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A severe predator-induced population decline predicted for endangered, migratory swift parrots (*Lathamus discolor*)

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ABSTRACT

Identifying the impact of introduced predators on endangered prey populations is critical for conservation management. Population viability analysis (PVA) becomes a valuable tool for quantifying such impacts when high quality life history data are available but, surprisingly, predictions from PVA of future population decline have seldom been used directly to assess conservation status. Here we synthesise new research on the unusual life history of the endangered swift parrot *Lathamus discolor*, an austral migrant that breeds in Tasmania, Australia. Swift parrots are challenging to monitor because (1) spatio-temporal fluctuation in food availability causes them to select entirely different breeding sites each year over a 10,000 km^2 range, and (2) they suffer high but variable rates of predation from introduced sugar gliders *Petaurus breviceps* depending on where they breed. 50.9% of nesting females on the main island of Tasmania were killed by sugar gliders while incubating eggs, but there was no predation from this source on offshore islands. Over four years 16.5% (0–29%) of the population bred on offshore islands. We use PVAs to examine the likely extent of future population decrease due to sugar glider predation, and demonstrate that the remaining swift parrot population is likely to decrease by 78.8–94.7% (mean over four models = 86.9%) over only three generations (12–18 years). Our models offer a rare example of the use of PVAs for assessing impending population decline and conservation status in species that are challenging to monitor. In this case they support a change of status for swift parrots from "Endangered" to 'Critically Endangered' under IUCN criteria.

1. Introduction

In anthropogenically altered landscapes, predators can have serious consequences on the viability of prey populations. Globally, introduced predators are a major driver of extinction (Clavero and Garcia-Berthou, 2005; Salo et al., 2007), but native predators can also have serious effects (Millus et al., 2007; Roemer et al., 2001). In modified landscapes, multiple threatening processes often occur in tandem (Brook et al., 2008), so that synergistic interactions between different threats (e.g., predation and habitat loss) accelerate prey population declines. Island endemics are particularly vulnerable to predators and have suffered high rates of extinction following the introduction of predators to their habitats (Duncan and Blackburn, 2007).

Identifying the causes of mortality and understanding their impacts on prey population viability is critical to successful conservation management (Lavers et al., 2010; Moorhouse et al., 2003; Whitehead et al., 2008). These impacts must be considered in the context of life history parameters (Bode and Brennan, 2011; McLoughlin and Owen-Smith, 2003). Detailed life history data are not available for most species (Morais et al., 2013; Norris, 2004), which is a problem for understanding how best to arrest decline in threatened populations (Christensen et al., 1996; Martin et al., 2012; Regan et al., 2005). However, when life history data are available, tools like population viability analysis (PVA) become valuable for understanding how animal populations might respond to environmental change (e.g., inflated mortality or habitat loss) and to identify where the best management options lie (Crouse et al., 1987; Drechsler et al., 1998). PVAs are computer simulation models that use demographic data to make quantitative predictions about population size over time and the likelihood of extinction (Beissinger and Westphal, 1998). PVAs are recognised as a potentially powerful tool in the assessment process for species conservation status (IUCN, 2012) and have been used to develop management strategies for several species (Crouse et al., 1987; Heinsohn et al., 2004). Somewhat surprisingly, predictions from PVA of future population decline based on current demographic

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data and the impact of threatening processes have seldom been used directly to assess conservation status.

Here we synthesise new research on the life history and distribution of endangered swift parrots *Lathamus discolor* (BirdLife International, 2008) and assess their population trajectory and conservation status using PVA. Swift parrots are austral migrants that breed on the large island of Tasmania to the south of continental Australia and over-winter in the south-east of the Australian mainland. They have a contentious conservation history (Allchin et al., 2013), are the subject of an Australian National Recovery Plan, and analysis of population viability has been identified as a key recovery action (Saunders and Tzaros, 2011). Until recently, few detailed demographic or ecological data have been available to help in understanding their population trajectory or conservation status. However recent research has revealed two important details about swift parrot ecology. First, spatio-temporal fluctuation in food availability drives unpredictable annual movements by swift parrots, causing the population to select entirely different breeding sites each year across a breeding range of approximately 10,000 km^2 (Webb et al., 2014). Second, nesting swift parrots suffer intense predation by sugar gliders *Petaurus breviceps* (Stojanovic et al., 2014b). Sugar gliders are native to continental Australia, but there is evidence to indicate that they were introduced to Tasmania as early as the 19th century (Gunn, 1851; Lindenmayer, 2002; Munks et al., 2004; Rounsevell et al., 1991). Webb et al. (2014) and Stojanovic et al. (2014b) highlighted that both the habitat requirement of swift parrots and the threatening processes occur over unusually complex spatio-temporal scales. Importantly, sugar gliders are present at all swift parrot breeding sites thus far monitored on the main island of Tasmania, but are absent from two smaller offshore islands (Bruny and Maria Islands) where the swift parrots sometimes breed (Fig. 1).

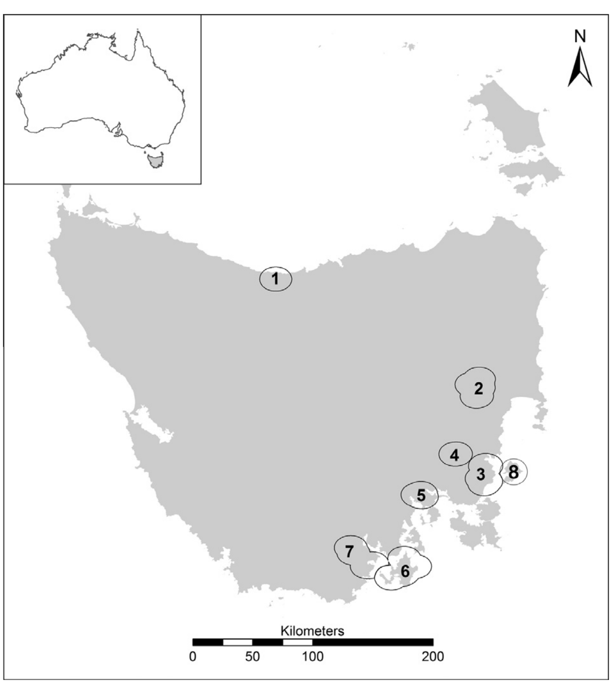

Fig. 1. Map of the study area, showing the regions where swift parrot nests were monitored in eastern Tasmania. The inset shows Tasmania (shaded) in relation to continental Australia. The regions and years in which they were utilised for nesting by swift parrots are: (1) Devonport; 2011, 2013 (2) the Eastern Tiers; 2011, 2013 (3) Wielangta; 2010 (4) Buckland; 2010, 2013 (5) the Meehan Range; 2010 (6) Bruny Island; 2011, 2012, 2013 (7) the Southern Forests; 2012, and; (8) Maria Island; 2010, 2011, 2012, 2013. Sugar gliders are known to occur in all regions except Bruny Island (6) and Maria Island (8).

In this study, we build on Stojanovic et al. (2014b) and Webb et al. (2014) by presenting PVAs incorporating up-to-date information concerning the highly variable and site-specific reproductive success and mortality of swift parrots. We specifically examine: (1) the impact of sugar glider predation on swift parrot population viability, and; (2) whether the current listing of swift parrots as 'Endangered' is still appropriate given these advances in knowledge. Our data and analyses are of broad importance because they show how PVA can be used for predicting severe population decline, and early assessment of conservation status, in species that are challenging to monitor because they are mobile, cryptic or uncommon across a large range.

2. Materials and methods

2.1. Study species

The swift parrot is a small (60–80 g), migratory bird whose main food is the nectar from several patchily distributed ephemerally flowering *Eucalyptus spp* (Higgins, 1999). Apart from a sea crossing to arrive at or depart from their Tasmanian breeding grounds, spatiotemporal variation in food availability causes the timing, direction, distance and destination of their movements to be highly irregular and unpredictable. Their over-wintering range is approximately one million square kilometres, and they can utilise *Eucalyptus* forest over approximately 10,000 square kilometres of eastern Tasmania for breeding (Saunders and Heinsohn, 2008; Webb et al., 2014). Swift parrots nest in tree cavities in the east coast forests of the Tasmanian mainland and nearby offshore islands (Stojanovic et al., 2012; Webb et al., 2012) within the distribution of their primary food trees (blue *Eucalyptus globulus* and black gums *Eucalyptus ovata*) (Brown, 1989). On the Tasmanian mainland where sugar gliders occur, Stojanovic et al. (2014b) reported that 83% of swift parrot nests failed due to predation compared to no losses from predation on glider-free offshore islands. Most cases (80.0%) of sugar glider predation at nests also resulted in the death of the adult female parrot in addition to her eggs. In this analysis we include an additional year of mortality data that has become available since the analysis presented in Stojanovic et al. (2014b).

Swift parrots rarely nest in the same places between years, and the population usually moves *en masse* to breed in entirely new localities (see Fig. 1 for inter-annual variability of breeding site choice). Thus they are likely to be exposed to different rates of mortality between years depending on whether or not sugar gliders are present. By monitoring sites spread across the entire Tasmanian breeding range of the swift parrot, Webb et al. (2014) showed that the proportion of birds nesting on islands (low predation habitat) versus the Tasmanian mainland (high predation habitat) varies annually. There is no evidence to suggest that the island breeding birds comprise a separate population. The proportion of the population that breeds on islands varies greatly between years because patterns of settlement across the study area by swift parrots mirrors the spatial configuration of food in a given year (Webb et al., 2014). Here, we use an additional year of spatial breeding data (2013/14) that has become available since Webb et al. (2014).

2.2. Mortality and fledging data

Swift parrot mortality and nesting success were estimated from the sample of 63 nests used in the mark analysis published by Stojanovic et al. (2014b). We updated these results by including one additional year of nest monitoring ($n = 48$ nests) in the analysis (i.e., four consecutive breeding seasons, 2010/11, 2011/12, 2012/13, 2013/14). We used the same analytical approach outlined in