



Snares Crested penguins (*Eudyptes robustus*) – photo credit Derek Lightbourne

Assessing the genetic health of crested penguins

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Past surveys have suggested that all crested penguin (*Eudyptes*) species are declining, despite three of the eight species being endemic to New Zealand and its sub-Antarctic islands. Recently, several studies have revealed important aspects of species biology and conservation implications in other New Zealand penguins (Little blue and Yellow-eyed). The genetic health of crested penguins however, is very poorly understood.

This project will assess genetic proxies for population size and provide new insights into the genetic health (including gene flow, genetic diversity, inbreeding and isolation by distance) of the three declining New Zealand endemic crested penguin species; Fiordland/Tawaki (*E. pachyrhynchus*), Snares (*E. robustus*) and Erect crested (*E. sclateri*).

We will use Diverse Arrays Technology (DArT-Seq), a cost-effective DNA sequencing technique that generates several thousand genetic markers per individual, allowing comparison within and between species. DArT-Seq is a powerful method that can pinpoint candidate genes important for adaptation to climate change. Such knowledge is integral for projecting the longevity of threatened species, such as crested penguins. High quality blood samples were kindly collected and made available to this project by Birds NZ members, the Tawaki project, NIWA and Te Papa Tongawera, under DOC collection permits.

The project proposed here will provide critical data for New Zealand endemic crested penguins, feeding into future conservation management strategies. Birds NZ have provided funding for genomic sequencing that will include samples from all three endemic crested penguin species.