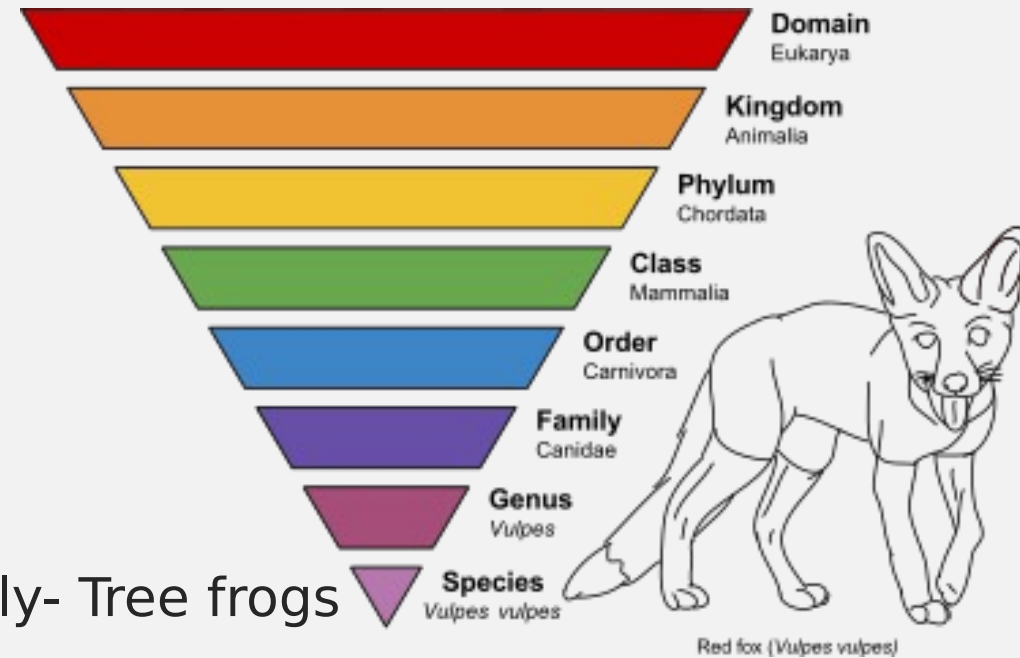


PHYLOGENETICS, CLASSIFICATION, AND BIOGEOGRAPHY OF THE TREE FROGS

Felicia Arias

BACKGROUND

- Anurans: frogs
- Phylogeny:
 1. Family
 2. Subfamily
 3. Genus
 4. Species
- Focus is on Hylidae family- Tree frogs



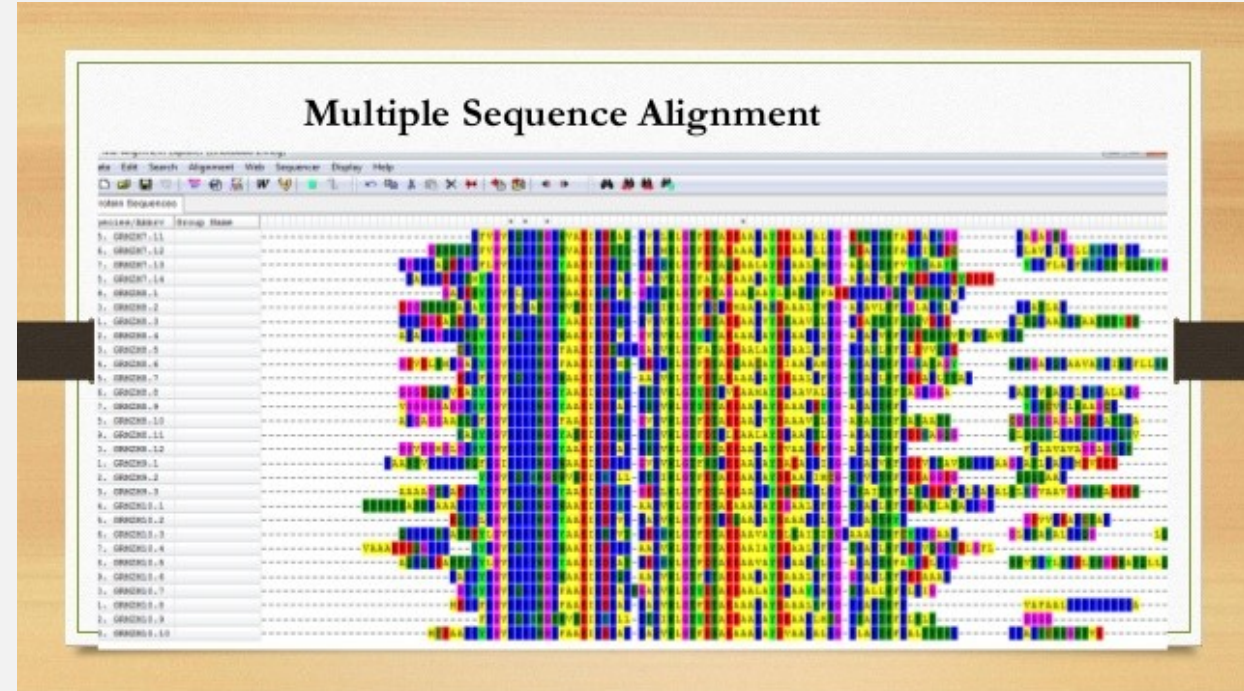
BACKGROUND

- In the past, classification based on morphological factors instead of molecular evidence
- Controversial classifications
- Amphibian Species of the World
- Ex. Wiens- 144 factors, 16S gene
- *Hyla cinerea*



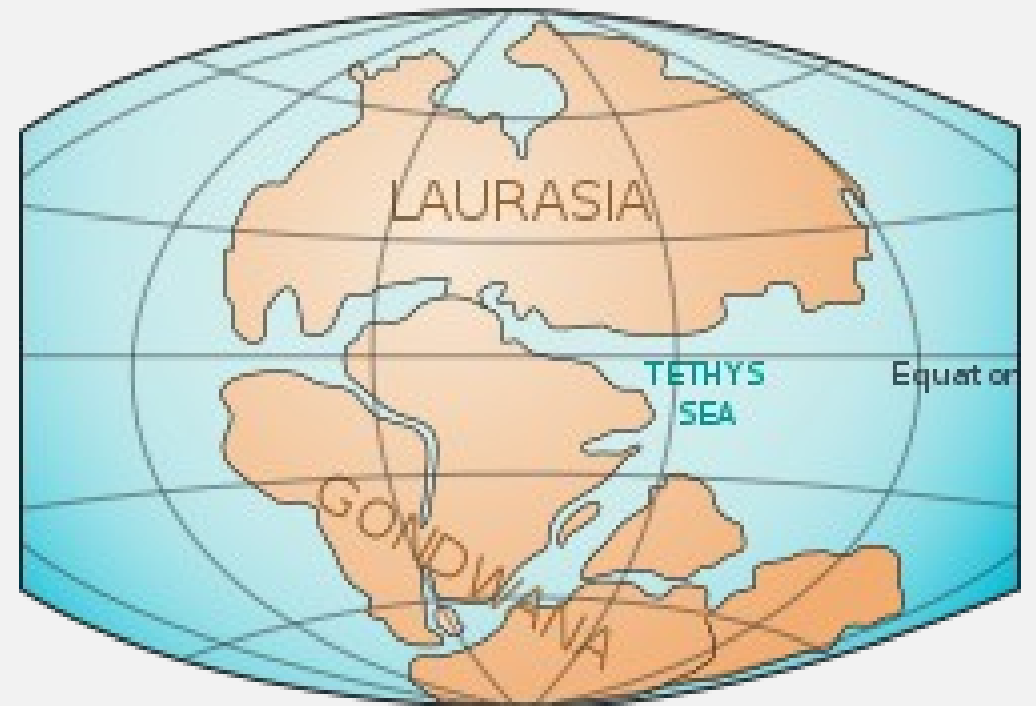
RESEARCH METHOD

- Molecular data
 - GenBank MEGA 5.2
- Sequence alignment construction
- Wiens and additional genes 503 species
 - 16, 128 aligned sites
 - 19 genes
- Studied alongside history of land



GONDWANA

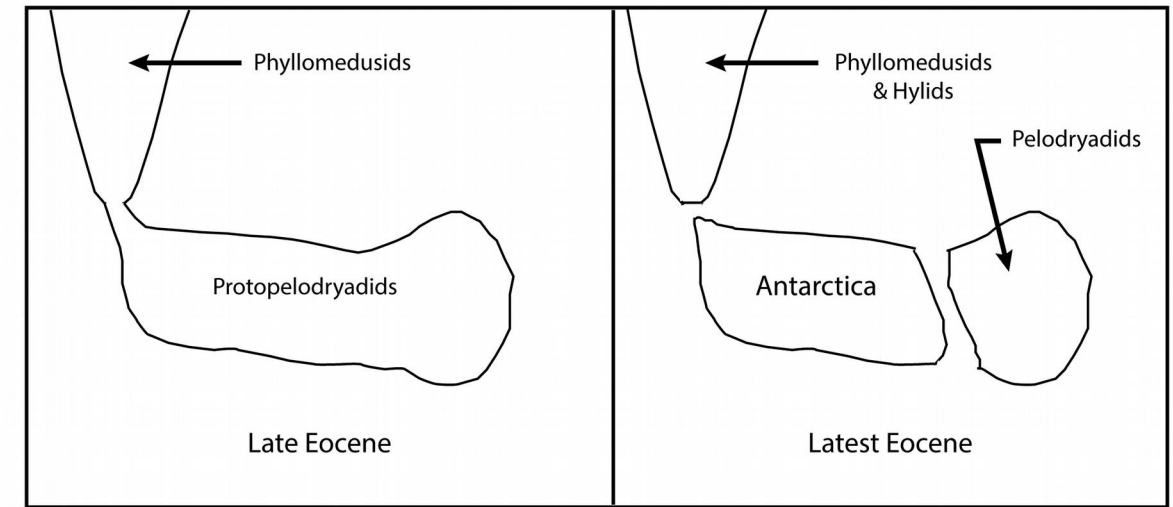
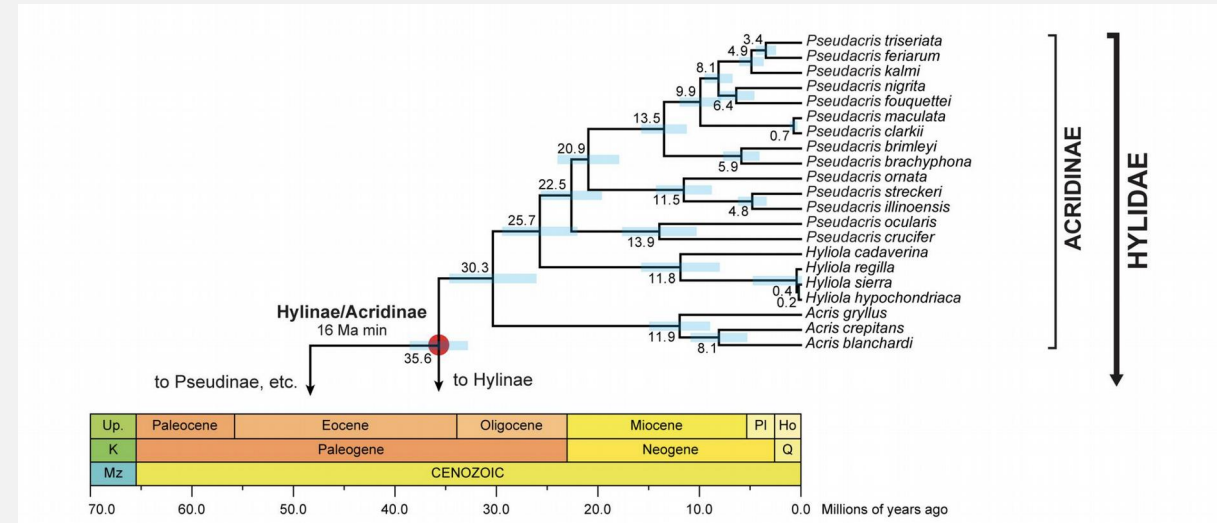
- Last supercontinent = Pangea
 - Broke into two continents; Laurasia (North) and Gondwana (South)
 - Separated by Tethys Sea
- Gondwana consisted of Africa, South America, India, Antarctica, and Australia



TRIASSIC
200 million years ago

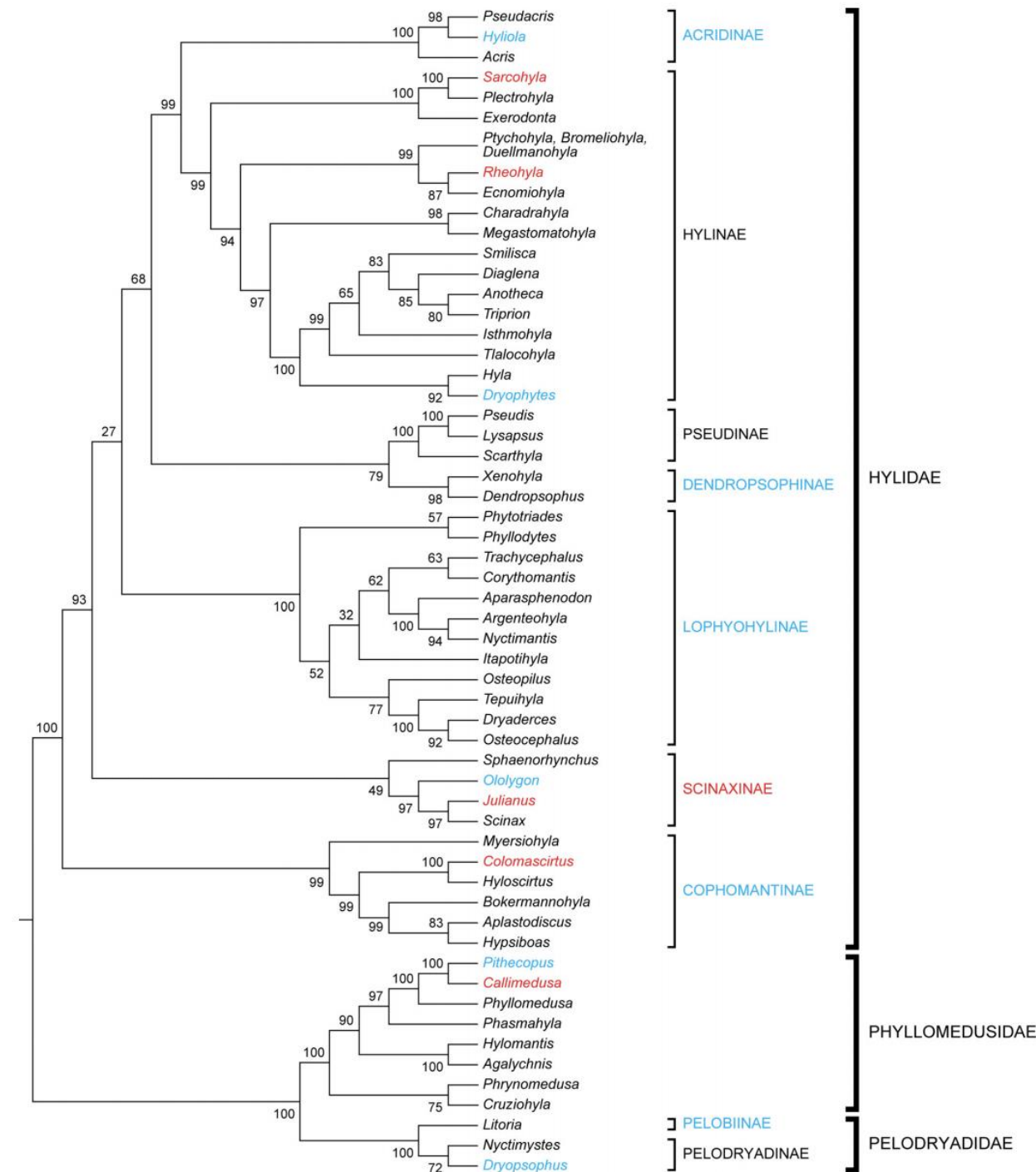
BIOGEOGRAPHY

- Supports Gondwana, after Pangea in Cretaceous period
 - Calculated times and confidence intervals for events
- Dispersal of pelodryadids to Australia



DISCOVERIES

- Transatlantic dispersal of arboranans from south America to Australia vs. transpacific dispersal event from south America to Australasia
- resurrected 5 subfamilies
 - New subfamily
 - Resurrected 6 genera
 - 5 new genera
- Subfamilies moved to family status



CRITICISMS

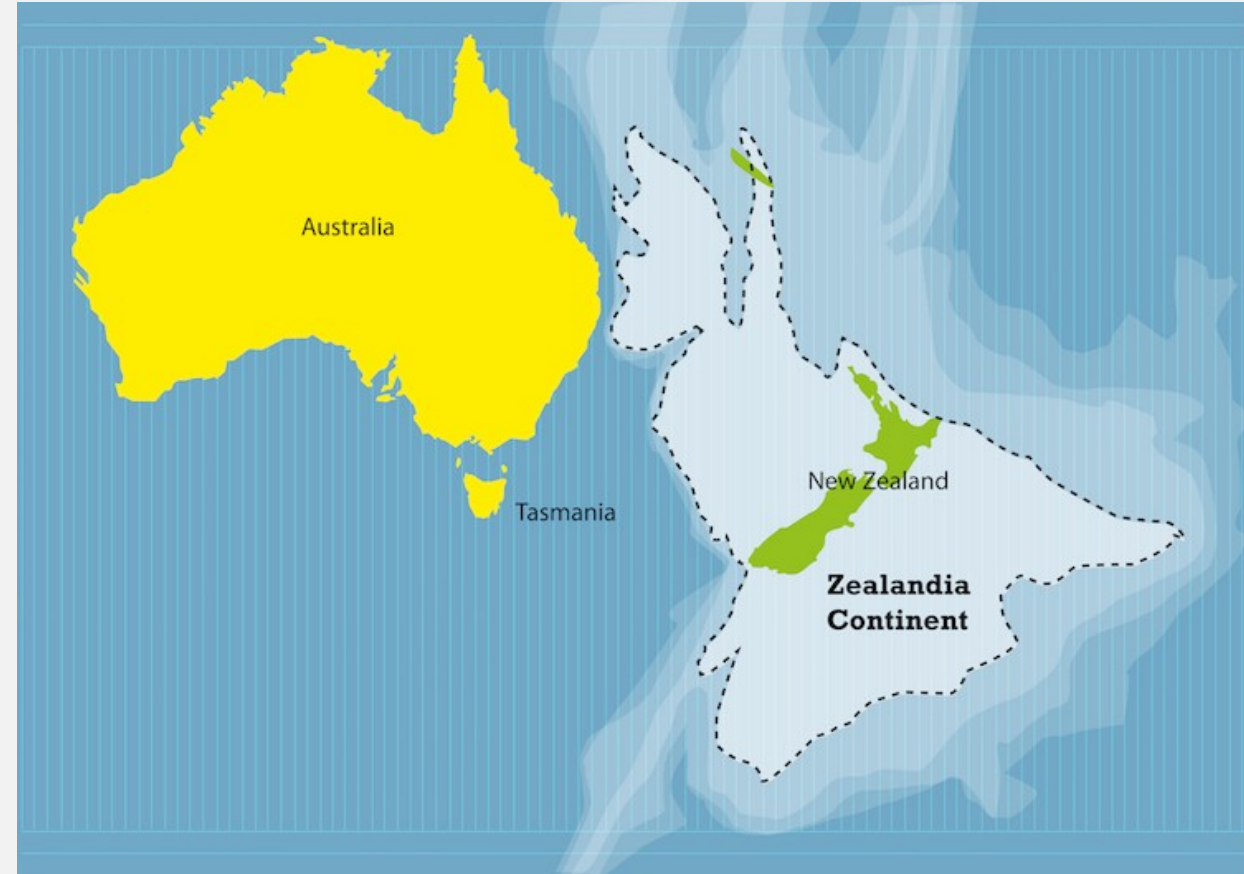
- Their method was similar to the Weins paper
- *Litoria graminea* and *L. sauroni*
- Acknowledge lack of genetic data
- Reliance on morphological factors for *N. Dux*



GOING UNDER DOWN UNDER? LINEAGE
AGES ARGUE FOR EXTENSIVE SURVIVAL
OF THE OLIGOCENE MARINE
~~TRANSGRESSION ON ZEALANDIA~~

BACKGROUND

- Zealandia is submerged continent
 - Separation 82 mya
 - Prevailing theories:
 - 1. Zealandia completely submerged, New Zealand rose
- 2. New Zealand has always existed and has never flooded
 - OMT = Oligocene Marine Transgression, submersion of Zealandia



METHODS

- Data collection was very thorough in order to get a wide range of possible dispersal dates
- Taxons and sister groups included rank of split, common group name, gene, and origin
- Most importantly, documented time of split (Mean, Min , and Max is time in MYA)
- Purpose for data collection is to tract divergence (split)

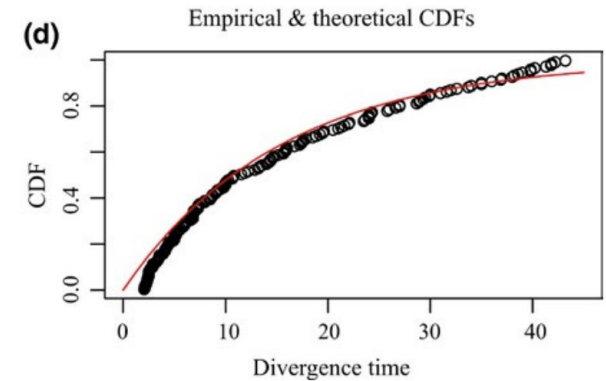
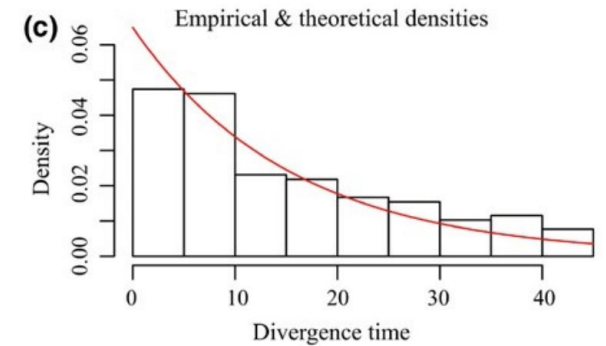
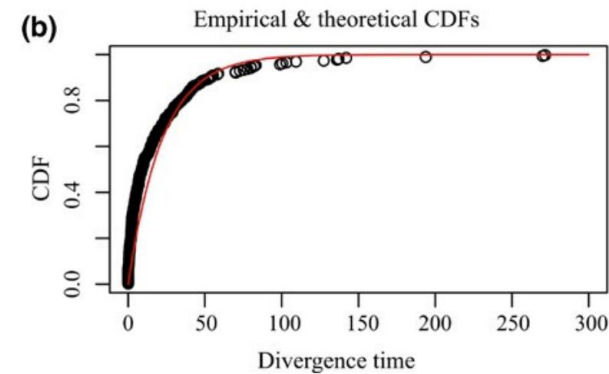
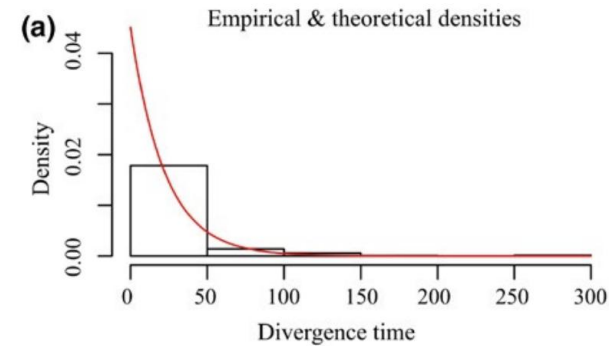
TABLE 1 Data set of published molecular clock estimates of divergence times between NZ lineages and their closest overseas relatives

NZ taxon	Sister group split	Rank of split	Common name/group	Genes	Calibration per Ma	Origin	Age				References
							AAR	Mean	Min	Max	
<i>Sphenodon</i>	Squamata	Order	Tuatara	RAG1	12 secondary	Archaic	n	271.5	268	275	Hugall et al. (2007)
<i>Craterostigma crabilli</i>	<i>C. tasmanianus</i>	Species	Centipede	Review	Several	Archaic	n	270	180	318	Giribet and Boyer (2010)
Leiopelmatidae	Ascaphidae	Family	Frog	95 nucl prot genes (+RAG1, CXCR4)	Fossils (20)	Archaic	y	193.8	178.6	207	Feng et al. (2017)
<i>Neopurcellia</i> , <i>Aoraki</i> , <i>Rakaia</i>	<i>Chileogovia</i> , <i>Purcellia</i>	Genus	Mite harvestman	cox1, 16S, 18S, 28S, H3	Fossils (2)	Archaic	y	142			Giribet et al. (2012)
<i>Paralamyctes</i> sp.	<i>Paralamyctes</i> sp.	Species	Centipede	Review	Several	Archaic	n	137			Giribet and Boyer (2010)
<i>Paraneophraps</i>	<i>Spinastacoides</i> , <i>Ombrostacoides</i>	Genus	Crayfish	16S, cox1, 18S, 28S	Fossils (6)	Archaic	n	136	109	160	Toon et al. (2010)
<i>Uropetala carovei</i>	<i>Phenes</i> , <i>Petalura</i> spp.	Genus	Petalurid dragonfly	cox1, cox2, cytb, 12S, 16S, 18S, 28S, H3	Fossils (4)	Archaic	y	127.4	80	175	Ware et al. (2014)
<i>Lepidothamnus laxifolius</i>	<i>L. fonckii</i>	Species	Mountain rimu	rbcL	Fixed rate	Archaic	n	109.3	70.1	148.5	Wardle et al. (2001)
<i>Griselinia littoralis</i> , <i>G. lucida</i>	Apiaceae, Myodocarpaceae, Araliaceae, Pittosporaceae	Family	Broadleaf	rpl16 intron, trnD-trnY-trnE-trnT	Fossils (6)	Archaic	y	103.06	90.2	115.84	Nicolas and Plunkett (2014)
<i>Nesamblyops</i>	16 genera	Genus	Carabid beetle	cox1, cox2, rnl+trnL+nad1, SSU, LSU	Fossil + island emergence + fixed clock <i>Carabus</i>	Archaic	n	100.4	70.4	134.5	Andújar et al. (2016)
<i>Schistochila (Scaphilae) glaucescens</i>	4 subgenera	Subgenus	Liverworts	rbcL, Rps4, trnL-F	Fossils (7) + plastid rate 0.05%	Archaic	y	98.92			Sun et al. (2014)
<i>Beaupresadites</i> spp. (†) to 1 Ma	<i>Beauprea</i>	Genus	Proteaceae	matK, rbcL, trnL intron, trnL-trnF, atpB, atpB-rbcL, rpl16 intron, ITS	Fossil pollen	Archaic	n	83	82.5	83.5	He, Lamont, and Fogliani (2016)
<i>Callaria</i> , <i>Gyrothyris</i> , <i>Neothyris</i> , 'Terebratella' sp.	Magellanic genera (4)	Genus	Long-looped brachiopod	cox1, SSU, LSU	Fossils (8)	Archaic	n	82	48	120	Cohen et al. (2011)
<i>Hemiandrus</i> spp. (6)	<i>Exogryllacris</i> , <i>Hypocaphoides</i> , <i>Penalva</i> , genus B, H. sp.	Genus	Ground weta	cox1, 28S	82 Ma plus relaxed cox1 insect rate 0.7%-1.2%	Archaic	n	80			Pratt et al. (2008)

(Continues)

DISCOVERIES

- More evidence for 2nd theory
- Shown by divergence charts
 - No drop
- Australia contributes to most of lineages on New Zealand
- Number has dwindled since drifting



DISCOVERIES

- Number of lineages high before Oligocene
- Zealandia submerged during Oligocene
- 74 lineages (Miocene) survived OMT

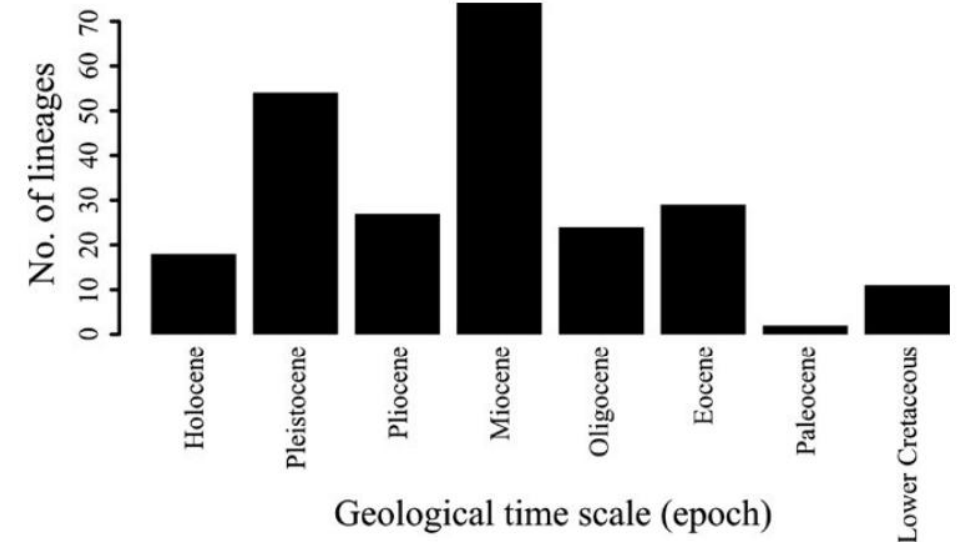


FIGURE 3 Histogram of divergence times grouped by epoch

CRITICISMS

- Fossil record is best suited for tracking continued existence after OMT
- Fossil record was not used for this paper
- Fossil record not completely reliable either
 - Early records can be lost

