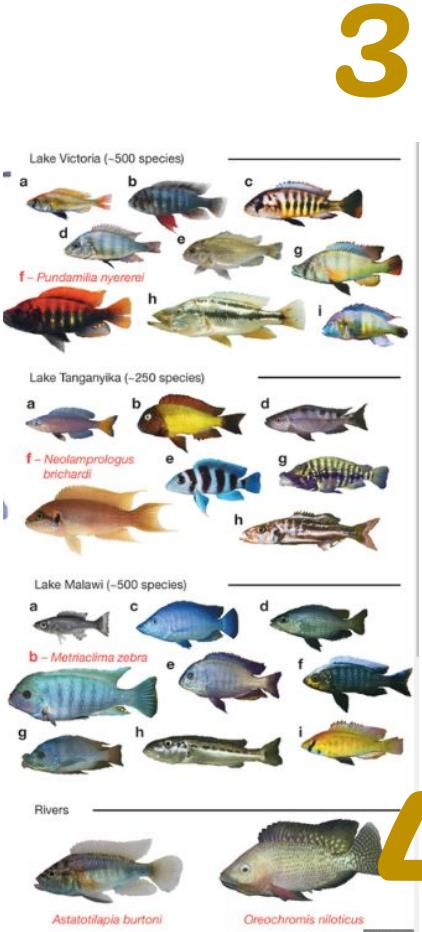
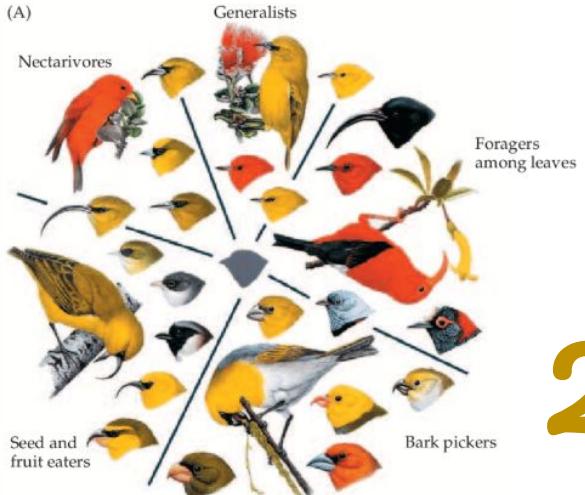
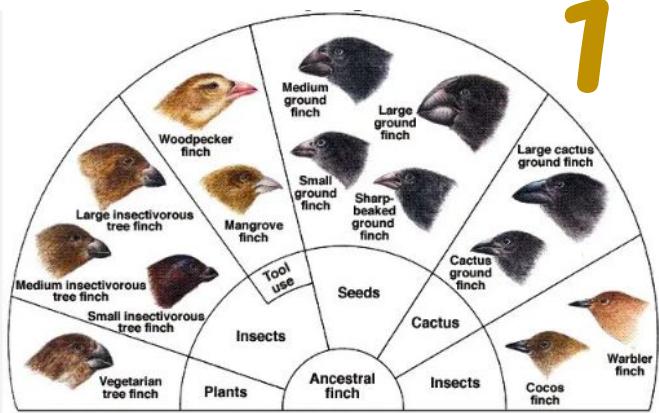


Practico 03

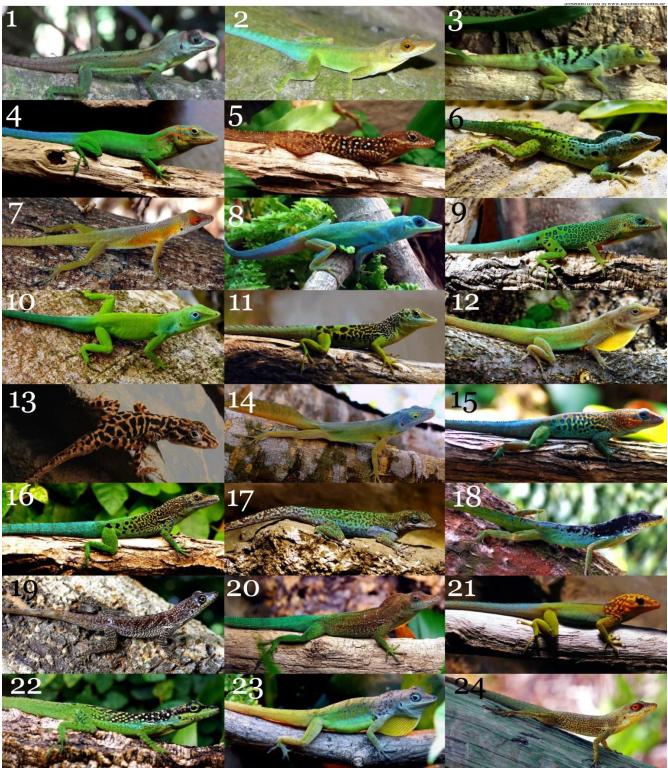
Patrones de Diversificación

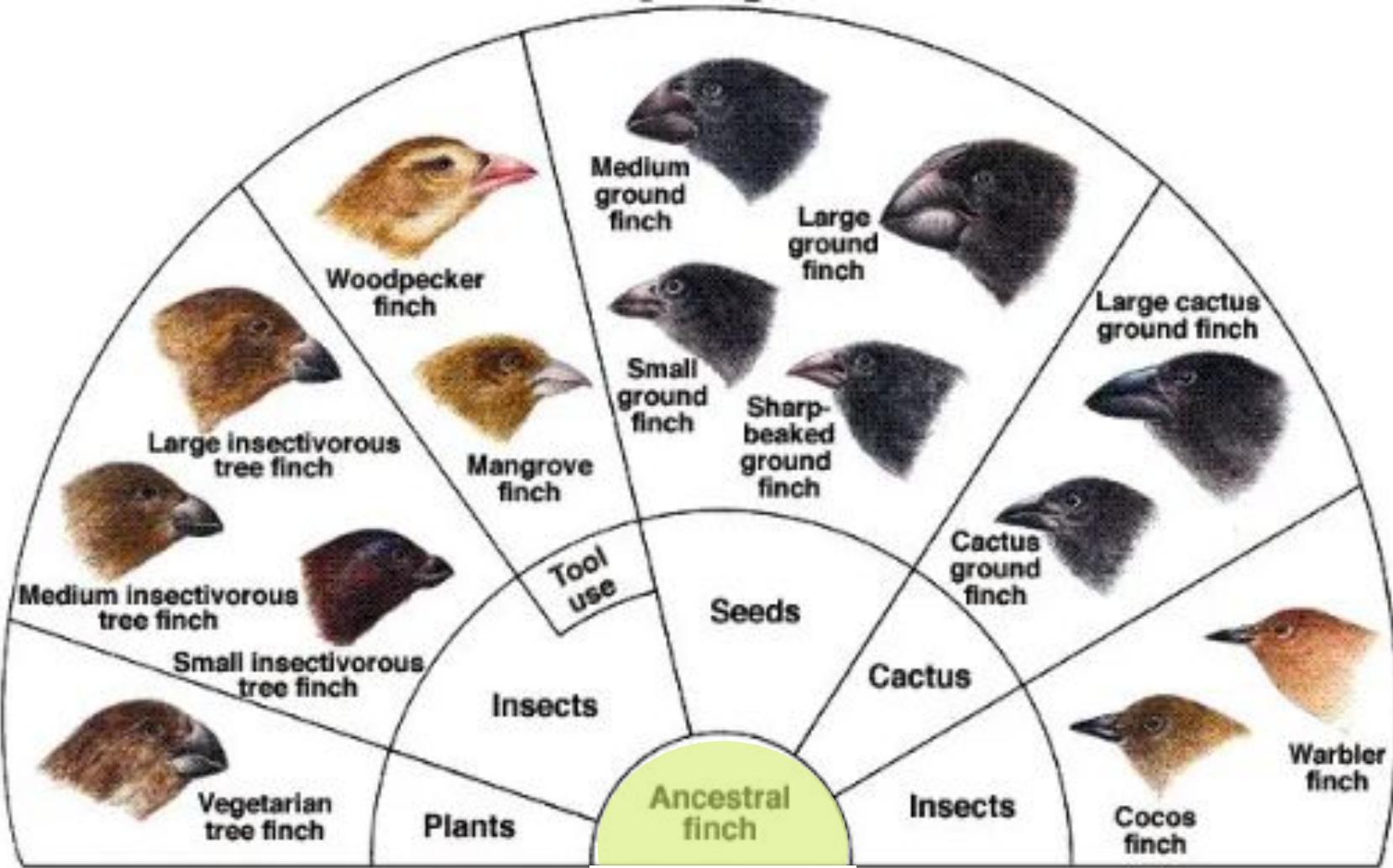
Agosto 2025

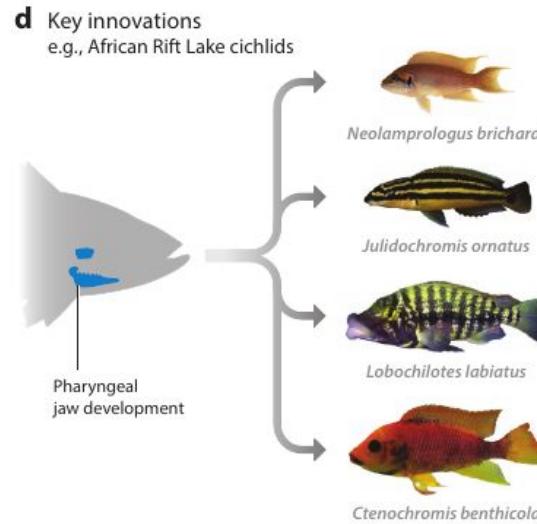
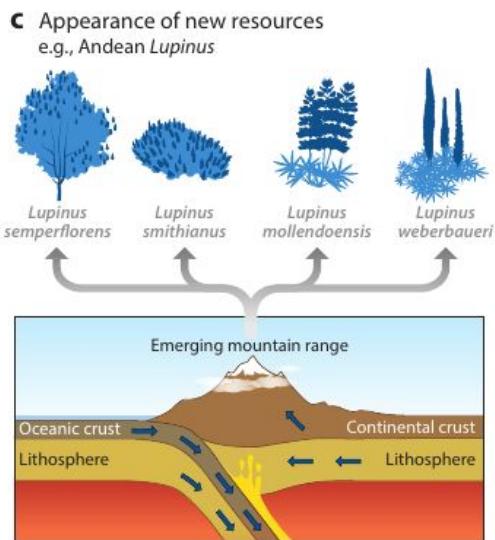
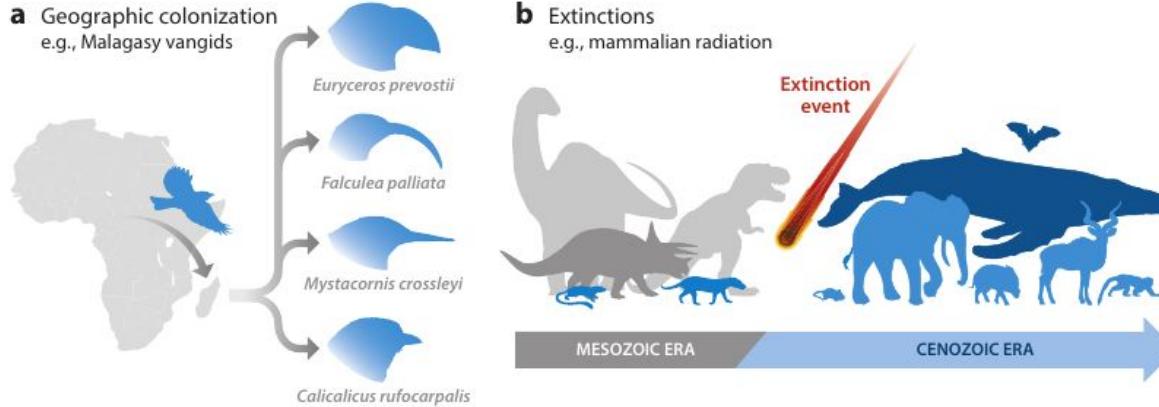
Curso Evolución 2025



1. Darwin's finches (genus *Geospiza*)
2. Hawaiian honeycreepers (family Fringillidae)
3. African cichlids (family Cichlidae)
4. Anolis lizards (genus *Anolis*)

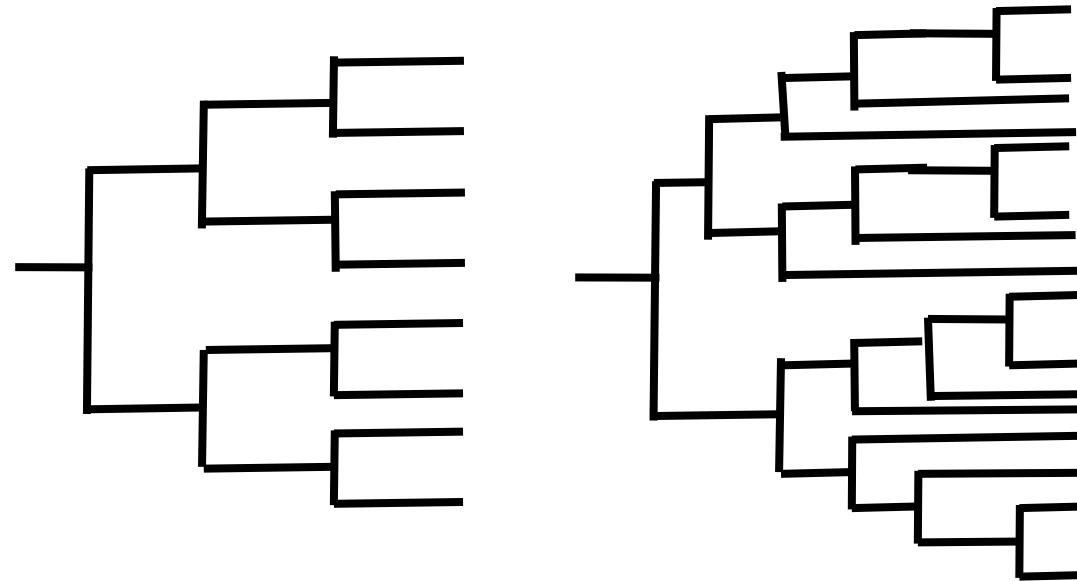




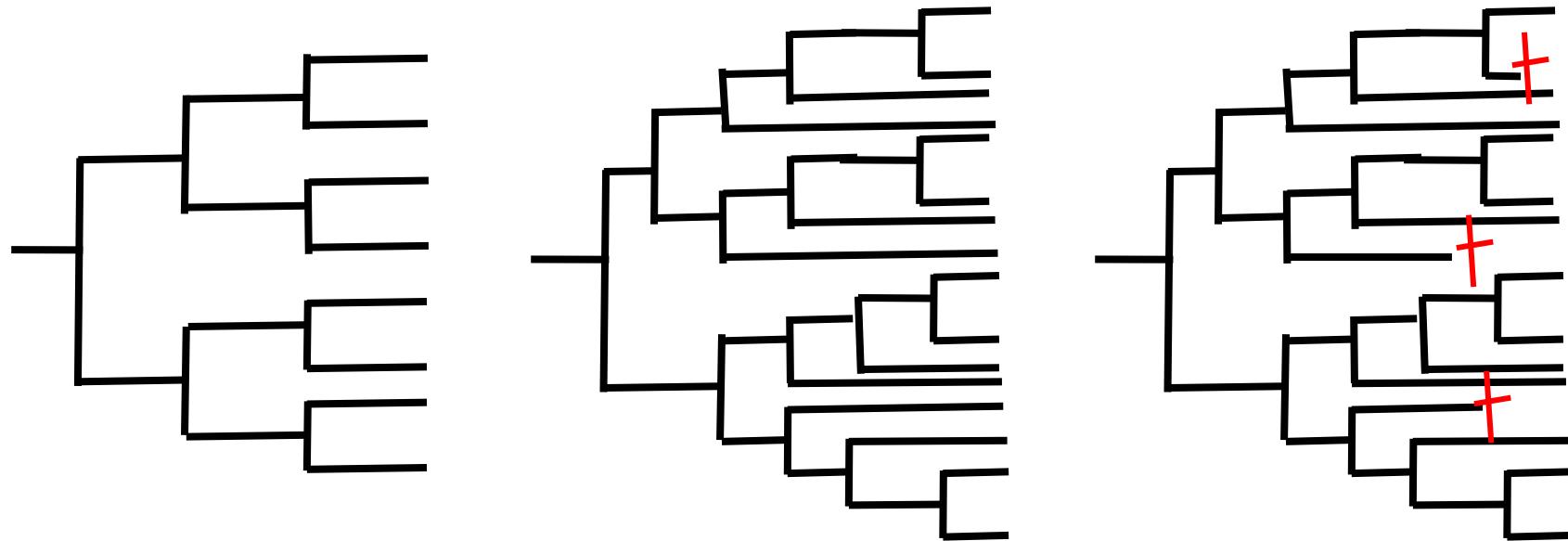


Queremos identificar un patrón.
Ahora...¿cómo lo detectamos?

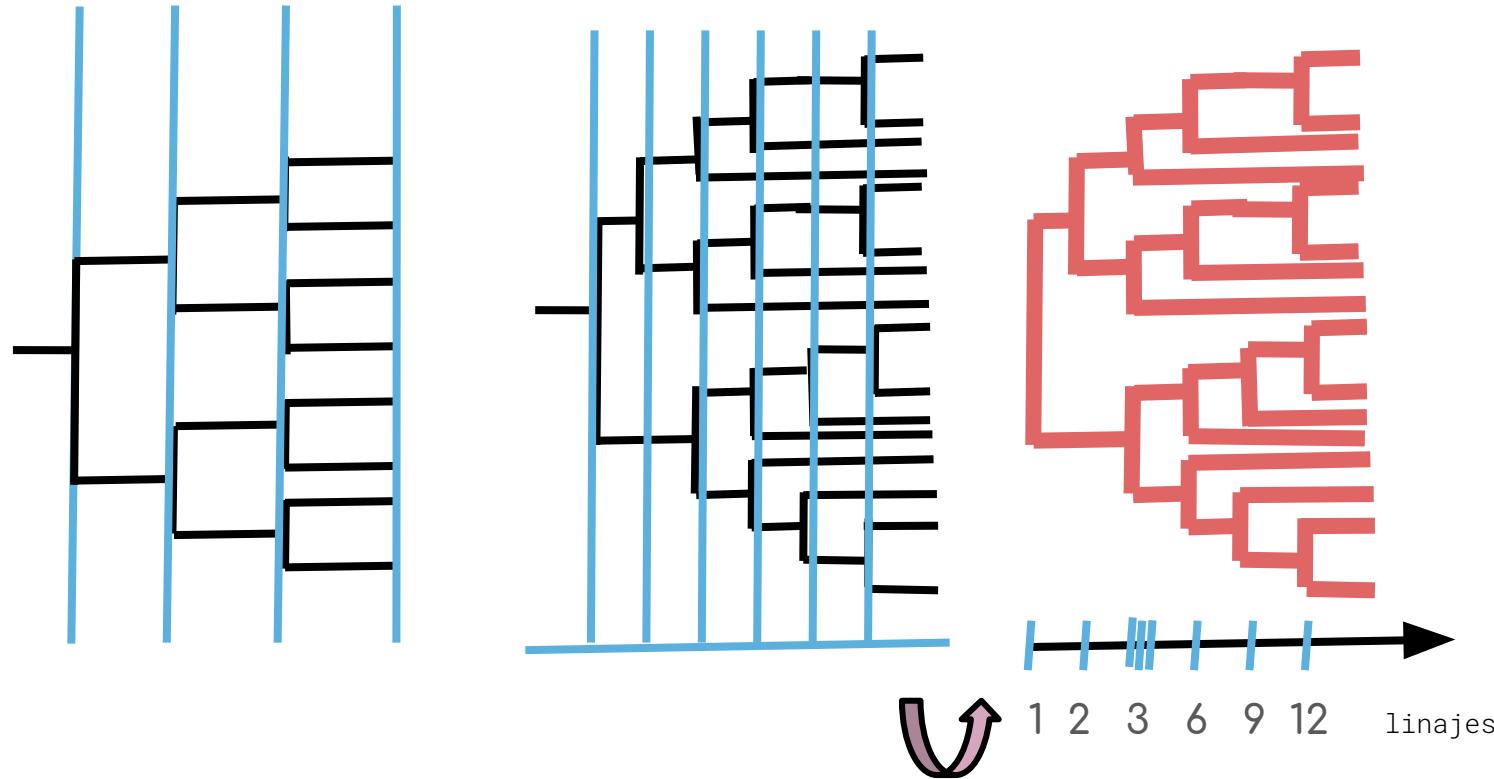
Un modelo de **nacimiento puro** es un modelo simple de evolución en el que la especiación ocurre a un ritmo constante y no hay extinción. Según un modelo de nacimiento puro, se espera que los intervalos entre nodos de una filogenia estén distribuidos uniformemente. Sin embargo, si la tasa de diversificación ha cambiado con el tiempo, los intervalos entre nodos estarán sesgados frente a lo esperado. El estadístico gamma mide este sesgo (o corrimiento) en los intervalos entre nodos.



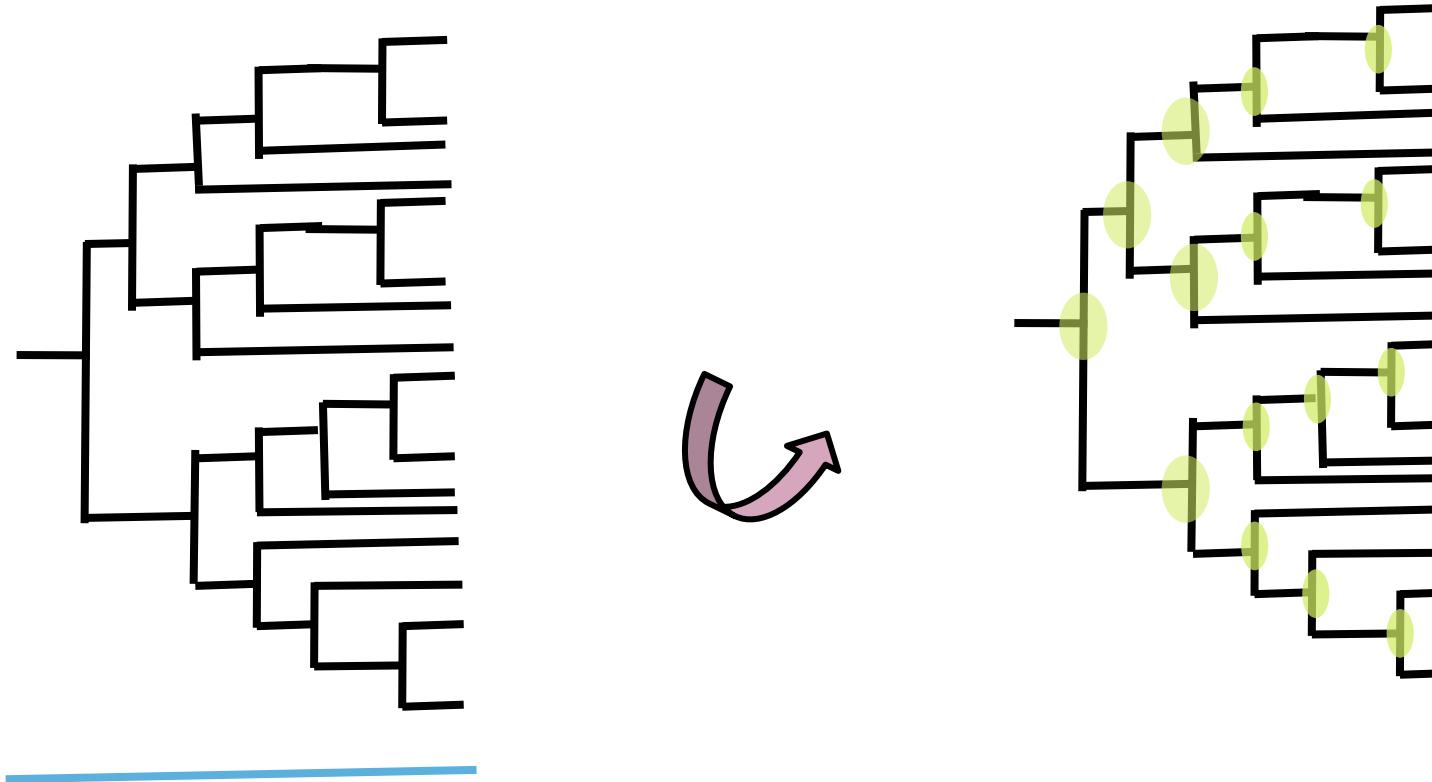
Luego del modelo de **nacimiento puro** (pure birth) surgieron modelos de **nacimiento y muerte** (birth-death) más "realistas"

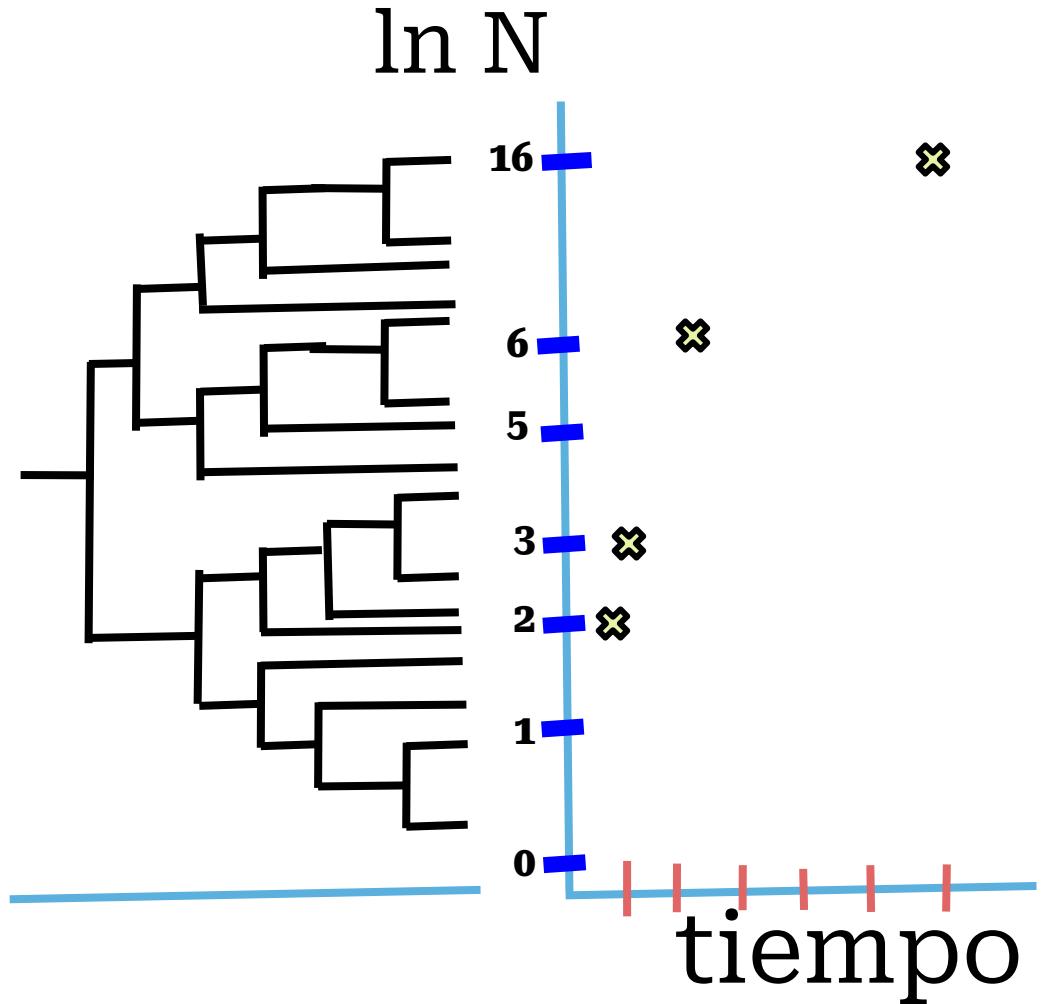


nos importa acá el **ritmo** de aparición de linajes



nos importa acá el **ritmo** de aparición de linajes
y el **número** de linajes





aplicación



Caribe



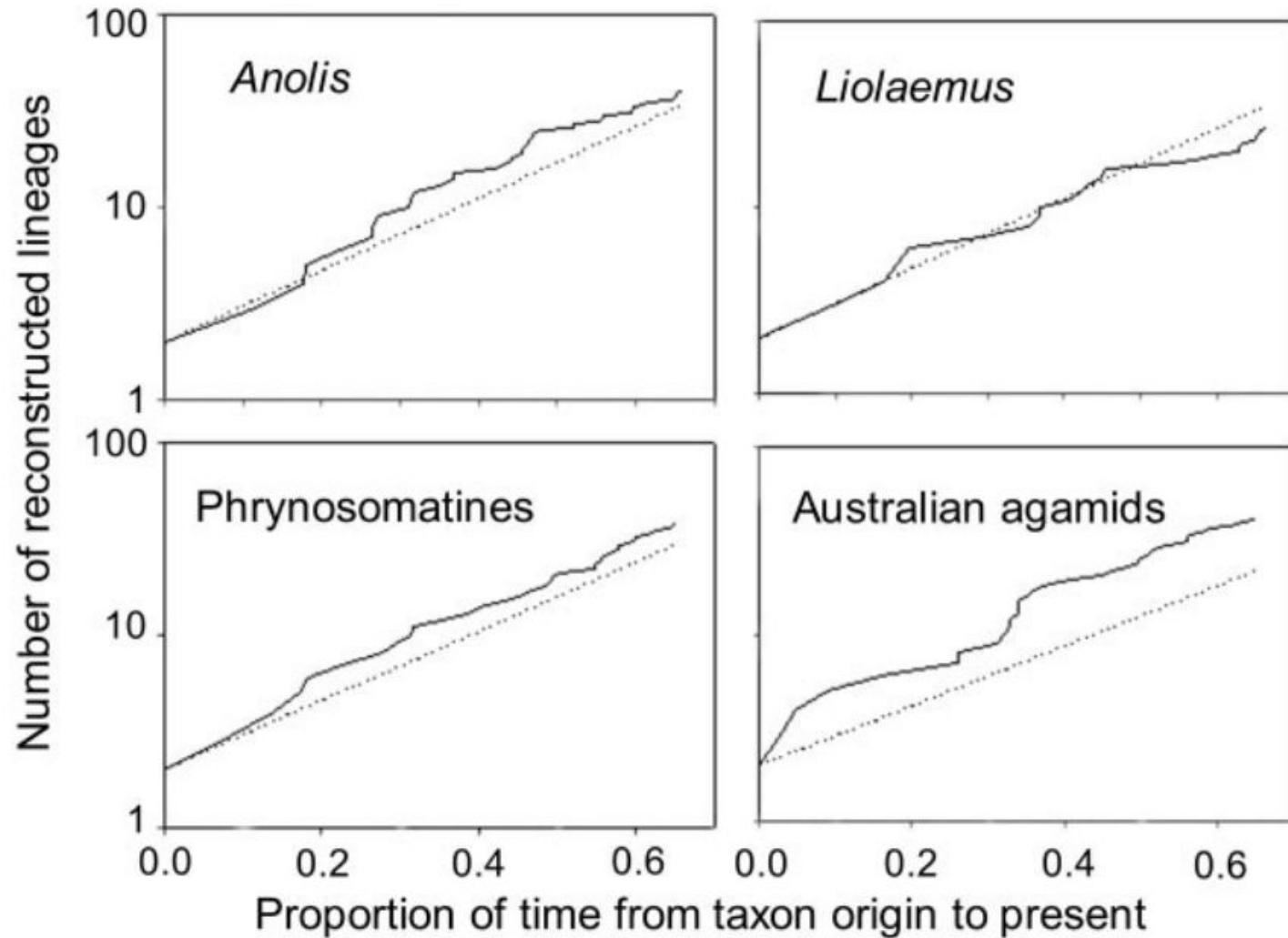
Sudamérica

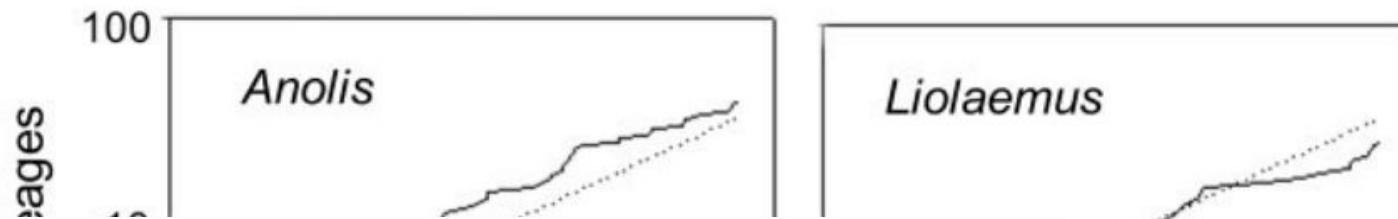


Am Norte



Australia





> Science. 2003 Aug 15;301(5635):961-4. doi: 10.1126/science.1084786.

Tempo and mode of evolutionary radiation in iguanian lizards

Luke J Harmon ¹, James A Schulte 2nd, Allan Larson, Jonathan B Losos

Phrynosomatines

Australian anamids

Fig. 1. Lineage accumulation curves for four lizard taxa compared with expectations under the null pure-birth model. Time is expressed as a proportion of the total time since the first cladogenetic event inferred for the taxon. Only the first two-thirds of each phylogeny is shown. Expected curves are obtained using an exponential model with the first branching in a clade set to time = 0 and the number of extant species (Table 1) set to time = 1. Solid line, actual number of reconstructed lineages for the clade; dashed line, expected number of lineages under the null pure-birth model.

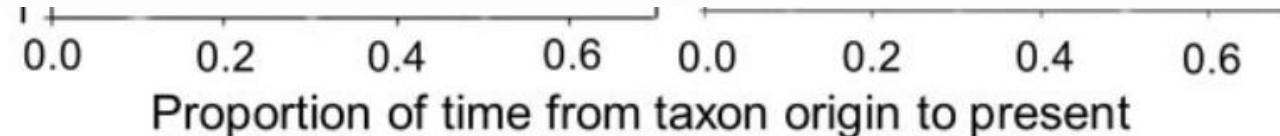


Table 1. γ statistics (20) and maximum-likelihood estimators (MLE) for the δ statistic (26) for the four lizard taxa included in the study. The γ statistic measures whether internal nodes of a phylogeny are closer to the root than would be expected under a model of constant diversification rates ($\gamma = 0$). Significant P values for a negative value of γ indicate a slowdown of the rate of cladogenesis over the history of the taxon. P values were adjusted for level of sampling with the Markov chain constant rates (MCCR) test with 1000 simulations (20). The δ statistic measures the extent to which rates of morphological evolution have changed through the history of the group, with values greater than 1 indicating accelerating evolution and values less than 1 indicating deceleration. P values were determined from likelihood-ratio tests against a model with constant rates of morphological evolution (26). Although MDI and δ statistic values are related ($r = 0.89$), Australian agamids do not show a slowdown in the rates of morphological evolution based on the δ statistic, as would be expected from the disparity-through-time analysis (Fig. 2). This is likely the result of missing taxa in the phylogeny. The majority of missing species are very closely related and morphologically similar to species that are included in the analysis; not including these species thus masks the overall pattern of a slowdown of morphological evolution. For this reason, we calculated MDI over only the first two-thirds of the disparity-through-time plots.

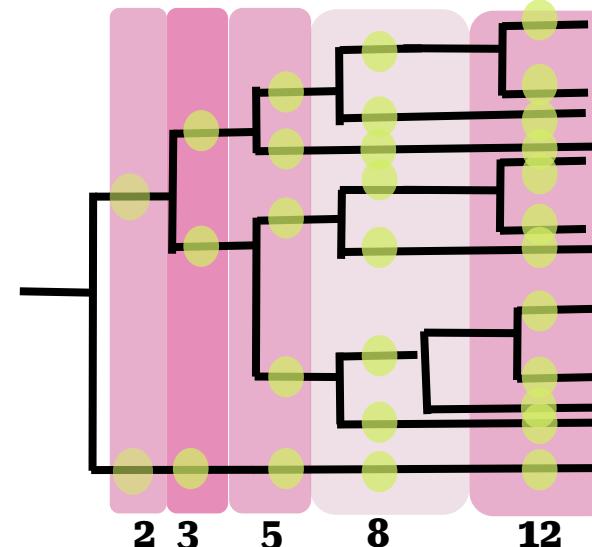
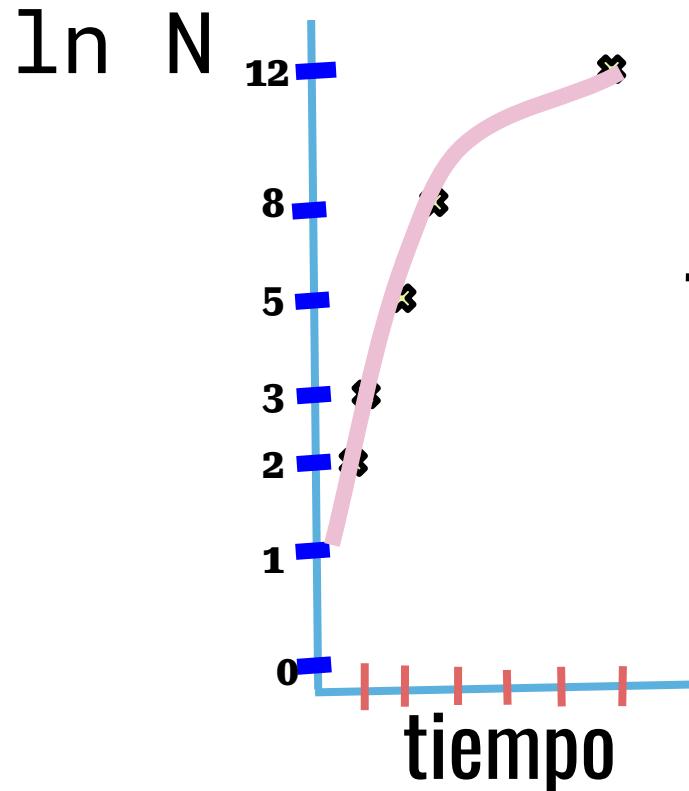
Clade	No. of species included in phylogeny	Total no. of species in clade	γ statistic	MCCR corrected P value	δ statistic (MLE)	P value
<i>Anolis</i>	112	147	-3.077	0.005	1.883	0.01
<i>Liolaemus</i>	69	149	-2.253	0.23	3.000	<< 0.0001
Phrynosomatines	71	124	-5.438	< 0.001	1.369	0.16
Australian agamids	69	79	-4.502	< 0.001	1.082	0.86

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gamma es una medida estadística que se utiliza para evaluar el ajuste de un modelo de nacimientos/muertes o tasa constante a un árbol filogenético. Se mide entonces la desviación de los intervalos entre nodos de una filogenia con respecto a una distribución uniforme, lo que sería de esperar en un modelo de nacimientos y muertes de tasa constante.

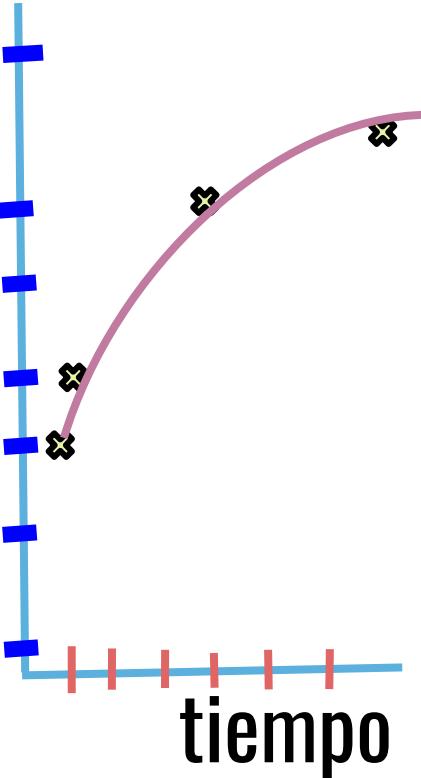
	phylogeny	in clade	statistic	P value	(MLE)	
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¿Cuál es la expectativa si aparecieron muchos linajes temprano y luego decrecen los eventos de especiación?



valores significativos son
 $\gamma \leq -1.645$
(test 1 cola $\alpha=0.05$)

ln N



Algunas puntuaciones...

- se suele usar el MCCR test para estimar el p-value de gamma (que corrige por spp faltantes en el árbol)
- para ver tasas de especiación y su asociación con otros rasgos etc se usan otras estrategias (y otros paquetes)
- para comparar o detectar distintas tendencias se usan otros métodos/paquetes.

The global diversity of birds in space and time

W. Jetz^{1*}, G. H. Thomas^{2*}, J. B. Joy^{3*}, K. Hartmann⁴ & A. O. Mooers³

8γ

LETTER

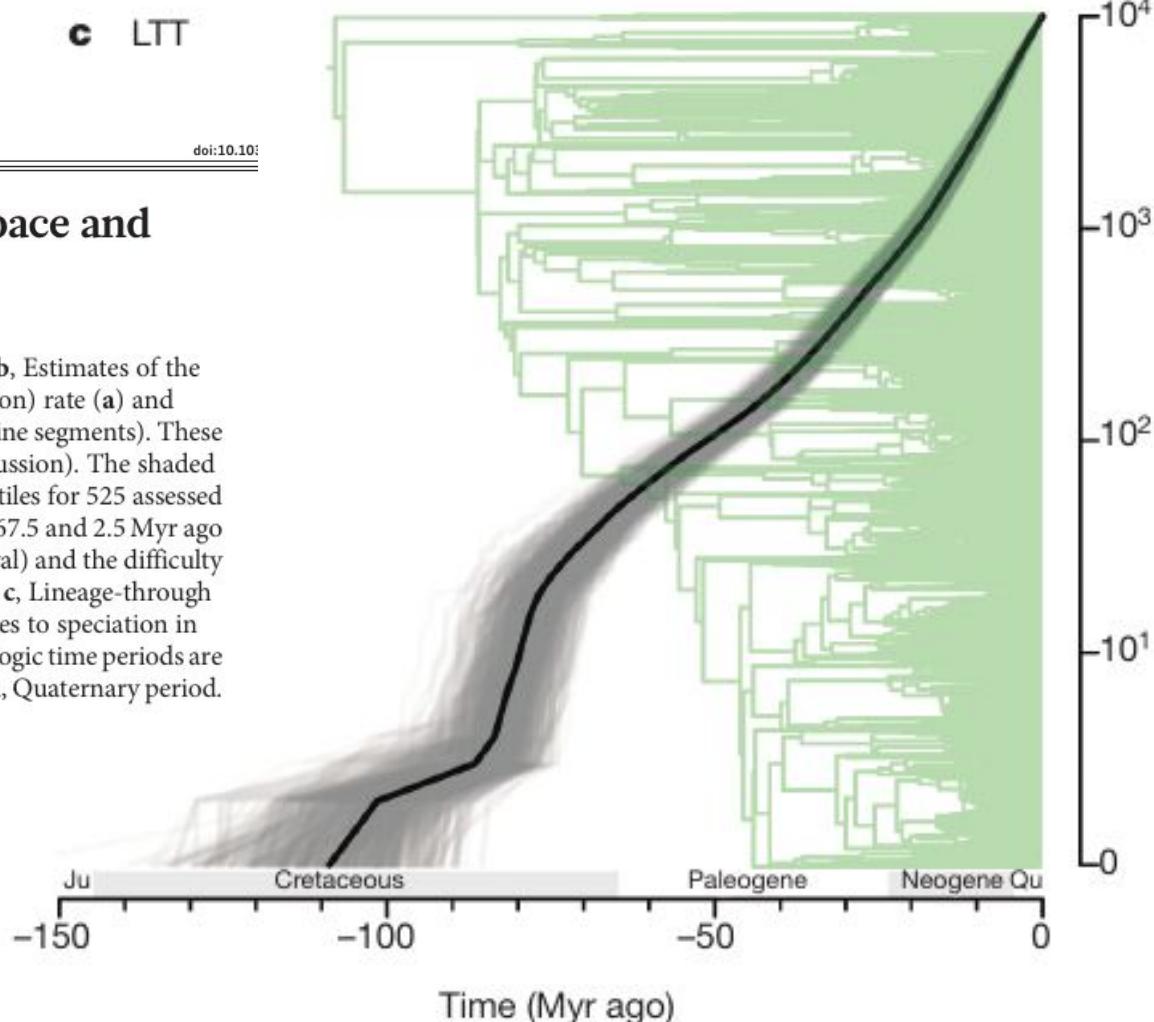
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doi:10.1038/

The global diversity of birds in space and

W. Jetz^{1*}, G. H. Thomas^{2*}, J. B. Joy^{3*}, K. Hartmann⁴ & A. O. Mooers³

Figure 1 | Diversification of all birds through time. a, b, Estimates of the tree-wide lineage net diversification (speciation – extinction) rate (a) and speciation rate (b), calculated in 5 million year intervals (line segments). These are estimated to be very similar (see Supplementary Discussion). The shaded region represents the area between the 5th and 95th quantiles for 525 assessed trees with the mean rate traced in black. Intervals outside 67.5 and 2.5 Myr ago are not shown due to lack of data (≤ 30 lineages per interval) and the difficulty of accounting for ongoing speciation events, respectively. c, Lineage-through time plot for 1,000 trees (in grey), with mean waiting times to speciation in black. Green background is the tree depicted in Fig. 2. Geologic time periods are delineated at the bottom of the plot. Ju, Jurassic period; Qu, Quaternary period.



the end

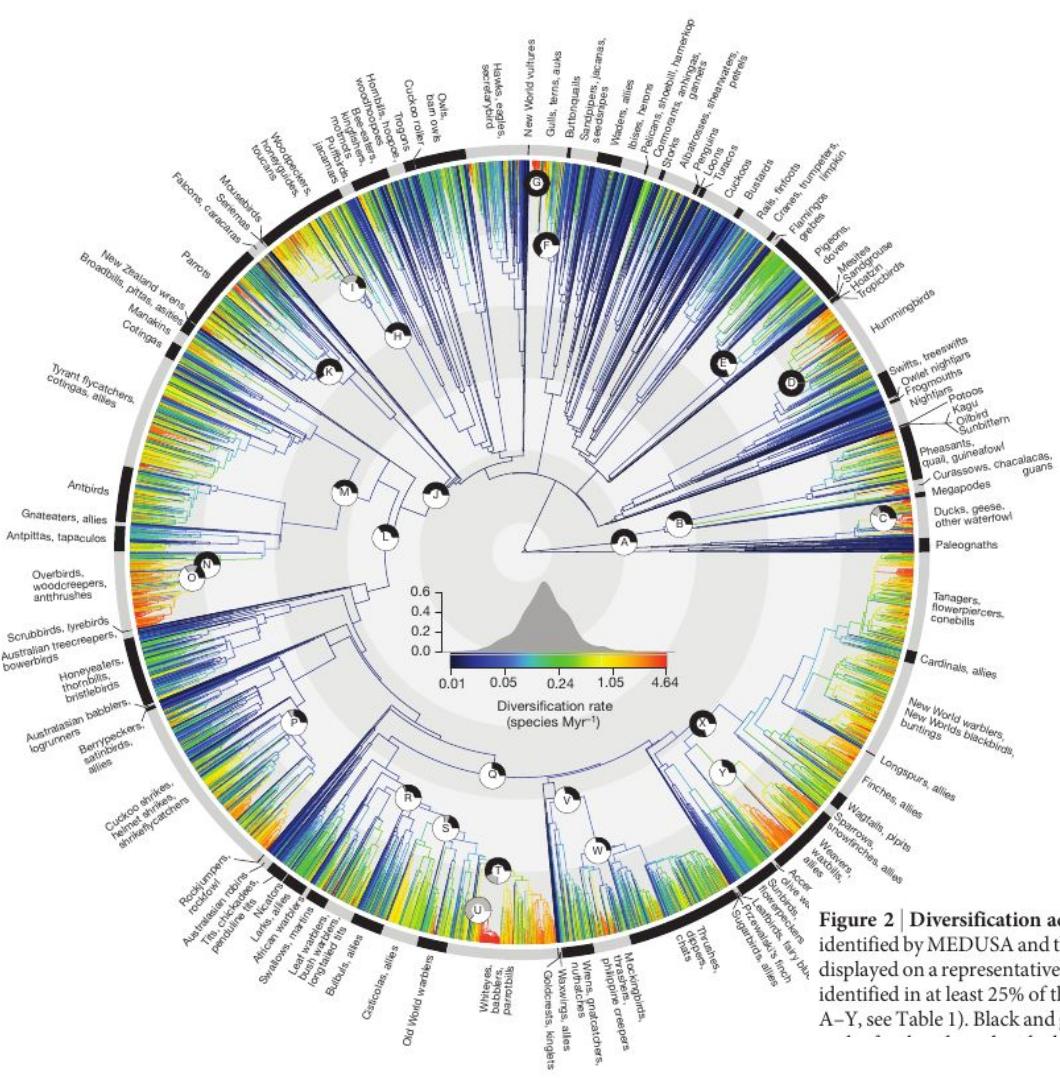


Figure 2 | Diversification across the avian tree. Diversification rate shifts identified by MEDUSA and the species level diversification rate metric (DR) are displayed on a representative avian tree. Nodes with shifts in diversification rate identified in at least 25% of the tested trees are indicated by pie-charts (labelled A–Y, see Table 1). Black and grey areas show the proportion of trees with a shift

Table 1 | Rate shifts found in at least 25% of sampled trees.

Node	English	Scientific	Age	r	Species
G	Select gulls	Select Laridae	4.6 (0.0)	0.74	44
U	White-eyes, select babblers	Zosteropidae, select Timaliidae	8.1 (0.1)	0.49	113
N	Ovenbirds, woodcreepers	Dendrocolaptidae, Furnariidae	17.8 (0.1)	0.28	285
[O]	- Ovenbirds	- Furnariidae	13.6 (0.1)	0.31	223
C	Select ducks, geese	Anseriformes	10.8 (0.1)	0.28	109
T	Babblers, white-eyes	Timaliidae, Zosteropidae	17.7 (0.1)	0.27	355
Y	Weavers, estrildid finches	Ploceidae, Estrildidae	21.9 (0.2)	0.24	278
H	Woodpeckers and allies	Ramphastidae, Indicatoridae, Picidae	36.4 (0.3)	0.17	361
[I]	- Woodpeckers	- Picidae	23.8 (0.2)	0.21	220
X	Passeroidea songbirds	Passeroidea	35.7 (0.1)	0.20	1,418
D	Select hummingbirds	Select Trochilidae	20.7 (0.1)	0.19	266