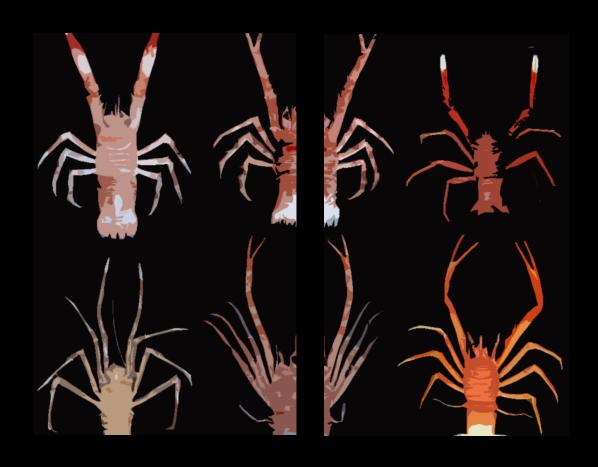
## Squat lobsters: a good example for taxonomy, evolutionary history and biogeography

Enrique Macpherson
Centro de Estudios Avanzados de Blanes (CSIC)



Decapoda	12029
Dendrobranchiata	551
Achelata	142
Chirostyloidea	206
Galatheoidea	715
Hippoidea	81
Lithodoidea	129
Lomisoidea	1
Paguroidea	1106
Enoplometopoidea	12
Glypheoidea	2
Nephropoidea	54
Brachyura	5688
Procarididea	6
Caridea	2572
Polychelida	38
Stenopodidea	68
Gebiidea	203
Axiidea	455



### **Ecological diversity**

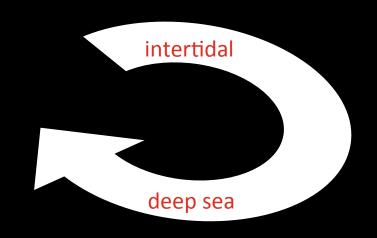




Kiwa hirsuta



*Allogalathea* sp.





Munidopsis sp.



Uroptychus sp.



Gastroptychus sp.

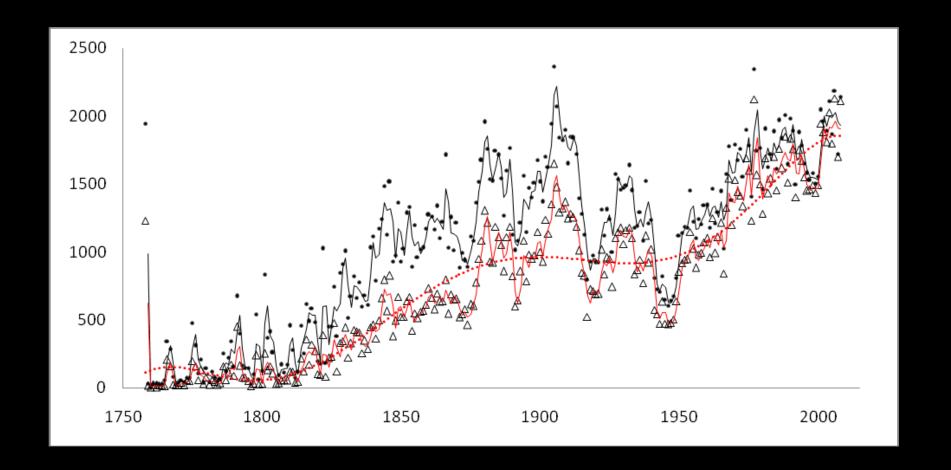
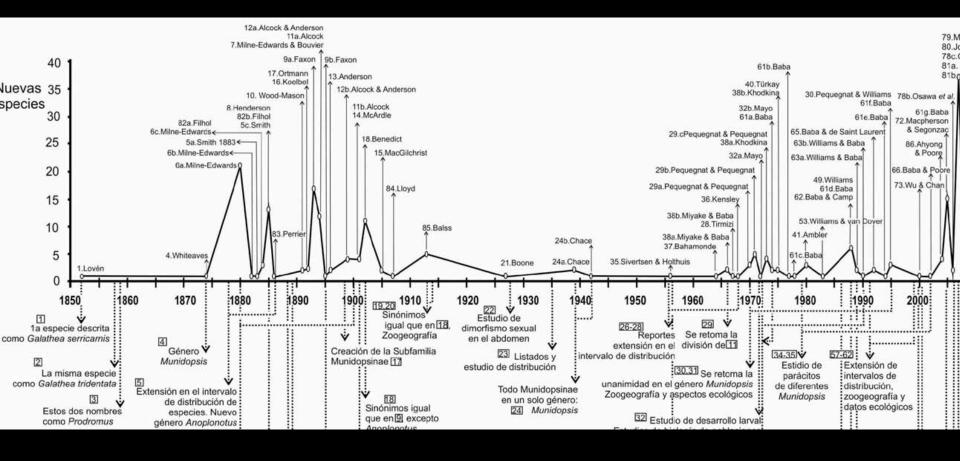
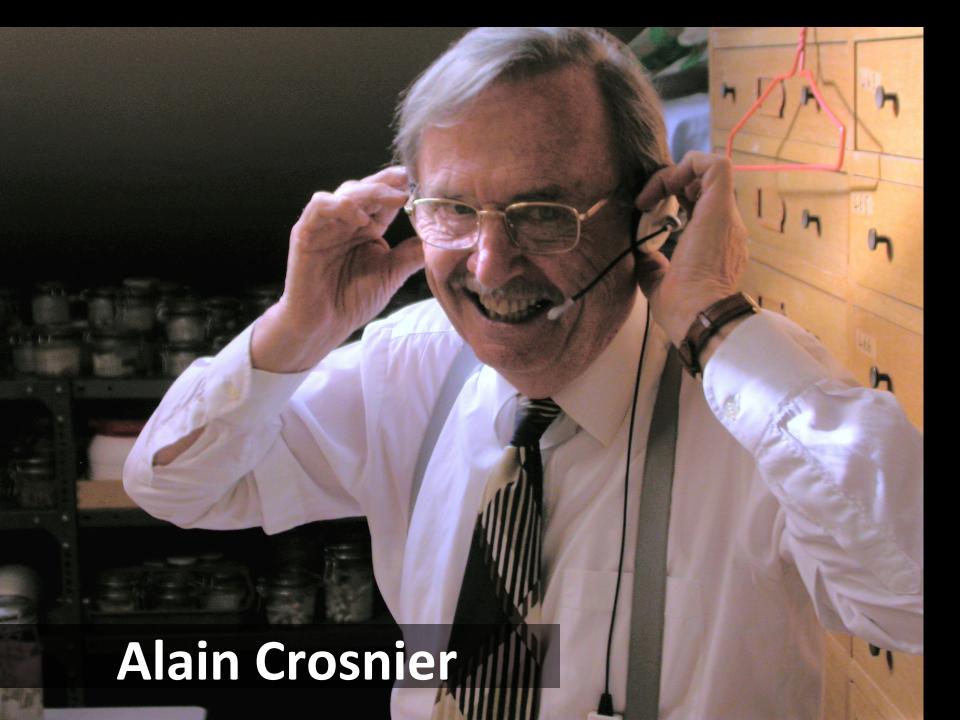


Figure 1. The number of nominal species described per year (•) vs currently recognised as valid ( $\Delta$ ). The solid lines are 2 year moving averages for nominal (black) and valid (red) species and the 6th order polynomial for valid species ( $r^2 = 0.858$ ; red dashed line). Data derived from the World Register of Marine Species on 2010-09-20.



# Munidopsis spp. Increase in sampling effort





#### **ZOOTAXA**





Catalogue of squat lobsters of the world (Crustacea: Decapoda: Anomura—families Chirostylidae, Galatheidae and Kiwaidae)

KEIJI BABA, ENRIQUE MACPHERSON, GARY C. B. POORE, SHANE T. AHYONG, ADRIANA BERMUDEZ, PATRICIA CABEZAS, CHIA-WEI LIN, MARTHA NIZINSKI, CELSO RODRIGUES & KAREEN E. SCHNABEL

#### **1718 times**

Abstract & excerpt (PDF; 20KB) free | Full article (PDF; 1600KB) open access

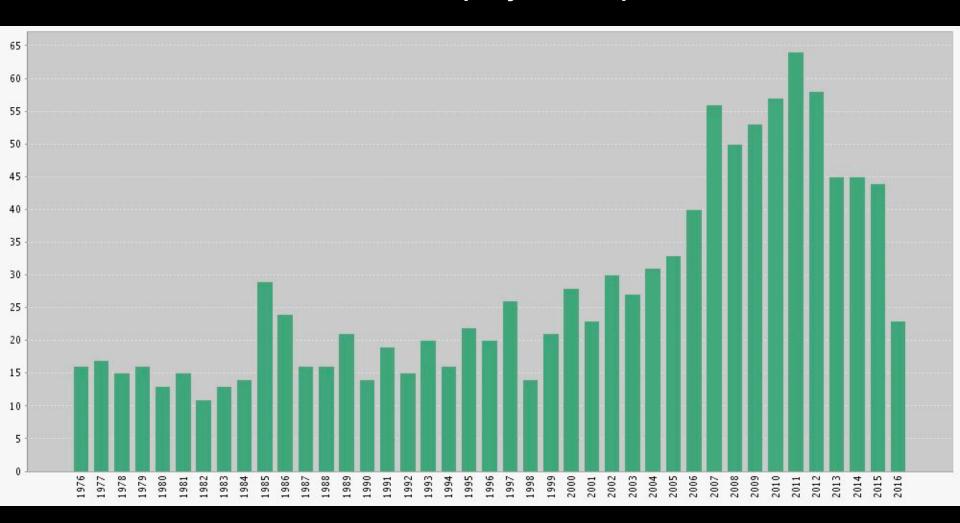
## SQUAT LOBSTERS



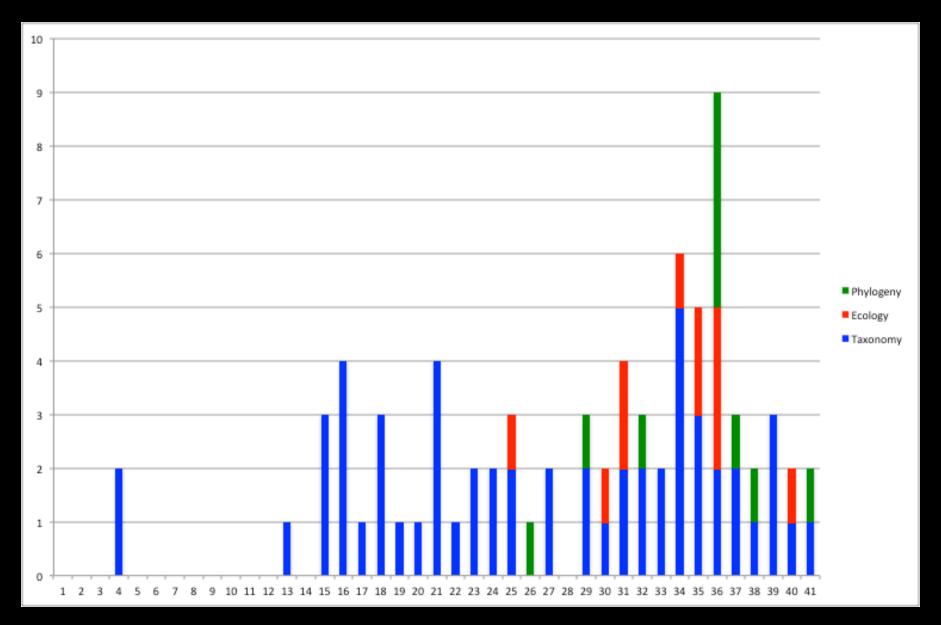
Editors

Gary CB Poore . Shane T Ahyong . Joanne Taylor

#### Publications per year on squats

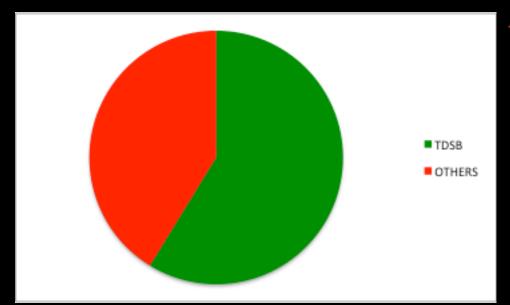


#### **Publications TDSB 1976-2016**





#### **Number of species from TDSB**





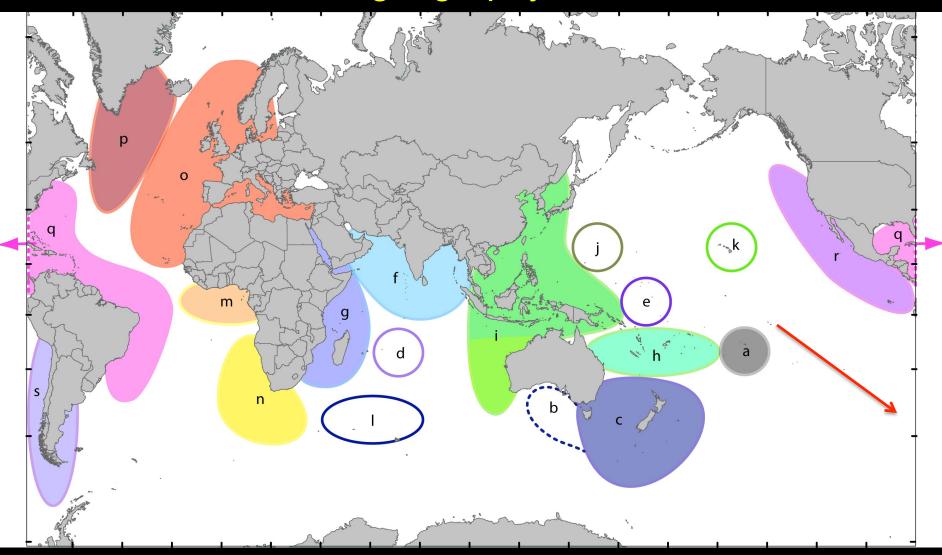




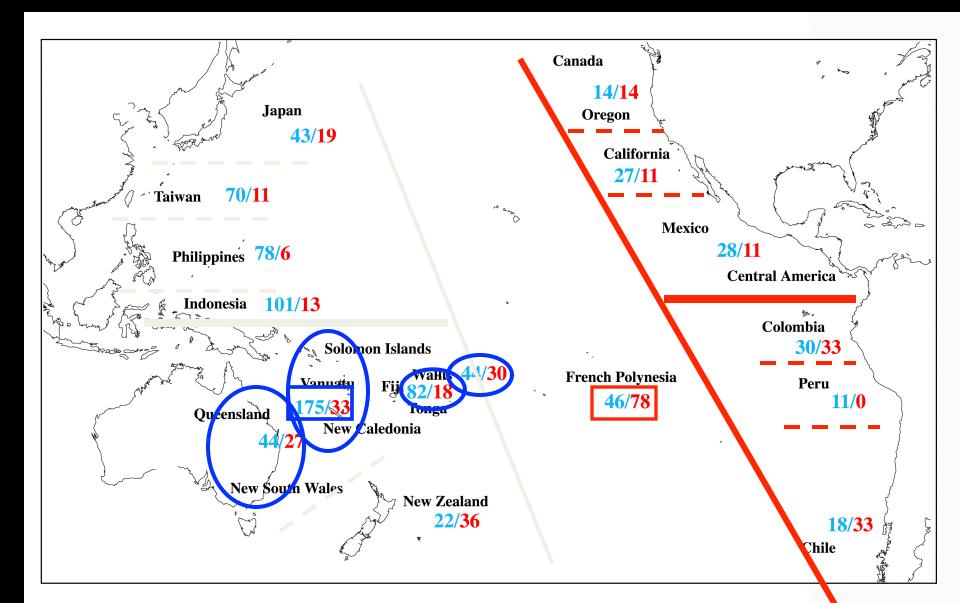




### Biogeography



#### Species richness/endemism



#### **CRYPTIC SPECIATION**

Species typically viewed as cosmopolitan are now recognized as complex species, with species showing more restricted distributions.

In the last years, cryptic species have been described for the family and this high number of species is probably still an underestimate of the family's true diversity.



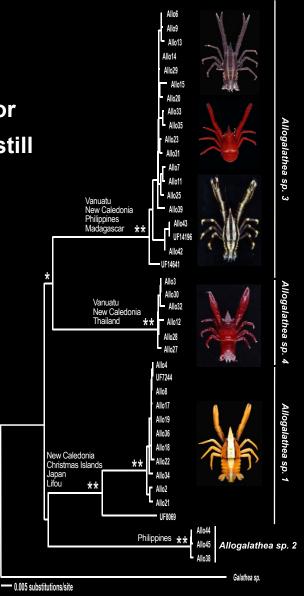


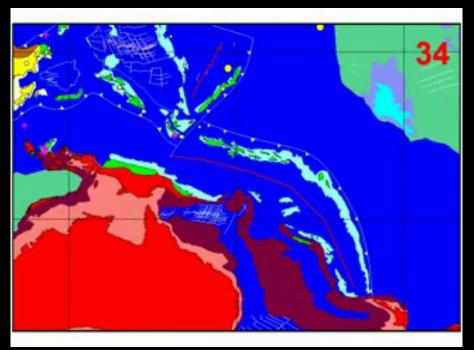
Figure 2. Localities and phylogenetic hypothesis based on the combined dataset. Two asterisks indicates Pp=1 and one asterisks indicates Pp=0.65

## SPECIATION PROCESS IN THE INDO-PACIFIC OCEAN: THE STATE OF THE ART

Speciation process has been studied in many species distributed in the Indo-Pacific Oceans, mainly in shallow waters or reef associated taxa.

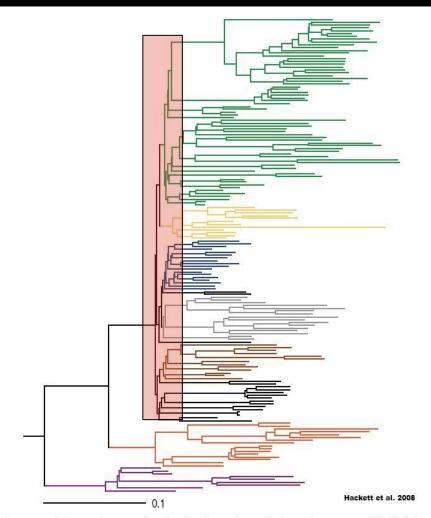


A pattern of increased diversification has been reported in these organisms, mainly associated with the period Oligocene-Miocene.



Is it likely to expect the same pattern for taxa associated with deeper waters?

#### **RAPID SPECIATION**



**Fig. 3.** ML phylogram demonstrating the short internodes at the base of Neoaves and highlighting certain extreme examples of rate variation across avian lineages. Colors are as in Fig. 2. Scale bar indicates substitutions per site. Figure S1 shows the phylogram with taxon names.

- -Characterized for a lack of resolution at the internal nodes of the phylogeny.
- -Reported in many different taxa (fishes, birds, crustaceans, mollusks, salamanders).
- -Plausible explanation for bush-like tree topologies.
- -Previously suggested in the family Galatheidae.







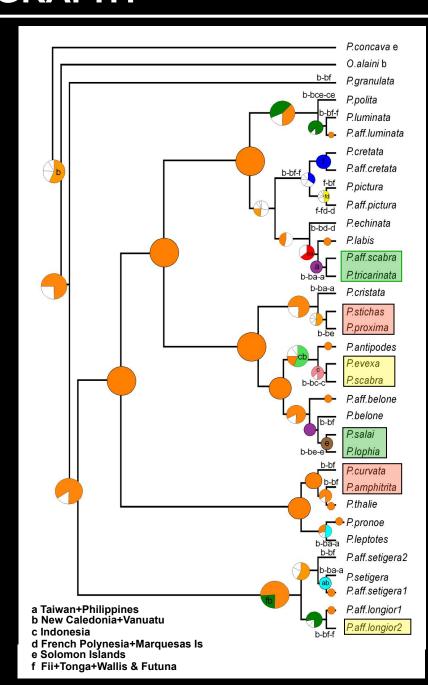


#### **BIOGEOGRAPHY**



The DEC model implemented in Lagrange 2.0 integrates the uncertainty in ancestral area reconstruction. Although NC + V is showed as the ancestral area in most of the nodes, other alternative reconstructions are proposed. Three different patterns were recovered:

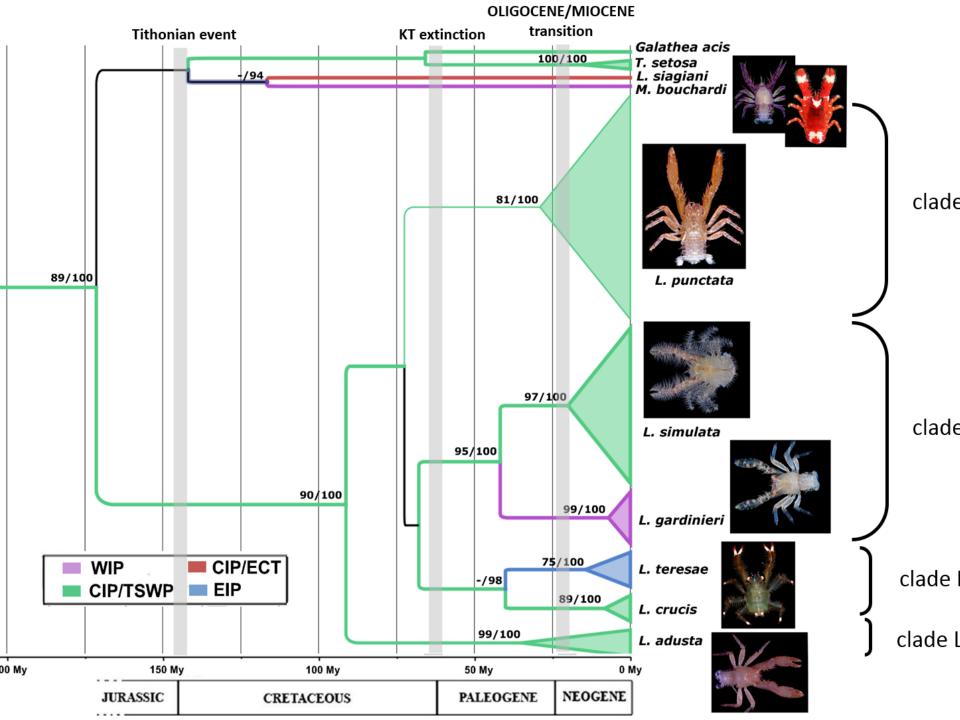
- 1) Dispersion-Expansion of the range
- 2) Dispersion-Expansion of the range-Extinction in the ancestral area
- 3) Dispersion-Expansion of the range-Extinction in the ancestral area-Speciation in situ

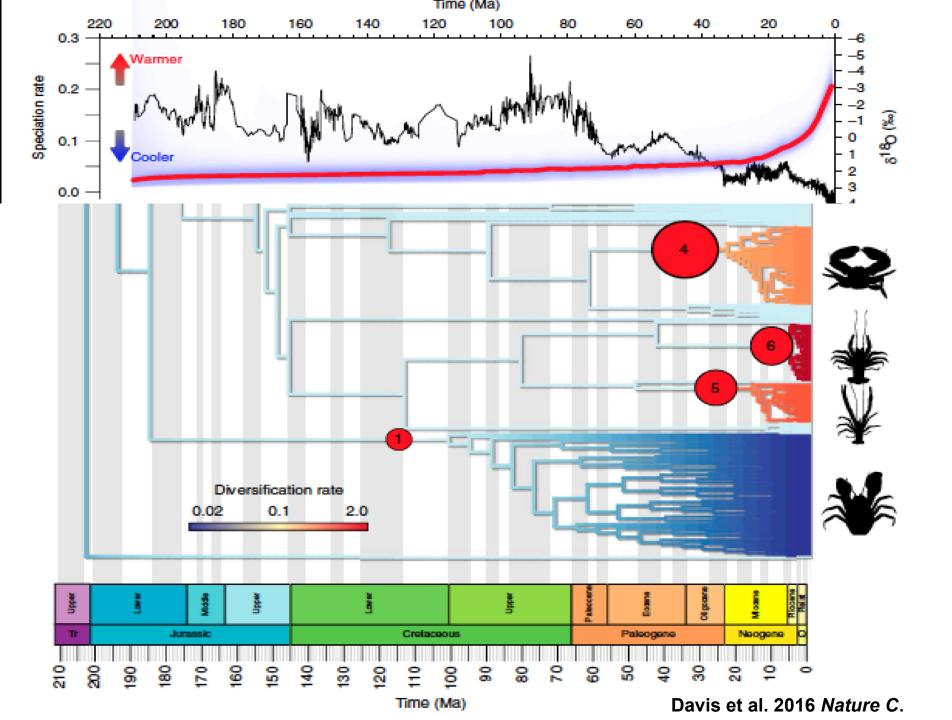


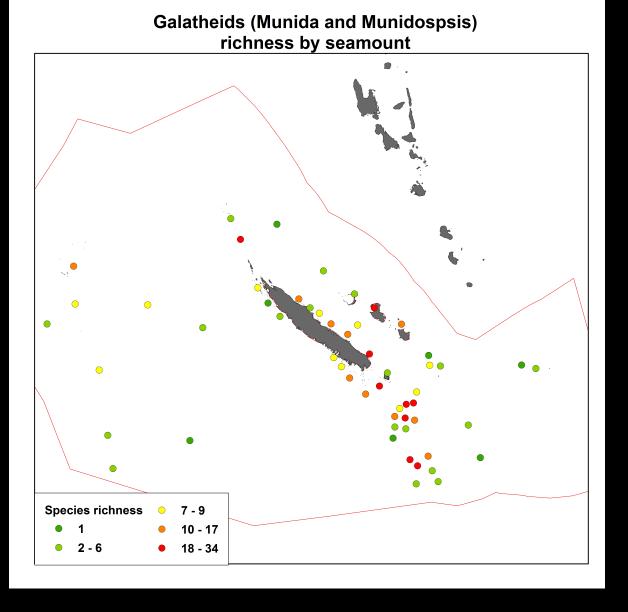
#### Genus Paramunida



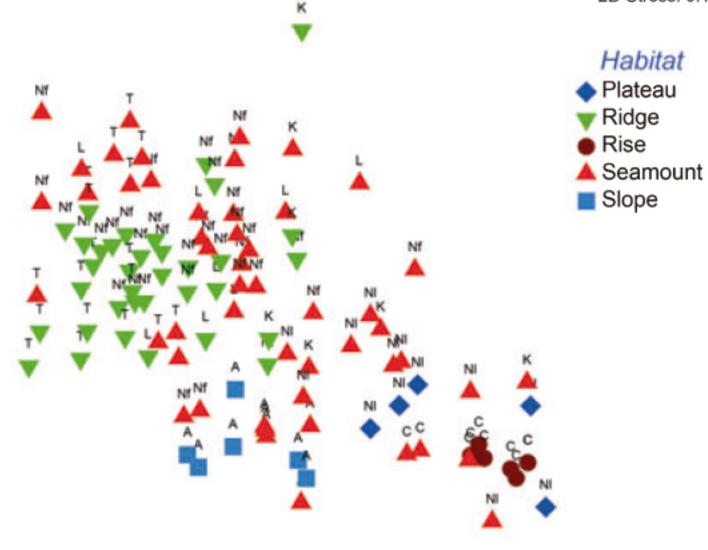
- The analyses of molecular data suggest an event of rapid speciation marked by several shifts in diversification rates and followed by a deceleration in the rate of lineage accumulation over the time.
- Based on mitochondrial average rates of molecular divergence, the diversification of the genus is dated between the Upper-Middle Miocene.
- New Caledonia was reported as the ancestral area of the genus.

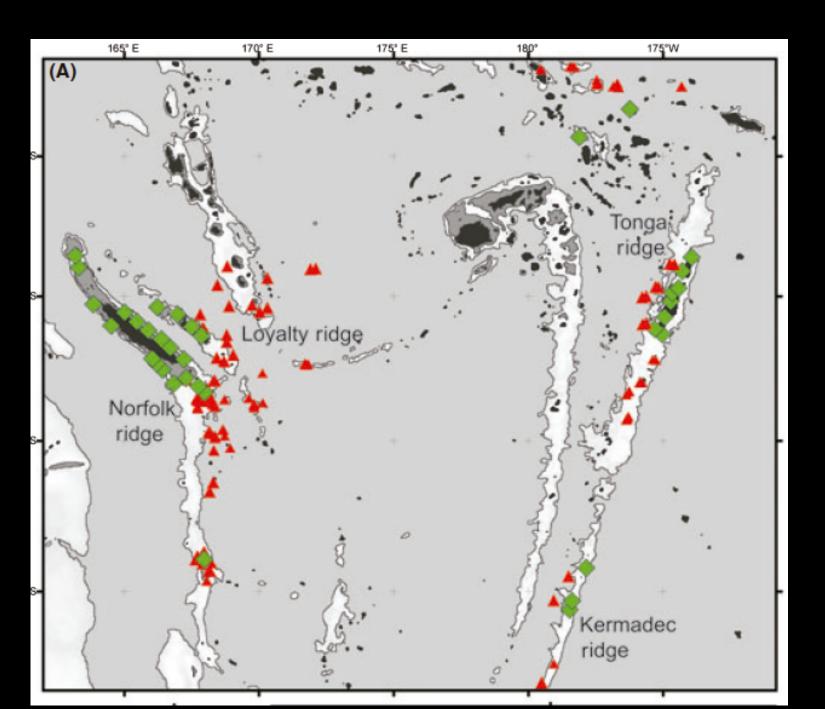


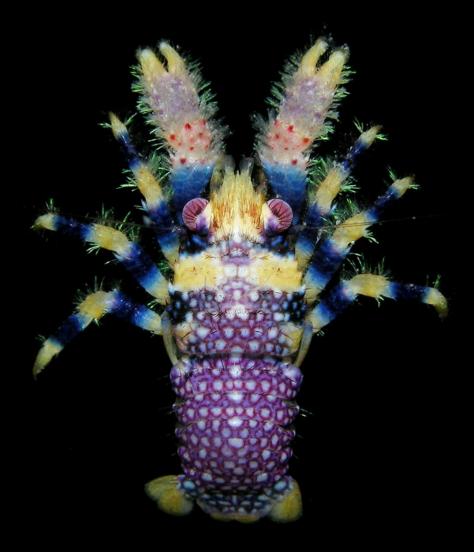




The limitation of gene flow between seamounts appears to be observed only for species with limited dispersal abilities.







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