Non-invasive sampling reveals low mitochondrial genetic diversity for a Critically Endangered island endemic species

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Abstract

As an island endemic with a decreasing population, the Critically Endangered Grenada Dove Leptotila wellsi is threatened by accelerated loss of genetic diversity resulting from ongoing habitat fragmentation. Small, threatened populations are difficult to sample directly but advances in molecular methods mean that non-invasive samples can be used. We performed the first assessment of genetic diversity of populations of Grenada Dove by a) assessing mtDNA genetic diversity in the only two areas of occupancy on Grenada, b) defining the number of haplotypes present at each site and c) evaluating evidence of isolation between sites. We used non-invasively collected samples from two locations: Mt Hartman (n=18) and Perseverance (n=12). DNA extraction and PCR were used to amplify 1,751 bps of mtDNA from two mitochondrial markers: NADH dehydrogenase 2 (ND2) and Cytochrome b (Cyt b). Haplotype diversity (h) of 0.4, a nucleotide diversity (π) of 0.4 and two unique haplotypes were identified within the ND2 sequences; one haplotype was identified within the Cyt b sequences. Of the two haplotypes identified; the most common haplotype (haplotype A = 73.9%) was observed at both sites and the other (haplotype B = 26.1%) was unique to Perseverance. Our results show low mitochondrial genetic diversity, a non-expanding population and clear evidence for genetically isolated populations. The Grenada Dove needs urgent conservation action, including habitat protection and potentially augmentation of gene flow by translocation in order to increase genetic resilience and diversity with the ultimate aim of securing the long-term survival of this Critically Endangered species.

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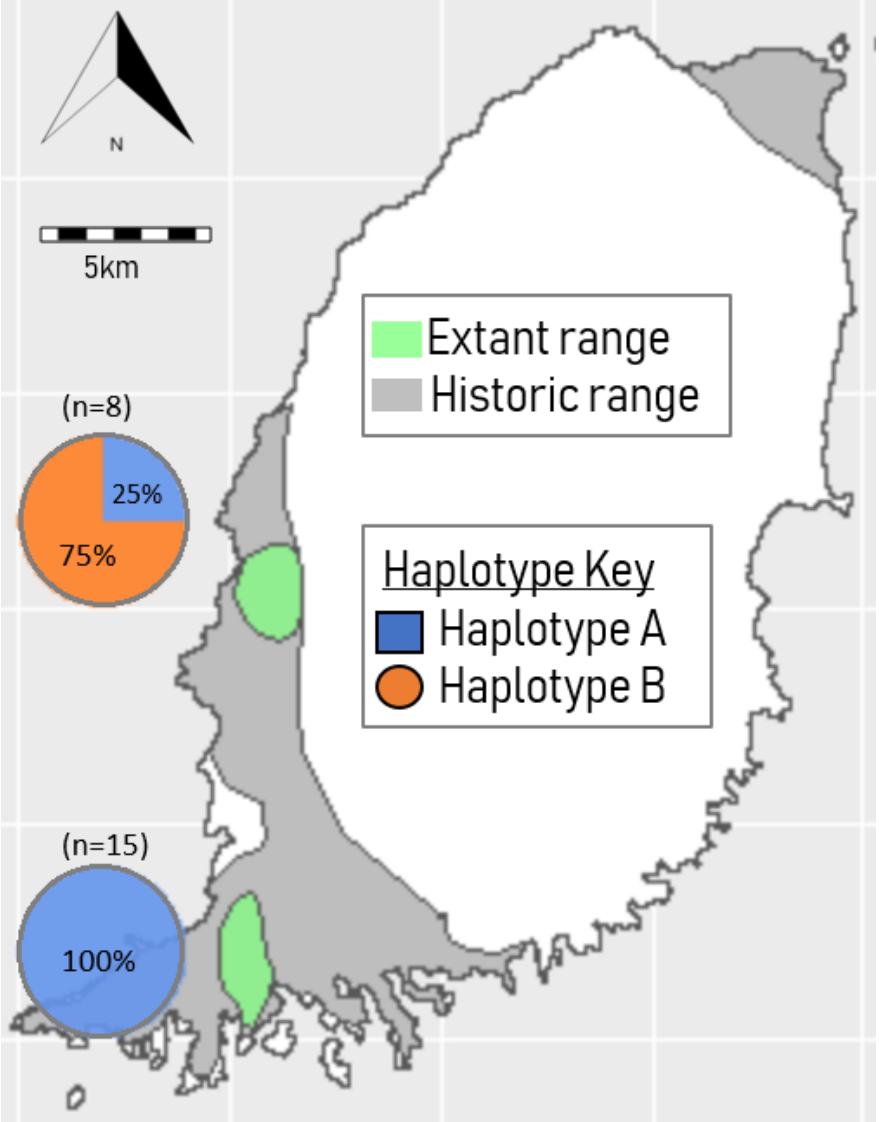

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