



# Rebuilding a model **tree**: evolution and genetic structure of *Rivacindela* tiger beetles (Coleoptera: Carabidae)

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LÓPEZ-LÓPEZ, A., VOGLER, A.P., GALIÁN, J.

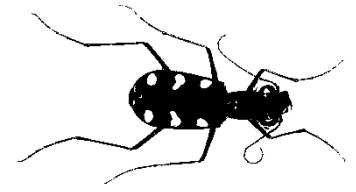
2016

# Introduction: tiger beetles

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*Cosmodela aurulenta*



# Introduction: *Rivacindela*

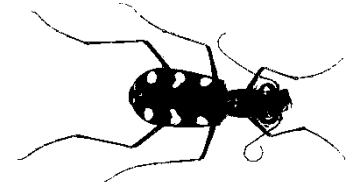
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*Rivacindela* sp, by Alan Henderson

# Introduction: *Rivacindela*

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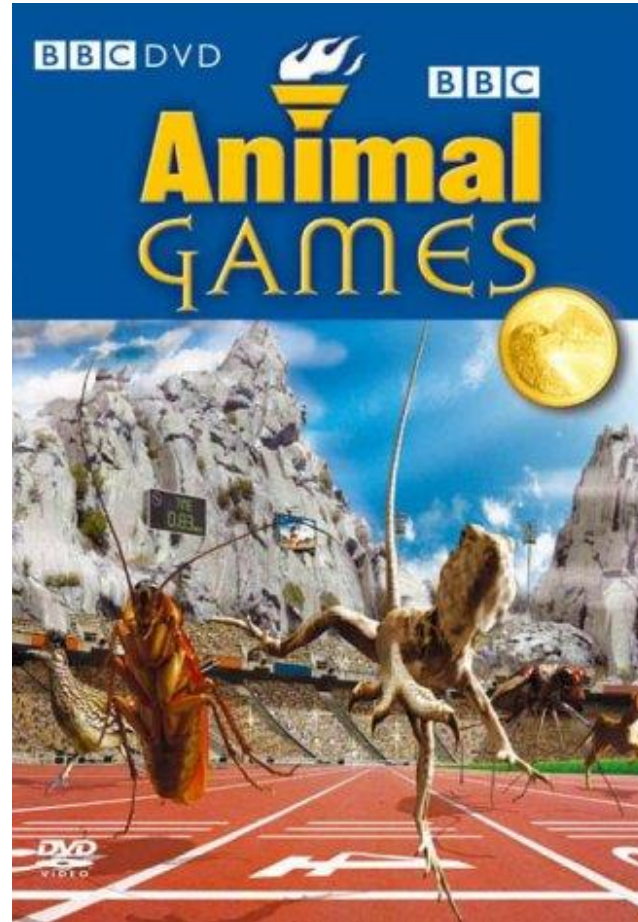
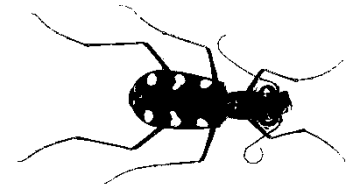
30 described species  
(Sumlin, 1997)

Flightless. Very fast hunters  
(Kamoun, 1996):

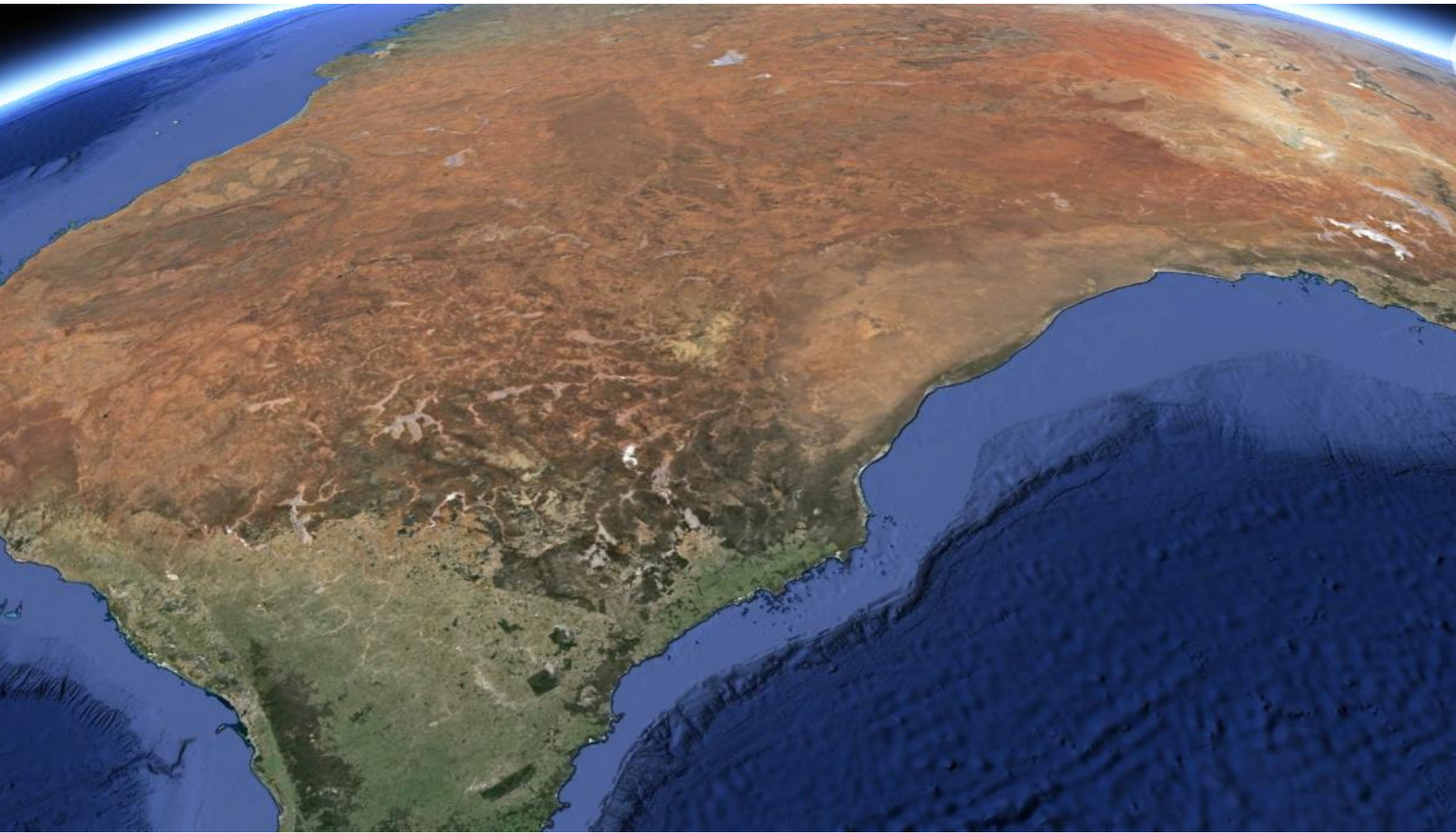
- *R. hudsoni*: 2.5 m/s
- *R. eburneola*: 170 body length/s

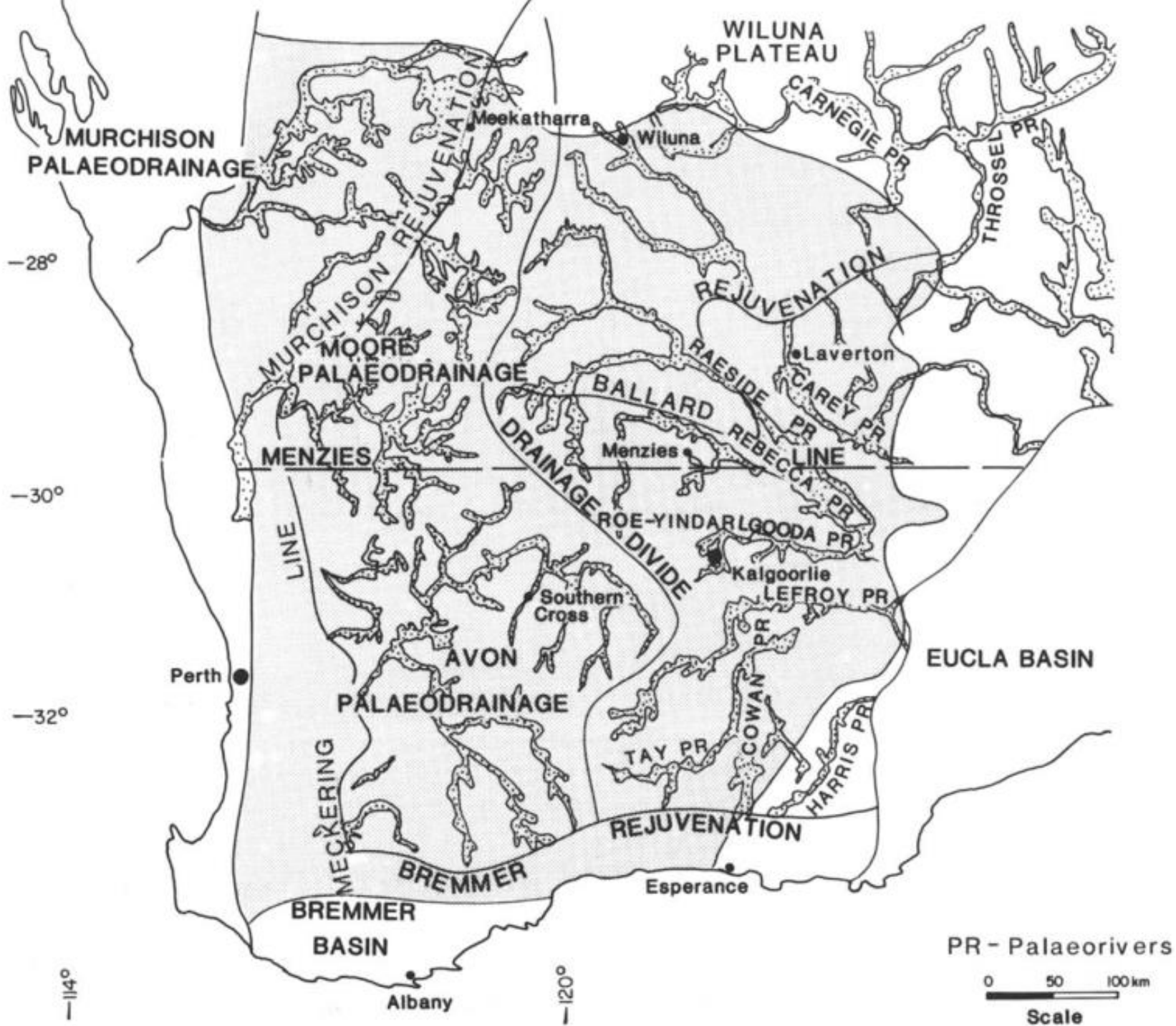
# Introduction: *Rivacindela*

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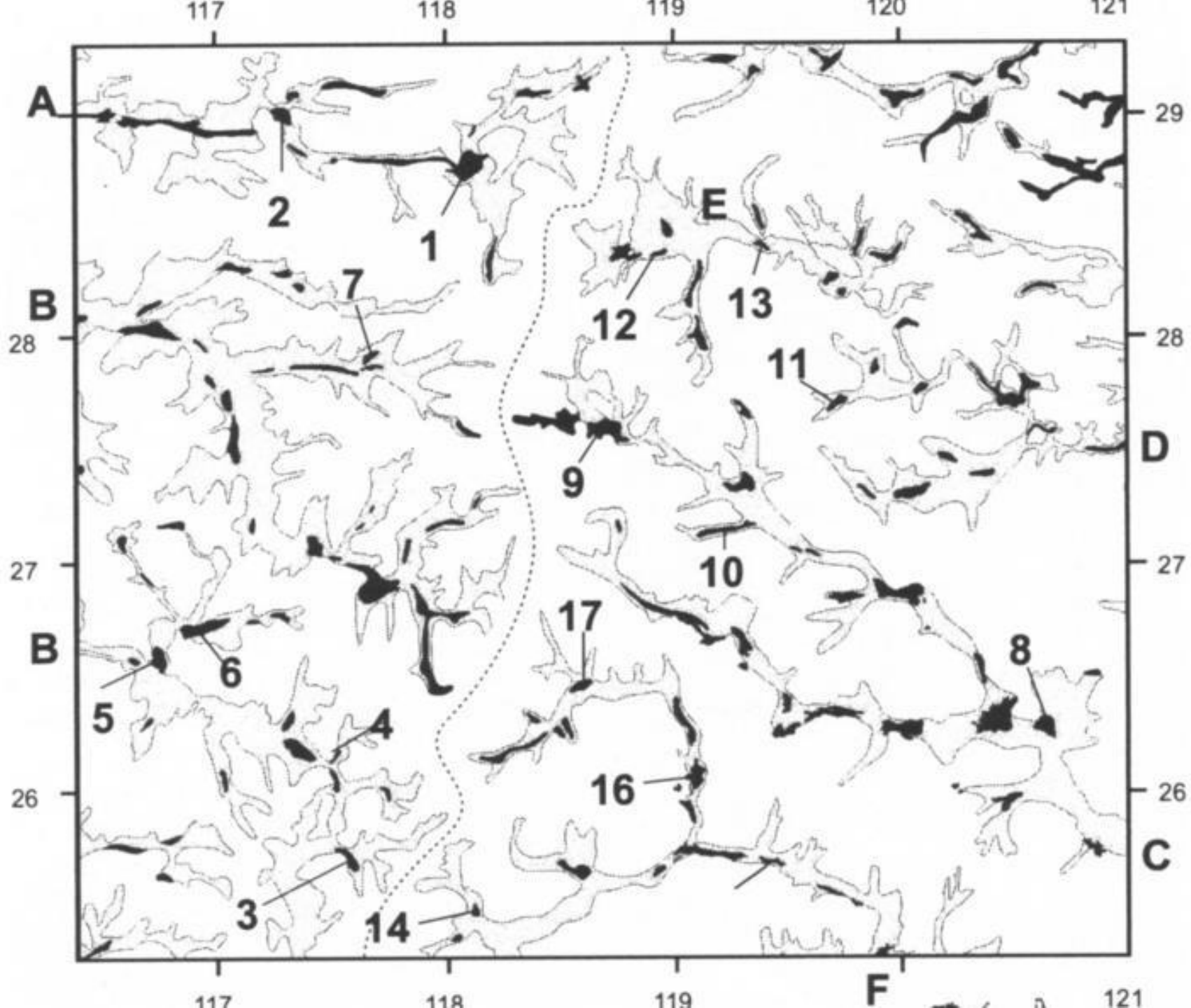






Image Landsat

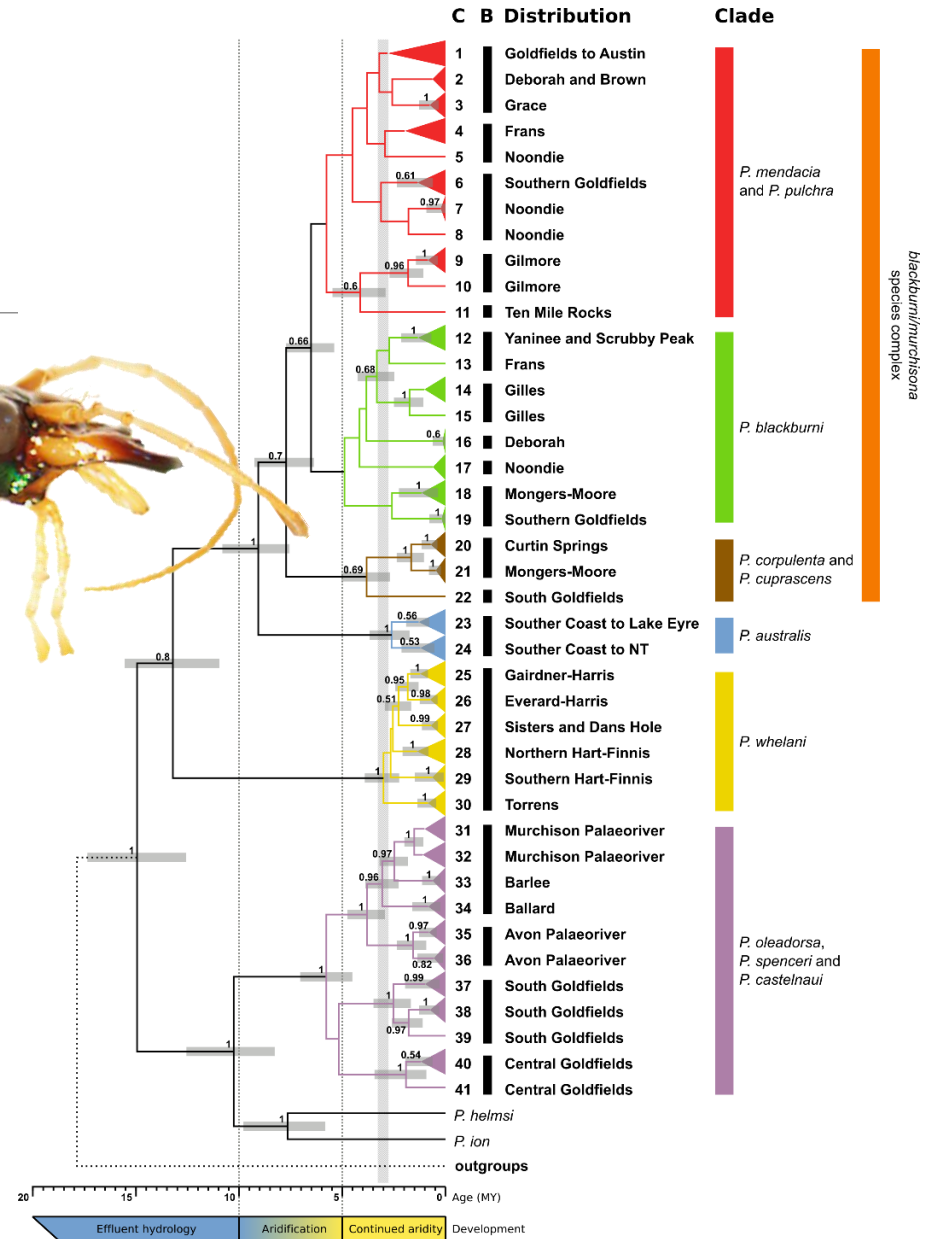


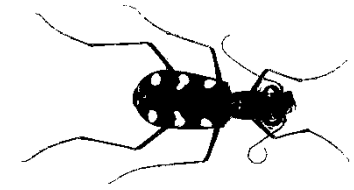


# Introduction



*Pseudotetracha sp*





# Introduction: the tree

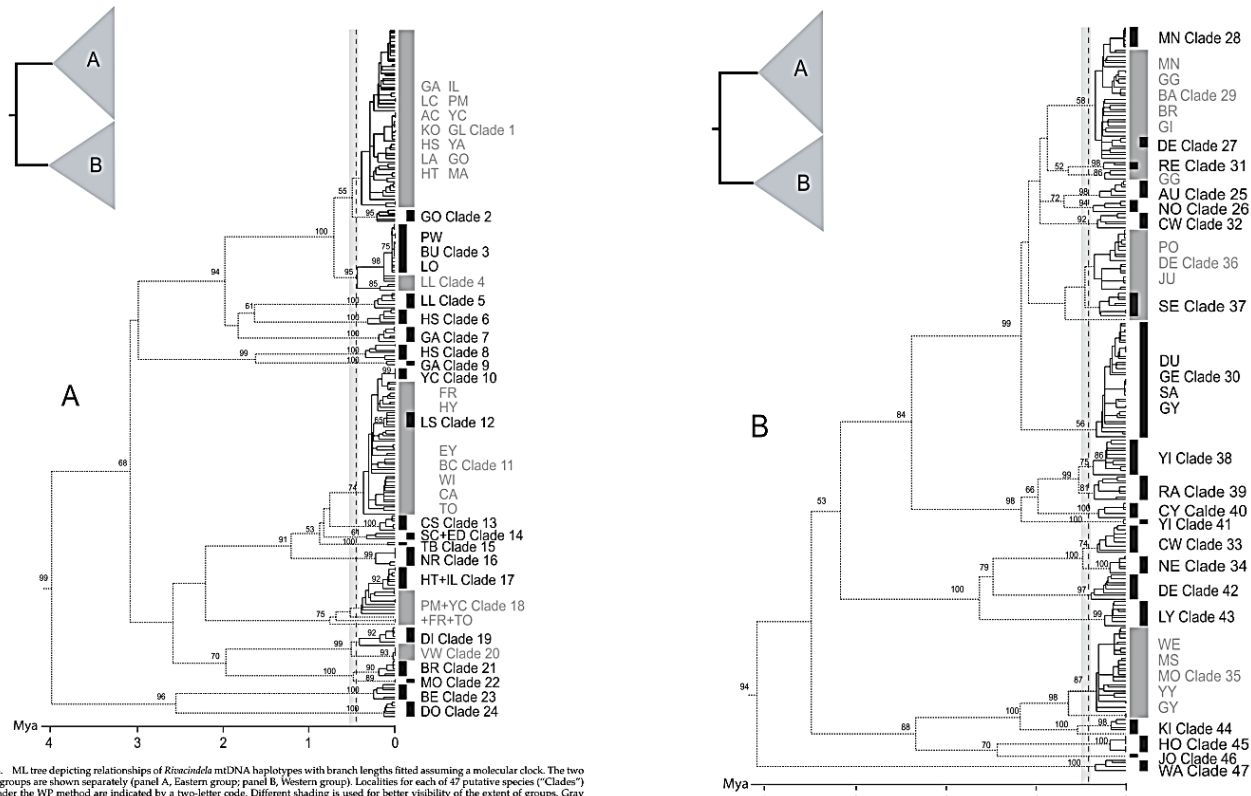
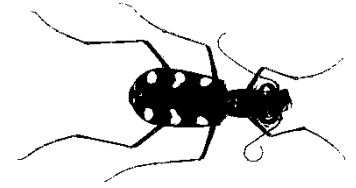


FIGURE 3. ML tree depicting relationships of *Ruscoides* mtDNA haplotypes with branch lengths fitted assuming a molecular clock. The two main sister groups are shown separately (panel A, Eastern group; panel B, Western group). Localities for each of 47 putative species ("Clades") obtained under the WP method are indicated by a two-letter code. Different shading is used for better visibility of the extent of groups. Gray bars and site names colours indicate widely distributed or paraphyletic species. The line style indicates whether branches were estimated as between-species branching (tippled) or within-species branching (solid) in the likelihood procedure. The dotted vertical line shows the maximum likelihood transition point of the switch in branching rates. The grey shading indicates the confidence limits for the transition point falling within 2 log-likelihood units of the ML solution (Material and Methods). Numbers above nodes represent bootstrap support values based on 100 pseudoreplicates and ratchet parsimony searches, shown only for the deep level clades. Bootstrap values under 50% are not shown. (Continued)

FIGURE 3. (Continued)

Pons et al. (2006)



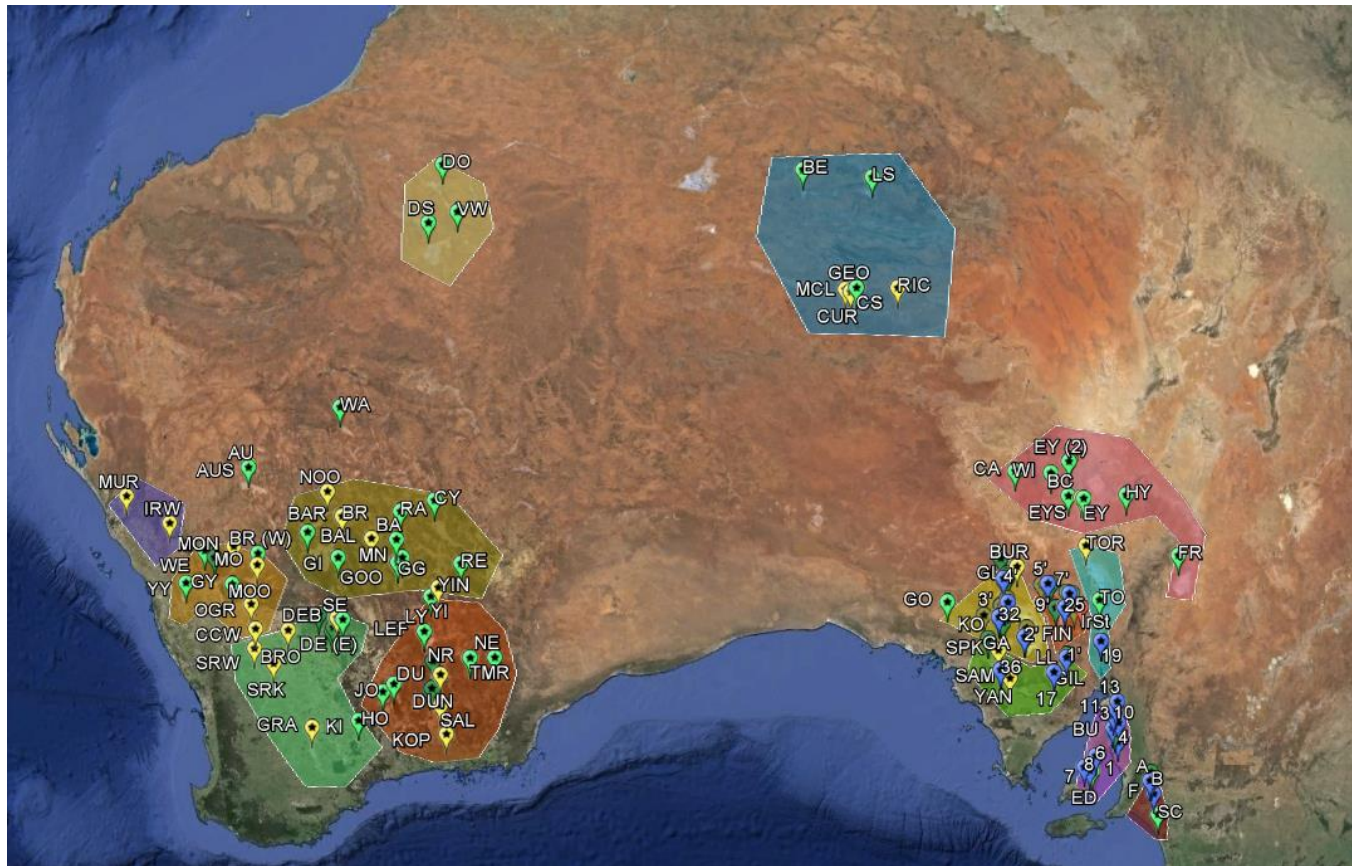
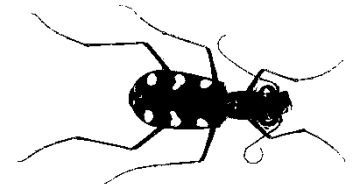


# Aims

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1. To **rebuild** the phylogenetic tree of *Rivacindela* using contemporary algorithms and including more samples.
2. To interpret the results in the light of past events, in order to determine which **historical processes** shaped the evolution and diversification of *Rivacindela*.
3. To **compare** these results with other tiger beetle genus occurring in salt lakes.

# Mat&Mets



199 samples

+

470 seqs (Pons)

**cob** + **COI** + **16S**

Phylogeny

**BEAST**

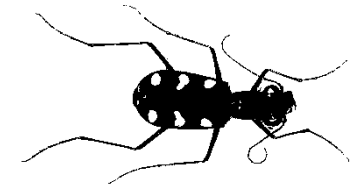
Phylogeography

**POPART**

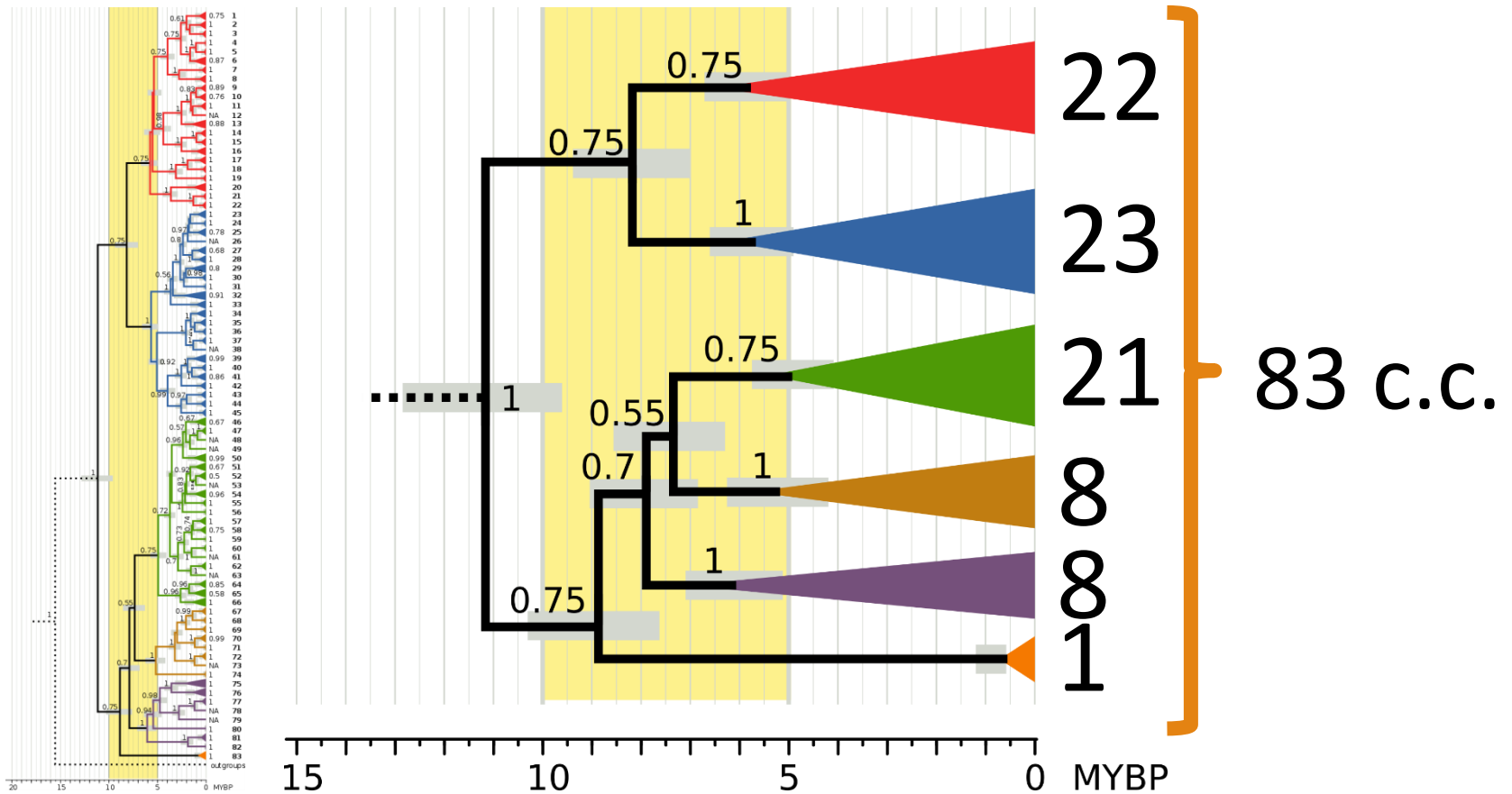
Sp. delimitation

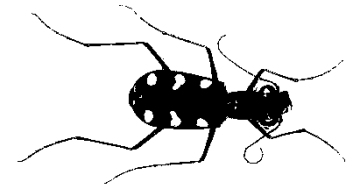
**GMYC**

**bPTP**

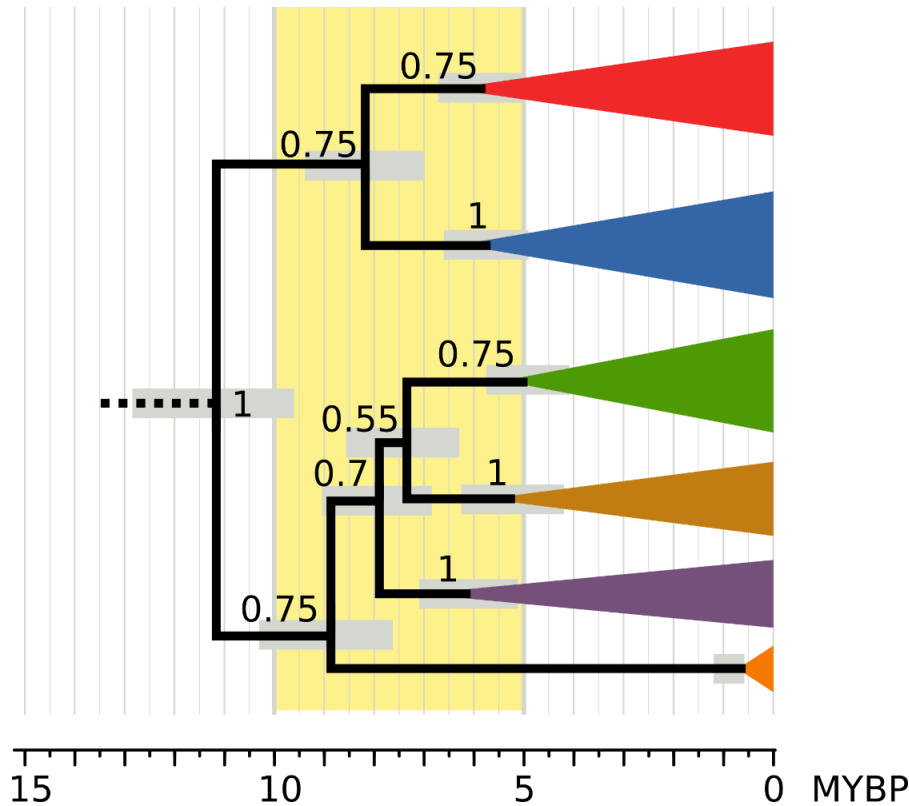


# Results&Discussion: phylogeny

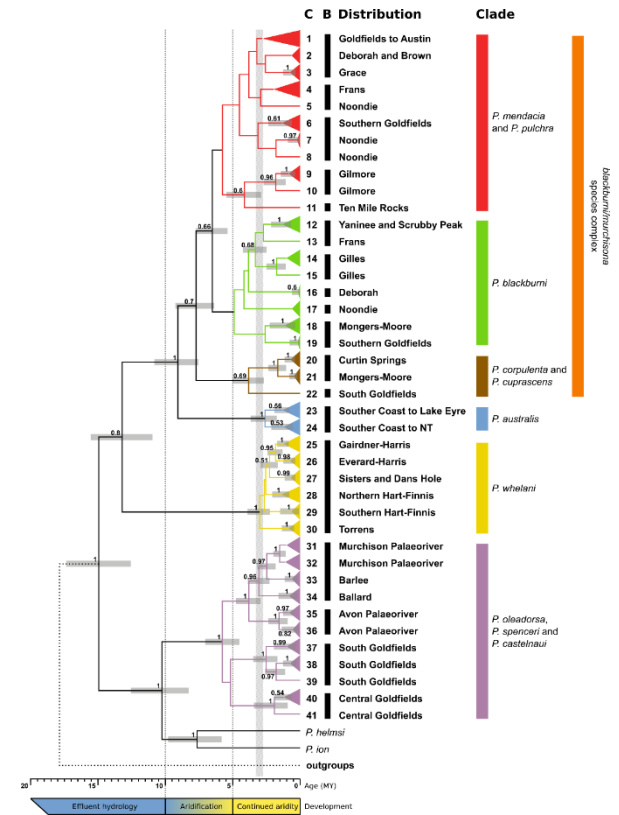




# Results & Discussion: phylogeny

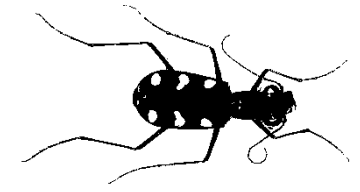


*Rivacindela*

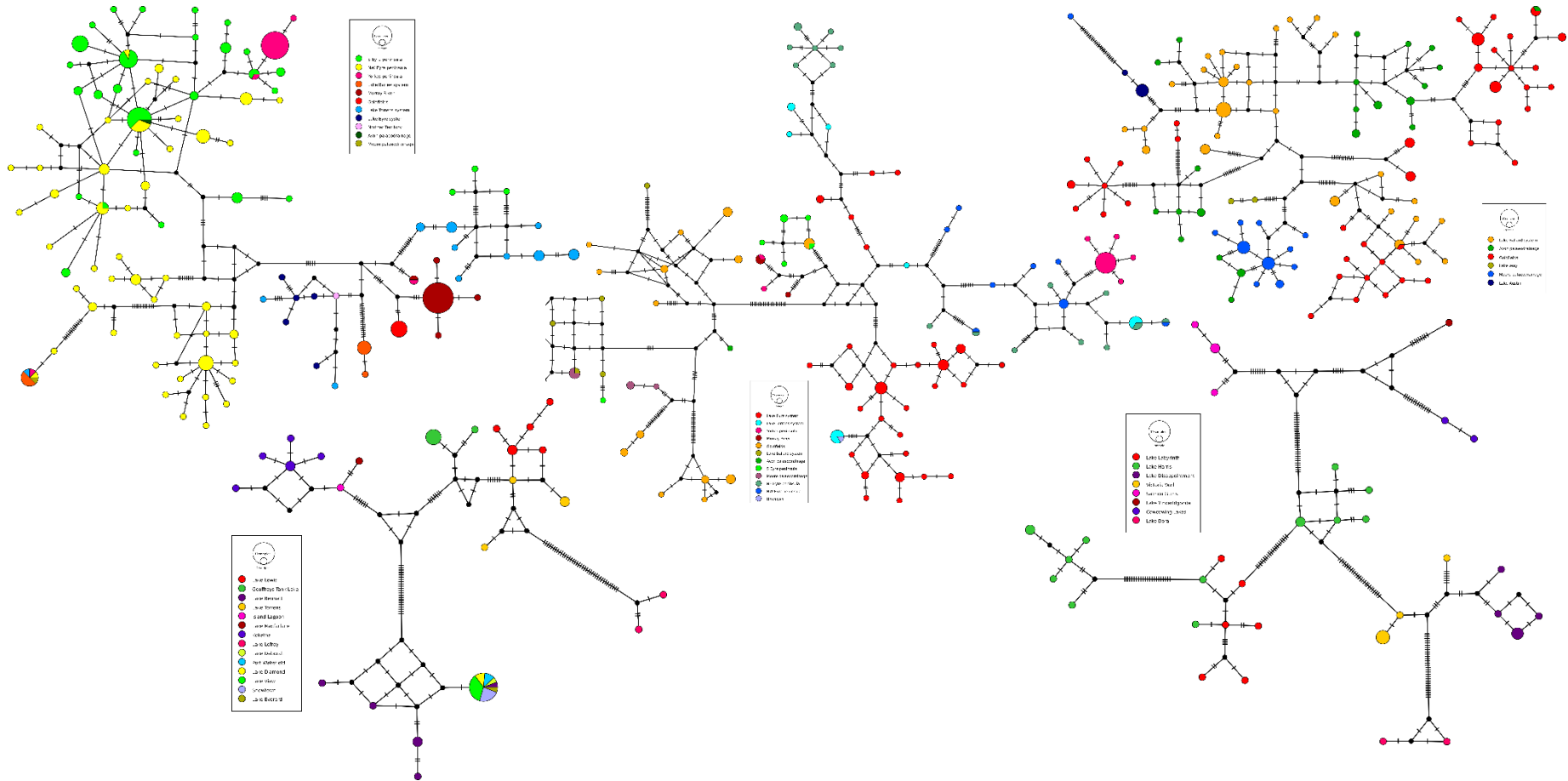


*Pseudotetracha*





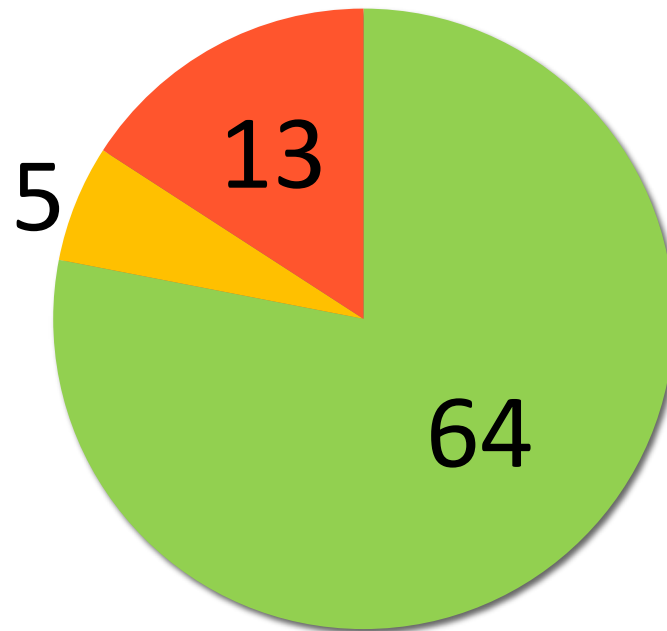
# Results&Discussion: phylogeography



# Results&Discussion: exclusive clades

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Samples



■ Pons (2001, 2003) ■ Mixed ■ Ours (2004, 2012)

# Conclusions

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- 1.** The aridification of Australia played a leading role in the diversification of *Rivacindela* by isolating lineages in separate lakes.
- 2.** The history of *Rivacindela* and *Pseudotetracha* are similar, with a few main lineages diverging 5-10 Mya and an increase in the branching rate once the aridification ended.
- 3.** An integrative revision of the genus is needed in order to assess its actual taxonomic composition.

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Región de Murcia **Proyecto: 19908/GERM/15**

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**Eduardo Díaz**  
**Peter Hudson**  
**Heather Atkin**





