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No evidence of inbreeding depression despite a historical severe bottleneck in the endangered Bermuda petrel (*Pterodroma cahow*)

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Abstract

The Bermuda petrel *Pterodroma cahow* is an island endemic seabird that belongs to the Procellariiformes, one of the most endangered orders of birds. Historical records suggest a significant population size decline following human settlement in Bermuda, bringing the species to near extinction. Since the 1950s, the population has been recovering aided by the implementation of an ongoing conservation plan. However, it still faces several threats, and negative genetic effects resulting from that drastic decline are to be expected, including inbreeding and genetic drift. We studied genetic diversity and levels of inbreeding, and their effects on individual fitness and mating choice. We also tested for a genetic signature of the recent demographic bottleneck. For this, we analyzed variation in thousands of nuclear single-nucleotide polymorphisms derived from double digest restriction site-associated DNA sequencing and 1 mitochondrial gene (cytochrome oxidase I). The results revealed that the Bermuda petrel suffered a recent genetic bottleneck and shows low mitochondrial diversity compared with other petrel species. Conversely, nuclear diversity was similar to that of other endangered petrels. Inbreeding levels were not high overall, although some individuals were highly inbred. However, we found no evidence that individual inbreeding or relatedness between mates affected hatching success, or that mate choice is influenced by kinship in this very small population.

Key words: ddRADseq, hatching success, HFCs, population genomics, *Pterodroma*

Introduction

A critical topic in conservation biology concerns the prevalence of inbreeding in small and isolated populations, particularly those restricted to islands, since inbreeding can have profound consequences on the viability of such populations (Kennedy *et al.* 2014; Huisman *et al.* 2016). Mating between close relatives leads to a genome-wide increase of homozygosity in the offspring, a consequence of most alleles being identical-by-descent. The increase of homozygosity at loci carrying recessive deleterious alleles, or decrease in heterozygosity at loci with heterozygote advantage, has a negative impact on individual fitness, known as inbreeding depression (Charlesworth and Charlesworth 1999). Individual heterozygosity (ideally averaged over many loci) has been frequently used as proxy for inbreeding (Townsend and Jamieson 2013) and when significantly correlated with fitness components (such as breeding success or survival) may indicate the presence of inbreeding depression. The impact of inbreeding depression on wild populations is still not well understood (Kardos *et al.* 2016), as it remains challenging to measure individual inbreeding levels in natural populations due to lack of accurate pedigrees or, until recently, the availability of a sufficiently large panel of markers to estimate genome-wide heterozygosity (Huisman *et al.* 2016).

A significant correlation of heterozygosity across loci (i.e. identity disequilibrium [ID]) will provide an indication of whether any heterozygosity-fitness correlations (HFCs) detected in a population may be caused by inbreeding depression (Szulkin *et al.* 2010; Kardos *et al.* 2014). HFCs can be driven by genome-wide heterozygosity (general effect) when ID is present in the population or by specific loci that are under selection and directly influence fitness (local effect) (Szulkin *et al.* 2010).

Demographic history can influence variation in genome-wide heterozygosity in a population, especially in scenarios of severe genetic drift, bottlenecks, and admixture (Szulkin *et al.* 2010). A population bottleneck is a likely cause of inbreeding

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