

Quantifying temporal changes in genetic diversity and mutational load in recently managed populations

Chiara Bortoluzzi, Gwendal Restoux, Michèle Tixier-Boichard

Abstract

Breeding programmes are systematic and structure breeding schemes aiming at changing the genetic make-up of a population based on objective performance criteria. In commercial settings, such as in pig and poultry production, breeding programmes have full control over all breeding activities. However, in the case of animal species kept for companion or leisure purposes, control over the breeding program by the breed associations is often loose. In this study, we used whole-genome sequencing data from two traditional French chicken breeds, the Gasconne and Barbezieux, to study the impact of starting a breeding program on the genetic diversity and mutational load in a non-commercial setting. To do so, we sampled for each breed 15 founders and 15 individuals 10 generations after. We observed that over 10 generations, recent samples show an overall reduction in heterozygosity ($\Delta\pi$ Gasconne: -0.0005; $\Delta\pi$ Barbezieux: -0.0001), mainly due an increase in medium (0.1-3 Mb) and long (>3 Mb) size regions of homozygous genotypes (runs of homozygosity, ROHs). This trend was particularly pronounced in the Gasconne breed, as also confirmed by the increased genomic inbreeding coefficient (ΔF_{ROH} : 0.07). Medium ($r = 0.67$; $p\text{-value}$: 8.303^{09}) and long ROHs ($r = 0.88$; $p\text{-value}$: $<2.2^{-16}$) were also found to be particularly enriched for deleterious mutations, although the proportion of these damaging sites was lower than that of benign (i.e. synonymous, tolerant) mutations. Our results suggest that setting up a breeding program in a non-commercial setting can help ensuring the long-term genetic survival of a population if inbreeding is properly managed.