

Effect of population bottlenecks on patterns of deleterious variation in small captive populations

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Predictions about the consequences of a small population size on genetic variation are fundamental to population genetics. As small populations are more affected by genetic drift, purifying selection acting against deleterious alleles is predicted to be less efficient, therefore increasing the risk of inbreeding depression. However, the extent to which small populations are subjected to genetic drift considerably vary depending on the nature and time frame in which bottleneck occurs. Domesticated species are an excellent model to investigate the consequences of population bottlenecks on genetic and deleterious variation, because their history is dominated by known bottlenecks and intense artificial selection. Here, we use whole-genome sequencing data from 97 chickens representing 39 traditional fancy breeds to directly examine the impact of past and recent population bottlenecks on patterns of deleterious variation in small populations. Overall, we find that populations recently established from larger populations have a higher proportion of deleterious variants relative to populations that have been kept at small population sizes for a long period of time. We also observe that most deleterious variants in recently bottlenecked populations are found in long tracts of homozygous genotypes, suggesting that deleterious variants have increased in frequency because of inbreeding. Our results indicate that the timing and nature of population bottlenecks can substantially shape the deleterious variation landscape in small populations.