



Conservation genomics identifies impact of trade in a threatened songbird



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ABSTRACT

In the last two decades, unsustainable levels of wildlife trade have led to an unprecedented biological crisis. Southeast Asia has become an epicentre for wildlife trade in general and specifically for the cage-bird trade, resulting in numerous regional extinctions. To assess the impact of regional extinction on the loss of genetic diversity in affected cage-birds, we obtained > 18,000 genome-wide markers across 60 Southeast Asian samples of the white-rumped shama (*Copsychus malabaricus*), a prized songbird that has gone extinct across wide swathes of its Southeast Asian range following heavy poaching. High levels of genomic uniformity across its mainland Southeast Asian range indicate that future reintroductions of birds from regions with less poaching could help bolster populations in regions with intense poaching pressure. Genomic assignment tests demonstrate that birds in the only Sundaic country with strict enforcement of poaching bans, Singapore, are a mosaic of both native populations and escaped cage-birds of mostly peninsular Malaysian origin, indicating that inadvertent reintroductions of caged shamas have led to the recovery of a local population that was nearly extinct and now constitutes a safe haven for the subspecies *tricolor*. Our study underscores the potential of genome-wide SNPs in identifying implications of trade on wildlife populations.

1. Introduction

Birds are amongst the most highly exploited vertebrates in the global wildlife trade (Bush et al., 2014). Their exploitation for the trade has resulted in the decline and decimation of populations worldwide (Collar et al., 1997; Eaton et al., 2015). Southeast Asia is characterized by its exceptional avian diversity (Dickinson and Christidis, 2014) but is at the same time the epicentre of the cage-bird trade (Sodhi et al., 2011). Birds in the region are commonly poached for both legal and illicit trade (Sodhi et al., 2011) to feed the burgeoning demand of hobby birdkeepers, especially in Indonesia (Jepson and Ladle, 2005; Shepherd et al., 2013). The trade has already caused extinctions and near-extinctions in the wild with regard to Sundaic bird species and subspecies, such as the Bali starling (*Leucopsar rothschildi*), black-winged myna (*Acridotheres melanopterus*), javan green magpie (*Cissa thalassina*), and the white-rumped shama (*Copsychus malabaricus*) (van Balen et al., 2000; Sodhi et al., 2011; van Balen et al., 2013; Chng et al., 2015; Eaton et al., 2015).

Known for its melodious song, the white-rumped shama is amongst the most popular and prestigious songbirds in the Southeast Asian cage-bird trade (Nash, 1993). The species has been reported to be in steep

decline across the Sundaic region and is believed to be extirpated on certain islands such as Java due to extensive poaching for the cage-bird trade (Shepherd et al., 2004; Eaton et al., 2015; Eaton et al., 2016). However, the dwindling numbers have only occurred in the last two to three decades, as the species was previously recorded as common throughout Southeast Asia (Bucknill and Chasen, 1927; Smythies, 1986; Thomas and Poole, 2003; Collar, 2005), especially in Indonesia (MacKinnon and Phillipps, 1993). Despite the sharp decrease in population, the species is currently still listed as Least Concern (BirdLife International, 2013) due to its vast distribution that ranges from the Indian subcontinent through mainland Southeast Asia and Sundaland (Eaton et al., 2016; Gill and Donsker, 2016) (Fig. 1a). The severe decline of wild shama populations in recent decades has led to proposals to list it on the Convention on International Trade in Endangered Species (CITES) appendix II or III to facilitate monitoring and control of the international trade of the species (Nash, 1993; Shepherd et al., 2004; Lee et al., 2016). Likewise, as many white-rumped shama subspecies are highly threatened by the trade, the species was considered to be amongst the top 12 priority birds for conservation in Asia (Lee et al., 2016).

The island nation of Singapore, located at the southern tip of the

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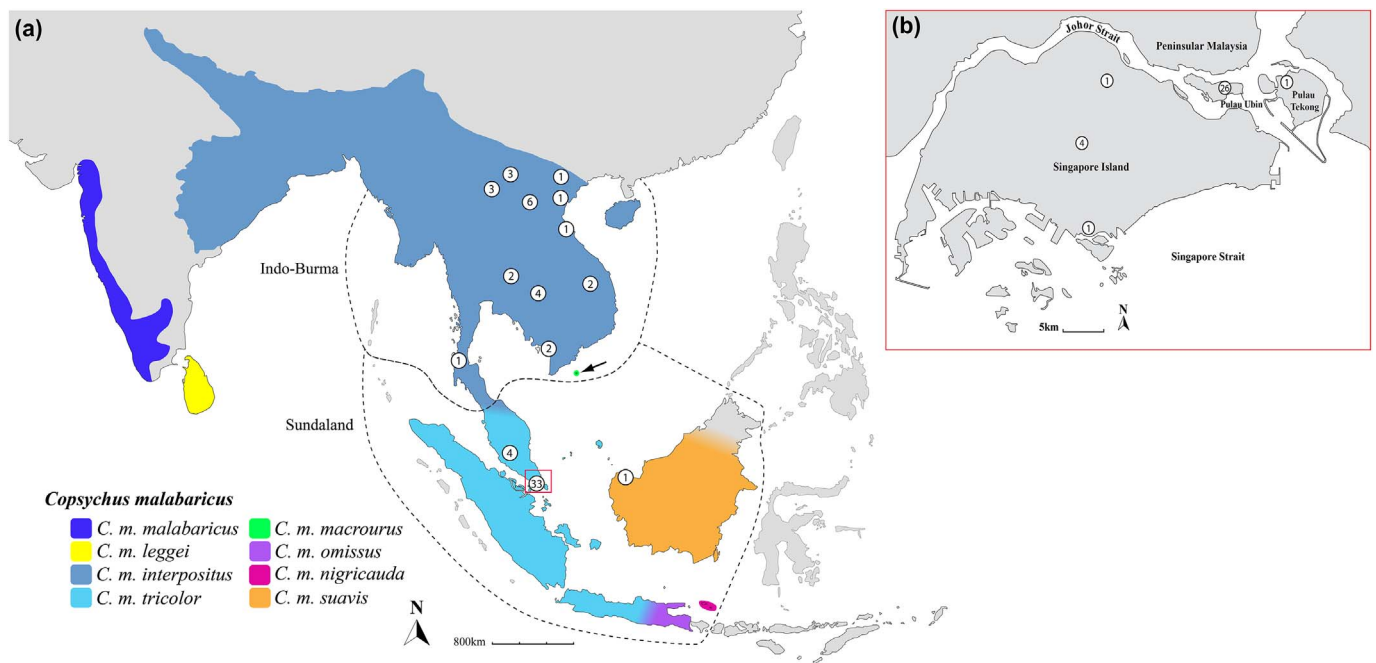


Fig. 1. (a) White-rumped shama (*Copsychus malabaricus*) distribution with ranges of eight subspecies indicated (Eaton et al., 2016; Gill and Donsker, 2016); Indonesian range according to Eaton et al. (2016). Sampling localities and number of individuals are indicated using white circles. The Southeast Asian range is further demarcated into the Indo-Burma and Sundaland regions using stippled lines (Mittermeier et al., 2004). Location of Singapore indicated by red rectangle. (b) Map of Singapore with sample locations and number of individuals. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Malay Peninsula (Fig. 1), is sometimes overlooked in conservation efforts of endangered terrestrial Sundanic animals because of its small size (719.1 km²) and heavy urbanization (Corlett, 1992). The small extent of remaining natural habitat in Singapore has meant that few species of conservation importance are represented here in significant numbers. However, as opposed to previous decades in which forest loss was the main driver of extinction, the emergence of wildlife trade as an important extinction agent has possibly rendered Singapore of critical importance, given that illegal poaching is low in this heavily urbanized country. The white-rumped shama is currently a local resident on the main island of Singapore and on the two offshore islands of Pulau Ubin and Pulau Tekong (Wang and Hails, 2007) (Fig. 1b). In the past, the species experienced a severe population decline, and prior to 1983 shamas were not observed on Singapore Island for many years (Lim, 1992; Wang and Hails, 2007), although they continued to be seen on Pulau Ubin and Pulau Tekong. Recent inventories have reported shama populations to be increasing again (Lim and Lim, 2009; Lim and Yong, 2011). However, it remains uncertain if the observed increase on Singapore Island has been due to the recovery of the native Singaporean population or releases from the cage-bird trade as shamas are known to have escaped into the local population (Lim, 1992; Collar, 2005; Wang and Hails, 2007).

With the introduction of white-rumped shamas from the cage-bird trade, there is a concern that native populations may suffer an infiltration of non-native genotypes. Individuals that escape from captivity may have been selectively bred for their vocal capabilities as well as aesthetic features (e.g. build and tail length) (Collar et al., 2012). Furthermore, shamas in the trade have also been brought into Singapore from elsewhere in Southeast Asia – Indonesia, Malaysia, Thailand (Nash, 1993), and Vietnam (ICA, 2015) – and may be genetically different from the Singaporean population.

Previous studies have investigated the genetic structure of the white-rumped shama and revealed genetic differentiation within the species (Lim et al., 2010; Lim et al., 2011). However, these studies have utilised only a single mitochondrial gene, which precludes the elucidation of fine scale population genetic structure. In this study, genome-wide single nucleotide polymorphisms (SNPs) from genomic reduced-

representation libraries were used to understand the population genomic patterns of connectivity and differentiation of the white-rumped shama in Southeast Asia in general and the populations in Singapore in particular. A specific aim was to detect whether individuals introduced from the cage-bird trade, with origins from elsewhere in Southeast Asia, are present in the wild Singaporean populations.

2. Material and methods

The usage of the terms Sundaland and Indo-Burma corresponds with Mittermeier et al. (2004)'s definition of biodiversity hotspots. The former region encompasses Peninsular Malaysia, Singapore, and the Greater Sunda Islands of Indonesia, while the latter region includes Cambodia, Laos, Myanmar, Thailand, Vietnam, and parts of eastern India and southern China (Fig. 1a). White-rumped shama species limits follow Eaton et al. (2016) for Sundaland and Gill and Donsker (2016) for the remaining range, with the insular taxon (*melanurus*) from the West Sumatran islands separated as an independent species and not further considered herein.

2.1. Sample collection

A total of 69 white-rumped shama samples, both breast muscle and blood, were obtained from across most of the Southeast Asian parts of the species range (Fig. 1, Supplementary material S1). Thirty-four of these refer to blood samples obtained from mist-netting activities across Singapore following the protocol of Sadanandan and Rheindt (2015) and in accordance with Institutional Animal Care and Use Committee regulations (B13-4738), whereas 33 constitute region-wide samples sourced from museum collections (Fig. 1, Supplementary material S1). Two additional breast muscle samples were collected from a captive individual from Jurong Bird Park (Singapore) and a wild individual found on the main island of Singapore (JBP002; Supplementary material S1). The latter was kindly contributed by a donor to Jurong Bird Park. Of the 34 blood samples from Singapore, four pertain to captive shamas from Jurong Bird Park that were mist-netted in open-flight

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