading IMAGE partner: WU

Other IMAGE partners involved: WR

Other non-IMAGE partners and actors involved: Fancy breeders for sampling

IMAGE WP and Task: WP2 & WP4 / Task 2.3, Task 4.2

Objectives and expected results/output:

The aim of the study was to characterize the genetic diversity, demographic history, and inbreeding of all recognized Dutch heritage breeds and most of the bantam forms, in order to provide recommendations on their conservation and genetic management. In particular, we investigated the process by which the bantamised breeds are formed, their degree of inbreeding and potential contribution to the total Dutch chicken genetic diversity. Based on the high heterogeneity in diversity displayed by the breeds considered in the study, we recommend the national gene bank to consider all traditional breeds as separate entities, including the bantam forms. Moreover, to capture the available genetic diversity, a sufficient number of individuals within each breed should be sampled to preferably embrace all breed-specific morphological standards. Although our study shows that genotype data can make up for the lack of traditional sources of information that inform breeding program, a systematic collection of pedigree data and phenotypes is required to monitor changes in genetic diversity in poorly managed populations subjected to rapid changes in breeding preferences.

Material and methods

A total of 480 individuals from 37 traditional breeds of chicken originating from The Netherlands were used, comprising true bantams, large fowls, and bantam counterparts. Gene bank sperm of four individuals of the breed North Holland Blue was provided by the Centre for Genetic Resources, the Netherlands (CGN). Sample collection took place over 13 years (1998-2011) and included also phenotype collection (feather color and pattern). Expected and observed heterozygosity, minor allele frequency, and inbreeding coefficient were averaged across all loci and individuals within a population, respectively. Genetic relationships were investigated through a Principal Component Analysis. To investigate changes in bantamisation we performed a population genetic admixture analysis. Runs of homozygosity were used to investigate the demographic history of all traditional breeds.

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Bortoluzzi, C., Crooijmans, R.P.M.A., Bosse, M. et al. The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity. *Heredity* 121, 564–578 (2018) doi:10.1038/s41437-018-0072-3