

Introducción a la filogenómica



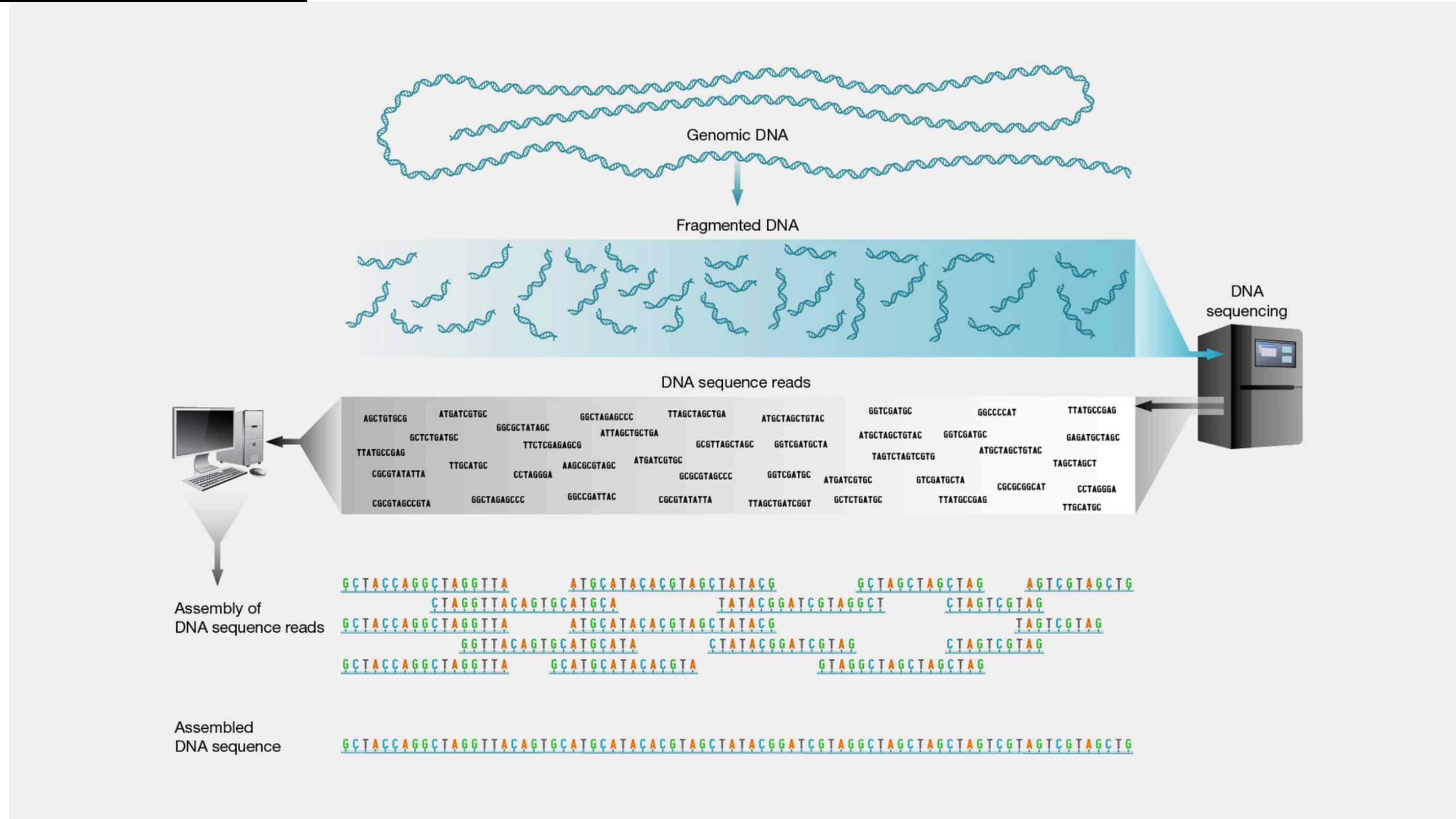
CENTRO DE
INVESTIGACIONES
BIOLÓGICAS DEL
NOROESTE, S.C.



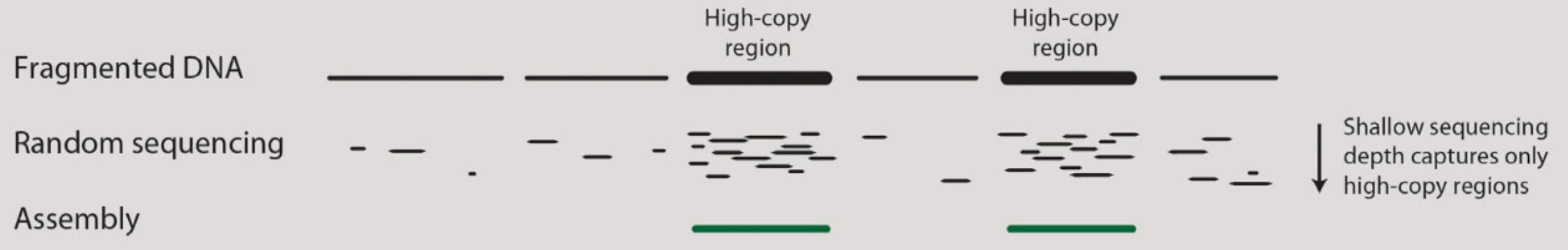
Genotecas

Día	Temas
23 de septiembre	<ul style="list-style-type: none">• Introducción a la Filogenómica. Conceptos básicos• Introducción al sistema operativo Linux
24 de septiembre	<ul style="list-style-type: none">• Métodos de construcción de librerías genómicas• Control de calidad, ensamble y alineamiento de secuencias
25 de septiembre	<ul style="list-style-type: none">• Método de Máxima Verosimilitud• Método de Inferencia Bayesiana
26 de septiembre	<ul style="list-style-type: none">• Modelo coalescente multiespecies• Evaluación de árboles de especies
27 de septiembre	<ul style="list-style-type: none">• Estimación de tiempos de divergencia• Evaluación de flujo genético

Genotecas



(A) Genome skimming



Regiones repetitivas. Baja profundidad.

- genes ribosomales
- mitocondriales
- plastoma.



Whole Plastome Sequencing Within *Silene* Section *Psammophilae* Reveals Mainland Hybridization and Divergence With the Balearic Island Populations

José Carlos del Valle^{1*}, Inés Casimiro-Soriguer¹, M^a Luisa Buidé¹, Eduardo Narbona¹
and Justen B. Whittall²

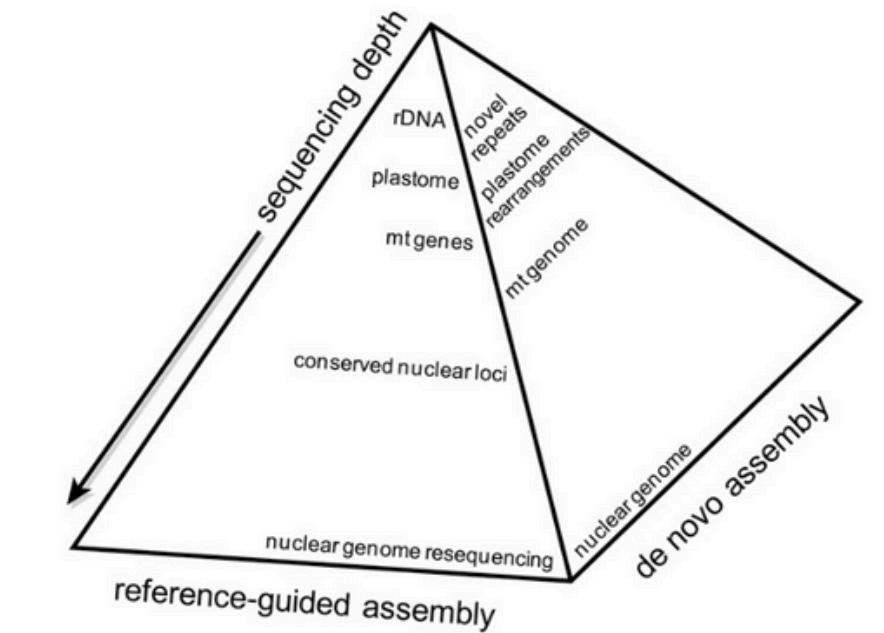
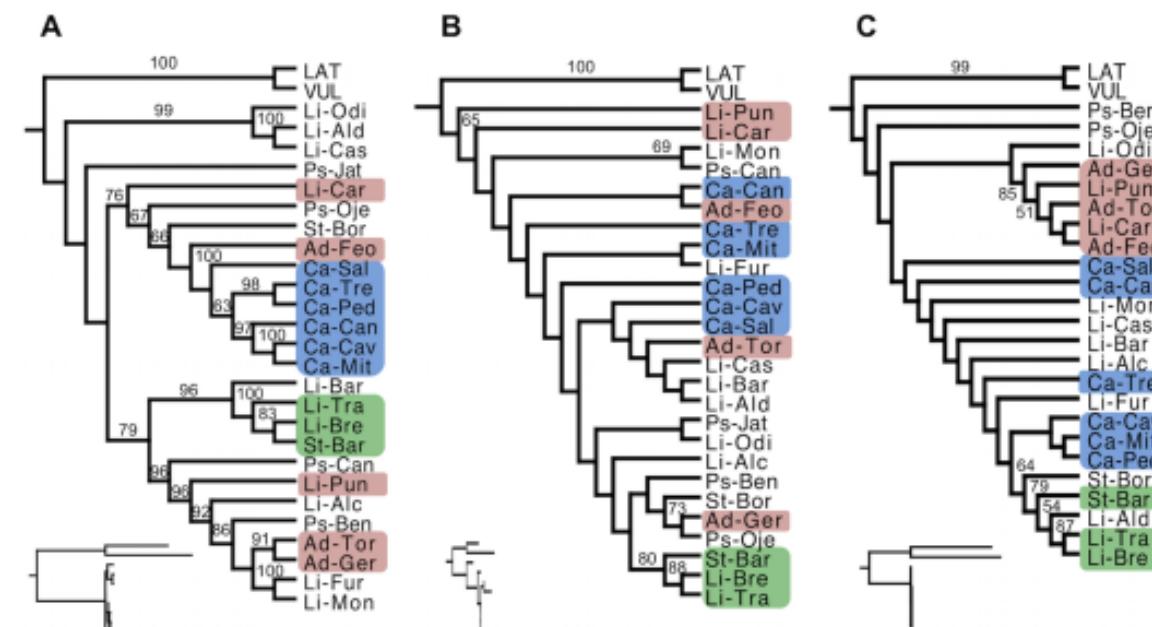
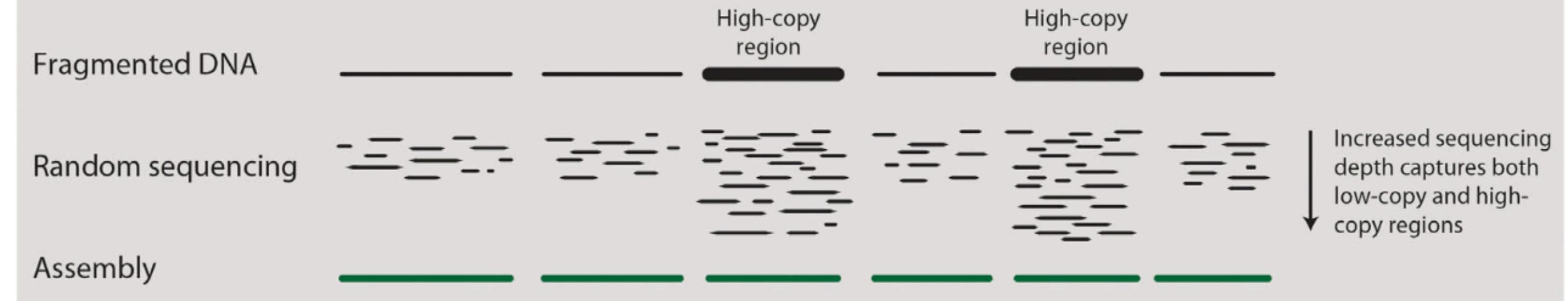


Fig. 1. The genomic iceberg: the relationship between genomic targets, the sequencing depth required to obtain them, and the most appropriate method of sequence assembly.

Straub et al., 2011

Genotecas

(B) Whole-genome sequencing

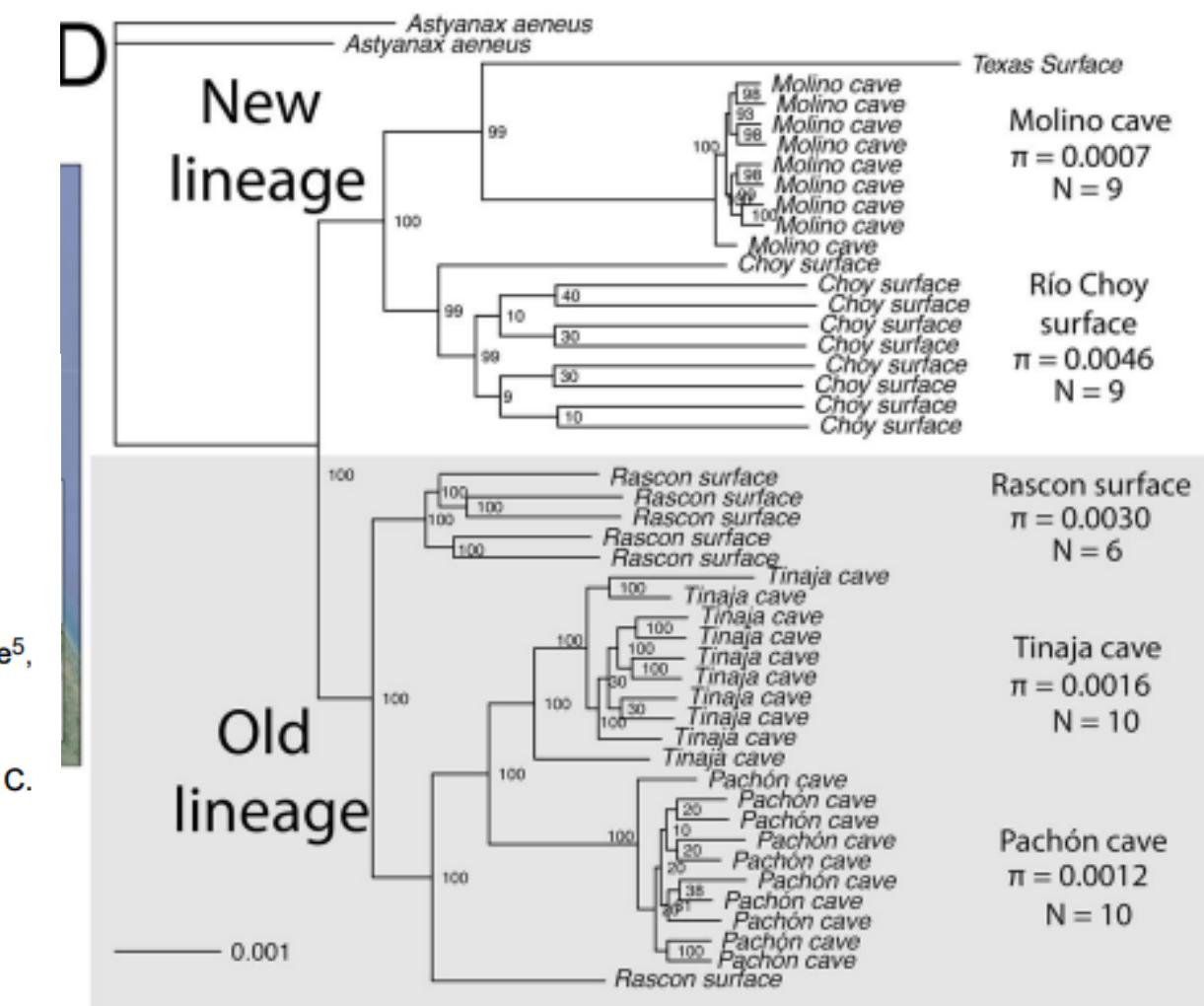


Mayor profundidad
Representación completa

Published in final edited form as:
Mol Ecol. 2018 November ; 27(22): 4397–4416. doi:10.1111/mec.14877.

The role of gene flow in rapid and repeated evolution of cave related traits in Mexican tetra, *Astyanax mexicanus*

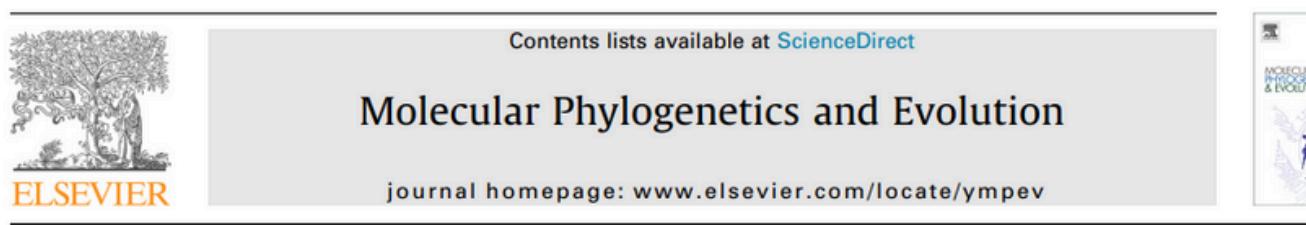
Adam Herman^{1,2}, Yaniv Brandvain¹, James Weagley³, William R. Jeffery⁴, Alex C. Keene⁵, Thomas J. Y. Kono⁶, Helena Bilandžija^{2,4}, Richard Borowsky⁷, Luis Espinasa⁸, Kelly O'Quin⁹, Claudia P. Ornelas-García¹⁰, Masato Yoshizawa¹¹, Brian Carlson¹², Ernesto Maldonado¹³, Joshua B. Gross¹⁴, Reed A. Cartwright^{15,16}, Nicolas Rohner^{17,18}, Wesley C. Warren¹⁹, and Suzanne E. McGaugh²



Genotecas

Expresión génica
Diferentes condiciones o tejidos.
(Wang et al., 2009)

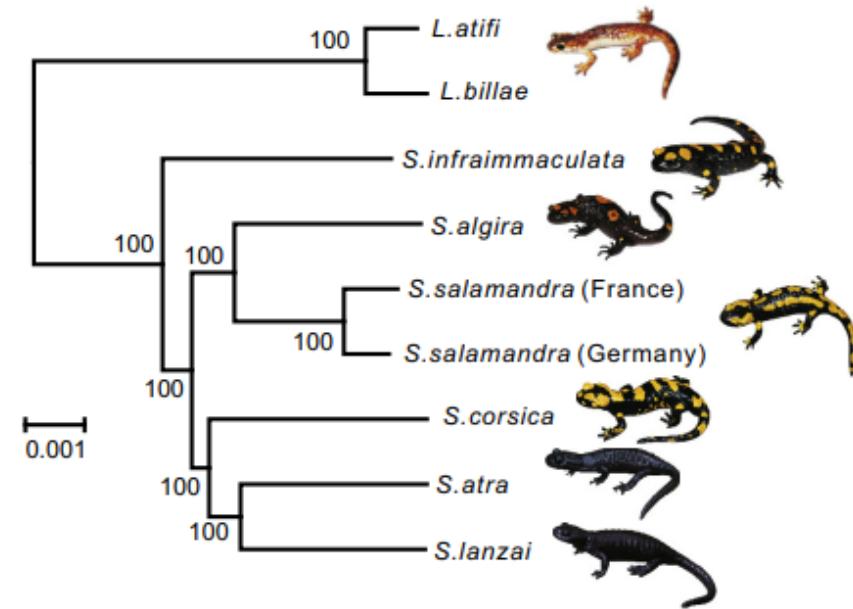
(C) RNA sequencing



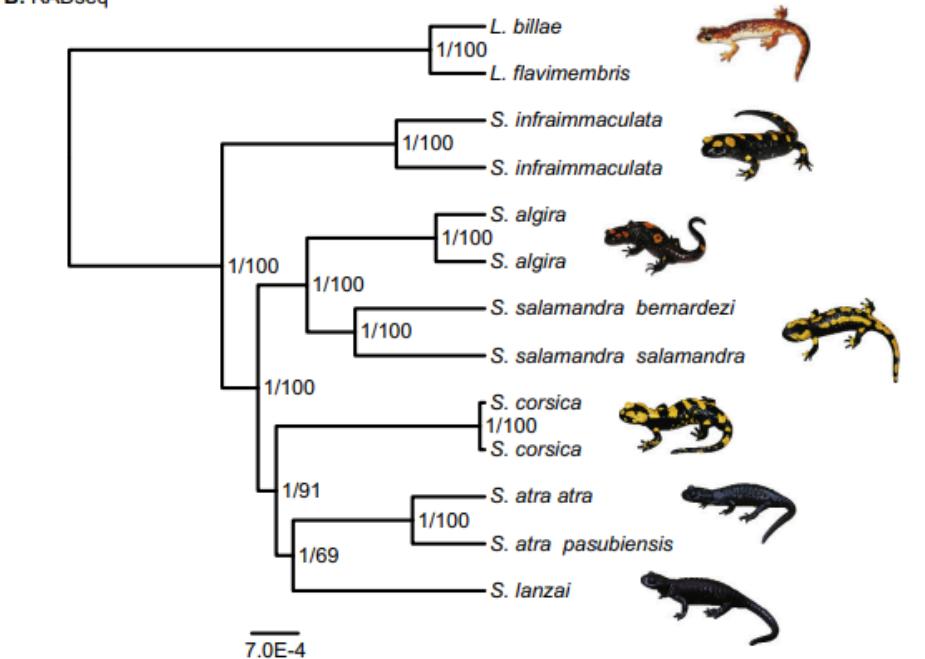
Inferring the shallow phylogeny of true salamanders (*Salamandra*) by multiple phylogenomic approaches

Ariel Rodríguez^{a,b}, James D. Burgon^c, Mariana Lyra^d, Iker Irisarri^e, Denis Baurain^f, Leon Blaustein^g, Bayram Göçmen^h, Sven Künzelⁱ, Barbara K. Mable^c, Arne W. Nolte^{i,j}, Michael Veith^k, Sebastian Steinfartz^a, Kathryn R. Elmer^c, Hervé Philippe^{l,m}, Miguel Vences^{a,*}

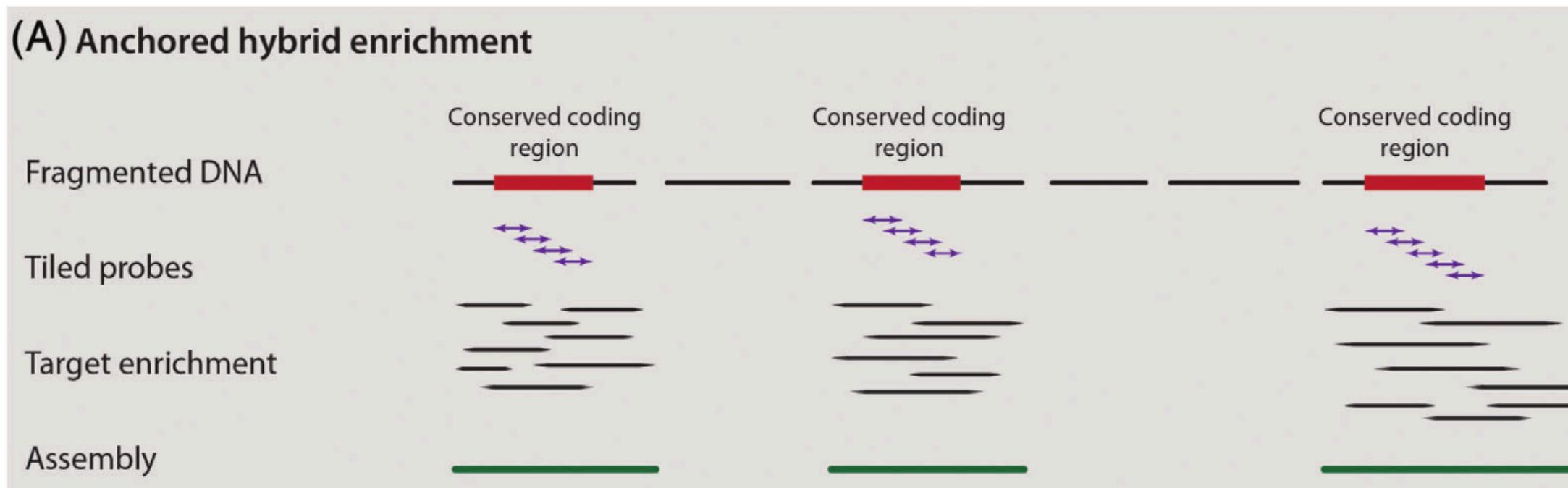
A. RNAseq



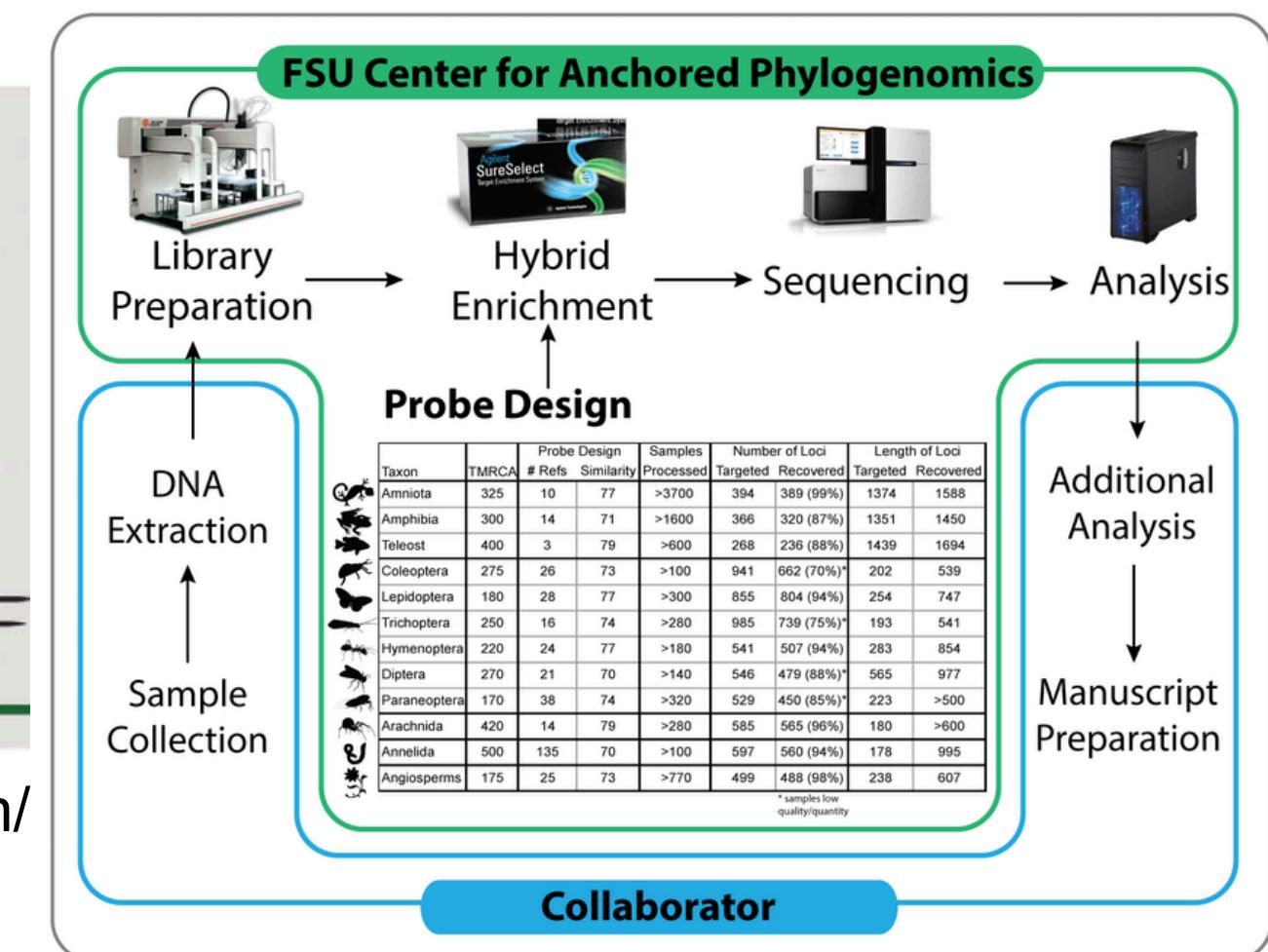
B. RADseq



(A) Anchored hybrid enrichment



anchoredphylogeny.com/

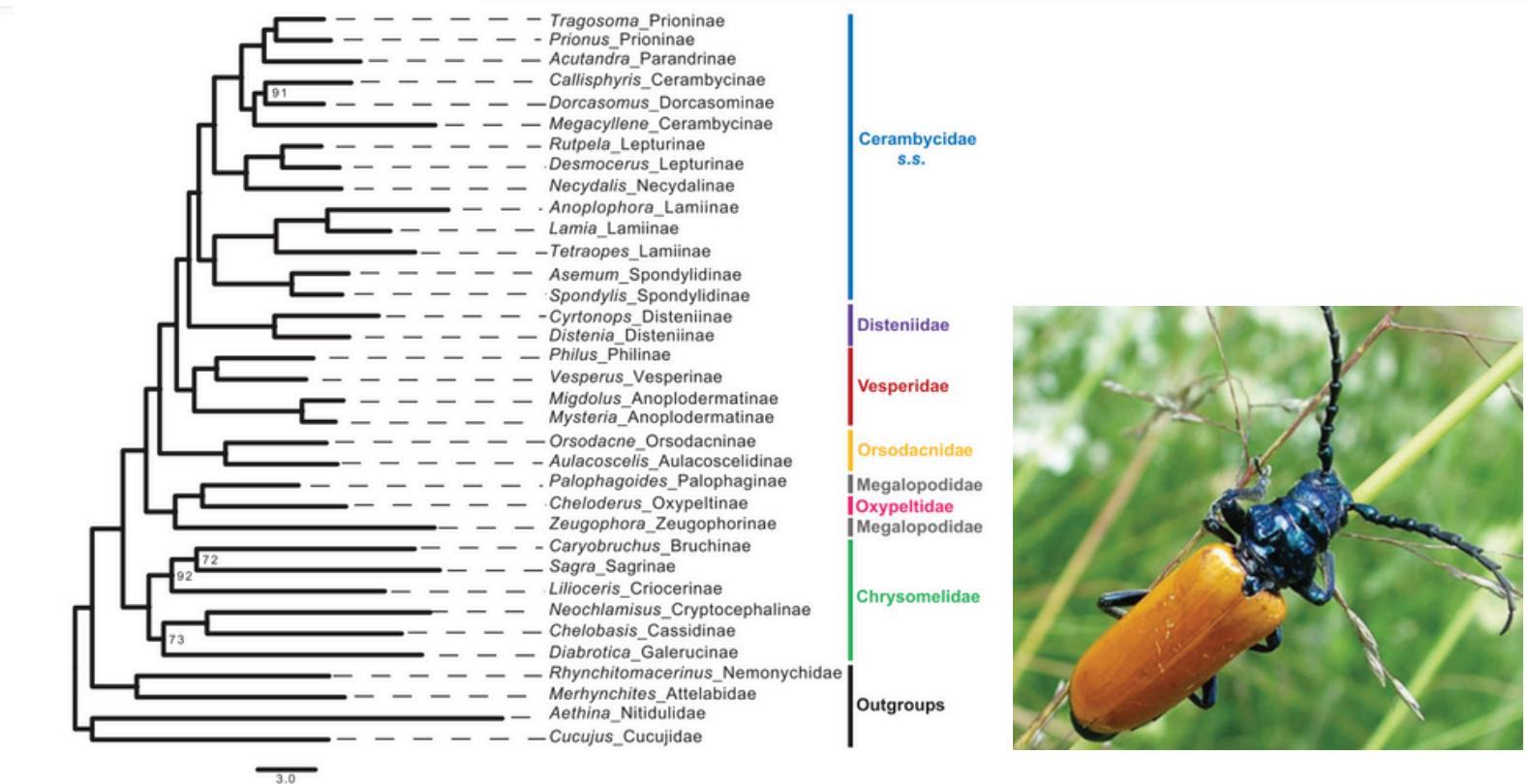


Systematic
Entomology

Systematic Entomology (2017), DOI: 10.1111/syen.12257

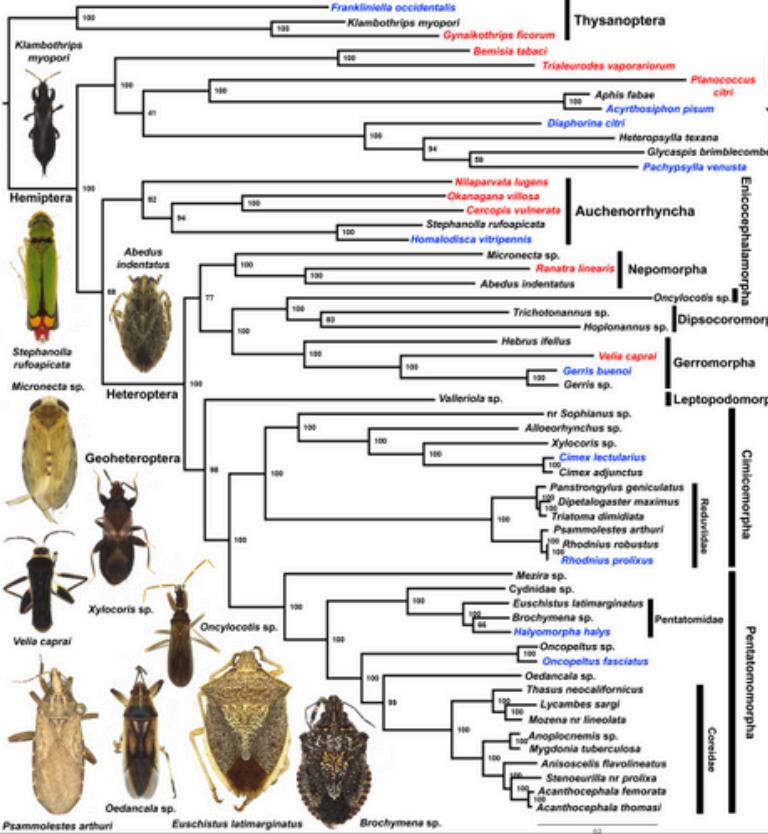
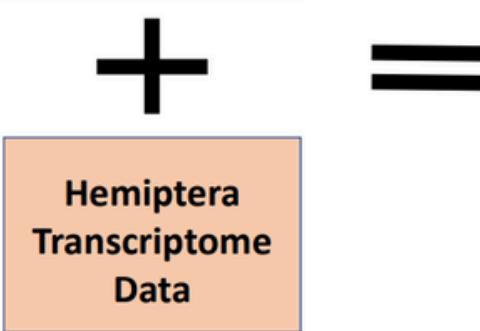
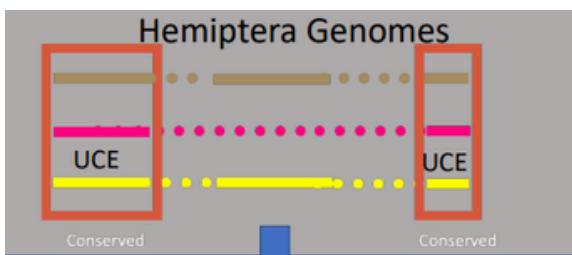
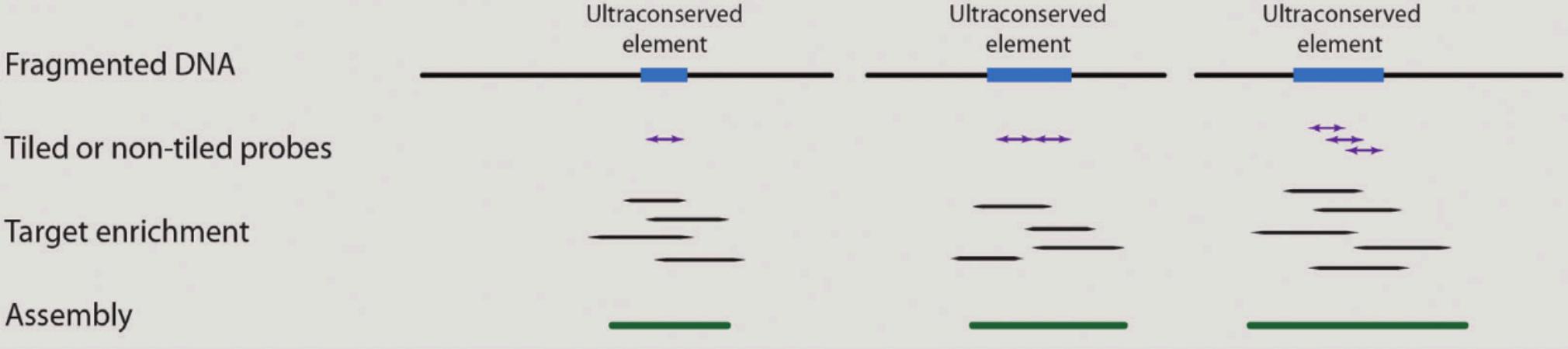
Anchored hybrid enrichment provides new insights into the phylogeny and evolution of longhorned beetles (Cerambycidae)

STEPHANIE HADDAD^{1,*}, SEUNGGWAN SHIN¹, ALAN R. LEMMON², EMILY MORIARTY LEMMON³, PETR SVACHA⁴, BRIAN FARRELL⁵, ADAM ŚLIPIŃSKI⁶, DONALD WINDSOR⁷ and DUANE D. MCKENNA¹



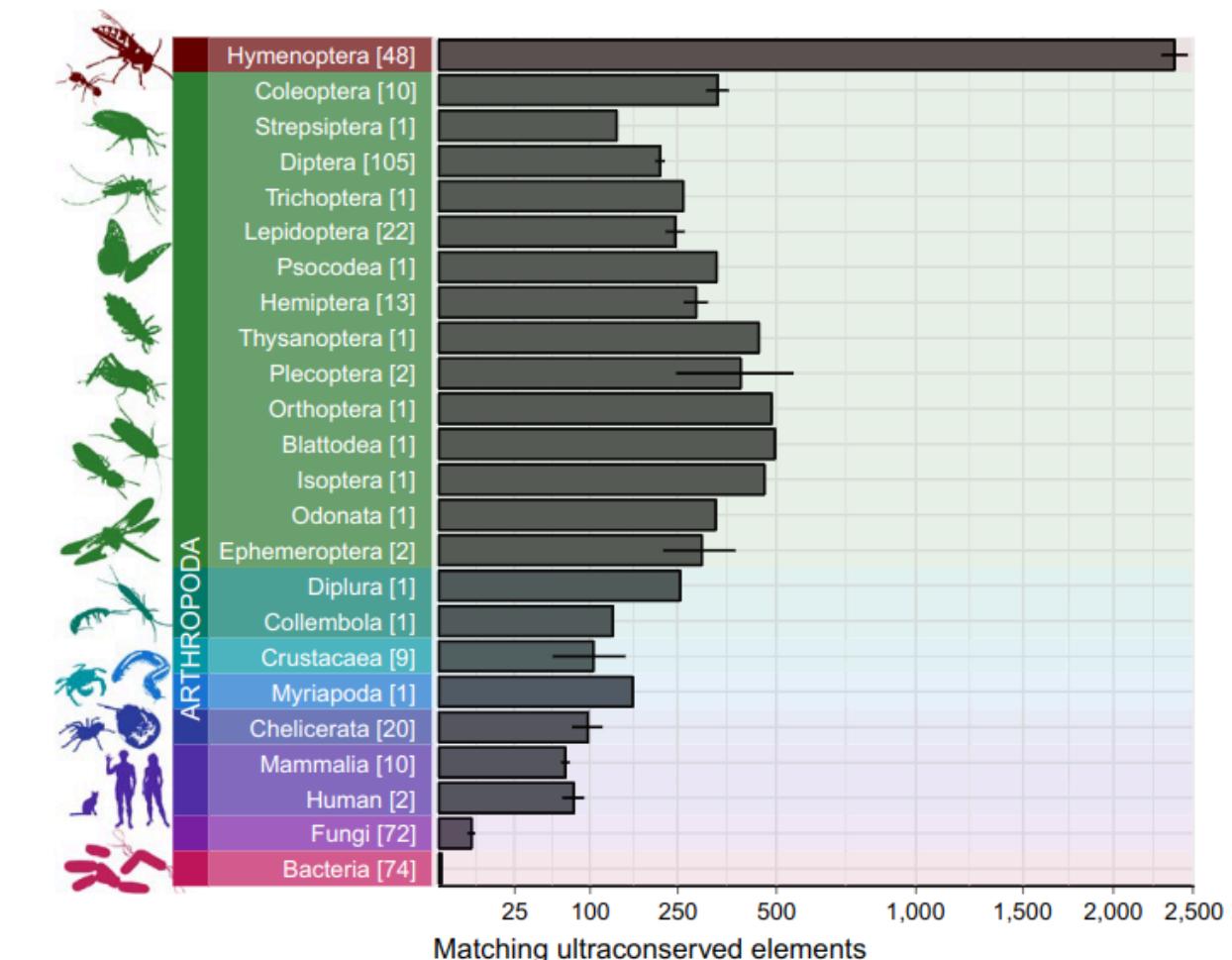
Genotecas

(B) Ultraconserved elements



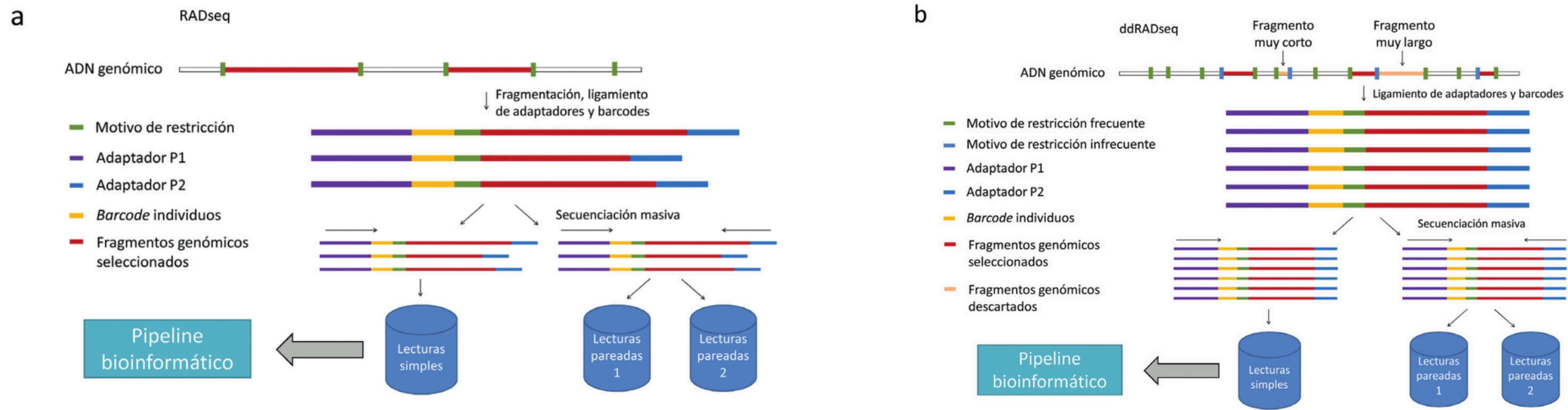
Insight from an ultraconserved element bait set designed for hemipteran phylogenetics integrated with genomic resources

Troy J. Kieran ^a , Eric R.L. Gordon ^{b c}, Michael Forthman ^d, Rochelle Hoey-Chamberlain ^b, Rebecca T. Kimball ^e, Brant C. Faircloth ^f, Christiane Weirauch ^b, Travis C. Glenn ^a

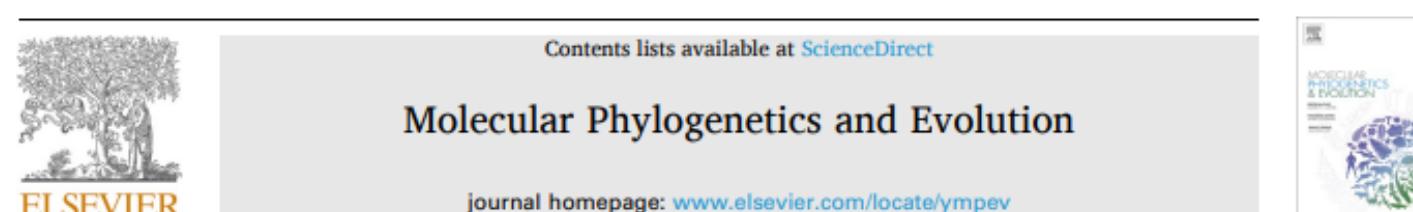


Bossert & Danforth, 2017

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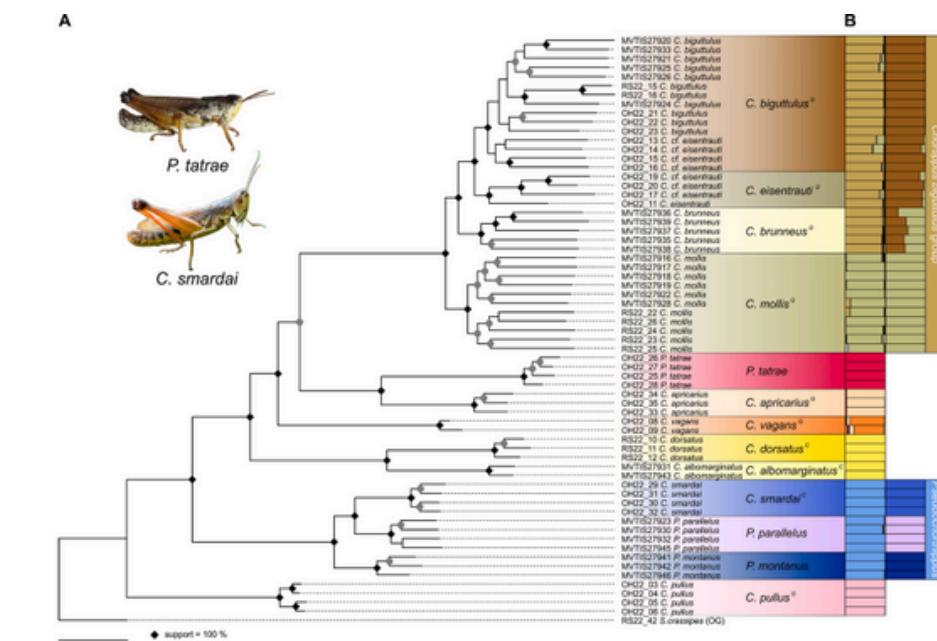
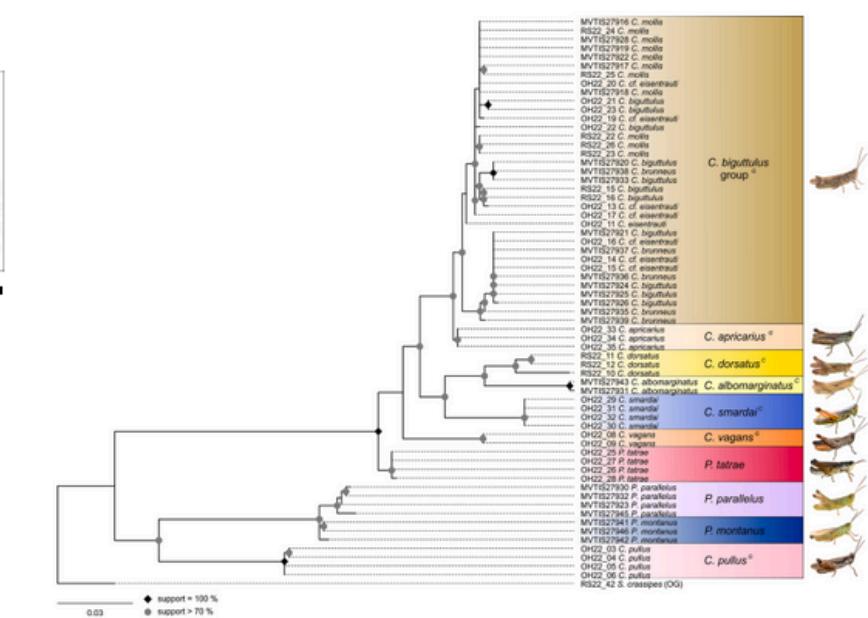


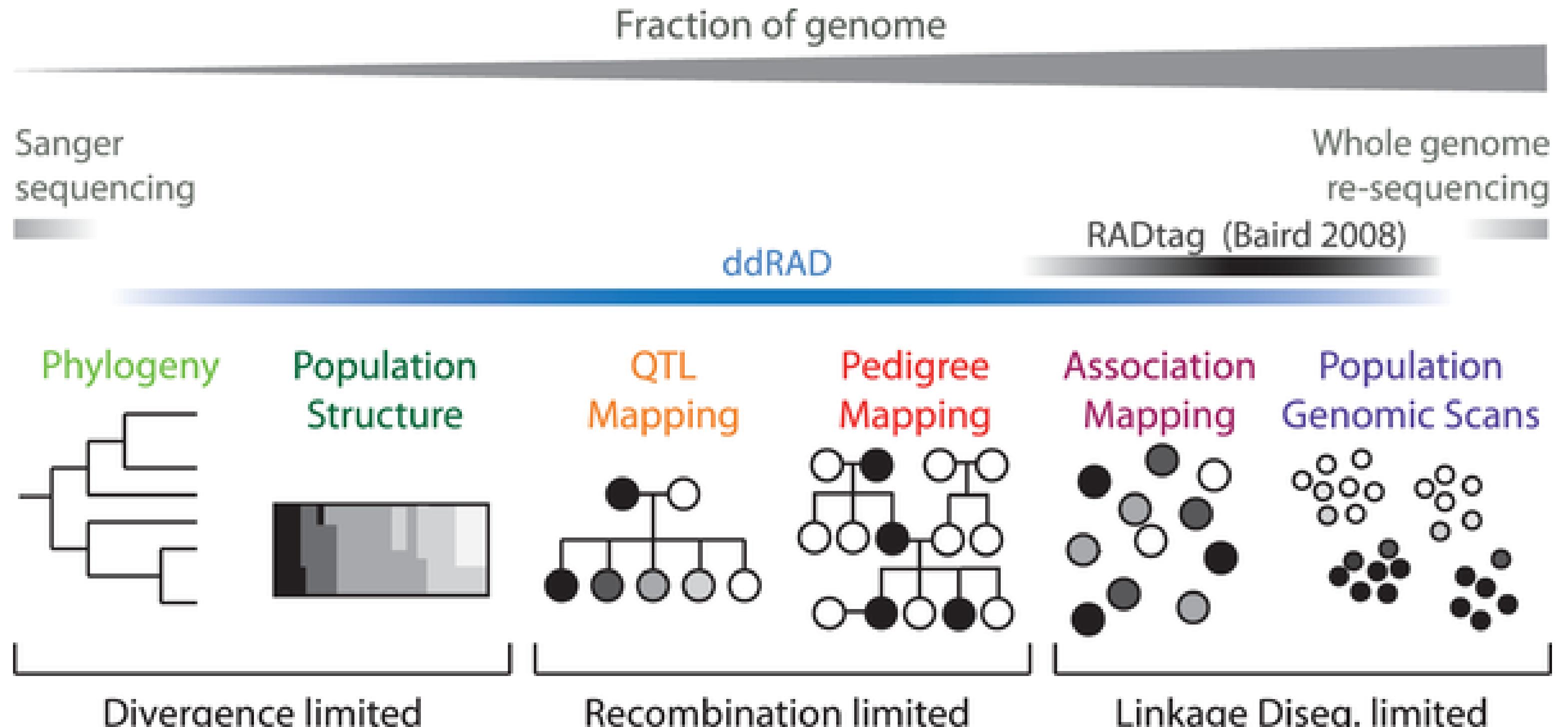
Lopez de Heredia, 2016



Phylogenetic insights into Central European *Chorthippus* and *Pseudochorthippus* (Orthoptera: Acrididae) species using ddRADseq data

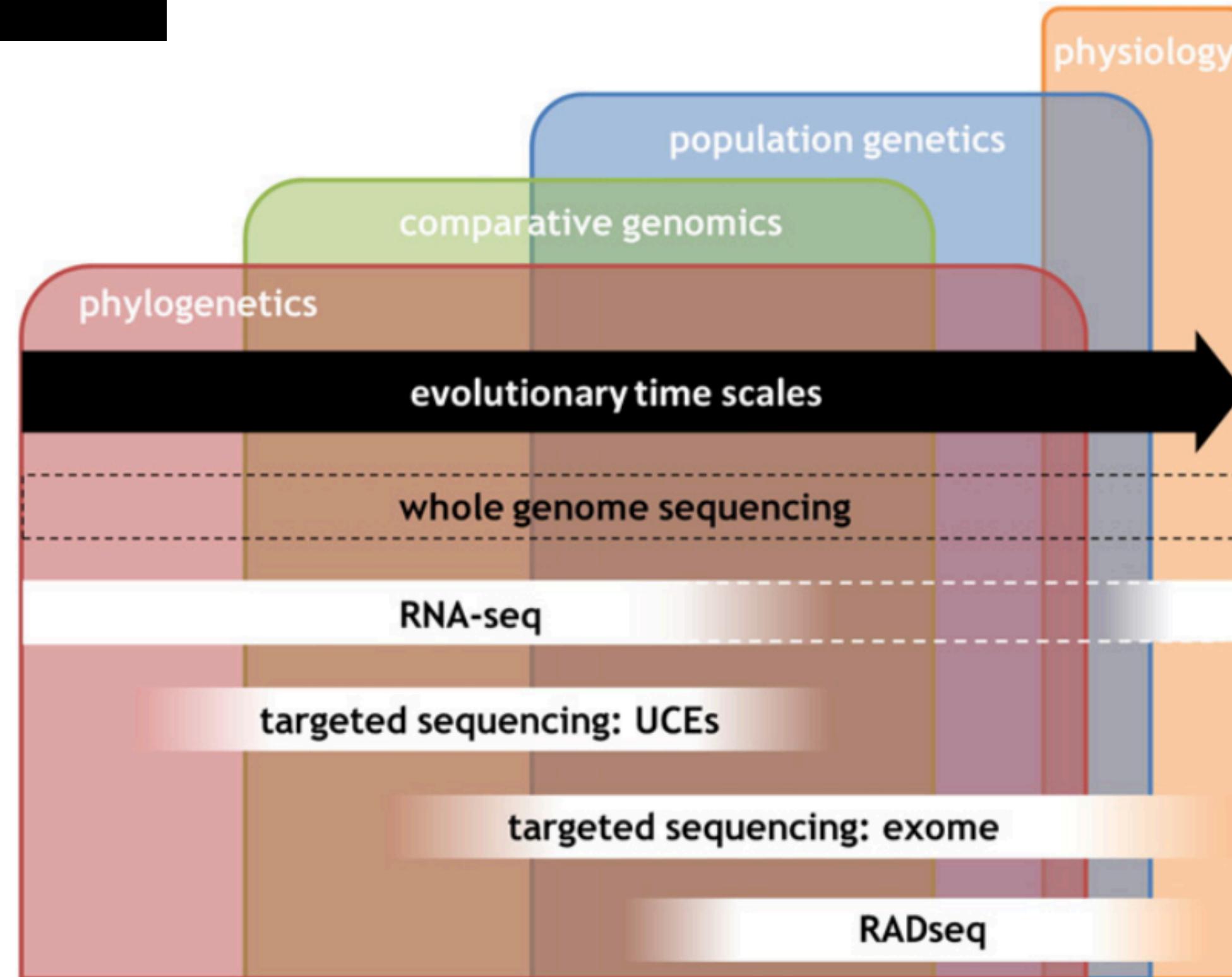
Robin Schmidt ^{a,*}, Christophe Dufresnes ^{b,c}, Anton Krištín ^d, Sven Künzel ^e, Miguel Vences ^a, Oliver Hawlitschek ^{f,g}





Peterson et al., 2012

Genotecas



da Fonseca et al., 2016

A moment of silence for all the samples that were lost



Header

Sequence

Quality

FASTQ

FASTQ

fastq header format (version > 1.8)

Sequence Header +Sequence ID

a b c d e f g h i j k

@HWI-ST486:166:C06K9ACXX:7:1101:1443:1995 1:N:0:ACAGTG

- a. unique instrument name**
- b. run id
- c. flowcell id
- d. flowcell lane
- e. tile number within the flowcell lane
- f. x-coordinate of the cluster within the tile
- g. y-coordinate of the cluster within the tile
- h. the member of a pair, 1 or 2 (paired-end or mate-pair reads only)**
- i. Y if the read fails filter (read is bad), N otherwise
- j. 0 when no control bits are on
- k. index sequence



FASTQ

ASCII _BASE=33 Illumina, Ion Torrent, PacBio and Sanger											
Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII
0	1.00000	33 !	11	0.07943	44 ,	22	0.00631	55 7	33	0.00050	66 B
1	0.79433	34 "	12	0.06310	45 -	23	0.00501	56 8	34	0.00040	67 C
2	0.63096	35 #	13	0.05012	46 .	24	0.00398	57 9	35	0.00032	68 D
3	0.50119	36 \$	14	0.03981	47 /	25	0.00316	58 :	36	0.00025	69 E
4	0.39811	37 %	15	0.03162	48 0	26	0.00251	59 ;	37	0.00020	70 F
5	0.31623	38 &	16	0.02512	49 1	27	0.00200	60 <	38	0.00016	71 G
6	0.25119	39 '	17	0.01995	50 2	28	0.00158	61 =	39	0.00013	72 H
7	0.19953	40 (18	0.01585	51 3	29	0.00126	62 >	40	0.00010	73 I
8	0.15849	41)	19	0.01259	52 4	30	0.00100	63 ?	41	0.00008	74 J
9	0.12589	42 *	20	0.01000	53 5	31	0.00079	64 @	42	0.00006	75 K
10	0.10000	43 +	21	0.00794	54 6	32	0.00063	65 A			

Q probabilidad de que la base sea incorrecta



Genotecas

