

Sunda shelf project

## **GRADUAL ENVIRONMENTAL CHANGE *VERSUS* SINGLE CATASTROPHE - IDENTIFYING DRIVERS OF MAMMALIAN EVOLUTION**

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The diversity of life is not evenly distributed across the planet. A few areas, so-called biodiversity hotspots, harbour the majority of all species. Although this pattern is well-described, a central question of evolution remains unresolved: *What are the drivers shaping high biodiversity, particularly in tropical rainforests?* Answering the question was impossible thus far, because at least one of three essential components was not available for study.

These are:

1. a fossil record as logfile of species' histories,
2. past climate data, needed to reconstruct changes in habitats, and
3. detailed knowledge about the ability of species to adapt to changing environments.

Recent methodological advances enable us now for the first time to investigate these three components simultaneously in a biodiversity hotspot where they are all attainable: the Sunda Shelf in Southeast Asia (SE Asia). By combining climate reconstructions, molecular genetic data and species distribution data from the Late Pleistocene (126-13.7 thousand years ago) to the present we can evaluate the impact of two key drivers shaping biodiversity: gradual climate change *versus* a single catastrophic event. The results will hopefully also allow us to assess the long-term consequences of the current (man-made) biodiversity crisis.

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### Project outcome (abstract of final report)

The project was set out in a biodiversity hotspot: the Sunda Shelf in Southeast Asia (SE Asia) and the bordering continental mainland. By combining climate reconstructions, molecular genetic data analysis and species distribution data from the Late Pleistocene to the present (based on contemporary habitat occupancy) we wanted to evaluate the impact of two key drivers shaping biodiversity: gradual climate change *versus* a single catastrophic event, which in SE Asia was the Toba super-volcano eruption ~73.5 thousand years ago. When possible, we studied pairs of sister species (as they derived from a common ancestor) that had either taken different ecological trajectories during speciation (generalist vs. specialist) or were now allopatrically distributed.

As a final conclusion we can state that evolutionary processes were more complex and more intertwined than envisioned in our hypotheses. There was no general pattern applicable to all species we had studied. Instead, we found phylogeographic histories and distributions to be species-specific and to have been impacted by either gradual climate change, single catastrophic events, or even additional barriers.

Our hypotheses predicted that the distribution of generalist species (and differentiation among their populations) under graduate climate change should be determined by adaptability only. Thus, they should be distributed across the Sunda shelf, because gene-flow among populations should have been possible during glacial periods (when low sea levels led to the emergence of Sundaland – a large landmass connecting all Sunda Islands and Thai/Malay Peninsula). This, however, was not what we found.

We regularly found clear distinctions into Sunda and continental mainland clades within species, but as dating revealed, surprisingly with different histories.

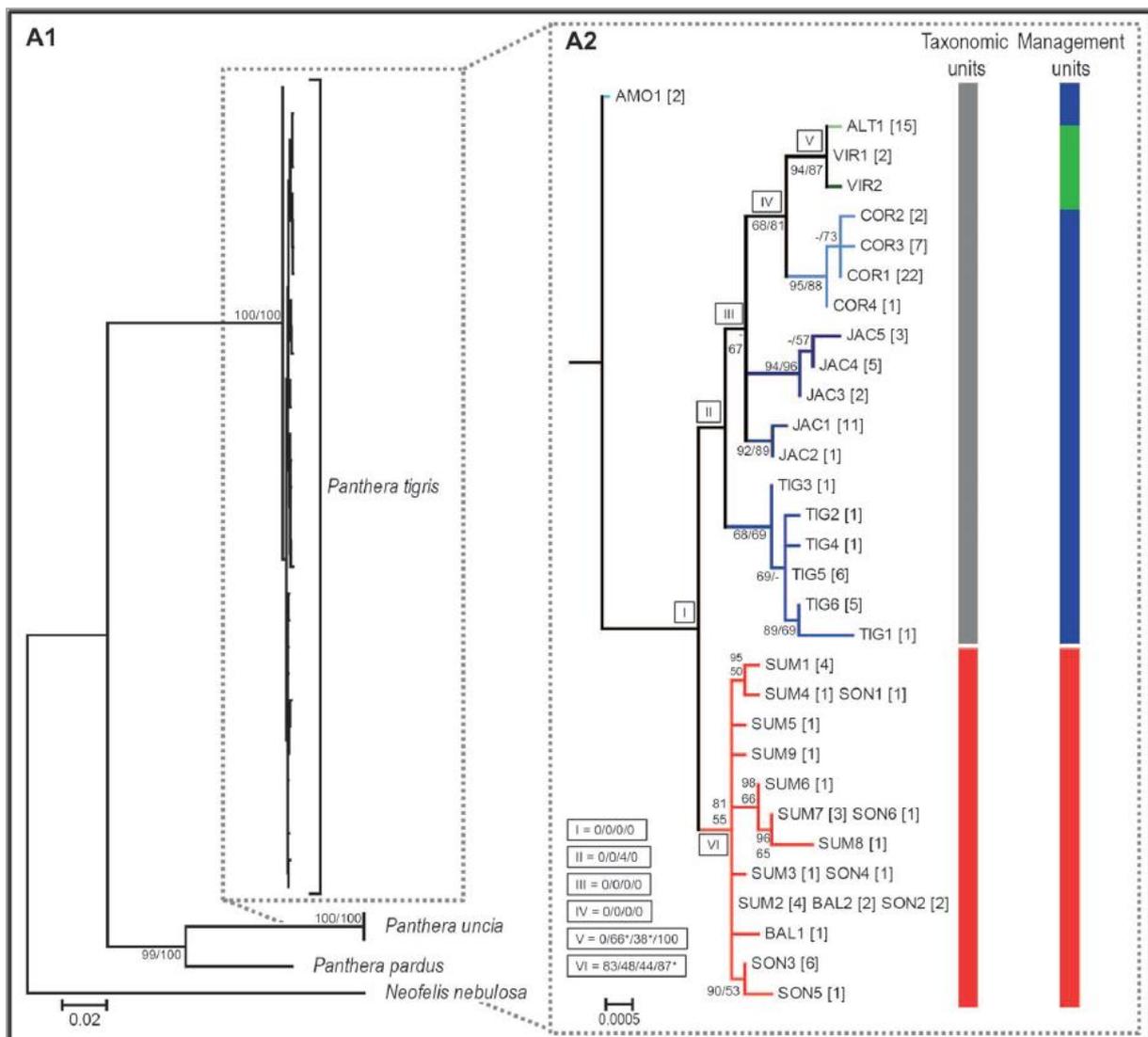


Fig. 2A from Wilting *et al.* (2015) Science Advances 1:e1400175 [Open Access]. Phylogenetic analyses of all nine putative subspecies using 3968 bp of mtDNA. (A1 and A2) Maximum likelihood (ML) tree of intraspecific variation among all putative tiger subspecies in relation to three pantherine cat species [snow leopard (*Panthera uncia*), leopard (*Panthera pardus*), and clouded leopard (*Neofelis nebulosa*)]. Values above or below branches show bootstrap supports for ML and Bayesian inference. (A1) ML tree including three pantherine cat species as outgroups. (A2) Enlargement of the ML tree part showing the tigers only. Roman numerals indicate bootstrap supports of nodes for skull {females} / skull {males} / skin / ecological preferences. Abbreviations for putative subspecies are given in Table 1 in the original paper. \* indicates that one additional putative subspecies clusters with this group.

Some generalist species (e.g. Leopard cat, Asian golden cat) had clades, whose age fitted well with the date of the Toba eruption, while other generalist species (e.g. red muntjac, *Rusa spec.*) had clades, whose age predated (by far) the volcano eruption and could only be explained by (at least temporal) presence of additional barriers such as the Isthmus of Kra, and the central Indian dry zone (red muntjac) or by gradual climate changes leading to a drier climate on Java compared to the other major Sunda Islands (*Rusa timorensis*).

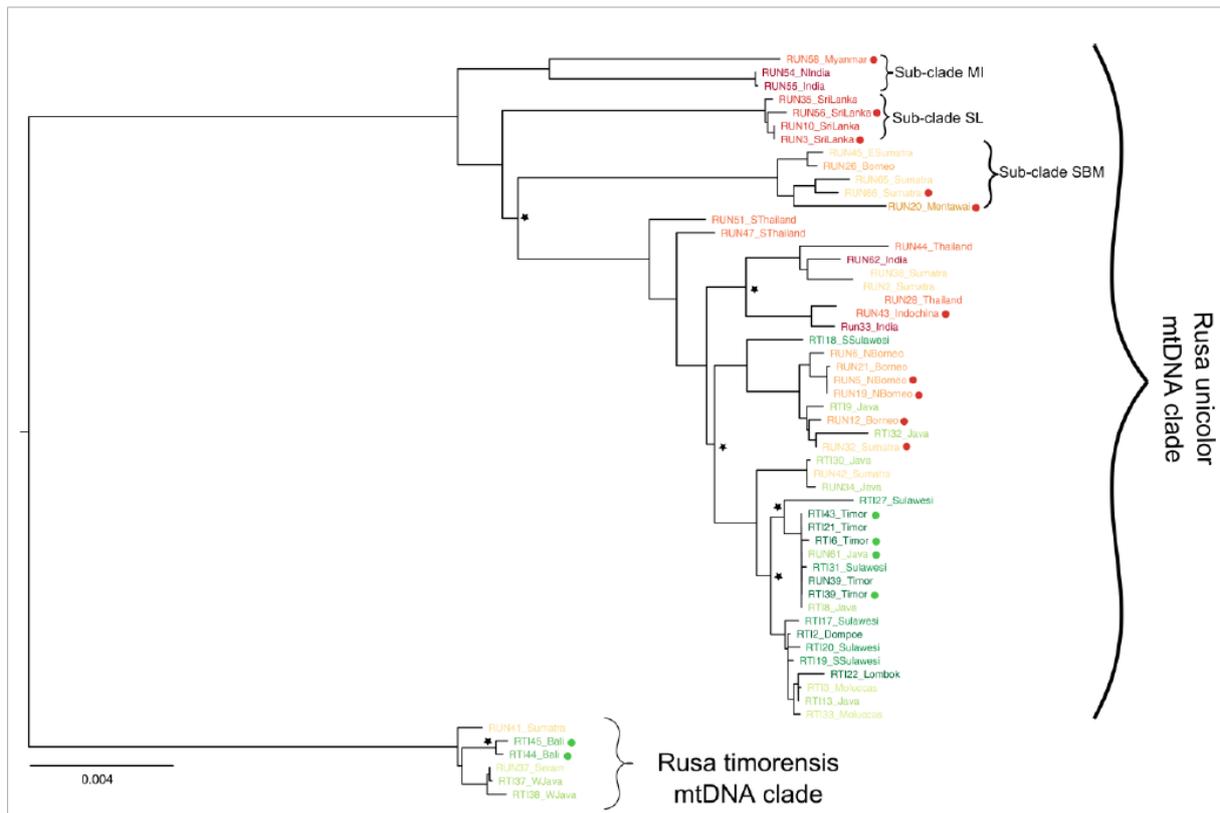
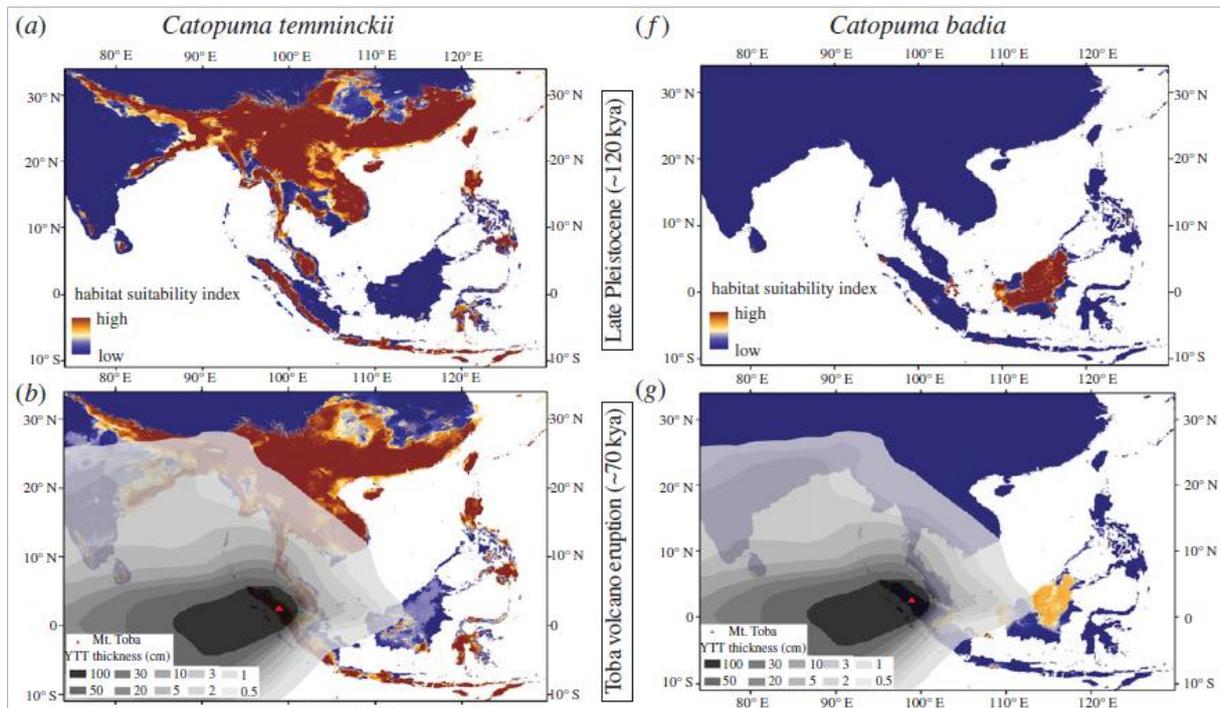


Fig. 3 from Martins *et al.* (2018) ECOL. EVOL. 8(3): 1465-1479. Mitogenome ML tree of both *Rusa* species. Colors on tips represent sampling location (as in Fig. 2 of the same paper) and stars represent split events with bootstrap values/Bayesian posterior probabilities lower than 90/0.95. Red and green dots represent samples for which we obtained nDNA; red dot: assigned to the *Rusa unicolor* genotypic cluster, green dot: assigned to the *Rusa timorensis* genotypic cluster. Major mtDNA clades and sub-clades are labeled with curved brackets. The scale bar indicates the number of substitutions per position.

For specialist species (e.g. Bay cat) we could confirm our hypothesis of gradual climate change having influenced the evolution of the species as they became patchily distributed following the patchy distribution of their habitat.



Upper part of Fig. 5 from Patel *et al.* (2016) R. Soc. open sci 3: 160350 [Open Access].

The figure depicts the projected distribution of the Asian golden cat (*Catopuma temminckii*, left) and the Bay cat (*Catopuma badia*, right) for two selected time periods (more time periods in the publication). Current distributions (to serve as 'occurrences' for model-fitting procedures) were taken from the IUCN/SSC Red List of Threatened species.

Analysis of climate data (by applying a newly developed nonlinear time series analysis technique) led to another quite surprising result: the identification of a seesaw relationship between the East Asian and the Australian summer monsoon at millennial to sub-centennial timescales (results of our cooperation partner PIK: Potsdam Institute for Climate Impact Research).

### Scientific output

Within the project we have so far generated 17 peer-reviewed manuscripts and one book chapter (together with our cooperation partner PIK). Different aspects of the project have been presented in 14 conference talks and 4 posters at 12 international conferences and colloquia. Within the project, so far three PhD theses, four master theses, and one scientific term paper have been completed.

1. Martins RF, Schmidt A, Lenz D, Wilting A, Fickel J (2018). Human mediated introduction of introgressed deer across Wallace's line: historical biogeography of *Rusa unicolor* and *R. timorensis*. *ECOL. EVOL.* 8(3): 1465-1479. DOI: 10.1002/ece3.3754 (IF: 2.44)
2. Salleh FM, Ramos-Madriral J, Peñaloza F, Liu S, Sinding MHS, Patel RP, Martins RR, Lenz D, Fickel J, Roos C, Shamsir MS, Azman MS, Lim BK, Rossiter SJ, Wilting A, Gilbert MTP (2017) An expanded mammal mitogenome dataset from

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3. [Patel RP](#), [Lenz D](#), [Kitchener AC](#), [Fickel J](#), [Förster DW](#), [Wilting A](#) (2017) Threatened but understudied – supporting conservation by understanding the genetic structure of the flat-headed cat. *Conservation Genetics*, early online, doi: 10.1007/s10592-017-0990-2.
4. [Patel RP](#), [Wutke S](#), [Lenz D](#), [Mukherjee S](#), [Ramakrishnan U](#), [Veron G](#), [Fickel J](#), [Wilting A](#), [Förster DW](#) (2017) Genetic structure and phylogeography of the Leopard cat (*Prionailurus bengalensis*) inferred from mitochondrial genomes. *JOURNAL OF HEREDITY* 108(4): 349-360. [OPEN ACCESS](#)
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#### *Book chapter*

1. [Martins RF](#), [Kampmann M-L](#), [Förster DW](#) (2017) Library preparation from degraded samples for non-Illumina platforms. Methods in Molecular Biology: aDNA Methods and Protocols, 2<sup>nd</sup> Edition, Springer Protocols. *in press*