Exercises in Marine Ecological Genetics

11. Phylogenetic inference

- Align sequences
- Infer phylogeny based on genetic distances
- Perform Maximum Likelihood analysis

Martin Helmkampf

https://github.com/mhelmkampf/meg25


Jake Wilton

Rays and sharks

- ~ 1200 species
- Crucial in many marine ecosystems e.g. as top predators
- High economic value
- Every third species threatened with extinction

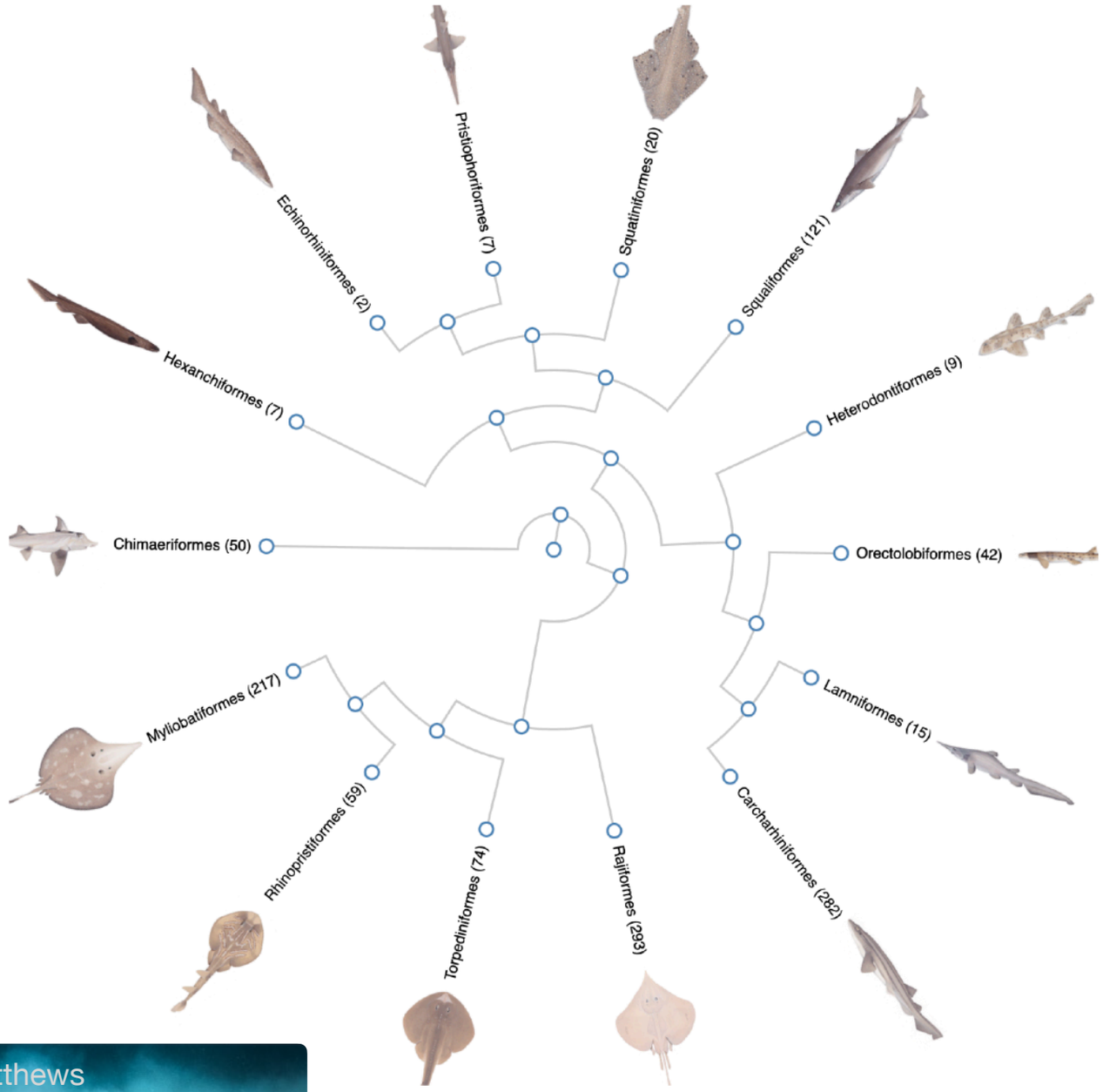


Photo: Albert kok


Photo: Toby Matthews

Sources: IUCN / Ocean Image Bank

Chondrichthyan Tree of Life

Threats

- Overfishing key driver of drastic decline
- Exacerbated by slow reproduction
- Lack of knowledge:
  > 25 % species discovered in last 20 years


Photo: Aina Fauzi

What is needed

- Improved management of fisheries and protected areas
- Better understanding of species distribution and genetic diversity of populations can help with spatial prioritization

Source: IUCN

Diversity of wedgefishes in Malaysia

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Kean Chong Lim

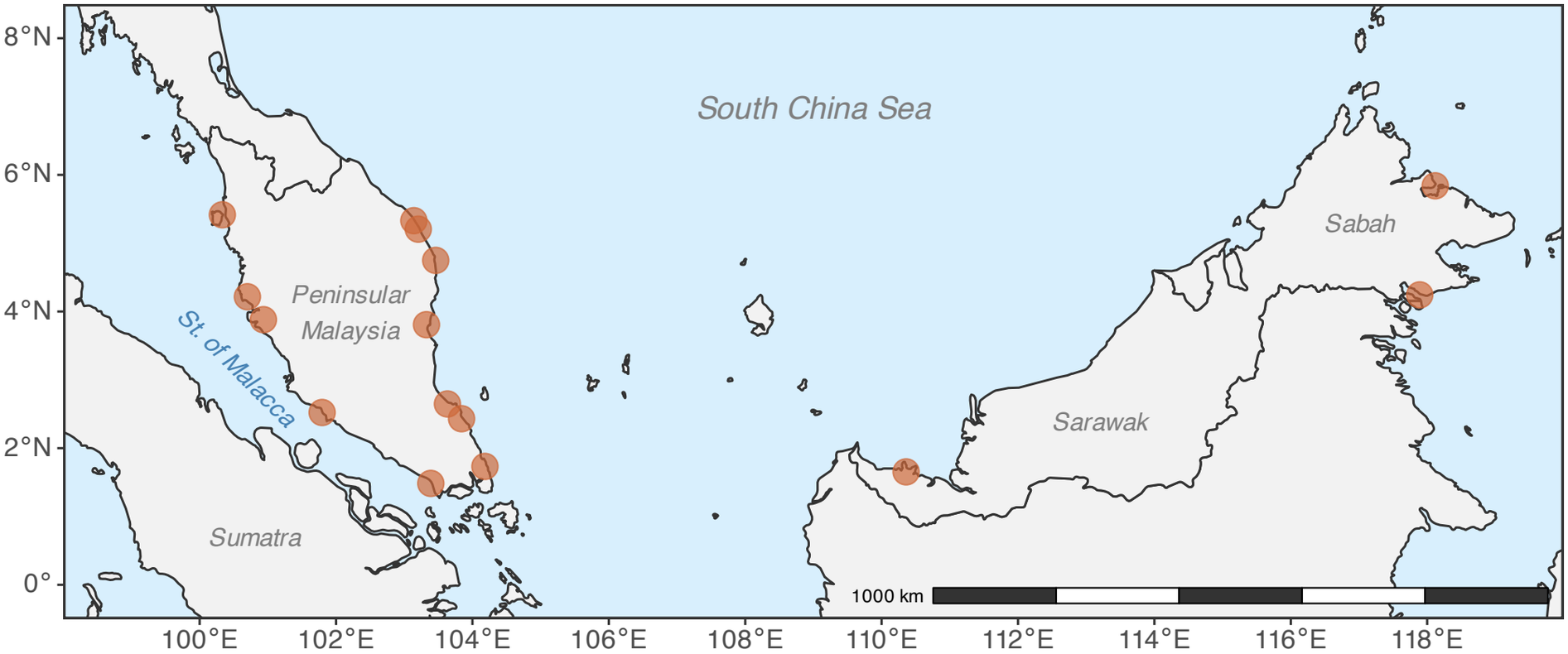
Amanda Jhu Xhin Leung

Serena Adam

- Wedgefishes are endangered but unprotected in Malaysia
- Limited knowledge of species distribution hinders effective management
- Objective: assess species diversity, distribution and genetic diversity across Malaysia

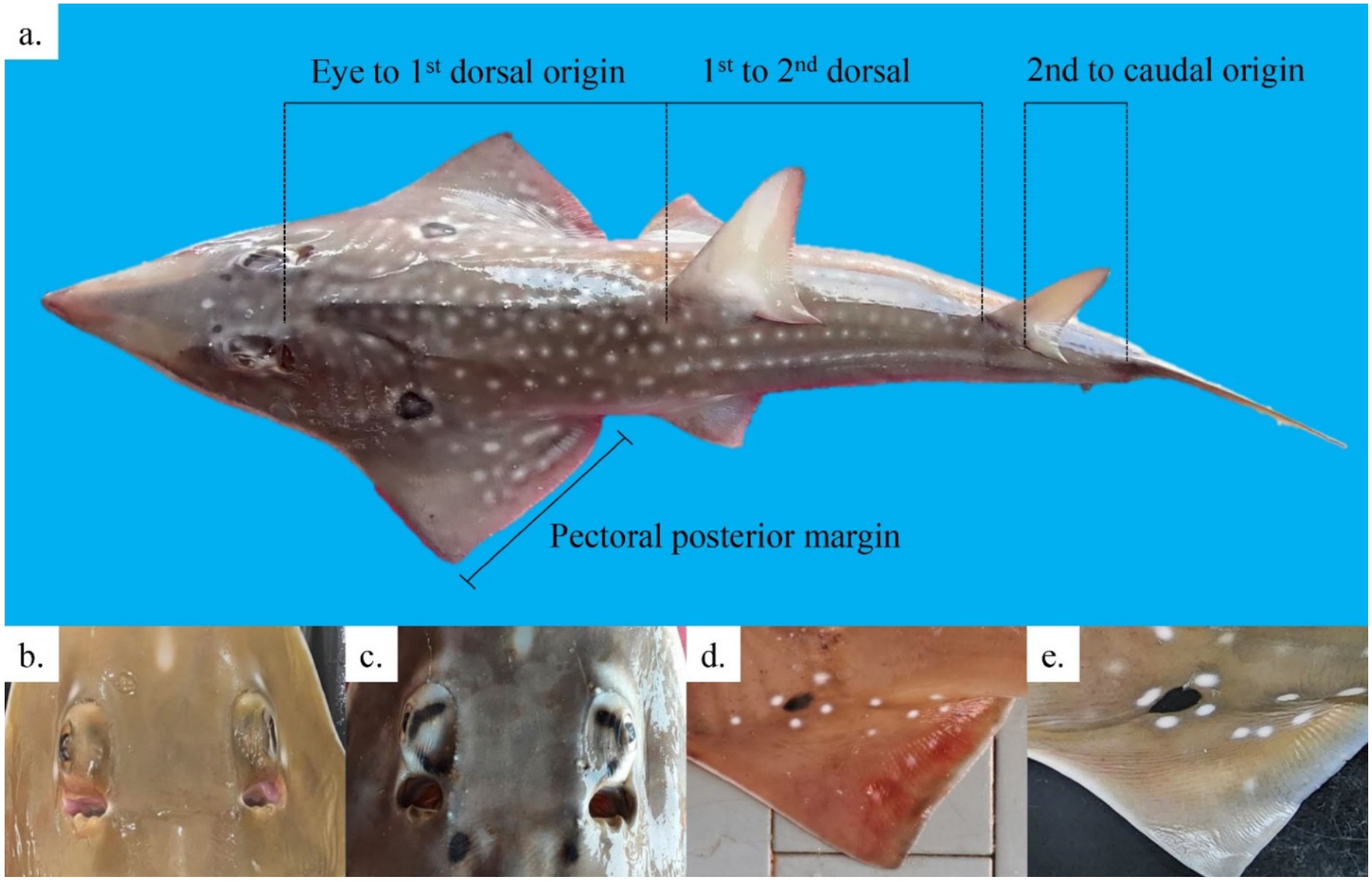
Photo: Ian Banks

Sampling sites



- 85 specimens
- 15 landing sites and markets
- *In situ* identification, photographs
- Tissue samples
- Sequencing of COI and ND2

Morphological characters



Eye / spiracle markings

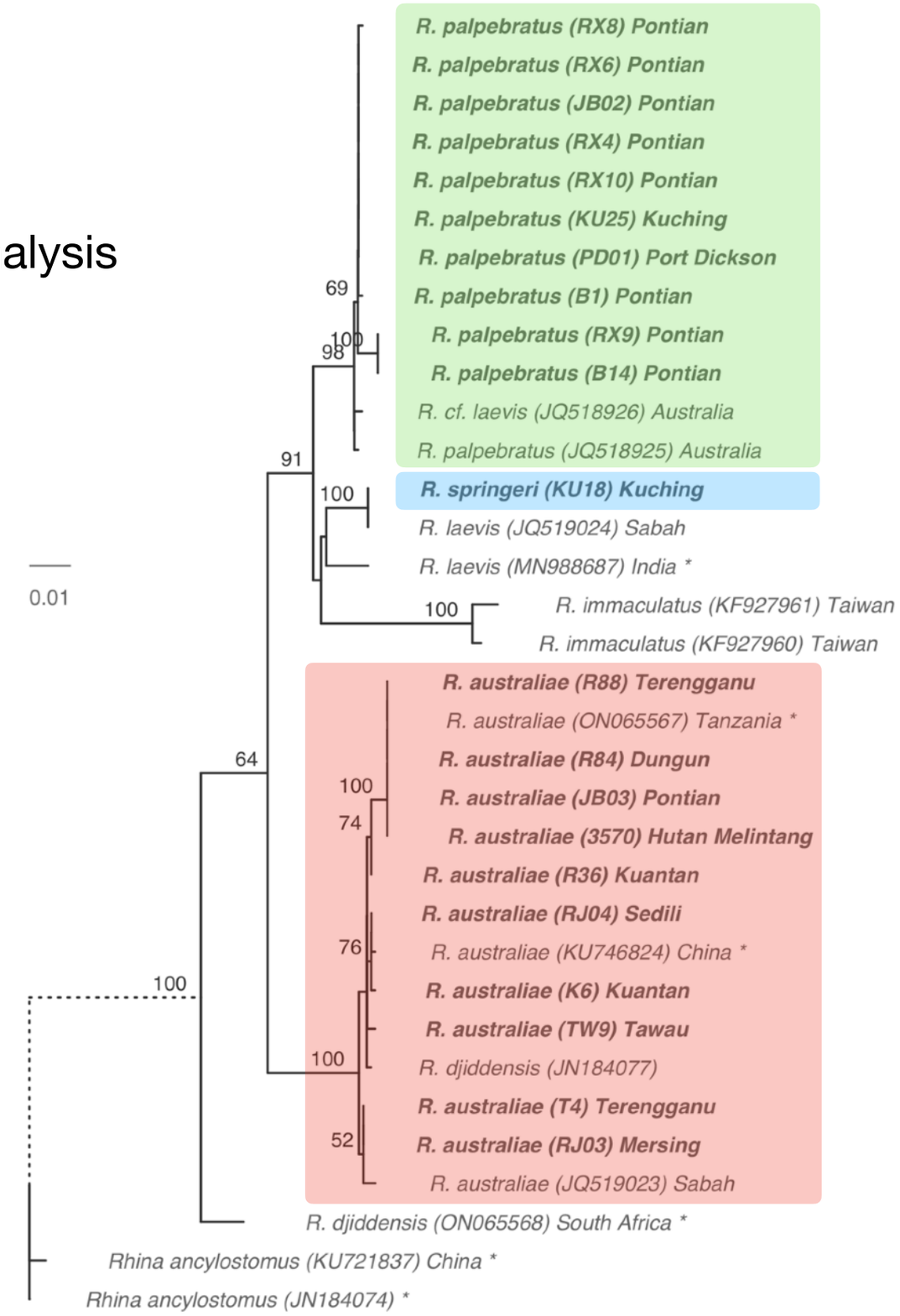
Pectoral fin spot pattern

Genetic validation

Maximum likelihood-based phylogenetic analysis

ND2 gene

All specimens could be assigned to species with high confidence



Comparison of species identification methods

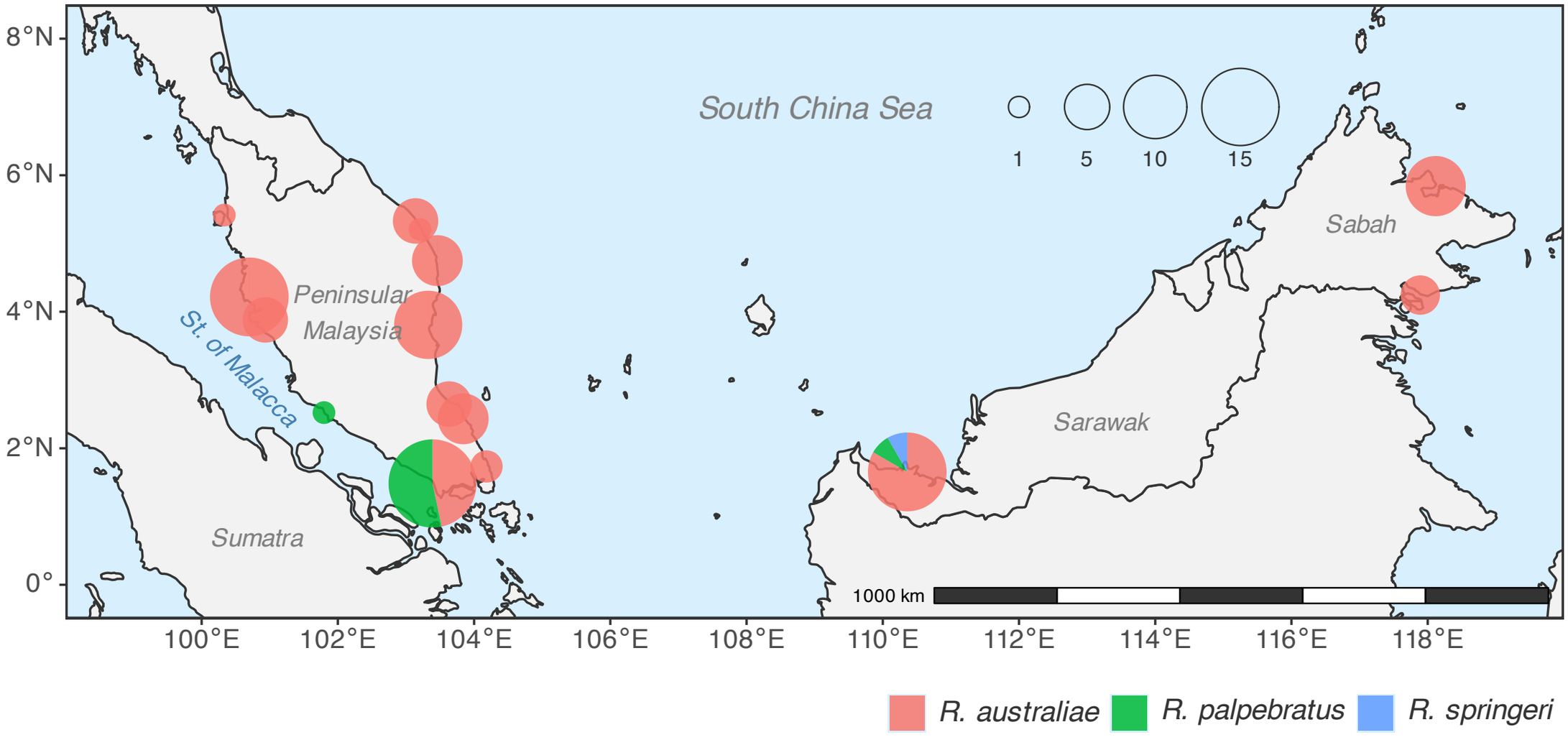
Species	Morphology	DNA barcoding
R. australiae	68	74
R. palpebratus	4	10
R. springeri	7	1
Unknown	6	0
Total		85

Underestimated by morphology

Overestimated by morphology

16 % of specimens were misidentified based on morphology alone

Species distribution



- *Rhynchobatus australiae* most common species
- First record of *R. palpebratus* in Malaysian waters

Phylogenetic inference

Summary

```
mafft input.fas > output.aln                                    # Align sequences

raxml-ng --all --msa input.aln --model MODEL --bs-trees n       # ML + bootstrap
```