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Toxic toad invasion of Wallacea: A biodiversity hotspot characterized by extraordinary endemism

Invasions of poisonous species can cause rapid population declines among native fauna because predators are naïve and often vulnerable to these toxins. The recent invasion of Madagascar by the poisonous Asian common toad, *Duttaphrynus melanostictus*, has sparked international attention (Kolby, 2014) as well as research and conservation efforts to predict the climate suitability of Madagascar for the invasive toads (Pearson, 2015; Vences et al., 2017), pinpoint the origin of the invasive lineage (Vences et al., 2017; Wogan, Stuart,

Iskandar, & McGuire, 2016), determining the toads' distribution, and educating local communities (Andreone, 2014). While the invasion in Madagascar has received much attention, an invasion of this same toad species on the islands of Wallacea in eastern Indonesia is ongoing but virtually unrecognized.

Wallacea is a distinct biogeographic realm characterized by thousands of oceanic islands harboring a highly endemic faunal assemblage (Sodhi, Pin Koh, Brook, & Ng, 2004). Most Wallacean islands

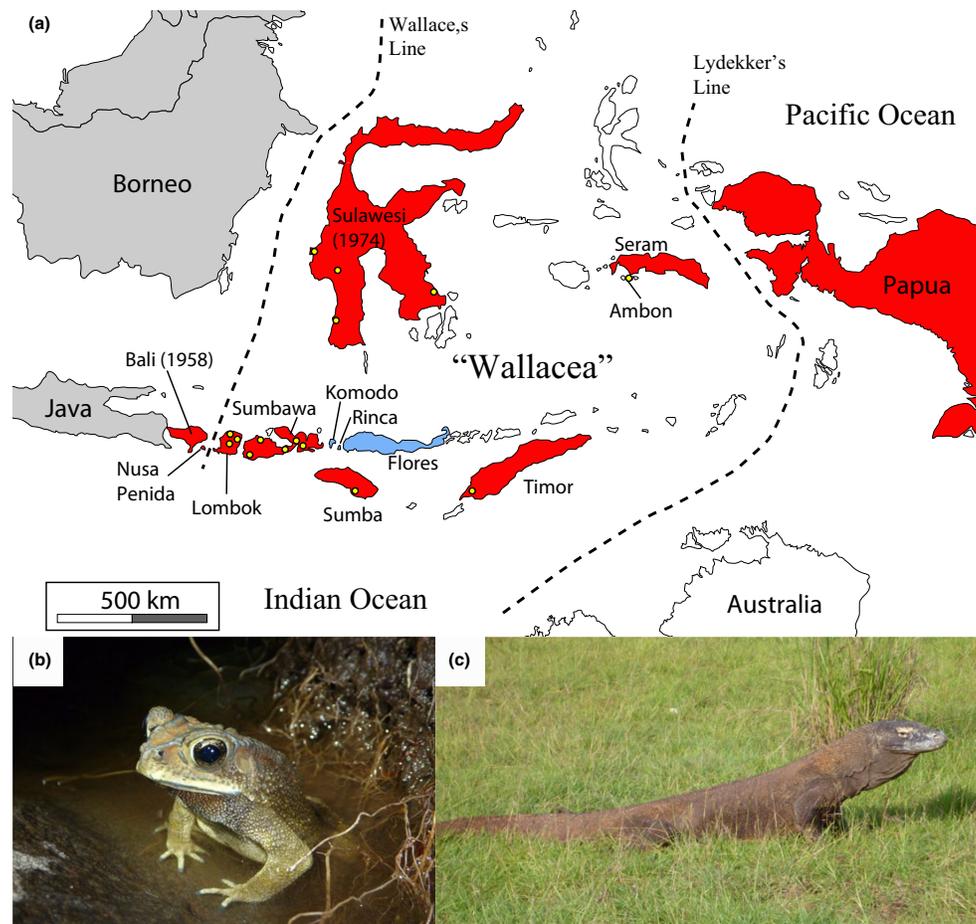


FIGURE 1 (a) Map of insular Southeast Asia depicting the range of *Duttaphrynus melanostictus*. Gray-shaded islands represent native range of *D. melanostictus*, red-shaded islands represent known introduced areas (with the year of introduction for some), and blue-shaded islands represent the range of *Varanus komodoensis*. Yellow dots represent sampling localities for genetic analysis. (b) A *D. melanostictus* from Lombok Island. (c) A *V. komodoensis* from Rinca Island

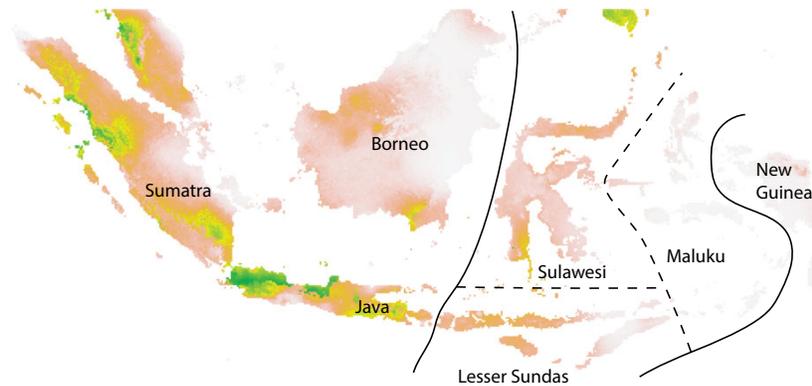


FIGURE 2 Environmental niche model of the Sunda Islands clade of *Duttaphrynus melanostictus* as defined by Wogan et al. (2016). Shades in green and yellow represent high suitability, and light colors represent low suitability

do not contain native toads, and because their fauna has not co-evolved with toads, many species are not adapted to deal with the toad toxins. This is just one more threat to the biodiversity of the Wallacean region, which is already facing an impending disaster due to deforestation and forest conversion, fires, hunting, and many other pressures (Sodhi et al., 2004). Asian common toads are native to SE Asia and the Sundaic Islands of Java and Sumatra, but presumably through human-mediated actions have recently (<50 years) invaded many of the islands of Wallacea including Sulawesi, Lombok, Sumbawa, Sumba, Timor, and others (AmphibiaWeb, 2016; Reilly et al., 2016). Based on limited sampling of invasive toads within Wallacea, Wogan et al. (2016) found that the point of origination was the Sundaic Islands, which suggests that local movement between islands has facilitated the spread of the toads.

With large mammalian predators absent from most of the Wallacean islands, the apex predators are varanid lizards and large snakes, both of which we have observed either dead or incapacitated in the field with *D. melanostictus* in their mouth or stomach (S. Reilly pers. obs.). Varanid lizards that are naturally sympatric with toads have evolved to cope with the potent toad toxins, while varanid lizards that are not naturally sympatric are highly susceptible to the toxins (Ujvari et al., 2013). The iconic Komodo Dragon (*Varanus komodoensis*), which has a restricted geographic range and small population sizes, is extremely susceptible to toad toxin (Ujvari, Mun, Conigrave, Ciofi, & Madsen, 2014). Recent survey work has now documented the first report of Asian common toads on the islands immediately west (Sumbawa) and south (Sumba) of the islands comprising the Komodo Dragon's range: Komodo, Rinca, and Flores (Figure 1). High levels of interisland boat traffic between Flores and the neighboring islands of Sumbawa, Sumba, and Timor pose a risk for the introduction of toads.

To establish some baseline data on the Wallacean invasion, we generated genetic data for additional invasive populations and then used our findings as a basis for building a climate suitability model. Our expanded sampling within Wallacea allows us to test if all of these populations share a common origin from within the Sundaic Islands. We sequenced mitochondrial DNA for 48 individual toads from six major islands throughout Wallacea (Figure 1; see Appendix S1 for detailed methods). We found that all of the newly

sequenced individuals shared a single haplotype with origins from within the Sundaic Islands of Java and Sumatra. To assess the potential climatic suitability for the invasive toads throughout Wallacea, we built an environmental niche model using 86 records of the insular clade from within their native range. We then projected the model to Wallacea (see Appendix S1 for detailed methods) so we could assess the potential range of invasive toads. We found that there is high predicted suitability throughout Wallacea, particularly in Sulawesi and the Lesser Sunda Islands, including the islands that encompass the range of the Komodo Dragon (Figure 2). This suggests that if the toads do indeed make it to these islands, that they will have an environment in which they could become established.

Our findings suggest that establishment of invasive toad populations throughout the Lesser Sunda Islands and within the range of highly endemic species such as the Komodo Dragon is not only possible, but likely unless specific efforts are made to prevent the further invasion of these toads throughout Wallacea. We recommend that increased protections are needed to prevent the establishment of toads on uninvaded islands for the sake of Komodo Dragon persistence. Furthermore, we need to begin monitoring the impacts of these introduced toads on the native predators on Wallacean islands.

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