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***Passeromyia indecora* causes hematophagous myiasis in captive-bred domestic pigeon (*Columba livia domestica*) squabs.**

Larval instars of the native dipteran *Passeromyia indecora* (Walker) (Diptera: Muscidae) induce subcutaneous hematophagous myiasis in nestling birds (Couri & Carvalho 2003). Infestations are often highly pathogenic, leading to host mortality or reductions in growth (Skidmore 1985; Poiani 1993). Associations between this generalist obligate parasite and several avian hosts have been documented (Pont 1974), but we report the first case from a captive-bred introduced species, the common pigeon, *Columba livia domestica* Gmelin. Incomplete larval taxonomy make the identification of *Passeromyia* Rodhain and Villeneuve challenging as current morphological descriptions (Skidmore 1985) do not allow for unequivocal species discrimination. The use of DNA barcoding provides an alternative diagnostic tool in the absence of a morphological-based approach and when rearing larvae is not feasible.

In mid spring 2015, myiasis in a two-day old, captive-bred pigeon squab was reported from a property in the dry tropics region of Bluewater, Queensland (19°09′37.7″S 146°33′57.7″E). A cluster of tiny maggots were collected from inside a puncture wound on its back approximately 2 mm in diameter and from inside both ears. Beneath the infested areas, the skin was swollen and abraded. Over the ensuing fortnight, maggots at various developmental stages were removed daily from the same individual and an additional infested squab subcutaneously at the base of new growing wing feathers. Several of the specimens collected from both squabs were submitted in ethanol to the laboratory for identification. Voucher specimens were lodged at the Queensland Museum (one first instar larva T207468, one third instar larva T207469).

Larvae collected from the two day old pigeon squab were identified as first instars of *Passeromyia* based on a feature unique to the genus at this life-stage: six long perispiracular filaments located dorsally (Skidmore, 1985). Larvae obtained from the same bird and a second squab over subsequent days were considerably larger and more mature. These were identified as third instar larvae due to their size (10 mm – 15 mm) and cephaloskeletal structure (Skidmore 1985). However, establishing a species-level identification of the specimens was not possible using the incomplete taxonomic descriptions and figures published by Skidmore (1985). While the larval life-history (sub-cutaneous blood-feeders) and geographic location (Queensland) from which our specimens were collected were indicative of *P. indecora*, it was important to establish a firm species identification. Molecular confirmation was therefore sought through the use of DNA barcoding.

DNA was isolated from one of the unidentified third instar larvae and from an adult fly of *Passeromyia longicornis* (Macquart) reared from a larva collected from a forty-spotted pardalote (*Pardalotus quadragintus* Gould) nestling on North Bruny Island, Tasmania (43°05′44.0″S 147°21′31.0″E) in October 2014. We performed standard PCR and sequencing using TY-J-1460 and C1-N-2191 primers according to Grzywacz *et al.* (2017) to obtain standard barcode fragments of mitochondrial cytochrome c oxidase subunit I. DNA sequences were blasted against those deposited in GenBank. The sequence we obtained for the unidentified larva (GenBank accession no. KY937945) was 100% identical with the sequence referring to *Passeromyia indecora* (GenBank accession no. KJ510635) (Kutty *et al.* 2014) and differed by more than 5% from the sequence we obtained for *P. longicornis* (GenBank accession no. KY937944). On this basis, we concluded that the material collected from the pigeon squabs were immature stages of *P. indecora*.

In Australia to date, *Passeromyia*-induced myiasis has been reported almost exclusively from wild native hosts (Pont 1974; Armstrong & Pyke 1991; Poiani 1993; Edworthy 2016, but see Green & Munday 1971). Here, we report the first infestation from an introduced host in a domestic setting, and provide the first record, to our knowledge, of a species of *Passeromyia* infesting a member of the host order Columbiformes. The prevalence of this group of highly adaptive, generalist parasites is not well known due to the scarcity of recent published accounts (Armstrong & Pyke 1991; Poiani 1993; Levot 2008; Edworthy 2016). For *P. indecora*, few data have accrued since early collections referenced in Pont's (1974) revision of the genus, although historical records show a widespread distribution across all states in Australia except Tasmania (Pont 1974). Our case is the first to be documented in Queensland for several decades and extends the host range for this dipteran parasite. The pathogenic effects of myiasis in these captive-bred pigeons were undetermined as both squabs were killed by an unrelated cause immediately after the collection of larvae. No further reports of myiasis were made following the outbreak and the implementation of control measures (e.g. burning of nest material).

From a biosecurity standpoint, the accurate and timely diagnosis of myiatic agents is important to ensure effective on-farm treatment and exclude exotic organisms. Despite the fact *Passeromyia* consists of only five species (two of which occur on mainland Australia and one in Tasmania), the larval taxonomy remains incomplete and inadequate for high-level diagnostics. Descriptions of the first instar stage are particularly deficient with only one of five species, *P. heterochaeta* (Villeneuve) documented (Skidmore 1985). Immature stage descriptions of *P. indecora* are limited to the second instar, derived from two specimens collected from a red-capped robin, *Petroica goodenovii* Vigors & Horsfield in NSW and some features of the third instar cephaloskeleton derived from seven puparia collected from a fairy martin, *Petrochelidon ariel* (Gould) in NSW (Skidmore 1985). The morphology of adult and pupal stages of *Passeromyia* are more comprehensive (Skidmore 1985), but rearing larvae is not always practical. DNA sequence data are available for *P. indecora* (Kutty *et al.* 2014) but molecular data for the genus are otherwise lacking. Expanding the taxonomy of immature stages of Australia's sole genus of avian myiasis-causing flies would greatly increase diagnostic capacity during outbreaks among captive-bred or production birds. An expanded molecular database would also provide an additional resource for diagnosticians.

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