

Evolución del genoma

Evolución Orgánica

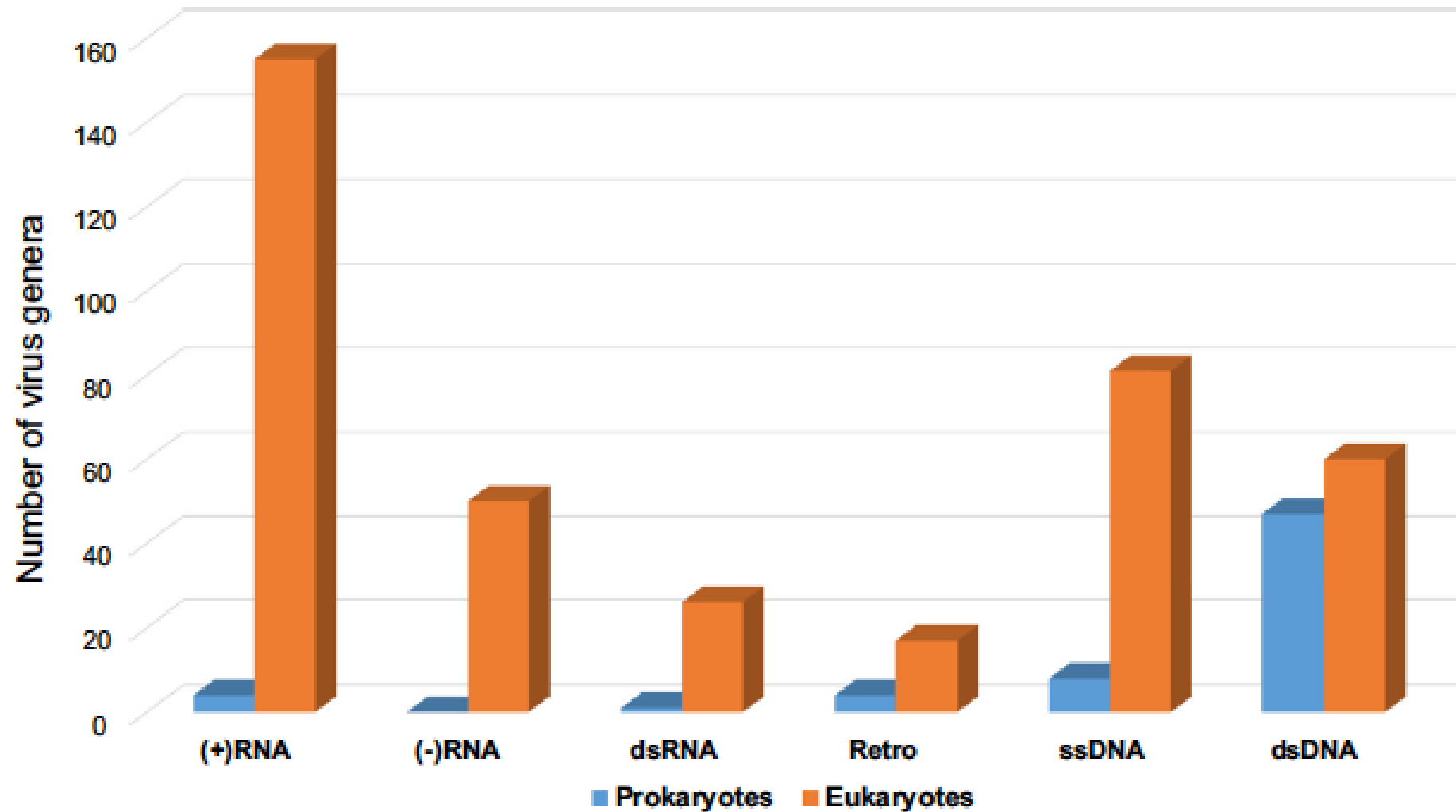
B-405

II Semestre 2024

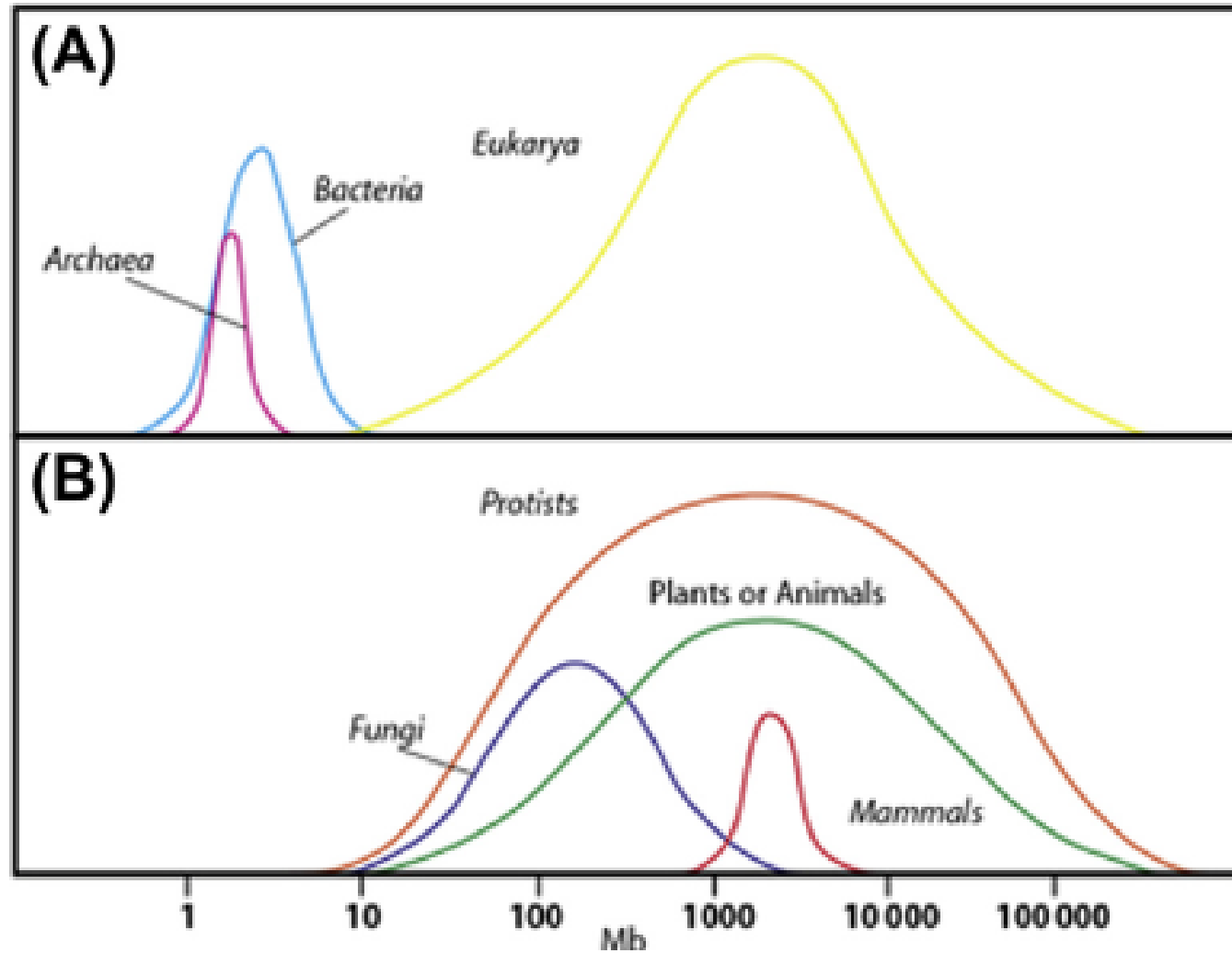
Temas a revisar

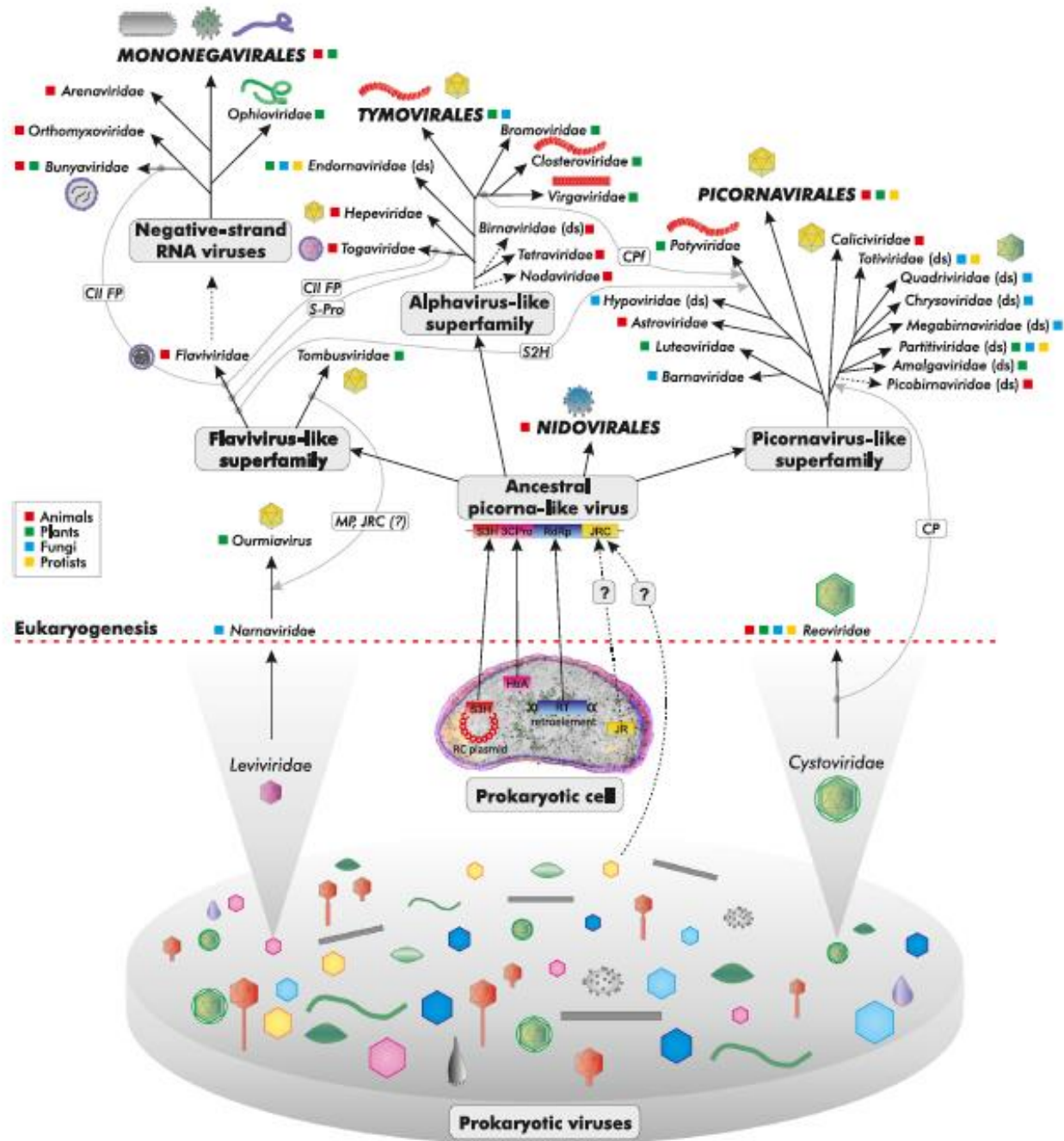
- Genomas virales, bacterianos y arqueanos
- Constitución de genomas eucariotas
- Aporte de fuentes externas al genoma eucariota
- Duplicación completa de genomas

Variación de tipos de genomas virales (Koonin, E.V. et al., 2015)



Variación de tamaños de genomas (Brunk & Martin, 2019)

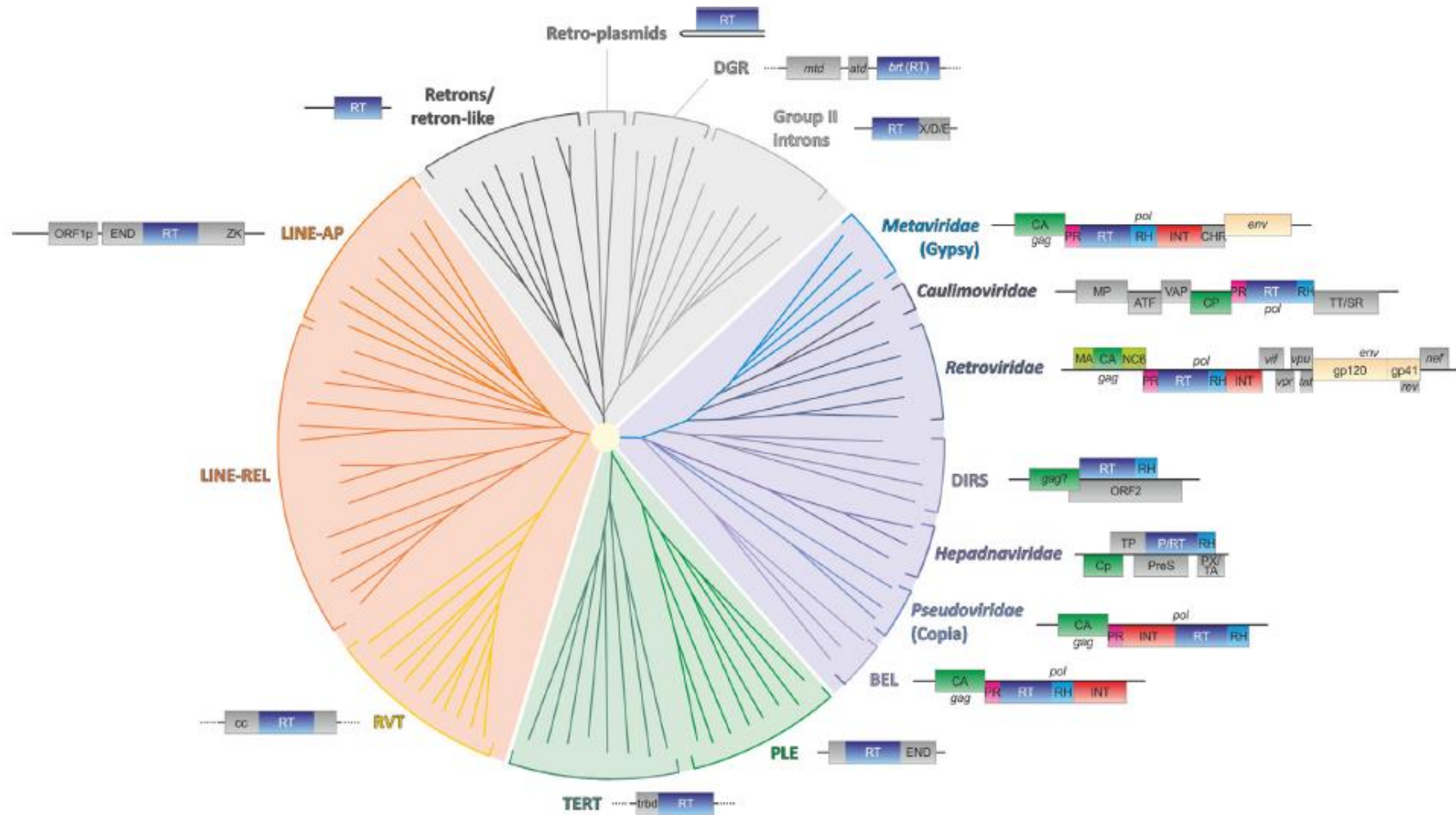


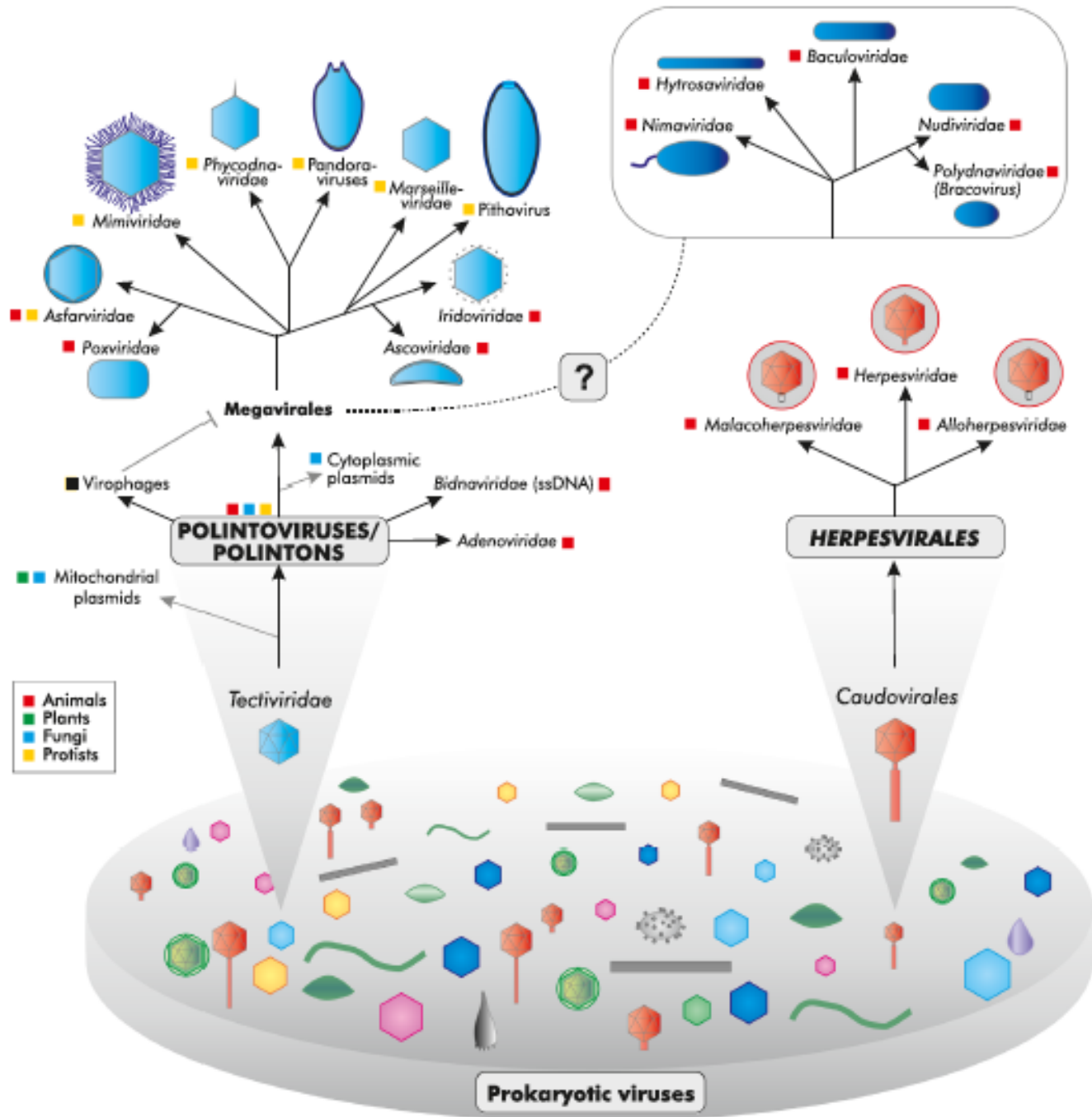


Origen de virus de eucariotas (Koonin, E.V. et al., 2015)

Evolución de retroelementos y retrovirus

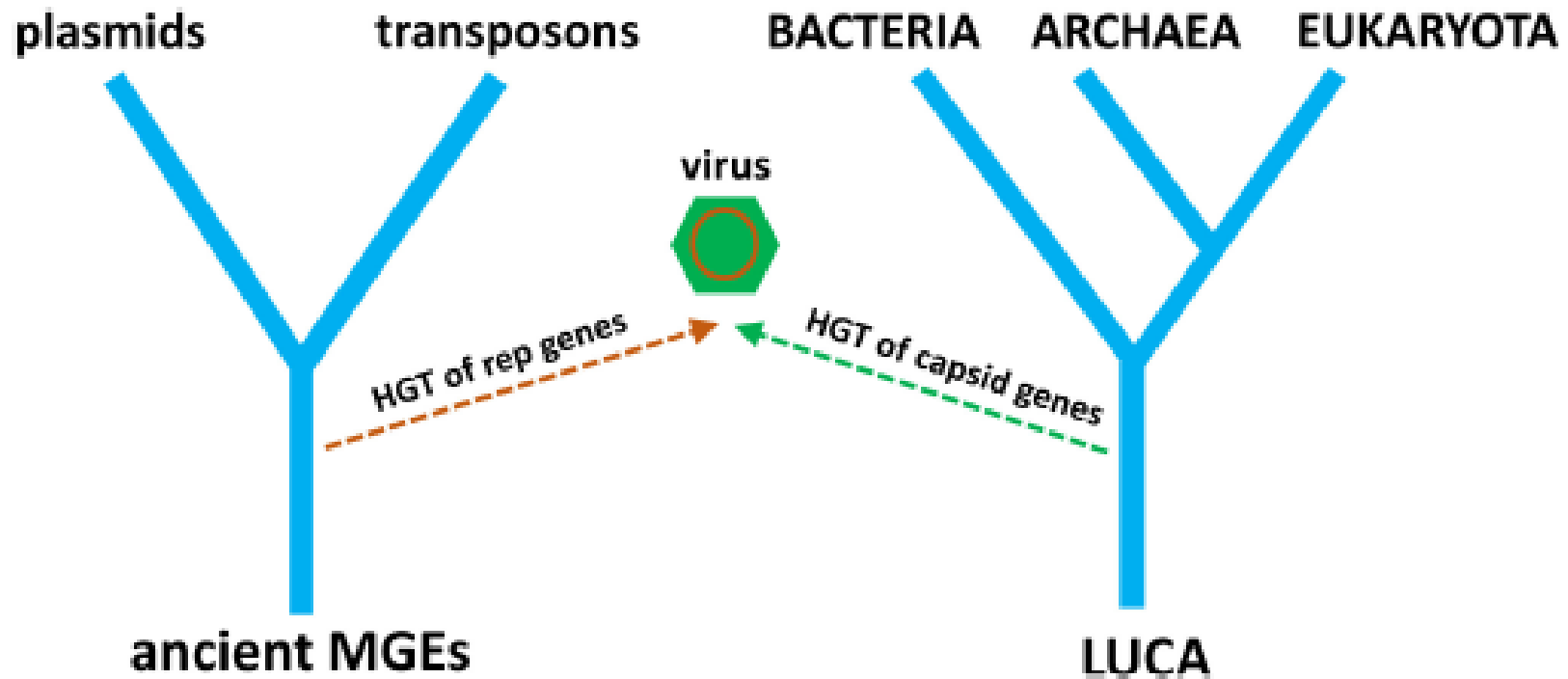
(Koonin, E.V. et al., 2015)





Evolución de virus dsADN a partir de dos grupos de bacteriofagos (Koonin, E.V. et al., 2015)

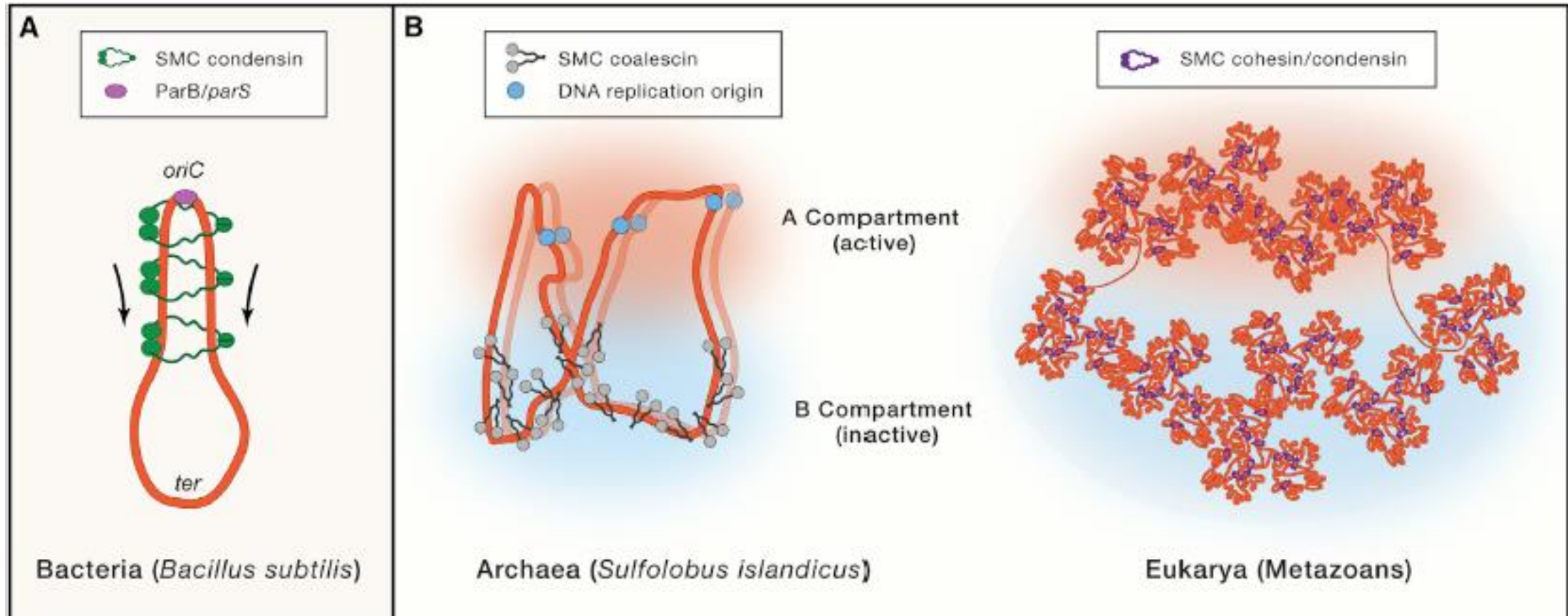
Origen quimérico de virus (Harris & Hill, 2021)



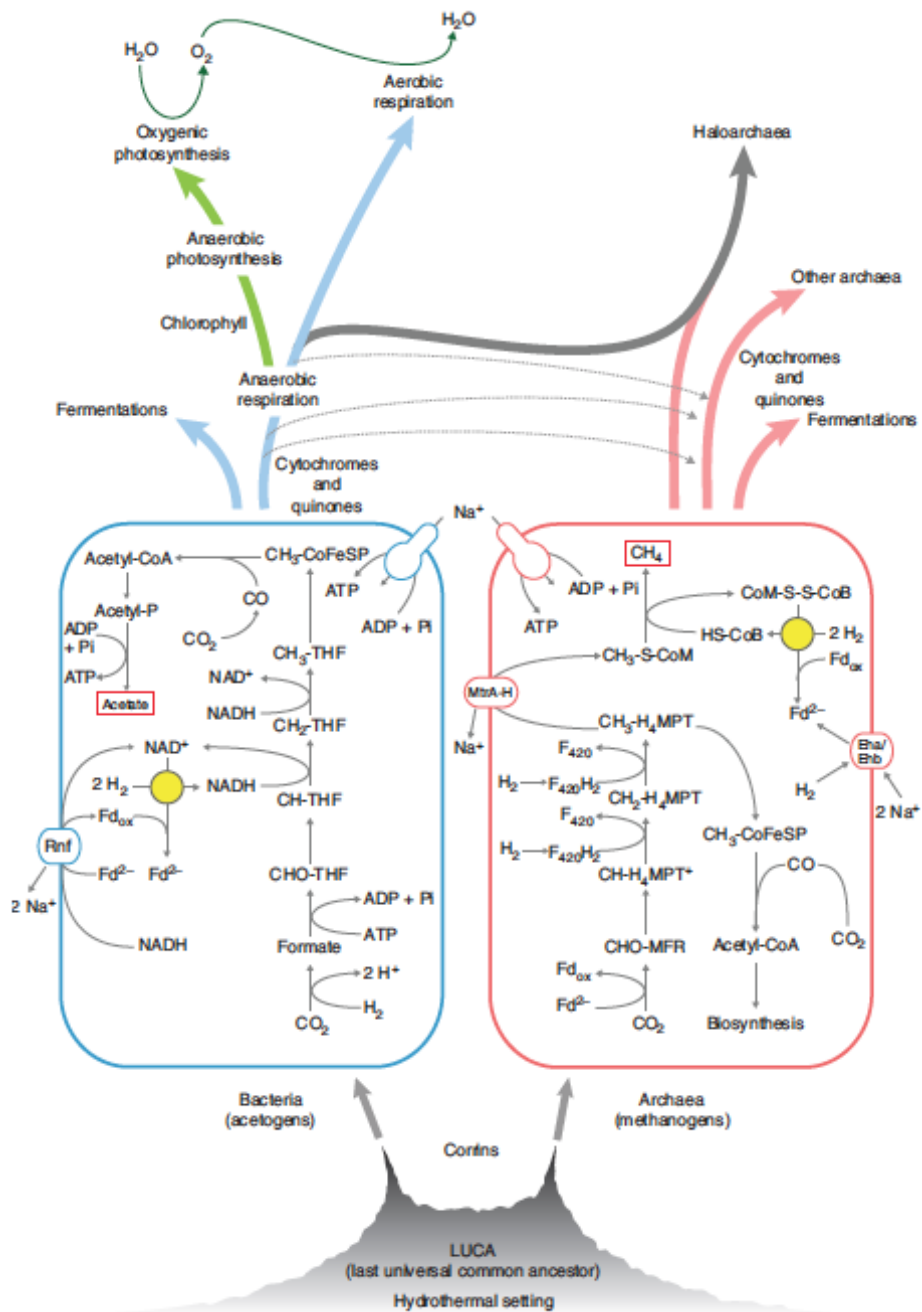
Genomas Procariotas

Organización de genomas en los tres reinos

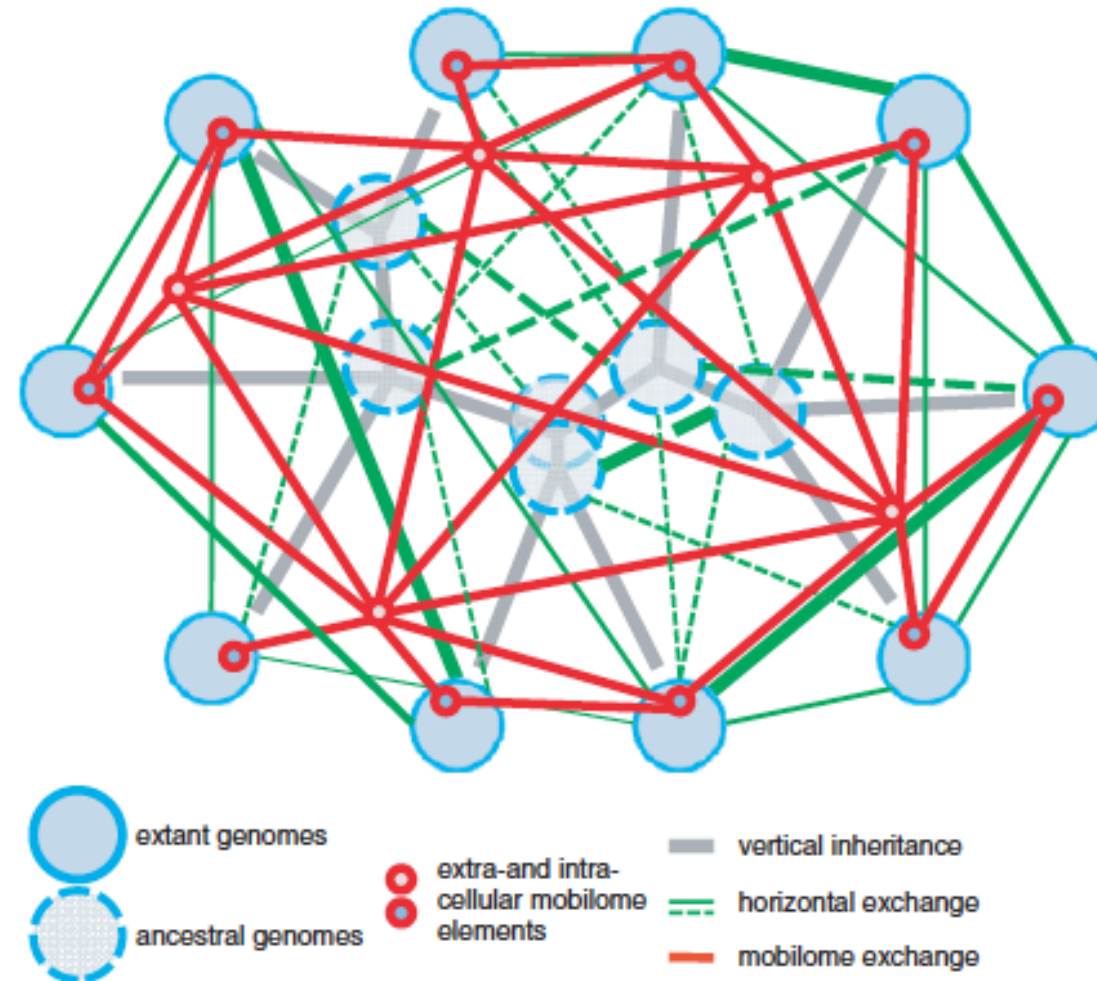
(Feng,X et al., 2019)



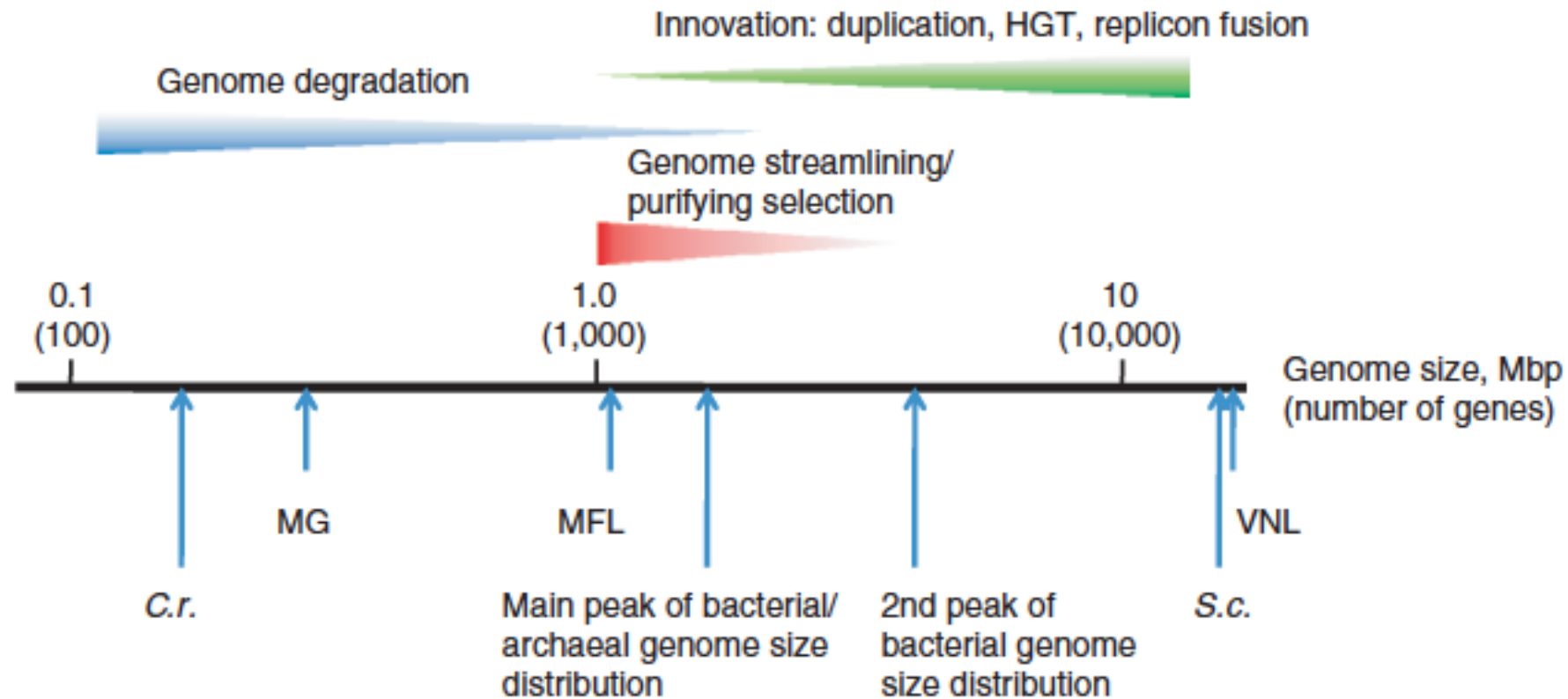
Posible evolución de bacterias a partir de ambientes hidrotermales vénticos (Martin & Sousa, 2016)



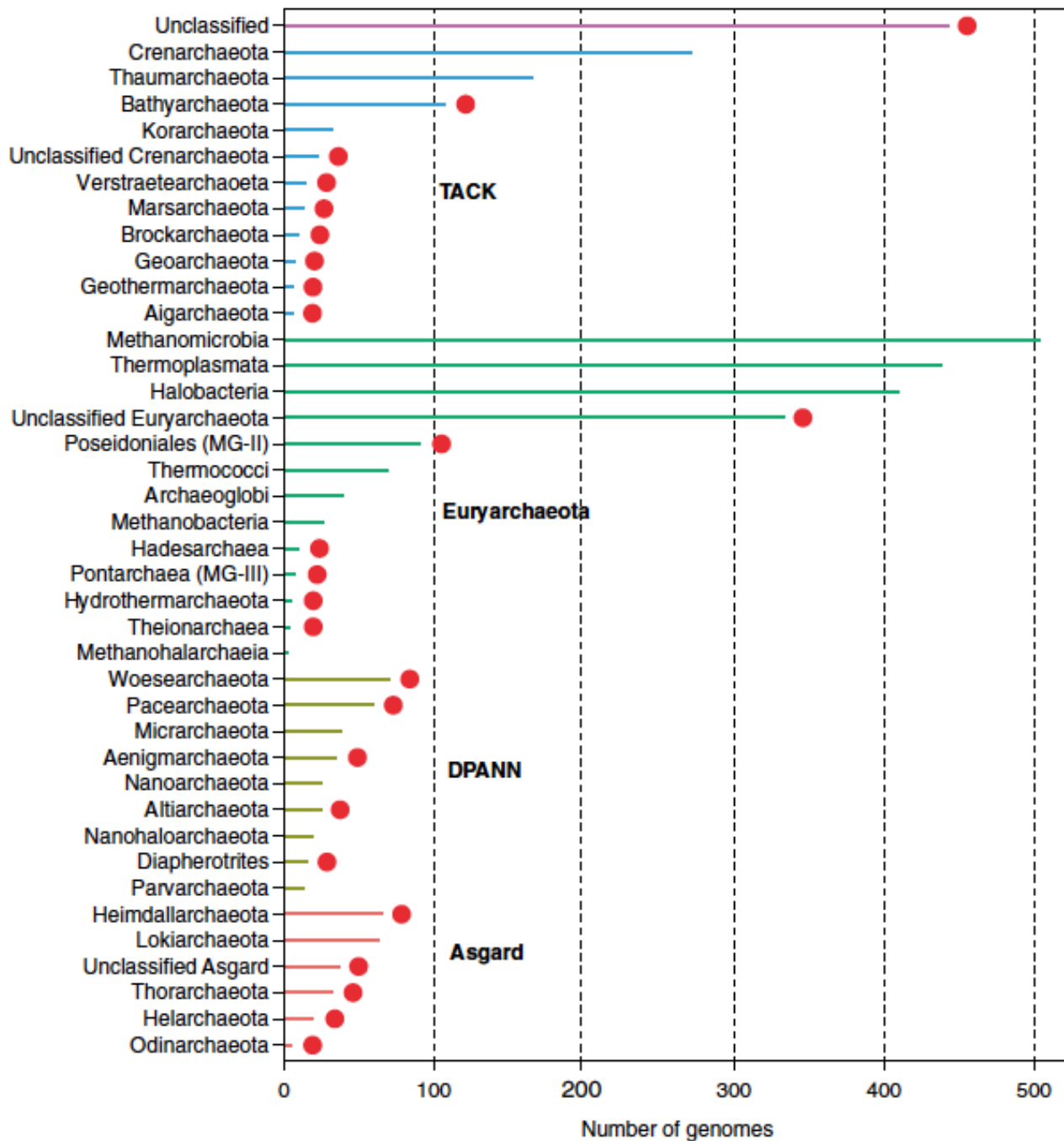
Posibles factores que contribuyen a la formación de genomas bacterianos (Kooning & Wolf, 2008)



Principales fuerzas evolutivas en procariotas y su efecto en tamaño del genoma (Kooning & Wolf, 2008)



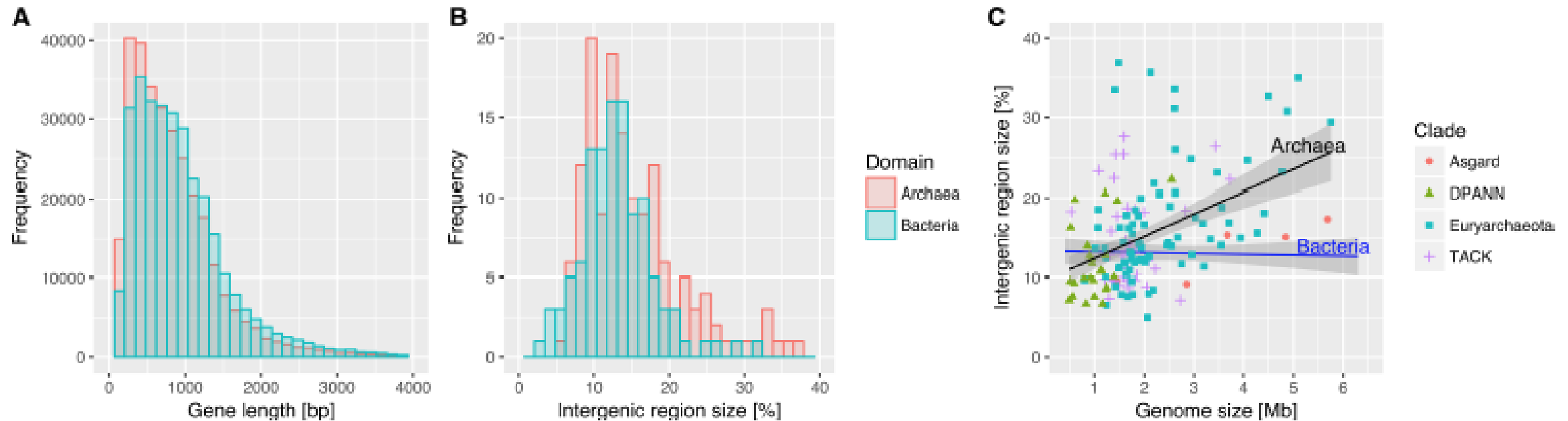
Genomas Arqueas

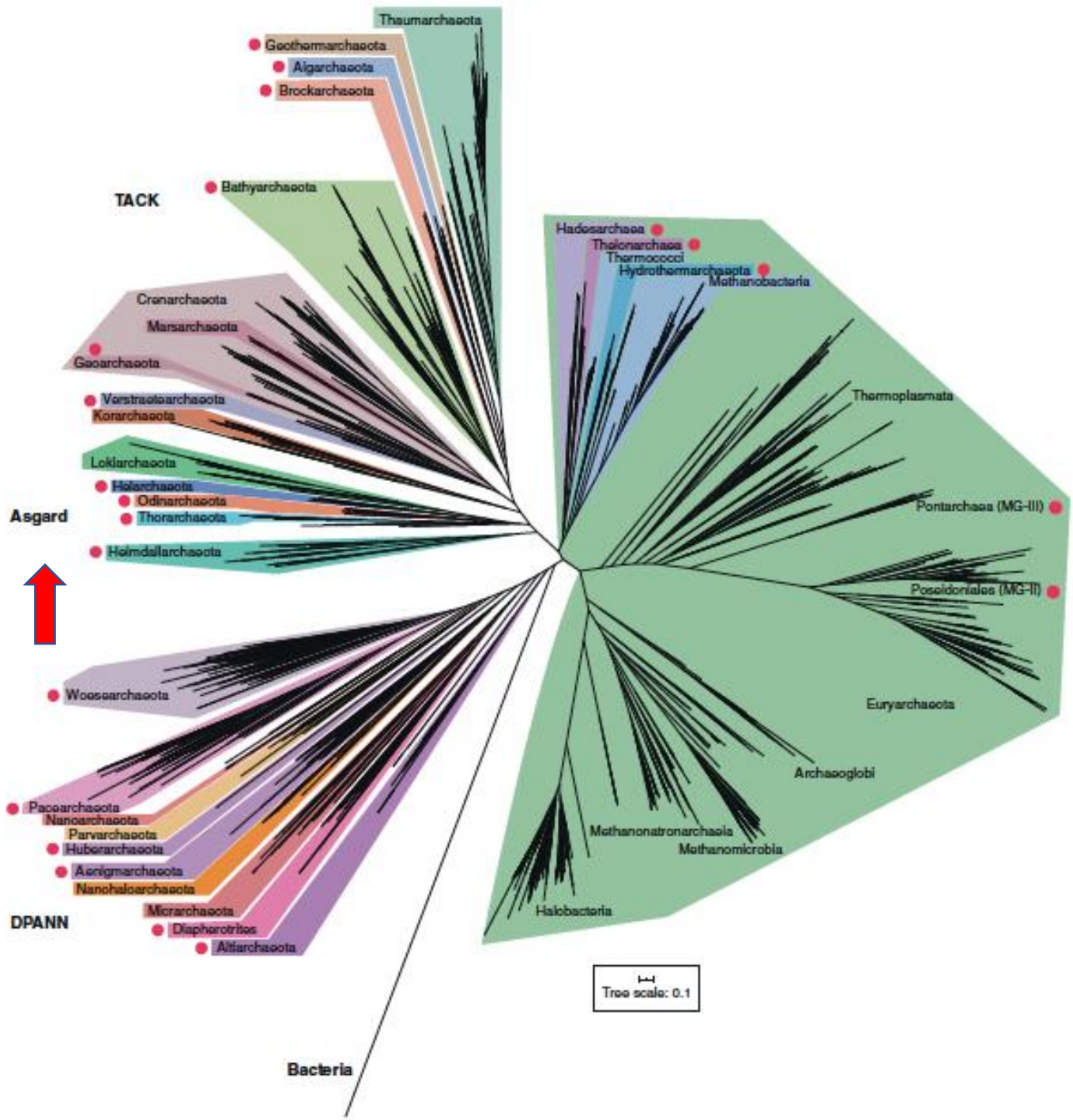


Número de genomas
 secuenciados de Arquea
 cultivables y no cultivables
 (pto. rojo) (Baker, B.J. et al., 2020)

Composición del genoma en Arquea y Bacteria

(Kellner et al. 2018)

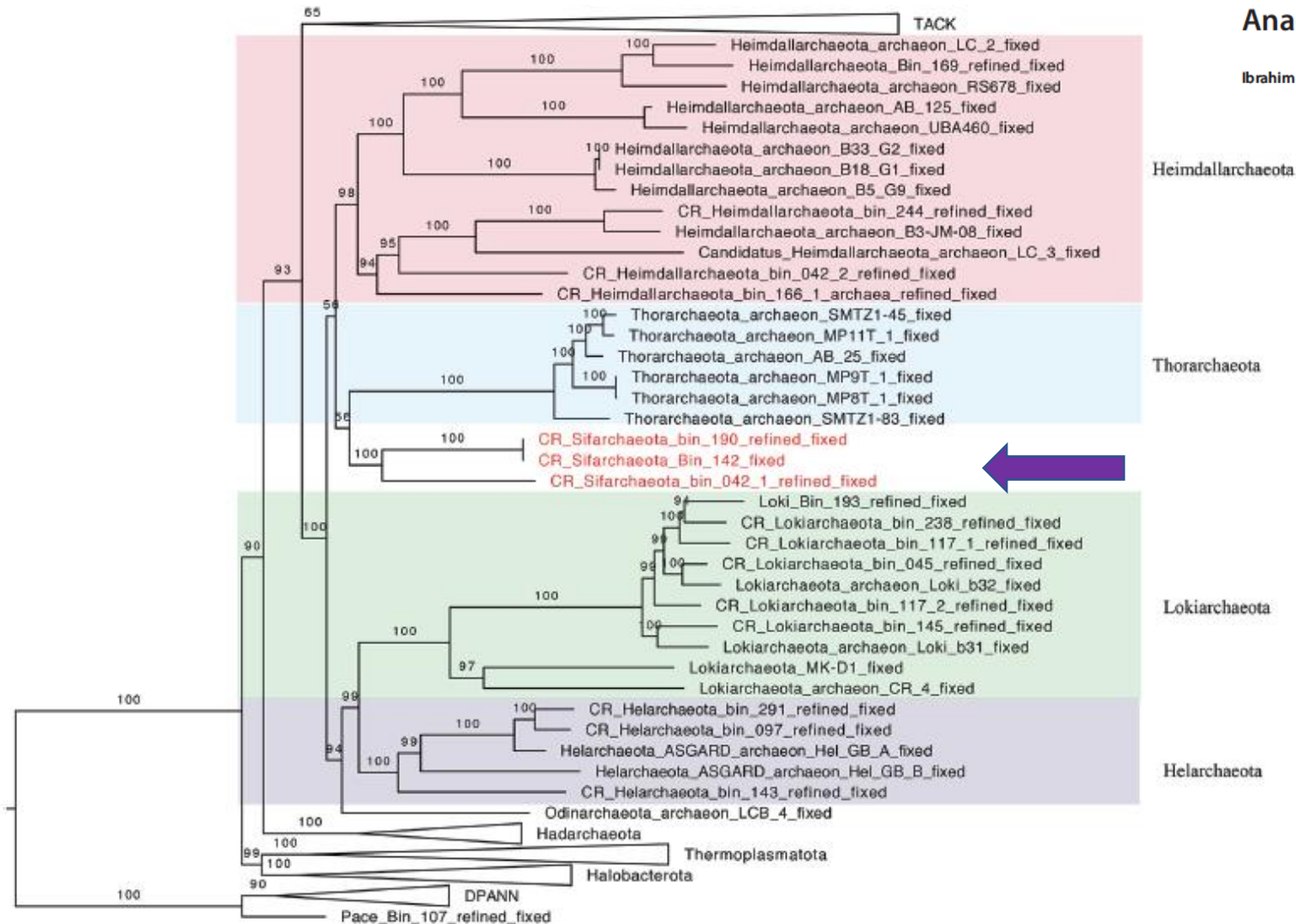




Filogenia de Arquea (Baker, B.J. et al., 2020)

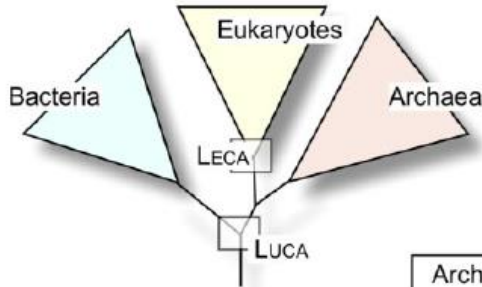
“Sifarchaeota,” a Novel Asgard Phylum from Costa Rican Sediment Capable of Polysaccharide Degradation and Anaerobic Methylophony

Ibrahim F. Farag,^a Rui Zhao,^a Jennifer F. Biddle^a

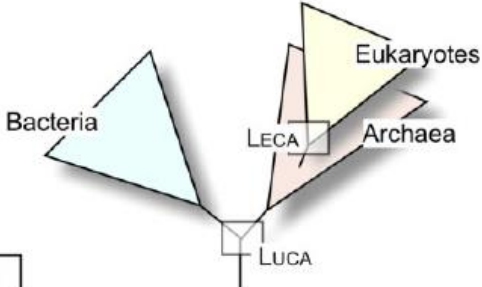


La hipótesis del origen de los eucariotes a partir de grupo ancestral de Arquea (Brückner & Martin, 2020; Nobs et al. 2022)

(a) Three domains

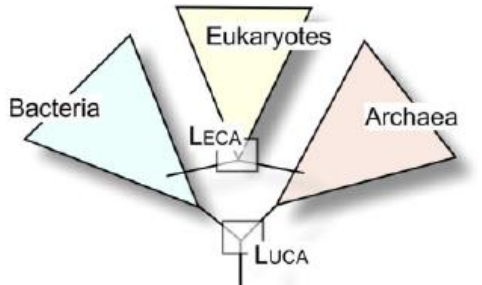


(b) Two domains

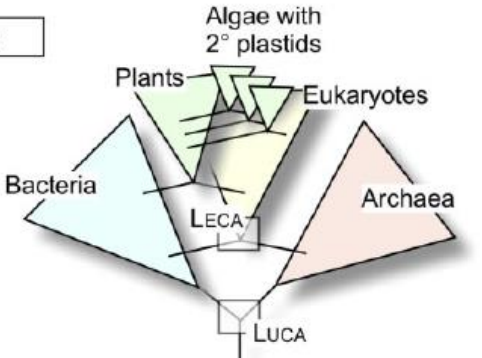


Archaeal origin

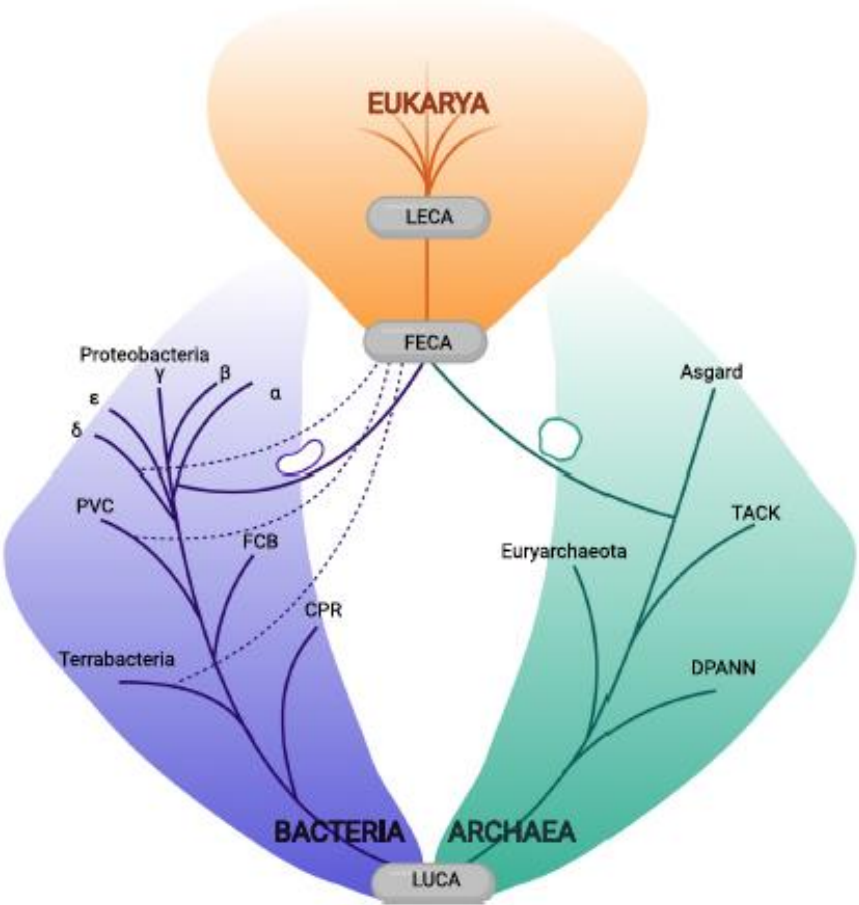
(c) Archaeal host plus mitochondria



(d) Archaeal host plus mitochondria and plastids

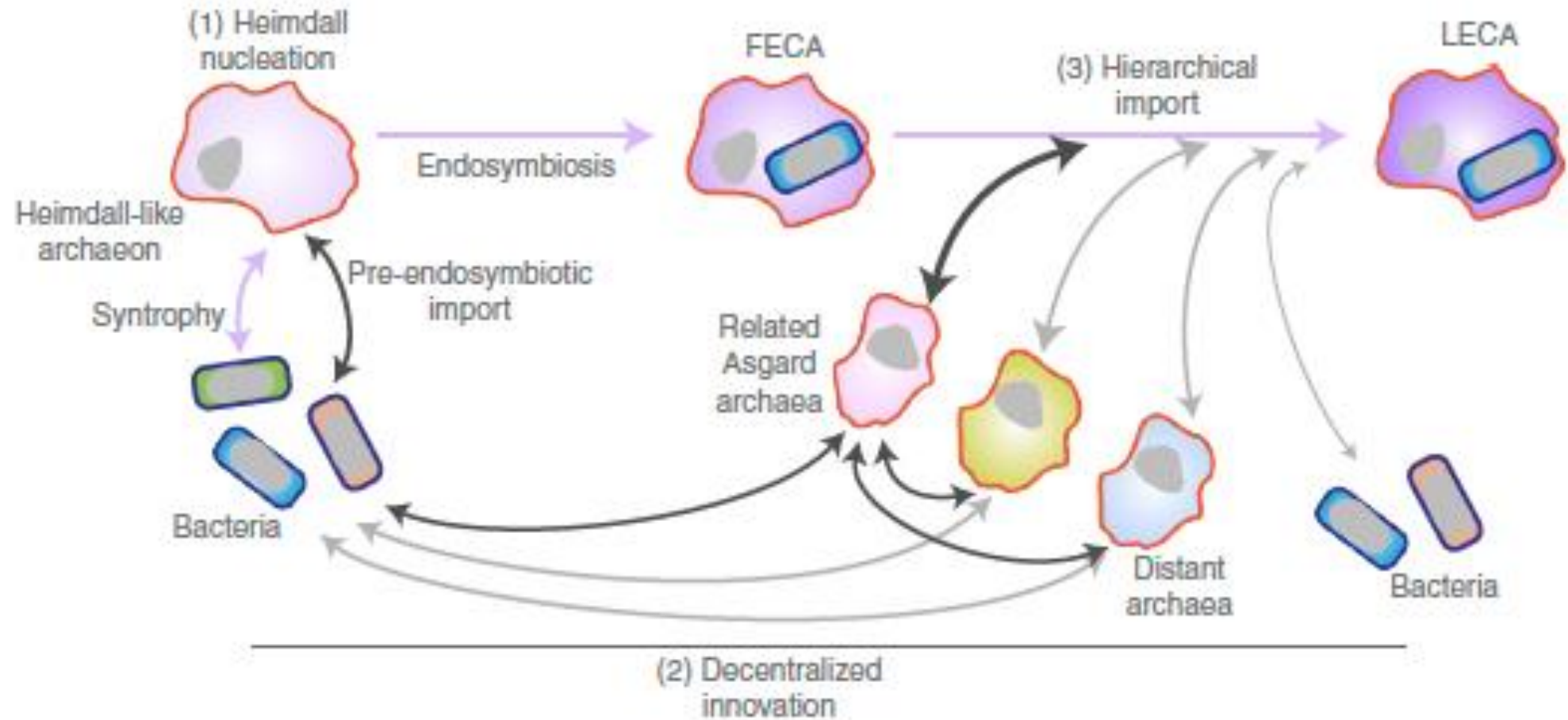


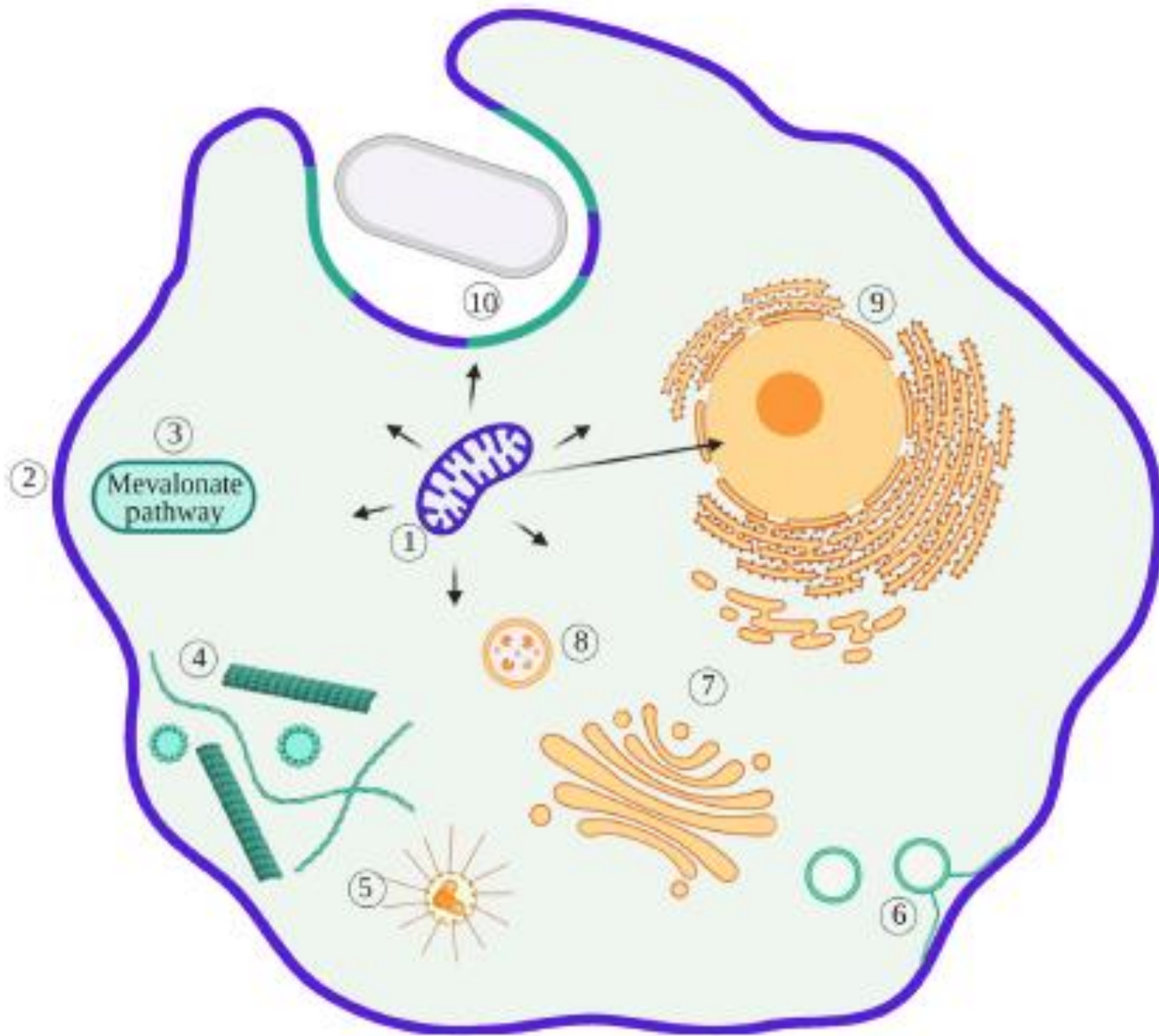
Symbiogenesis



Genomas Eucariotas

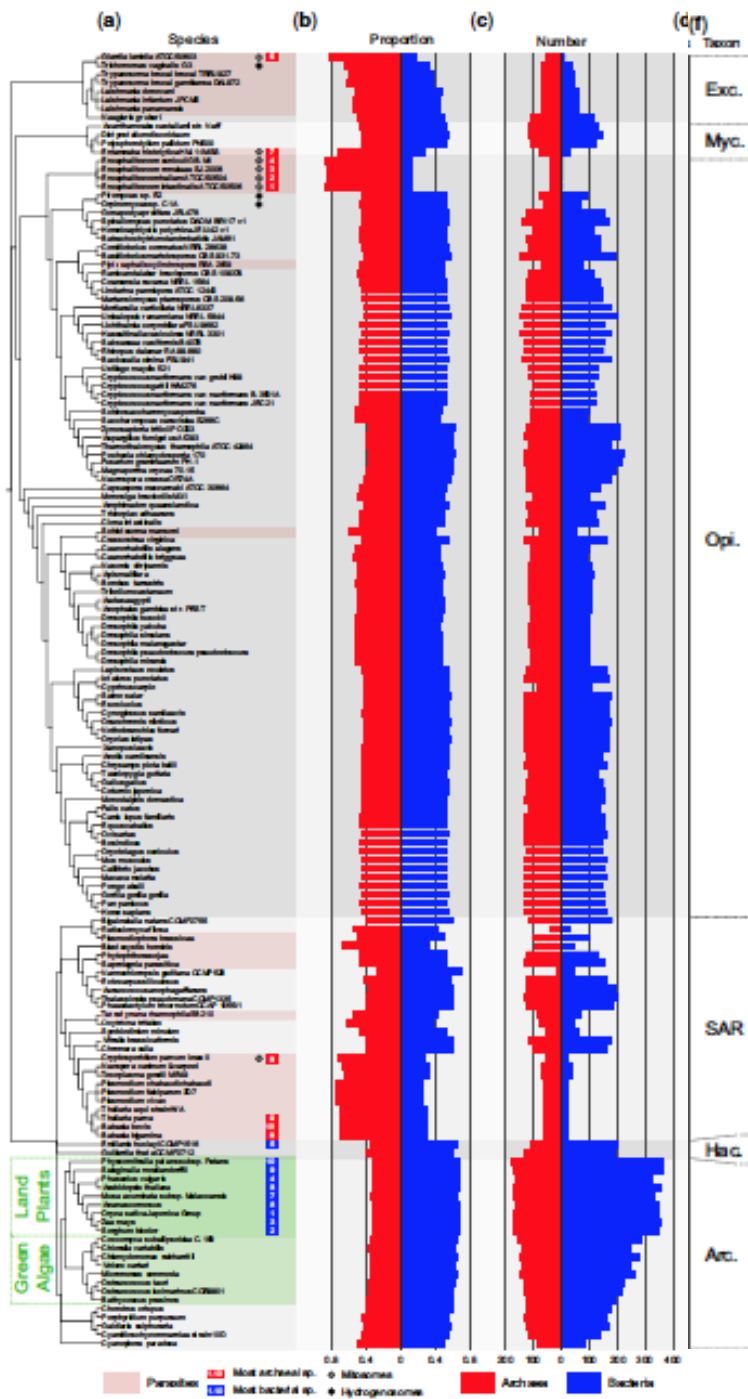
Modelo de origen de eucariotas (Wu et al. 2022)





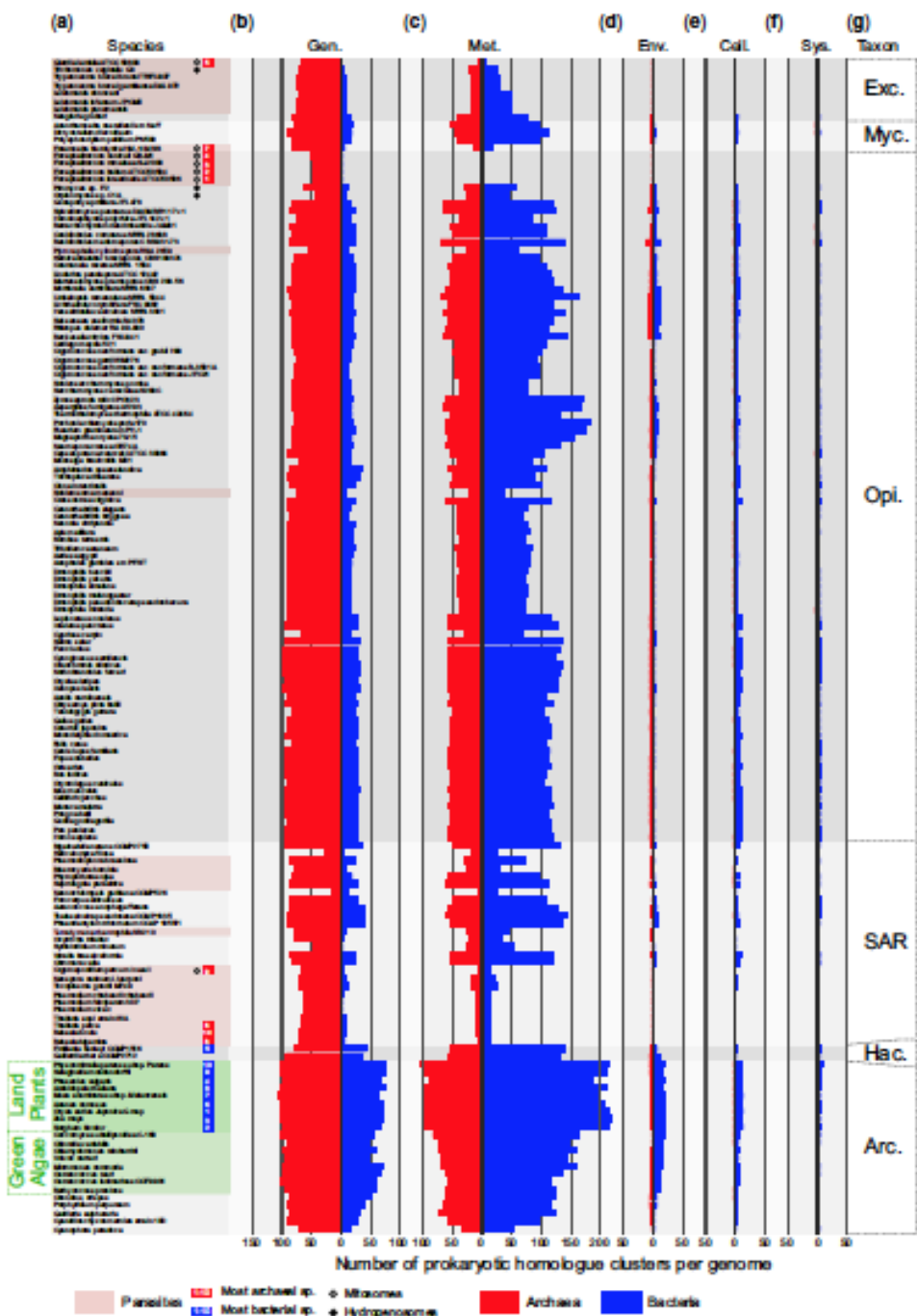
Esquema Último Ancestro Común Eucariota ("LECA") con contribuciones bacterianas (morado), arqueas (verde claro) e innovaciones eucariotas (amarillo).

(Nobs et al. 2022)



Genes bacterianos (azul) y de arquea (rojo) en el genoma eucariota (Brückner & Martin, 2020)

Group	Archaeal	Bacterial
All eukaryotes	0.44	0.56
All without plastids ^a	0.47	0.53
All with plastids ^b	0.39	0.61
Land plants	0.33	0.67
Opisthokonts	0.46	0.54
Hacrobia	0.38	0.62
SAR	0.50	0.50
Archaeplastida	0.36	0.64
Mycetozoa	0.50	0.50
Excavata	0.58	0.42
Parasites ^c	0.62	0.38



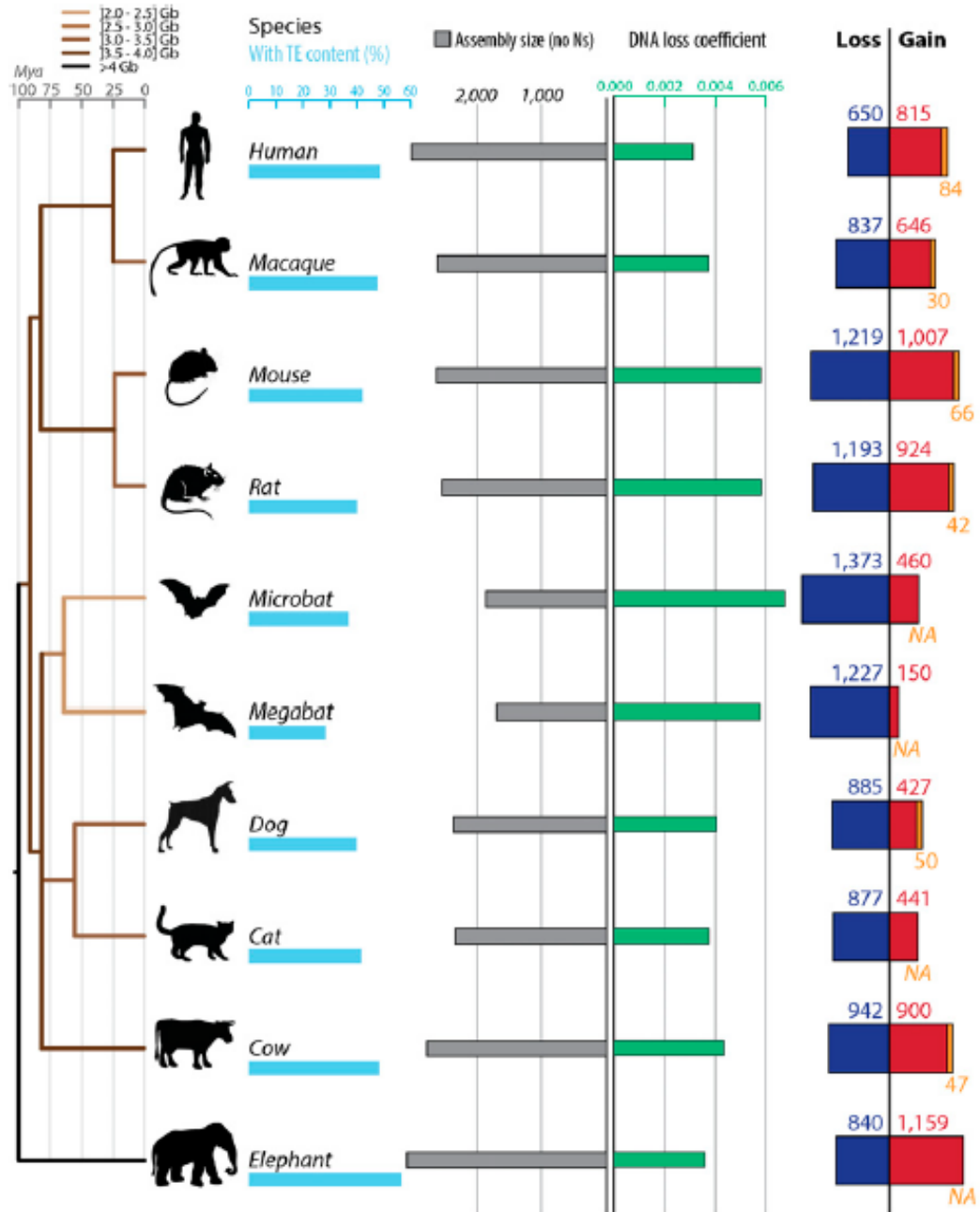
Categorías funcionales (Brückner & Martin, 2020)

-Secuencias de 19 millones proteínas de: 150 eucariotas y 5655 procariontas

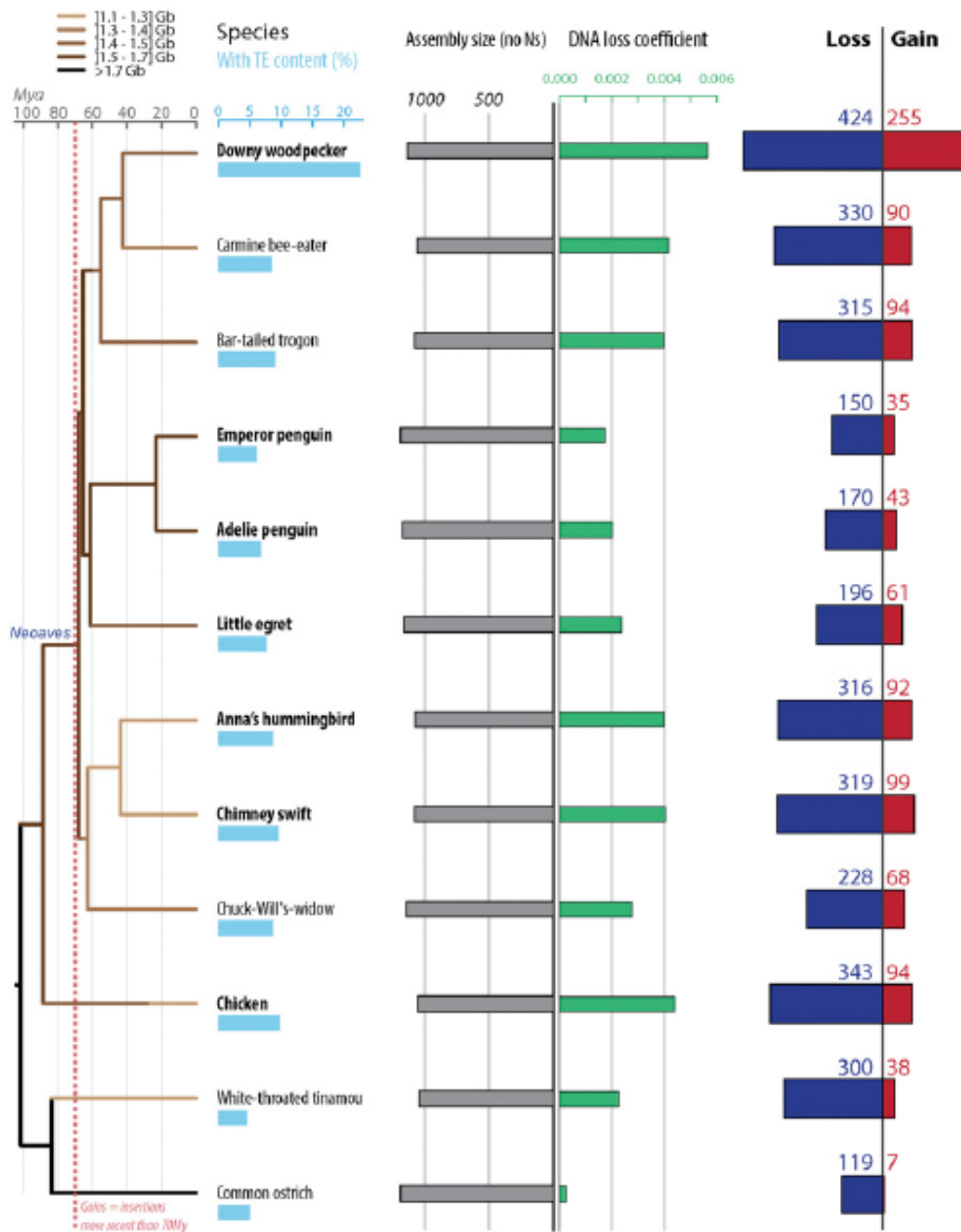
-**Gen**: Sistemas genéticos; **Met**: Metabolismo; **Env**: Procesamiento ambiental; **Cell**: Procesos celulares; **Sys**: Sistema organismal

Datos sobre genomas entre diferentes grupos indica una diversidad grande (Elliot & Gregory, 2015)

parameter	animals	land plants	fungi	protists
genome size				
assembled genome size (Mbp)	1153.98 ± 100.18 (n = 149)	1065.82 ± 176.86 (n = 83)	3498 ± 1.74 (n = 218)	61.11 ± 9.76 (n = 70)
estimated genome size (Mbp)	1294.71 ± 110.65 (n = 149)	1498.43 ± 232.52 (n = 83)	35.71 ± 1.92 (n = 218)	75.51 ± 21.49 (n = 70)
discrepancy (Mbp)	165.107 ± 25.73 (n = 127)	448.83 ± 206.26 (n = 80)	26.38 ± 12.34 (n = 6)	100.82 ± 87.56 (n = 10)
average database genome size (Mbp)	4176.06 ± 112.36	6120.79 ± 107.58	65.89 ± 5.31	n.a.
maximum database genome size (Mbp)	129 907.74 (n = 5635)	148 852 (n = 8257)	5800 (n = 1916)	n.a.
gene content				
number of protein-coding genes	18 943 ± 451.82 (n = 139)	35 577 ± 1641.08 (n = 80)	9953 ± 315.16 (n = 202)	12 589 ± 1148.69 (n = 70)
total amount of coding DNA (Mbp)	27.58 ± 1.26 (n = 90)	39.23 ± 1.81 (n = 64)	13.059 ± 0.56 (n = 97)	18.55 ± 2.16 (n = 49)
coding % of estimated GS	10.4 ± 1.12 (n = 90)	7.86 ± 0.87 (n = 64)	46.66 ± 1.62 (n = 97)	42.31 ± 3.23 (n = 49)
average exon length (bp)	218.8 ± 9.28 (n = 70)	256.35 ± 6.06 (n = 55)	498.77 ± 41.21 (n = 72)	600.05 ± 53.37 (n = 40)
total amount of exonic DNA per gene (bp)	1489.54 ± 35.65 (n = 91)	1159.98 ± 27.49 (n = 63)	1392.89 ± 24.72 (n = 89)	1497.27 ± 54.49 (n = 49)
average intron length (bp)	2172.5 ± 255.34 (n = 72)	430.091 ± 28.08 (n = 50)	133.34 ± 6.87 (n = 80)	204.37 ± 20.44 (n = 44)
average number of introns per gene	5.05 ± 0.47 (n = 26)	3.94 ± 0.38 (n = 20)	1.72 ± 0.24 (n = 50)	2.61 ± 0.66 (n = 27)
total amount of intronic DNA per gene (bp)	8191.5 ± 2033.71 (n = 25)	1804.45 ± 287.43 (n = 18)	201.23 ± 25.23 (n = 38)	1047.99 ± 472.46 (n = 19)
total gene region size (introns + exons) (bp)	9533.11 ± 2050.22 (n = 25)	2956.72 ± 302.28 (n = 18)	1655.47 ± 48.73 (n = 30)	2487.97 ± 552.27 (n = 17)
repetitive content				
repeats as % of assembly GS	27.35 ± 1.83 (n = 102)	50.6 ± 3 (n = 54)	14.38 ± 1.75 (n = 92)	19.45 ± 3.98 (n = 26)
total amount of repetitive DNA (Mbp)	459.41 ± 69.96 (n = 102)	946.23 ± 202.51 (n = 54)	8.81 ± 1.76 (n = 92)	24.88 ± 7.56 (n = 26)
TE % of assembly GS	23 ± 1.85 (n = 100)	38.88 ± 2.44 (n = 61)	13.59 ± 2.75 (n = 74)	13.84 ± 3.19 (n = 28)
base pair composition				
GC %	37.68 ± 0.55 (n = 76)	36 ± 0.62 (n = 31)	45.73 ± 0.58 (n = 161)	47.24 ± 1.76 (n = 56)

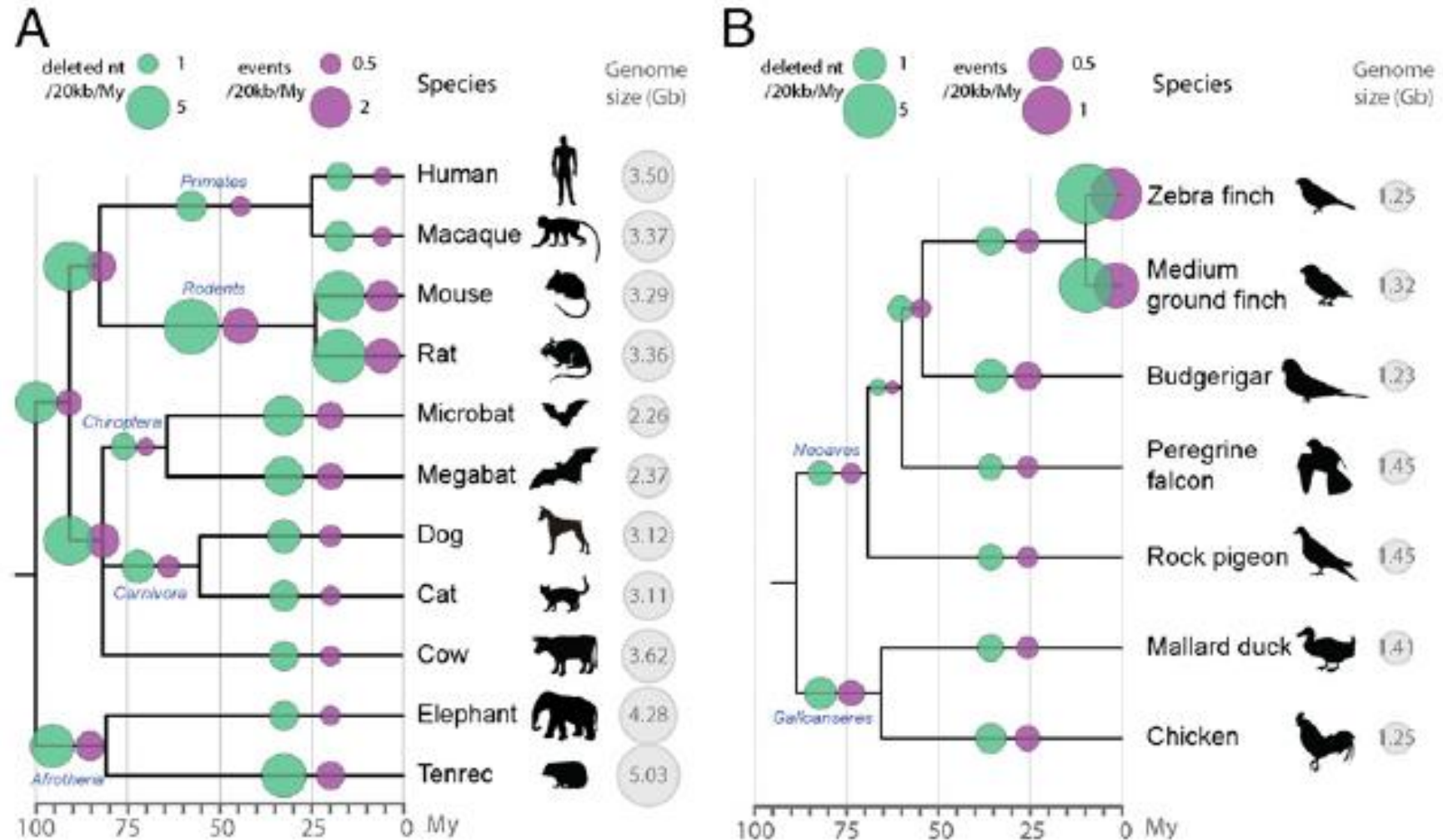


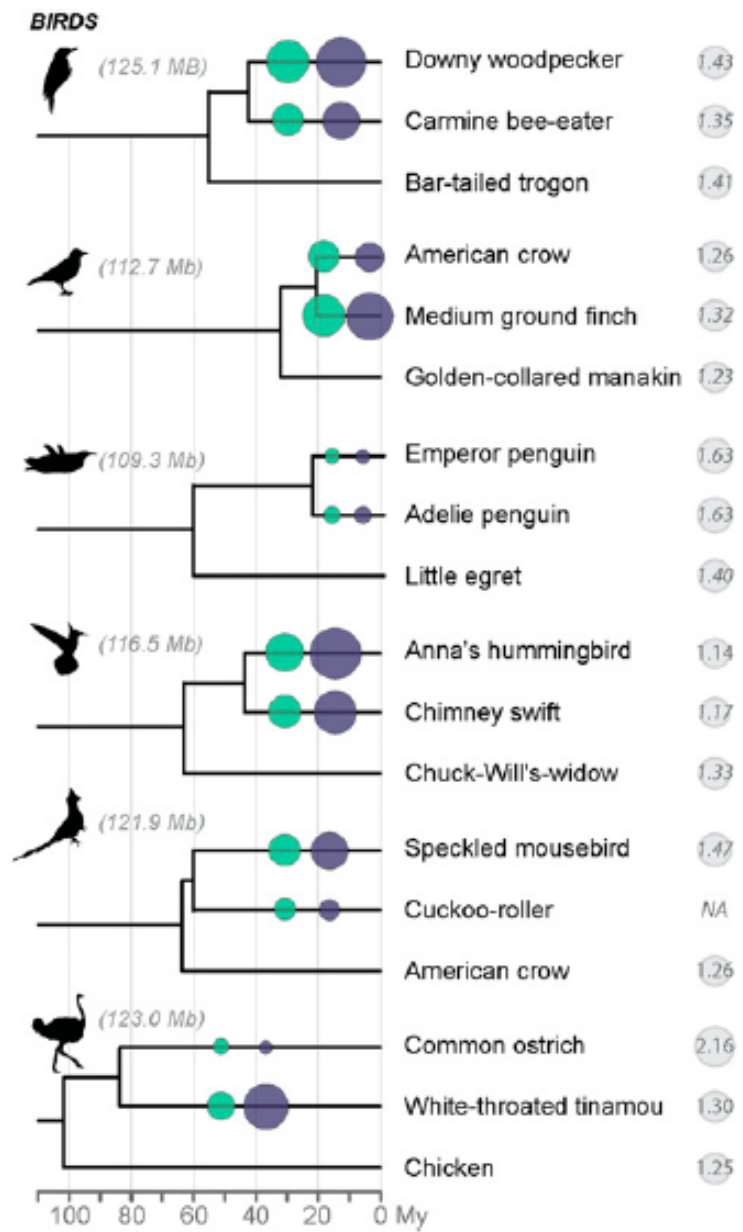
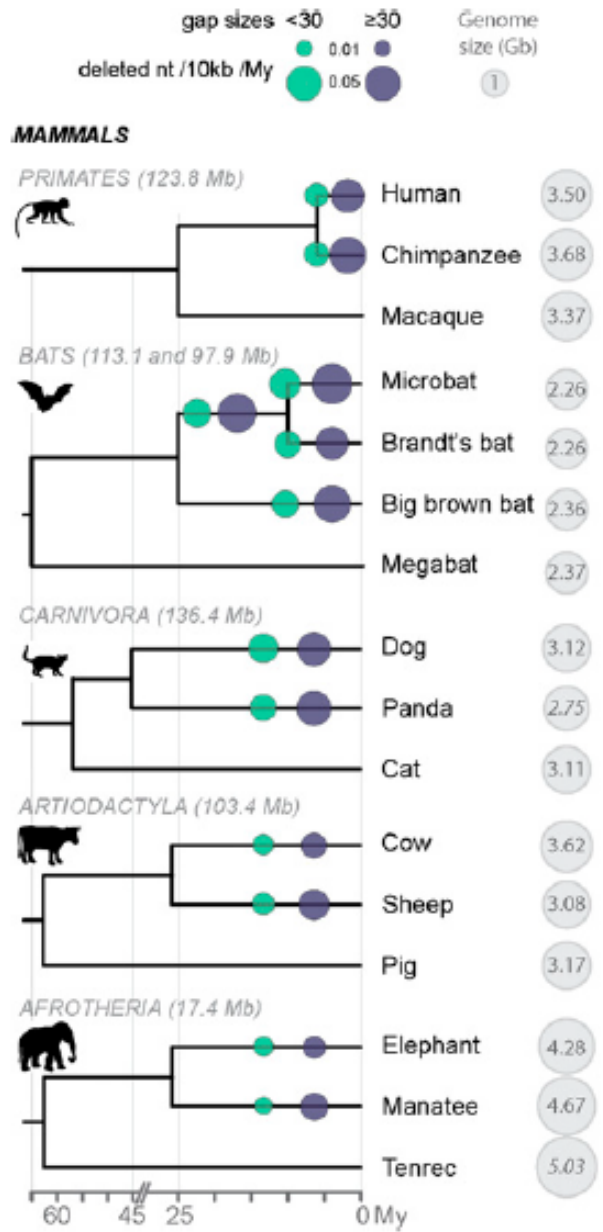
Caso 1 Aves: Pérdida y ganancia de ADN en 10 linajes de mamíferos (Kapuska, A. et al., 2017)



Caso 1 Aves: Pérdida y ganancia de ADN en 12 linajes de aves (Kapuska, A. et al., 2017)

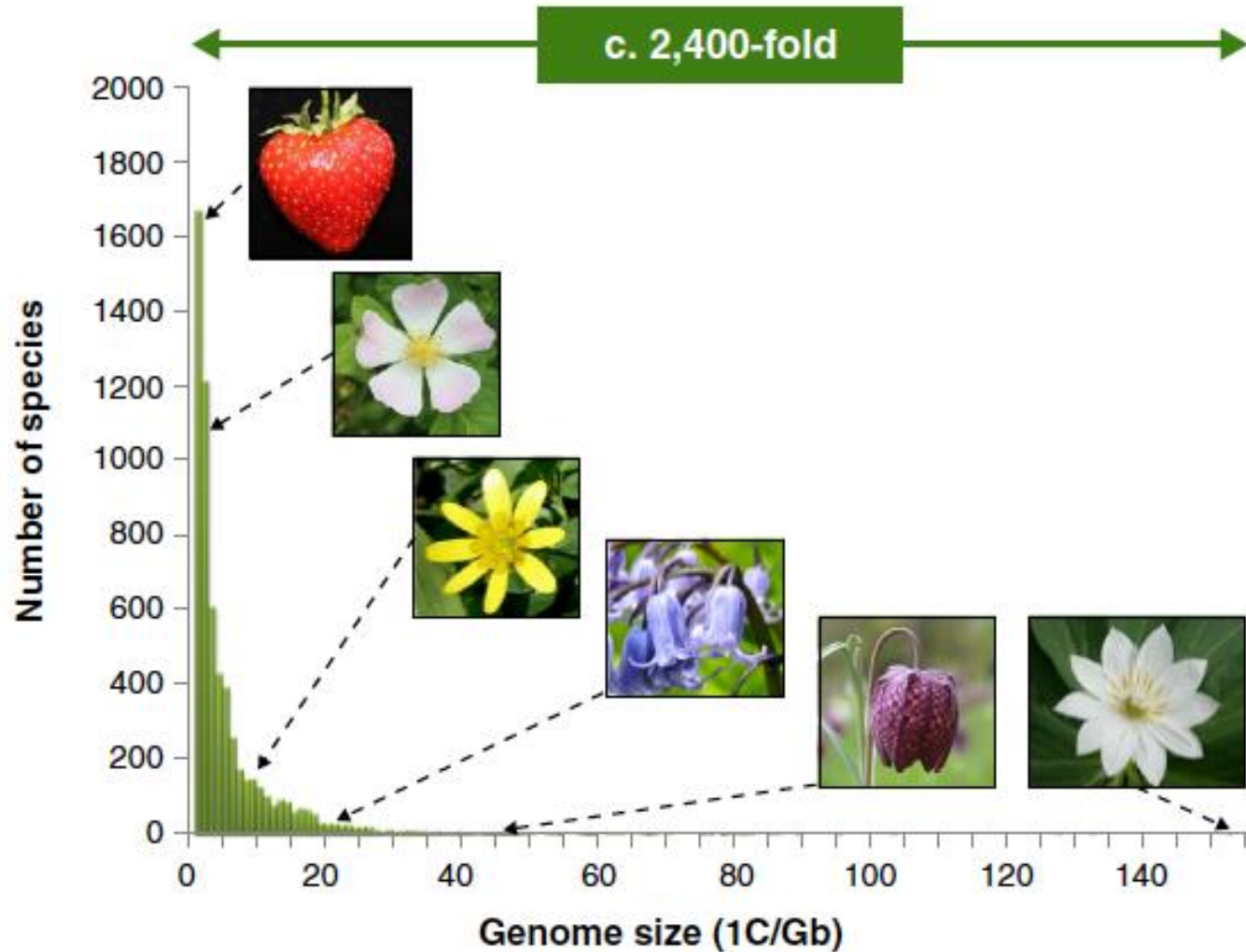
Caso 1 Aves: Tasa de microdeleciones y número de eventos en amniotas (Kapuska, A. et al., 2017)



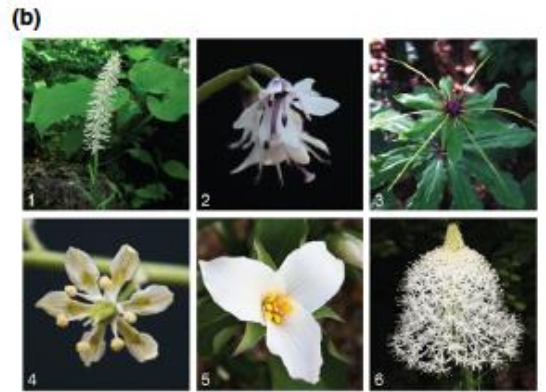
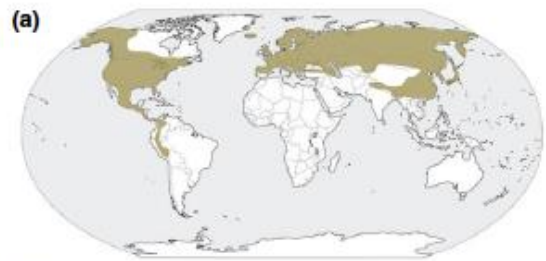
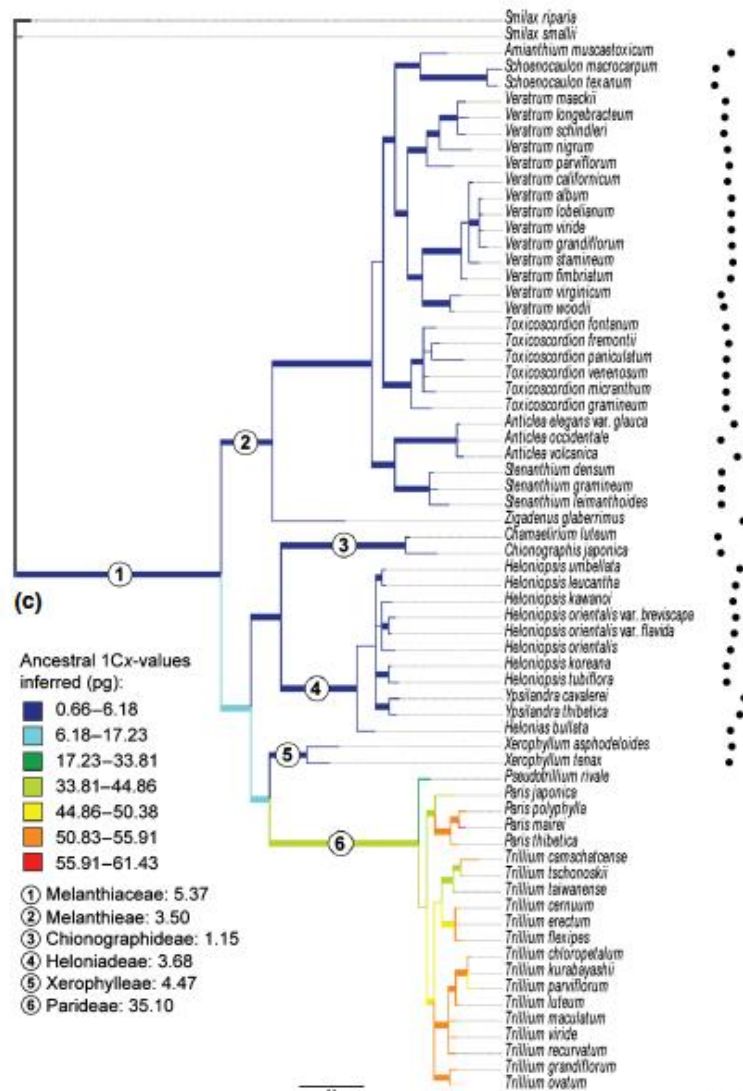


Caso 1 Aves: Tasa de deleciones de tamaño medio y número de eventos en amniotas (Kapuska, A. et al., 2017)

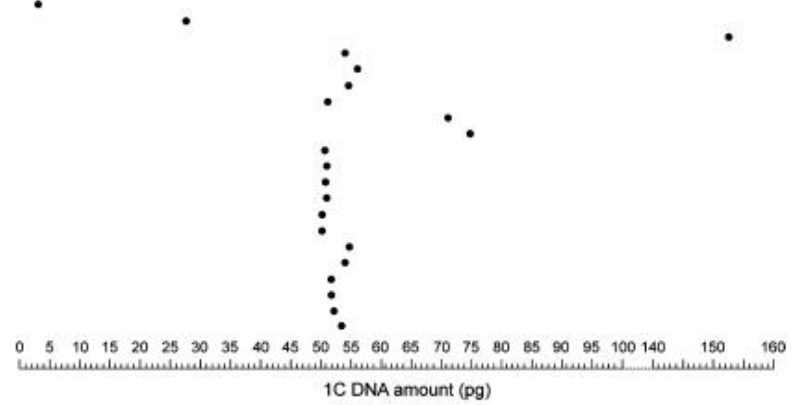
Variación en tamaño genoma en plantas (Dodsworth, S. et al., 2015)

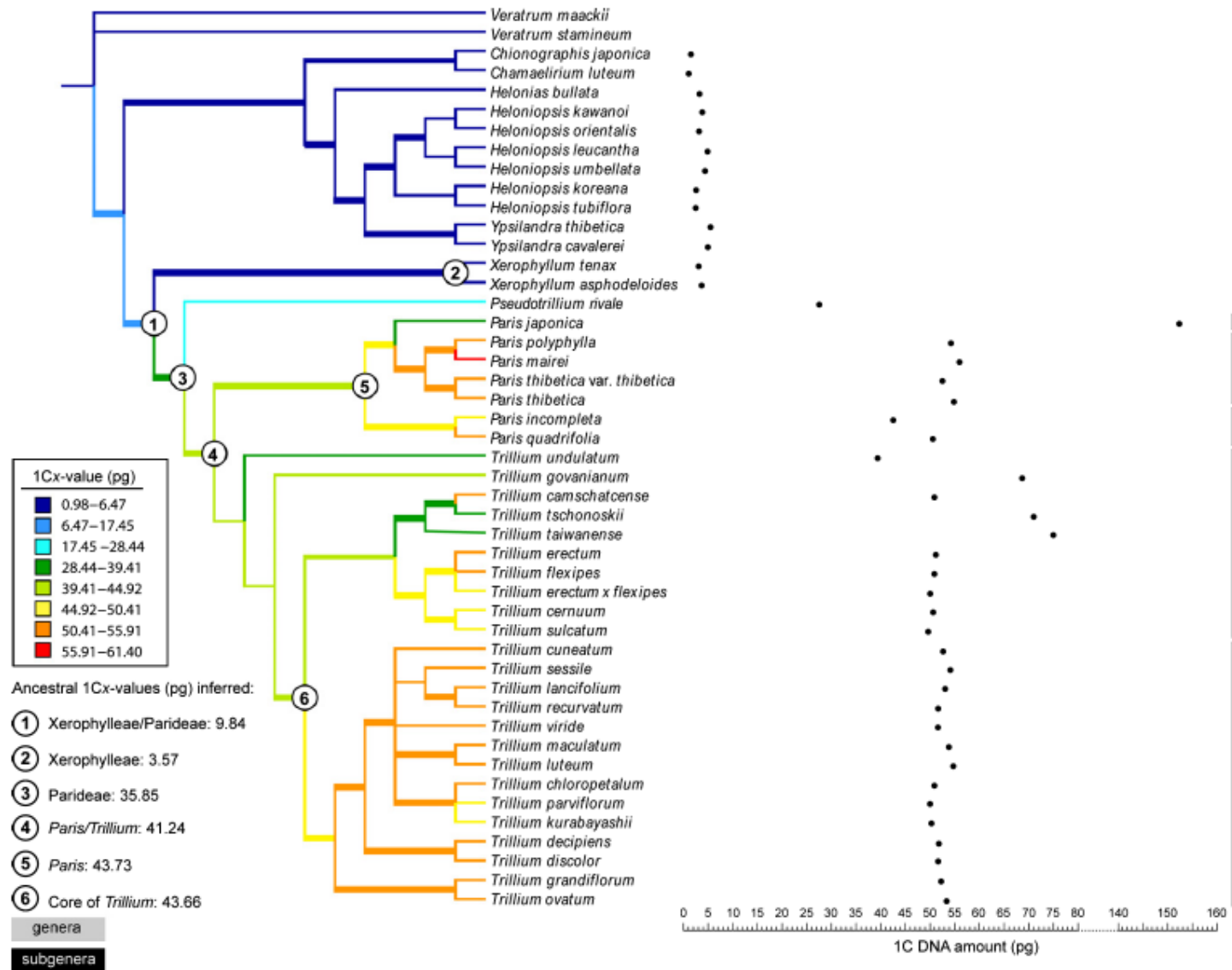


- <i>Fragaria x ananassa</i>	0.60 Gb
- <i>Rosa canina</i>	1.39 Gb
- <i>Ranunculus ficaria</i>	9.12 Gb
- <i>Hyacinthoides non-scripta</i>	20.73 Gb
- <i>Fritillaria meleagris</i>	46.26 Gb
- <i>Paris japonica</i>	148.8 Gb

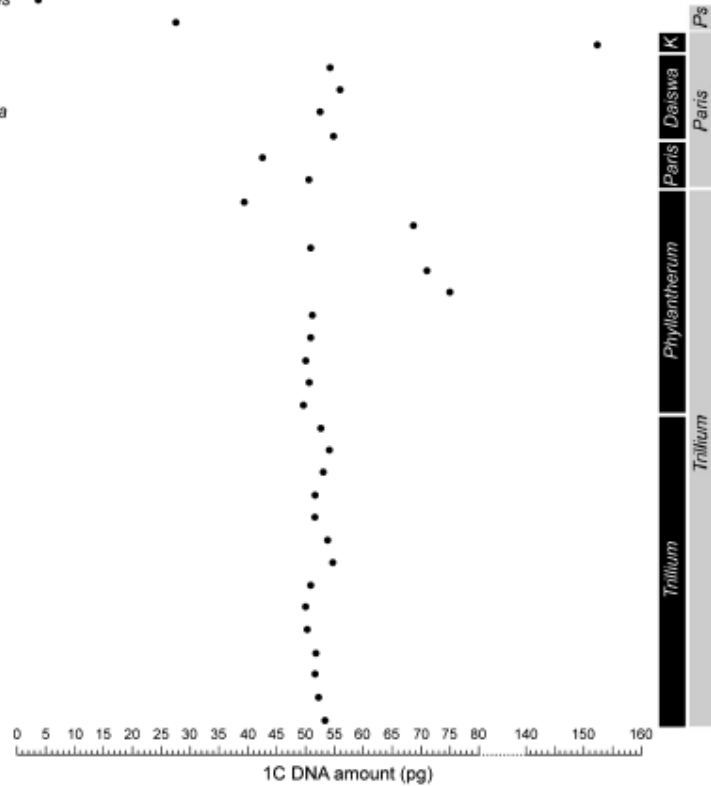


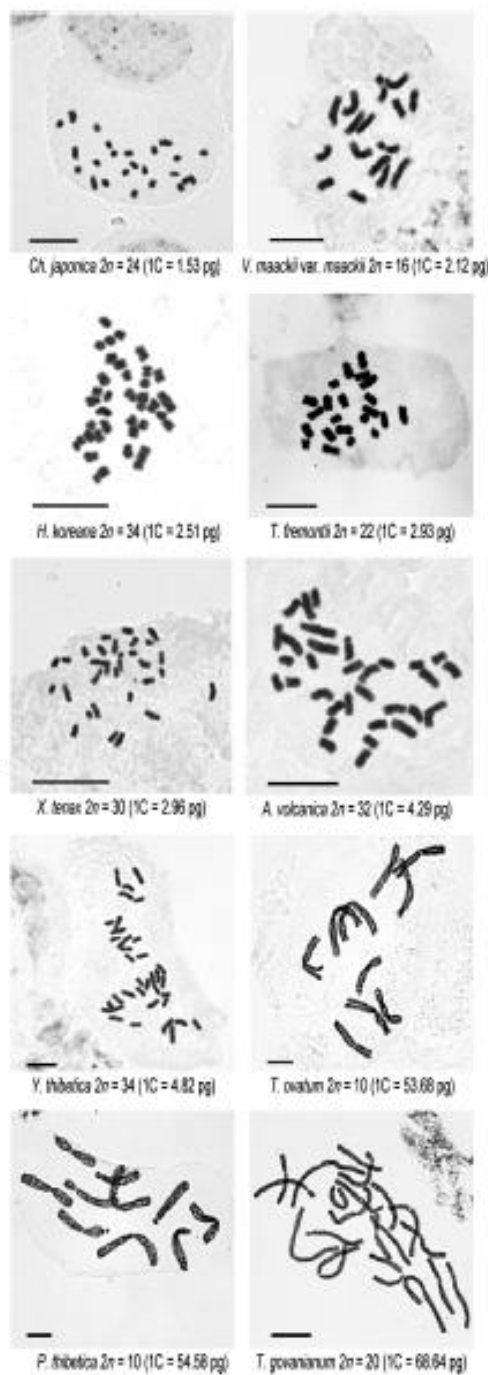
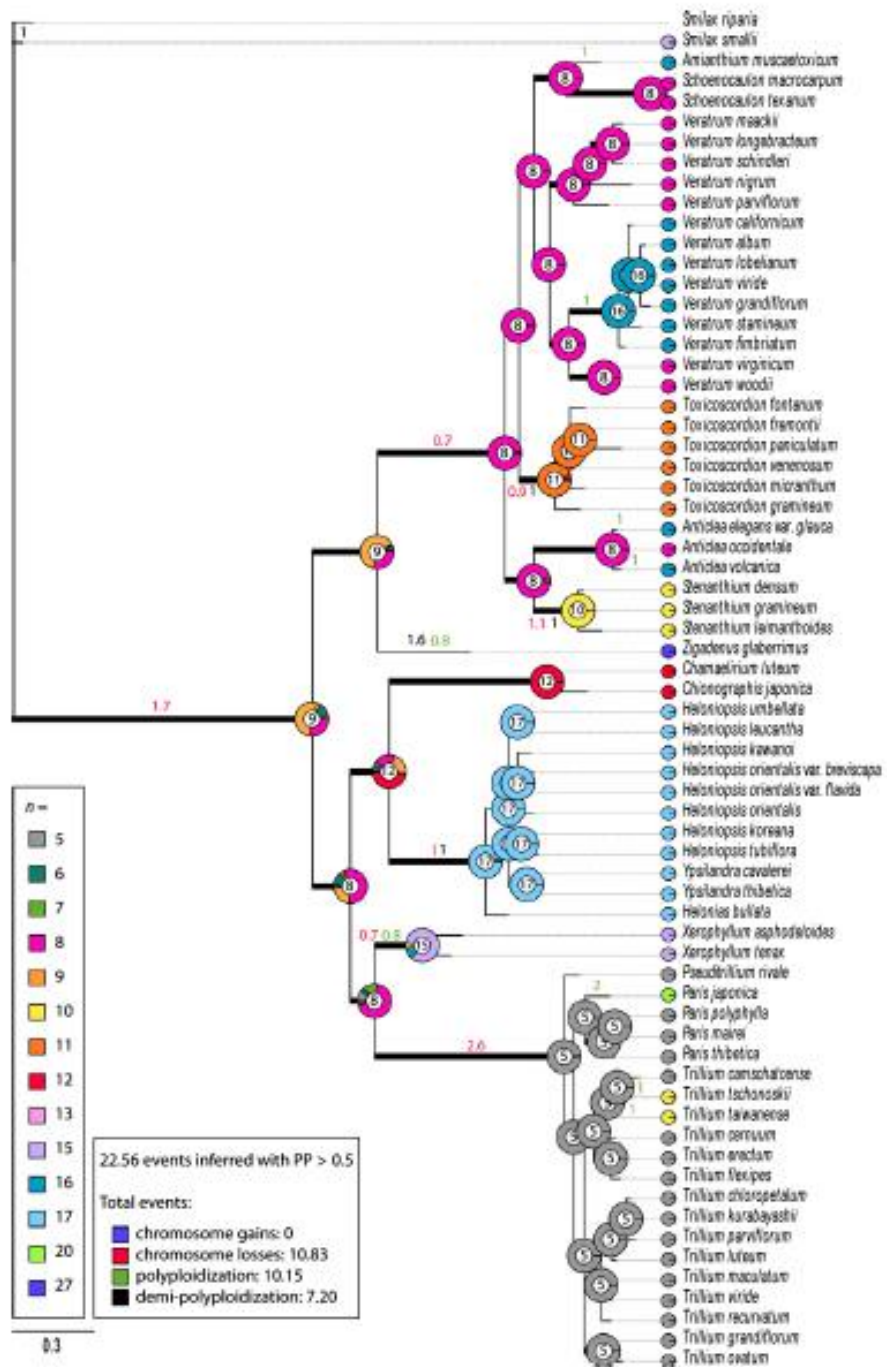
Caso 2: Familia Melanthiaceae con eventos reducción/aumento en tamaño genoma (Pellicer, J. et al., 2013)





Caso 2 Familia Melantheriaceae: Cambios en tamaño de genoma en tribu Parideae (Pellicer, J. et al., 2013)



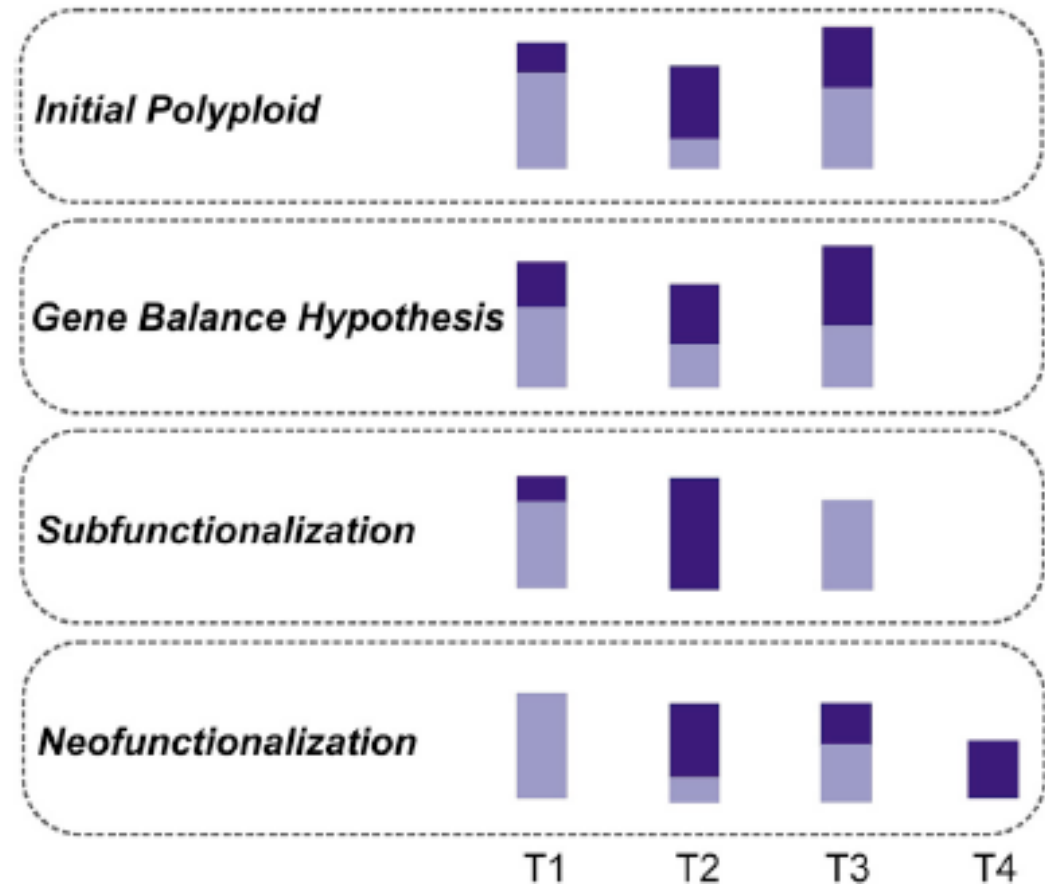
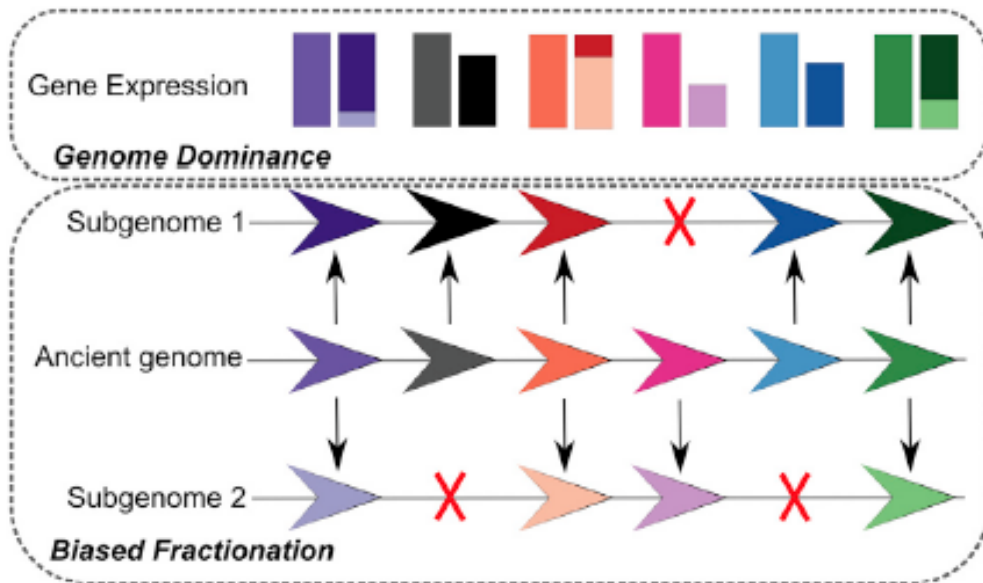


Caso 2 Familia Melanthaceae: Diversidad de número cromosómico

(Pellicer, J. et al., 2013)

Fraccionamiento/dominancia de genes (izq) y patrón de expresión (der) en genomas duplicados

(Liang & Schnable, 2018)

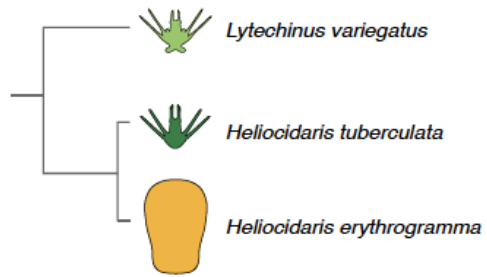


Caso 4 Erizos de mar: Cambios en la cromatina originando nuevos rasgos por presión selectiva (Davison et al., 2022)

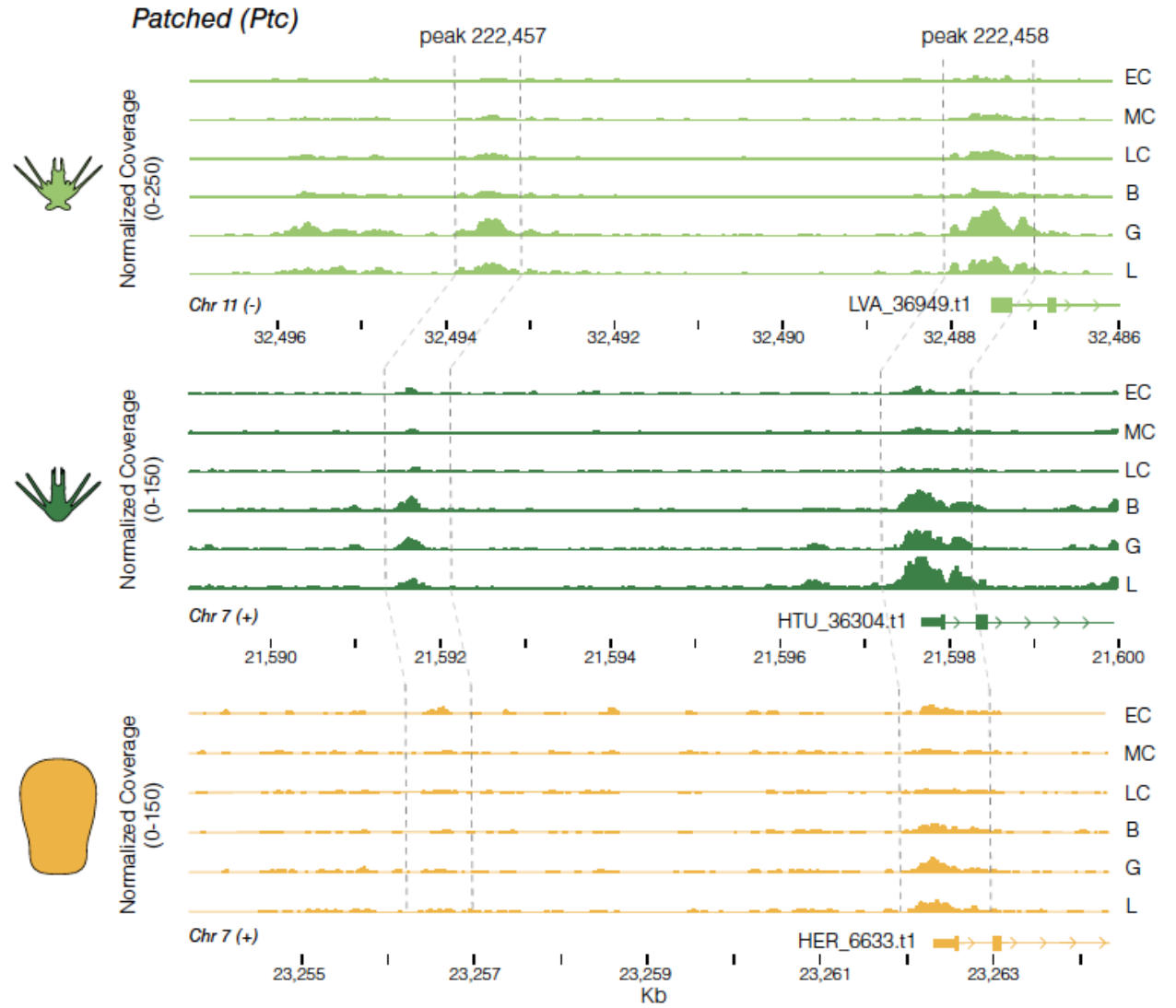
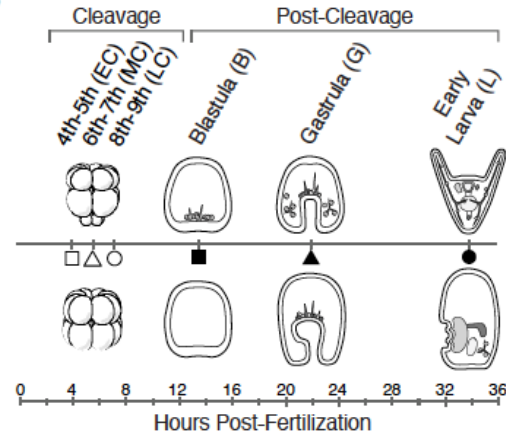
- El papel de los cambios evolutivos en la configuración de la cromatina sobre la expresión génica y los rasgos (desarrollo).
- Estudio del genoma de erizos de mar:
 - *Heliocidaris erythrogramma* (lecitotrofa)
 - *H. tuberculata* (planktotrofa)
 - *Lytechinus varieagatus* (distante planktotrofa)
- Cambios en elementos reguladores a menudo correlacionan con patrones de expresión divergentes de genes (ie. desarrollo), sugiriendo que las modificaciones evolutivas han sido consecuencia de evolución fenotípica
- Se demostró que presión selectiva impuesta por cambios en la historia del Desarrollo remodelaron rápidamente los elementos cis de genes del desarrollo principales para generar nuevos rasgos y programas embriónicos.

Caso 4 Erizos de mar: Cambios en la cromatina originando nuevos rasgos por presión selectiva (Davison et al., 2022)

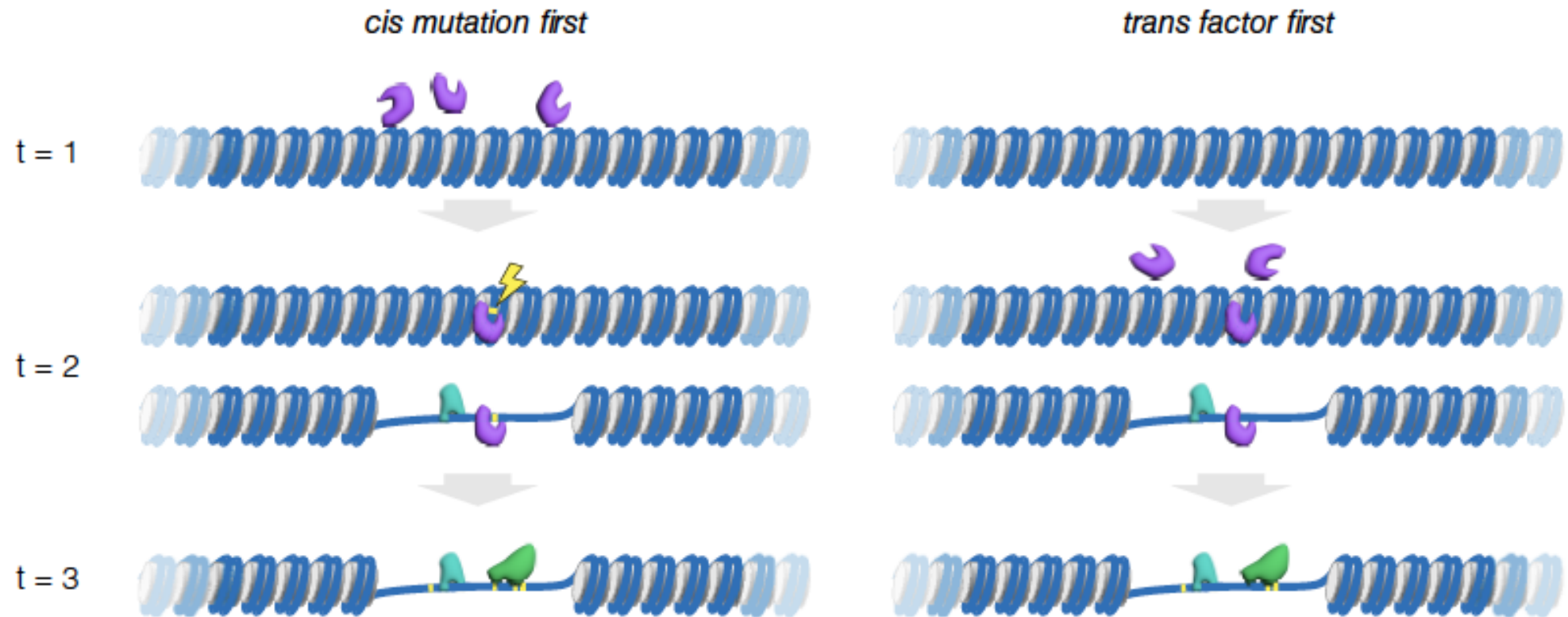
A



B



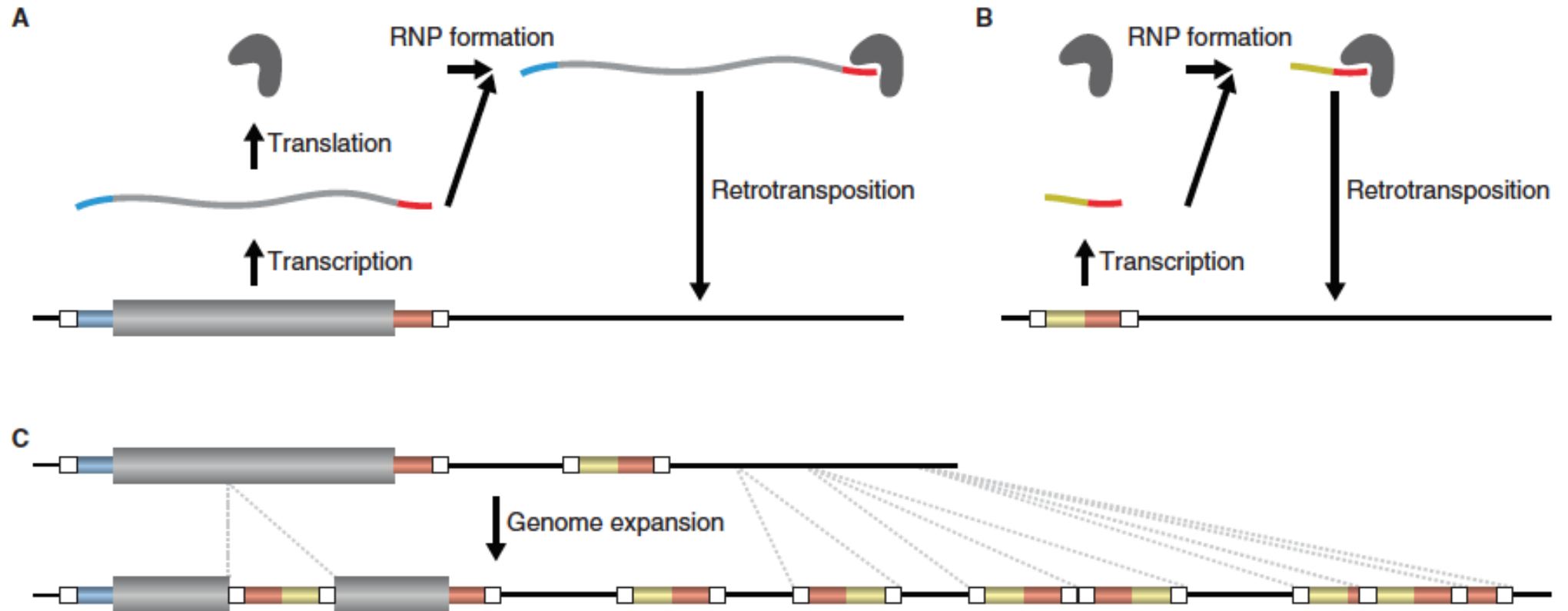
Caso 4 Erizos de mar: Cambios en la cromatina originando nuevos rasgos por presión selectiva (Davison et al., 2022)



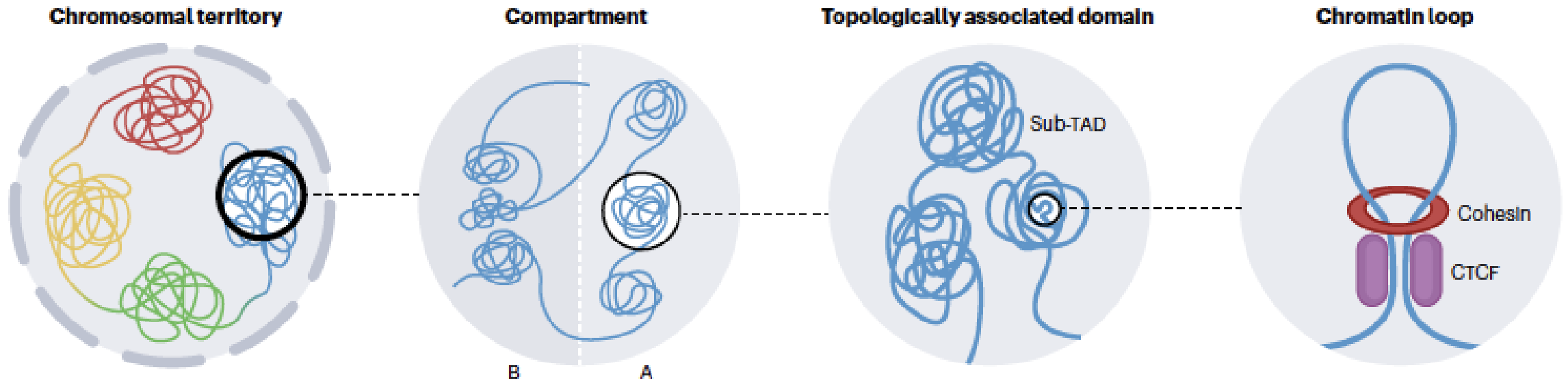
Modelo de apertura de una región de la cromatina

Los elementos transponibles dirigen el tamaño del genoma

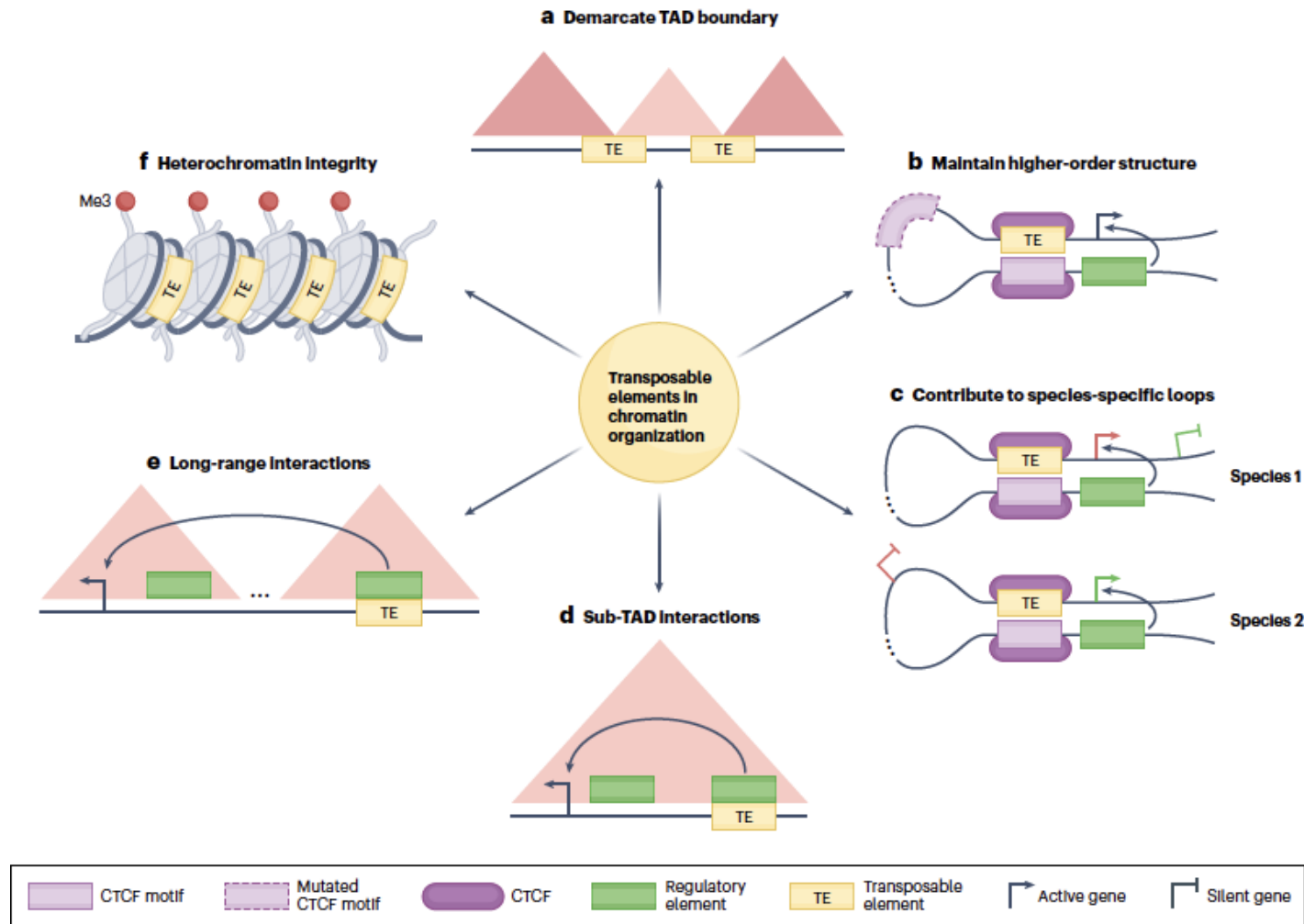
(Suh, A. 2019)

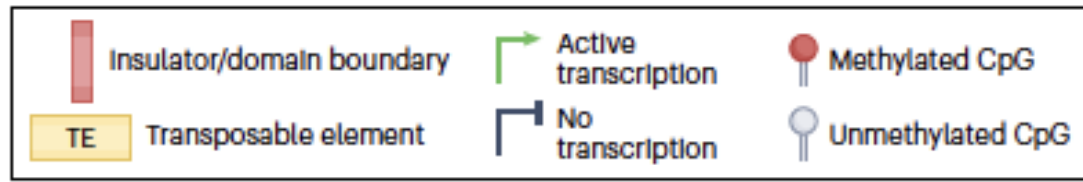
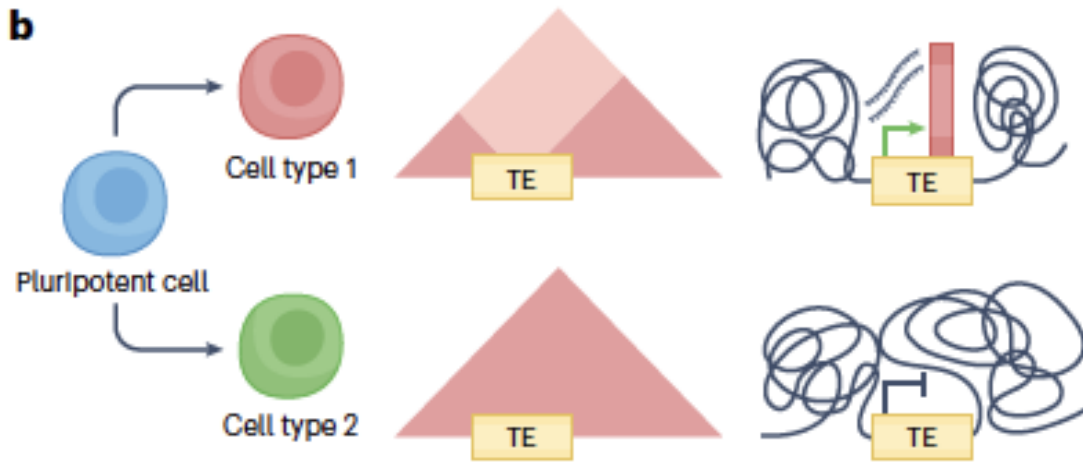
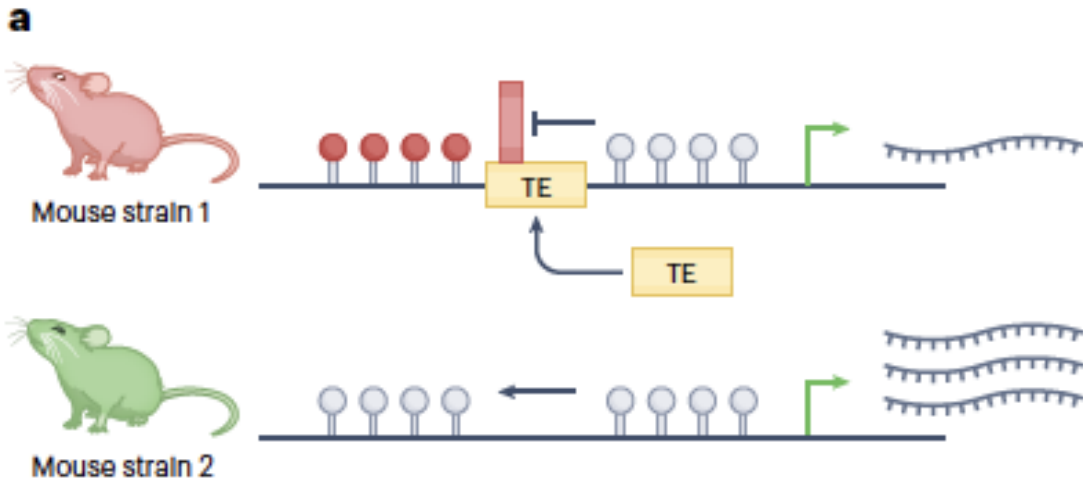


Estructura 3D del genoma en mamíferos (Lawson et al., 2022)



Papel de los ET en la organización de la cromatina (Lawson et al., 2022)





Papel de los ET en la organización de la cromatina

(Lawson et al., 2022)

2.97 ± 0.1



Euarchontoglires
 3.4 ± 0.4

Laurasiatheria
 2.8 ± 0.4



Afrotheria
 5.5 ± 0.6



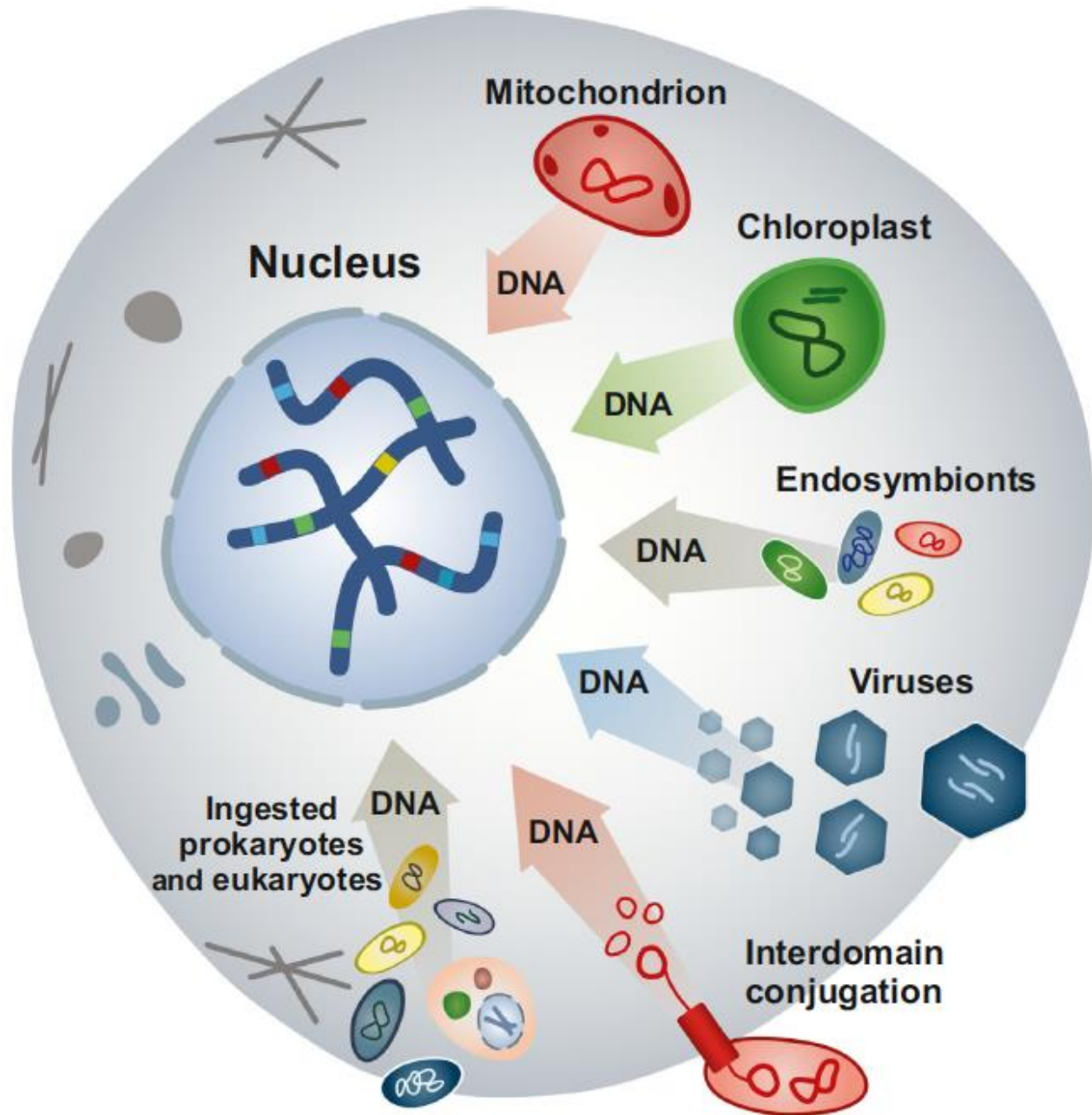
Xenarthra
 4.5 ± 0.5



4.07 ± 0.58



Tamaño de genomas en vertebrados (Redi & Capanna, 2012)

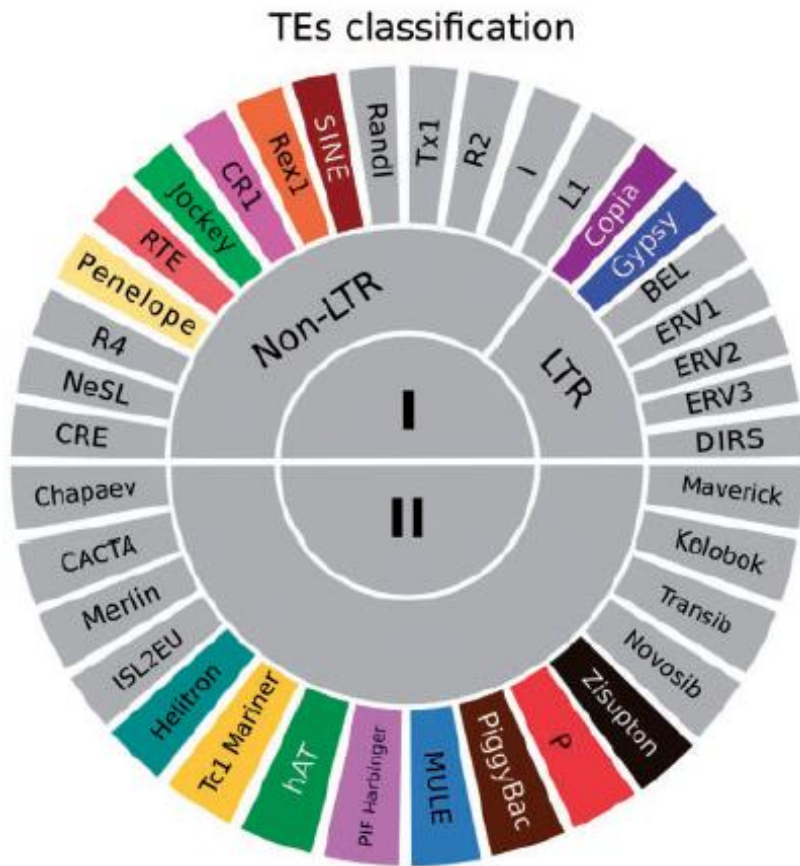


Posibles fuentes de transferencia lateral de genes en eucariotas (Sibbald, S. et al. 2020)

Transferencia Horizontal de ET en eucariotas y Animalia

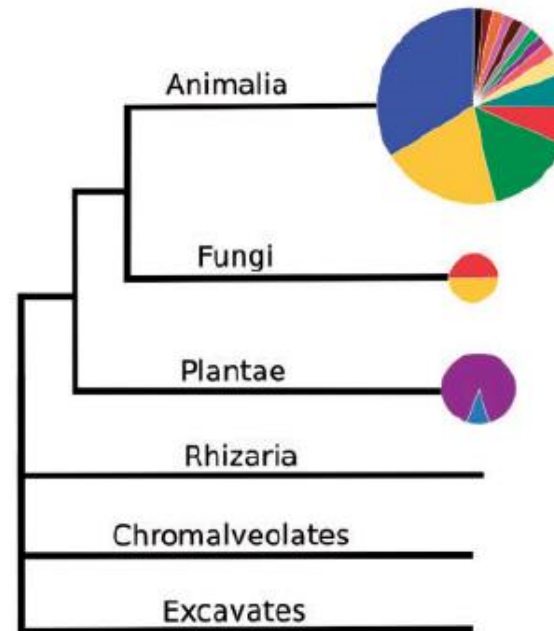
(Wallau, G.L. 2012)

B



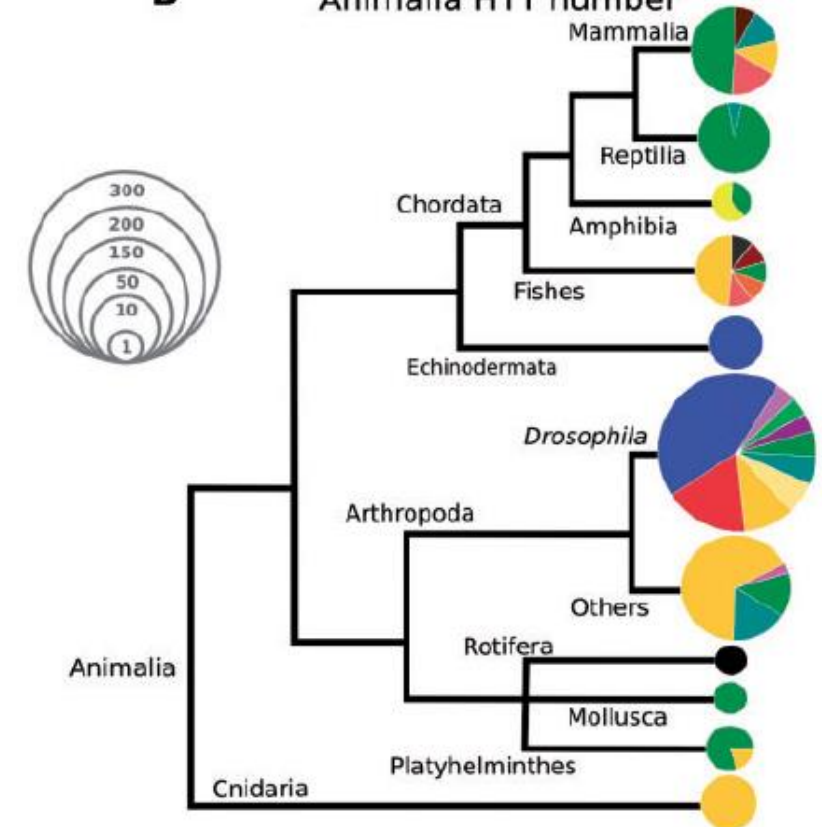
C

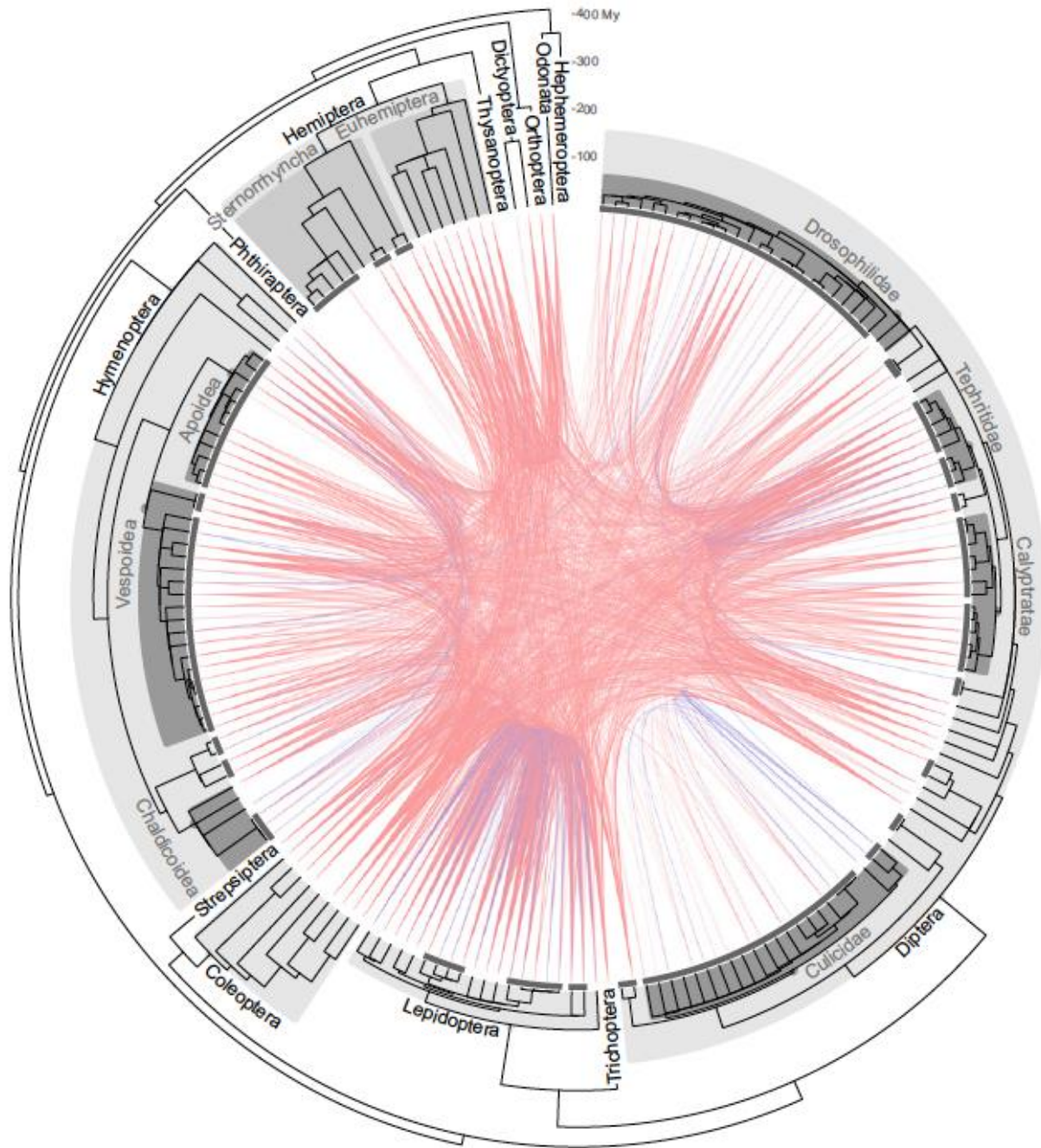
HTT number



D

Animalia HTT number





Transferencia horizontal de ET (THET o "HTT") en insectos

(Peccoud, J. et al., 2017)

Origination Events

- 1 Formation of composite SVA SINEs
- 2 Formation of composite LAVA SINEs
- 3 Dimerization of FLAM, FRAM to form ALU SINEs
- 4 Dimerization of ID and B1 to form ID-B1 SINEs
- 5 *De novo* origination of FLAM SINEs
- 6 *De novo* origination of FRAM SINEs
- 7 *De novo* origination of B2 SINEs
- 8 *De novo* origination of B3 SINEs
- 9 *De novo* origination of Ped-1 SINEs
- 10 *De novo* origination of ID SINEs
- 11 *De novo* origination of pB1 SINEs
- 12 *De novo* origination of ID-Spe SINEs
- 13 *De novo* origination of CAN SINEs
- 14 *De novo* origination of CHR SINEs
- 15 *De novo* origination of VES SINEs
- 16 *De novo* origination of MEG SINEs
- 17 *De novo* origination of AfroSINE SINEs
- 18 *De novo* origination of anARTE SINEs
- 19 *De novo* origination of Mon-1 SINEs

Horizontal Transfer Events

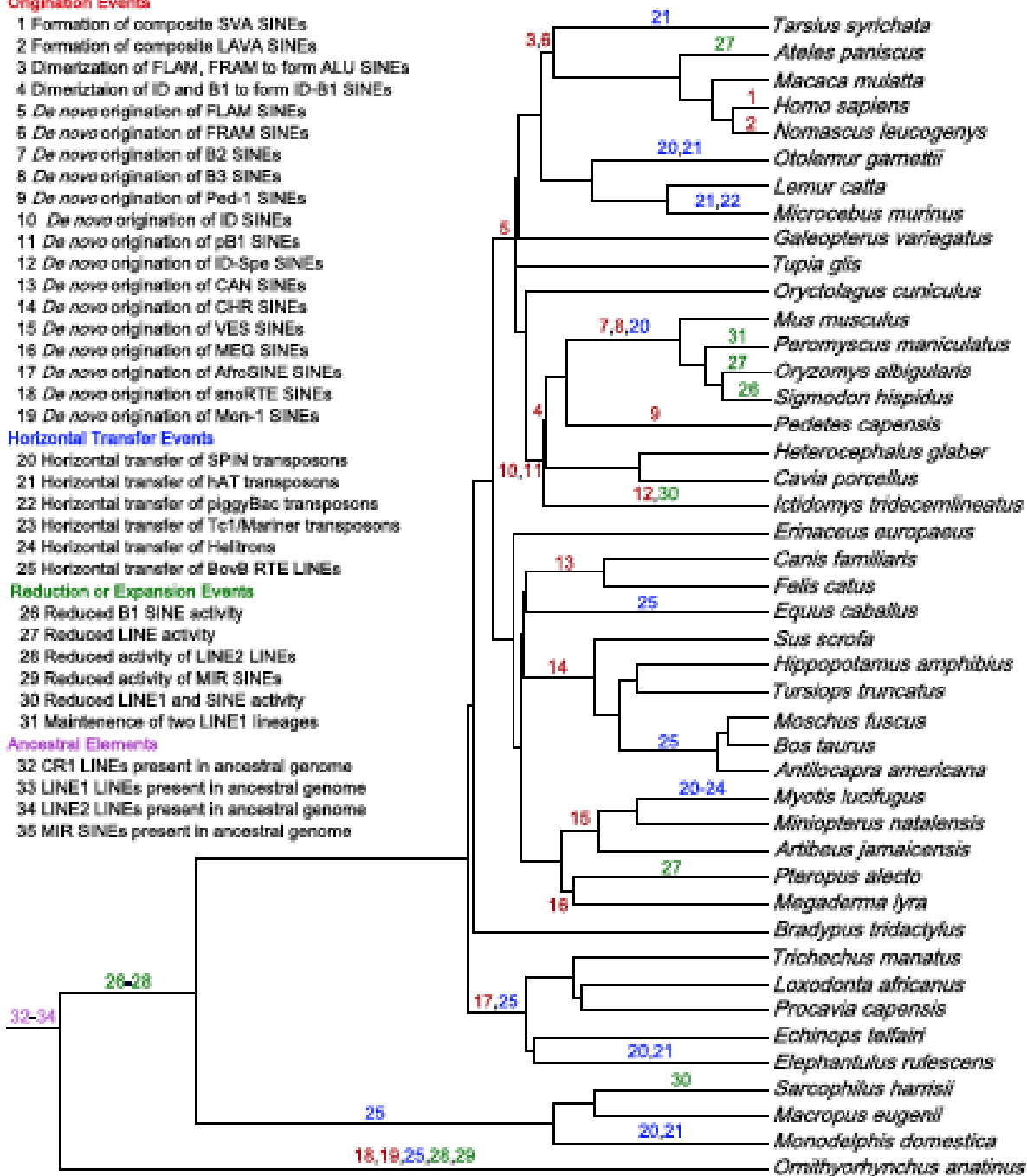
- 20 Horizontal transfer of SPIN transposons
- 21 Horizontal transfer of hAT transposons
- 22 Horizontal transfer of piggyBac transposons
- 23 Horizontal transfer of Tc1/Mariner transposons
- 24 Horizontal transfer of Helitrons
- 25 Horizontal transfer of BovB RTE LINEs

Reduction or Expansion Events

- 26 Reduced B1 SINE activity
- 27 Reduced LINE activity
- 28 Reduced activity of LINE2 LINEs
- 29 Reduced activity of MIR SINEs
- 30 Reduced LINE1 and SINE activity
- 31 Maintenance of two LINE1 lineages

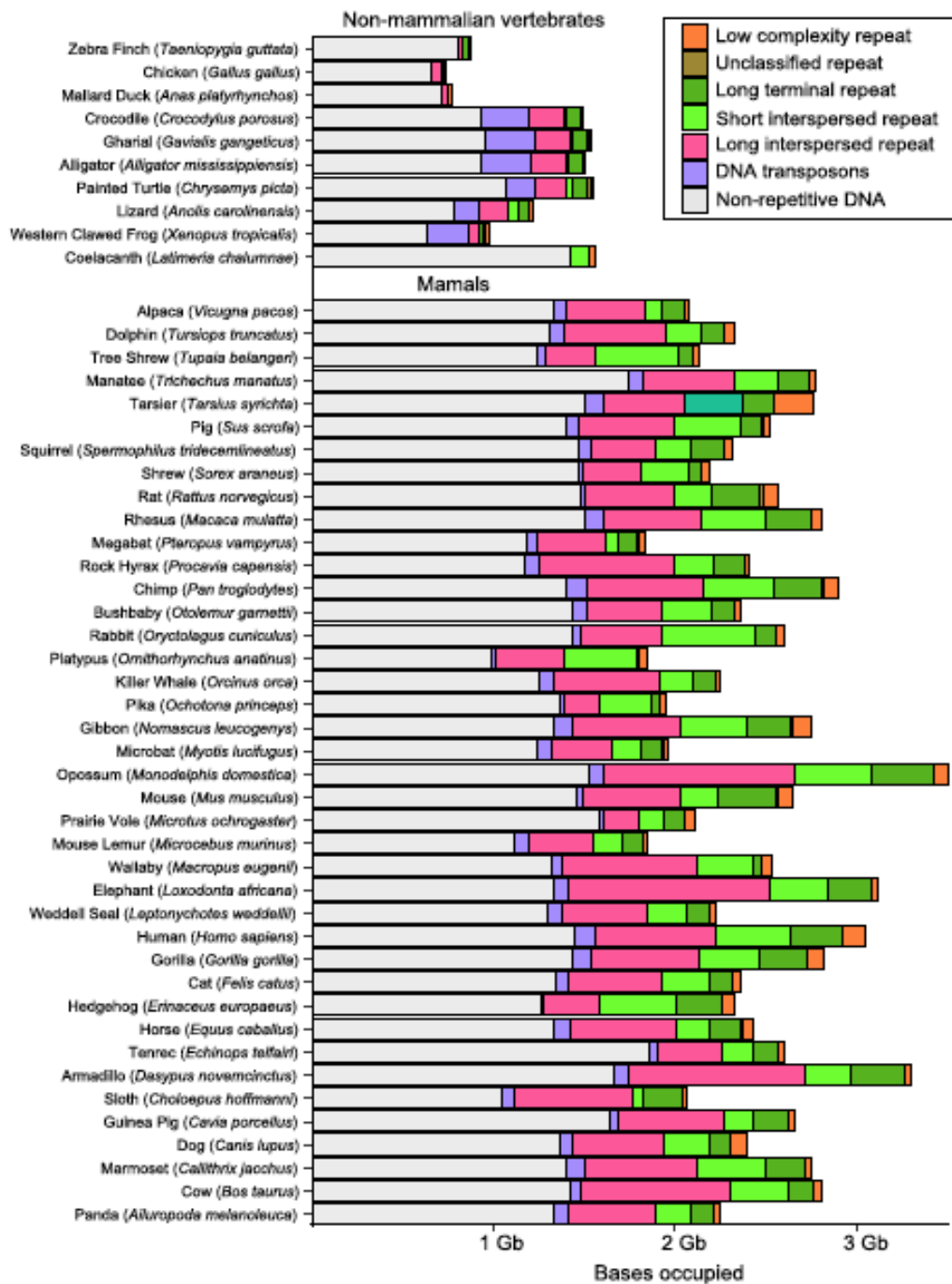
Ancestral Elements

- 32 CR1 LINEs present in ancestral genome
- 33 LINE1 LINEs present in ancestral genome
- 34 LINE2 LINEs present in ancestral genome
- 35 MIR SINEs present in ancestral genome



Principales transiciones de ET en genomas de mamíferos

(Plat II, R.N. et al. 2018)



Contenido de ET en genomas de mamíferos y otros vertebrados (Plat II, R.N. et al. 2018)

Hipótesis sobre la evolución del tamaño del genoma

(Blommaert, J. 2018)

