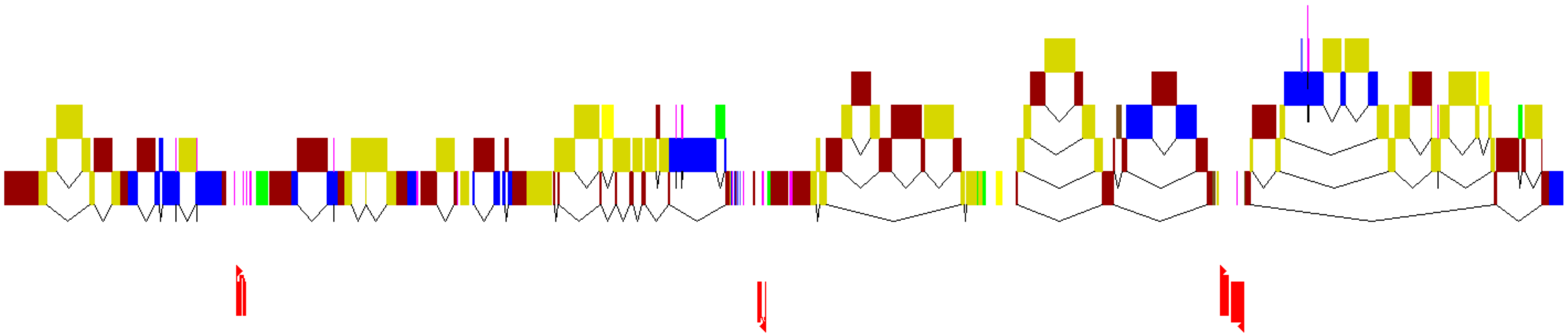
Transposable elements in invasive species



Invade the invader…

Introduction on TEs

Untangling evolutionary forces shaping TE content

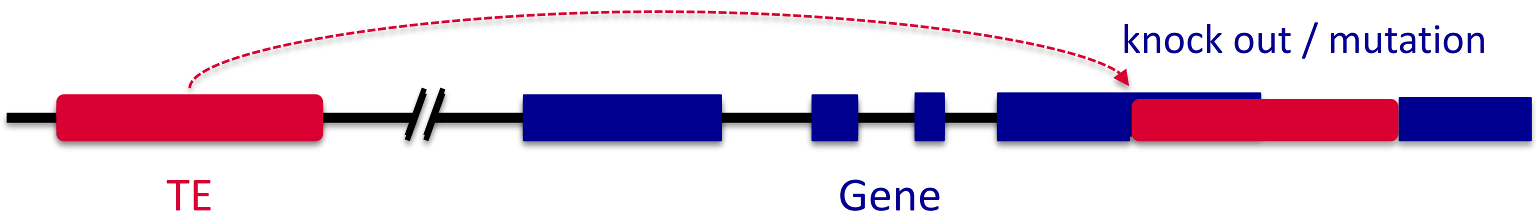
- TEs amplification
- TEs accumulation
- Balance TEs insertion/loss

TE content: the prism of invasive species

Role of TEs throughout the invasion

Transposable elements

= mobile genetic DNA



Transposition

Mutagenic

Neutral

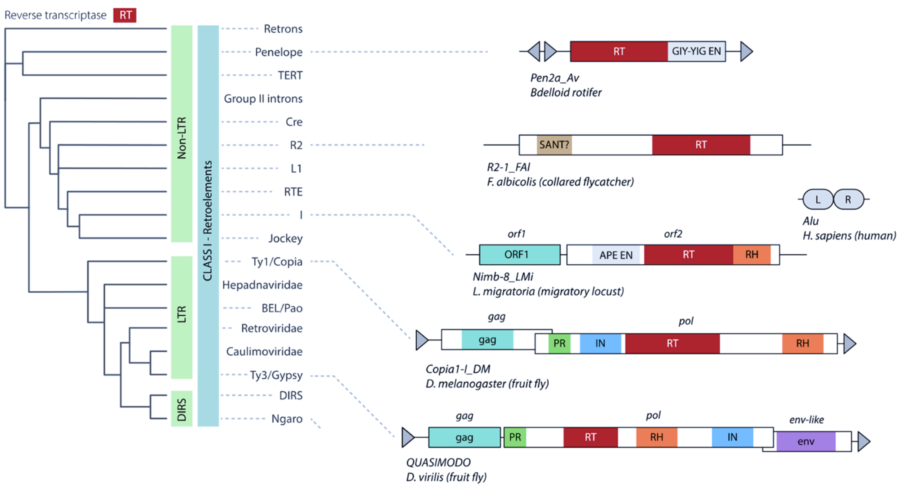
Selected

Lethal

Transposable elements

= mobile genetic DNA

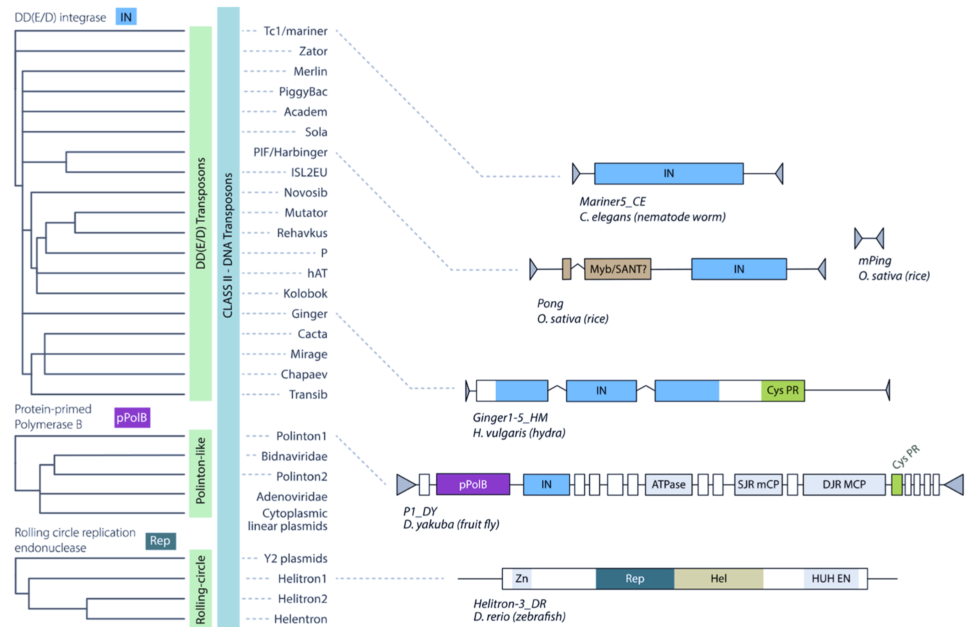
Class I : Retrotransposons



'RNA intermediate'

Copy and paste

Class II : DNA transposons



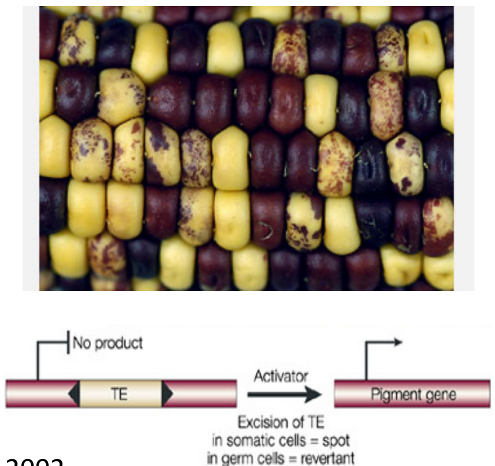
'DNA intermediate'

Cut and paste

Wells, 2021

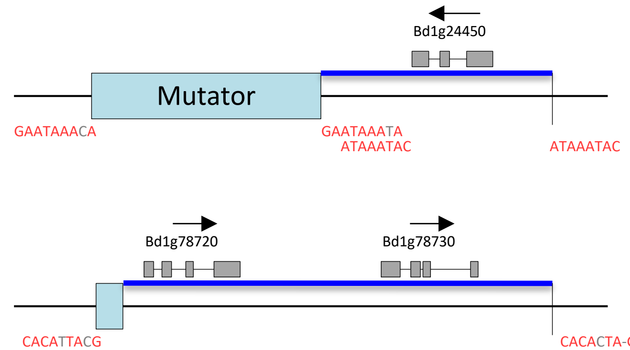
TEs effect on genes

Genes mutations



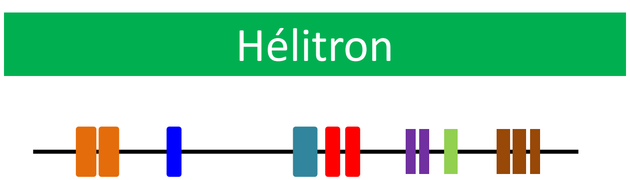
Feschotte et al., 2002

Genes movement and duplication



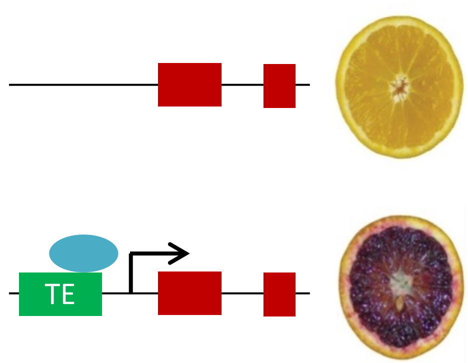
Wicker et al., 2010

Genes creation

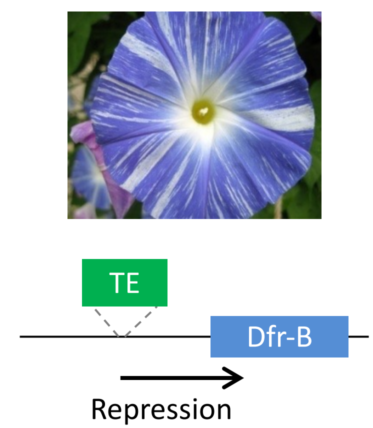


Yang et al., 2009

Reprogramming of genes expression

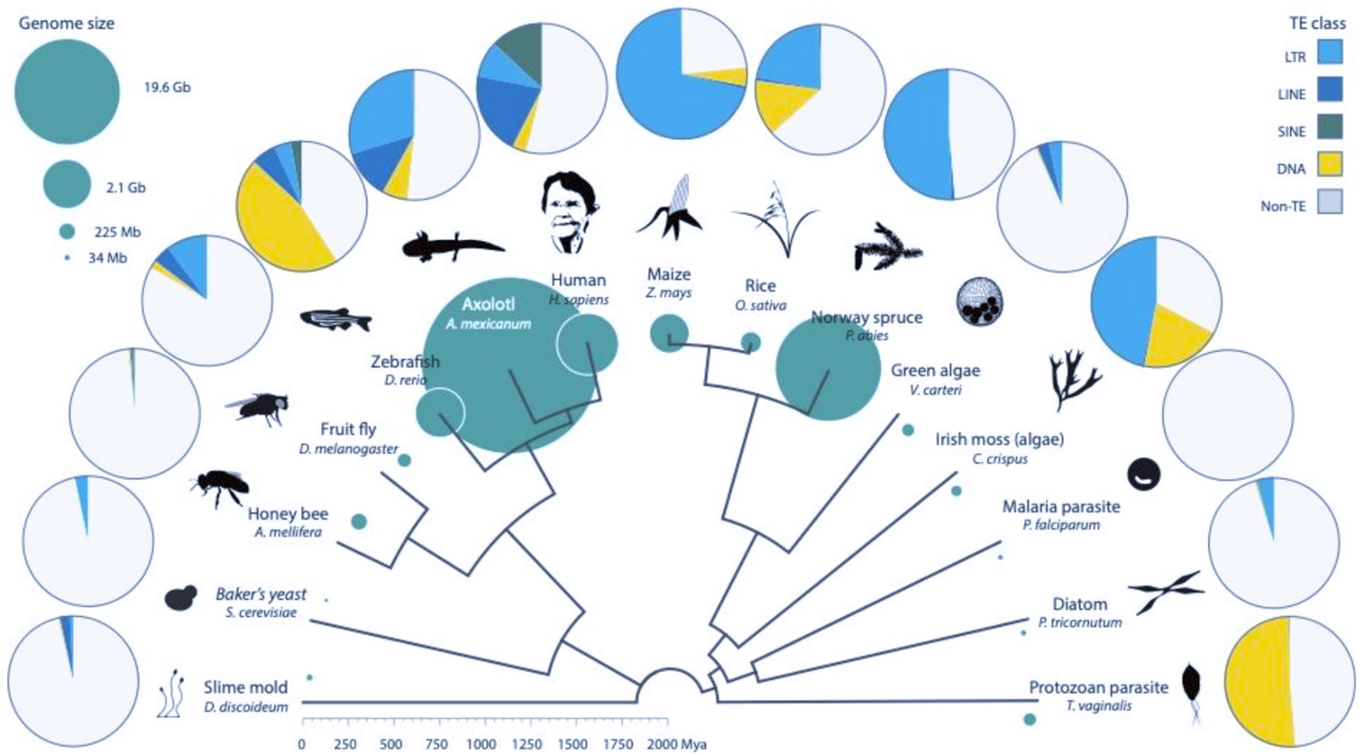


Butelli et al., 2012



Iida et al., 2004

Variable success of TEs across species



1. Why the TEs content is so variable between species?

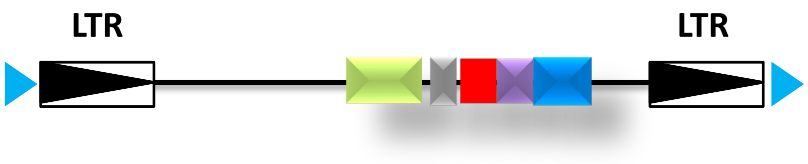
2. Why certain TE types seem to be particularly successful in certain taxonomic groups.

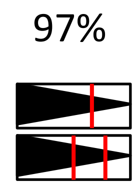
Wells, 2021

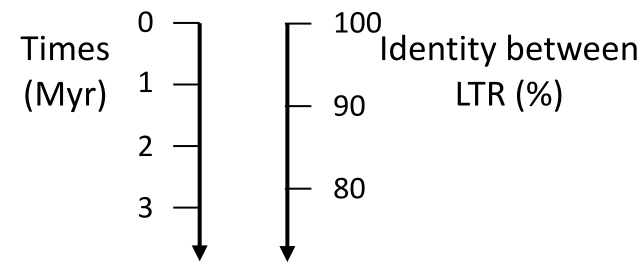
TEs amplification model: “burst” and “latent”

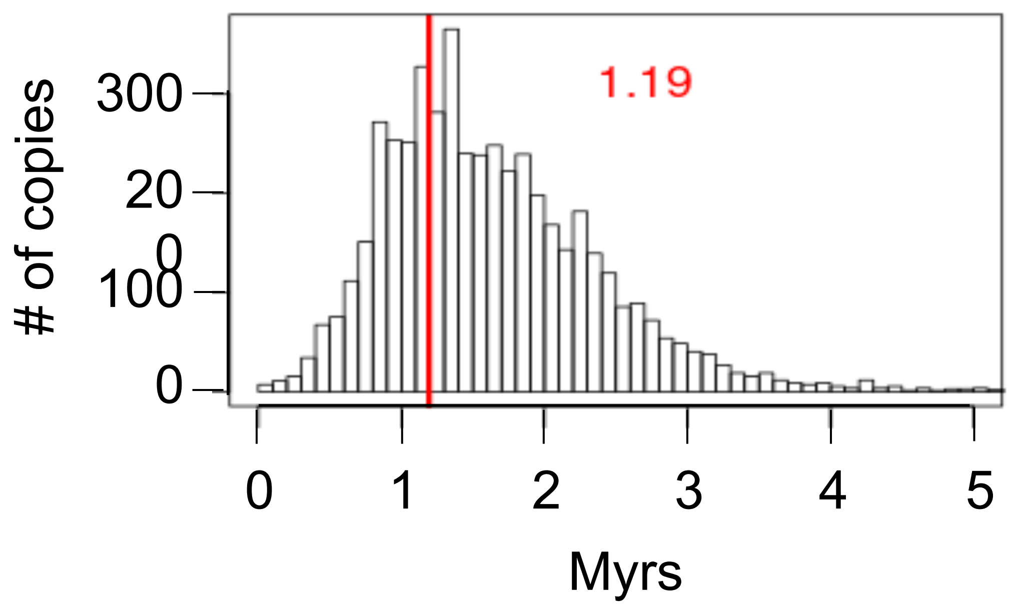
Burst of transposition

= TEs are periodically active



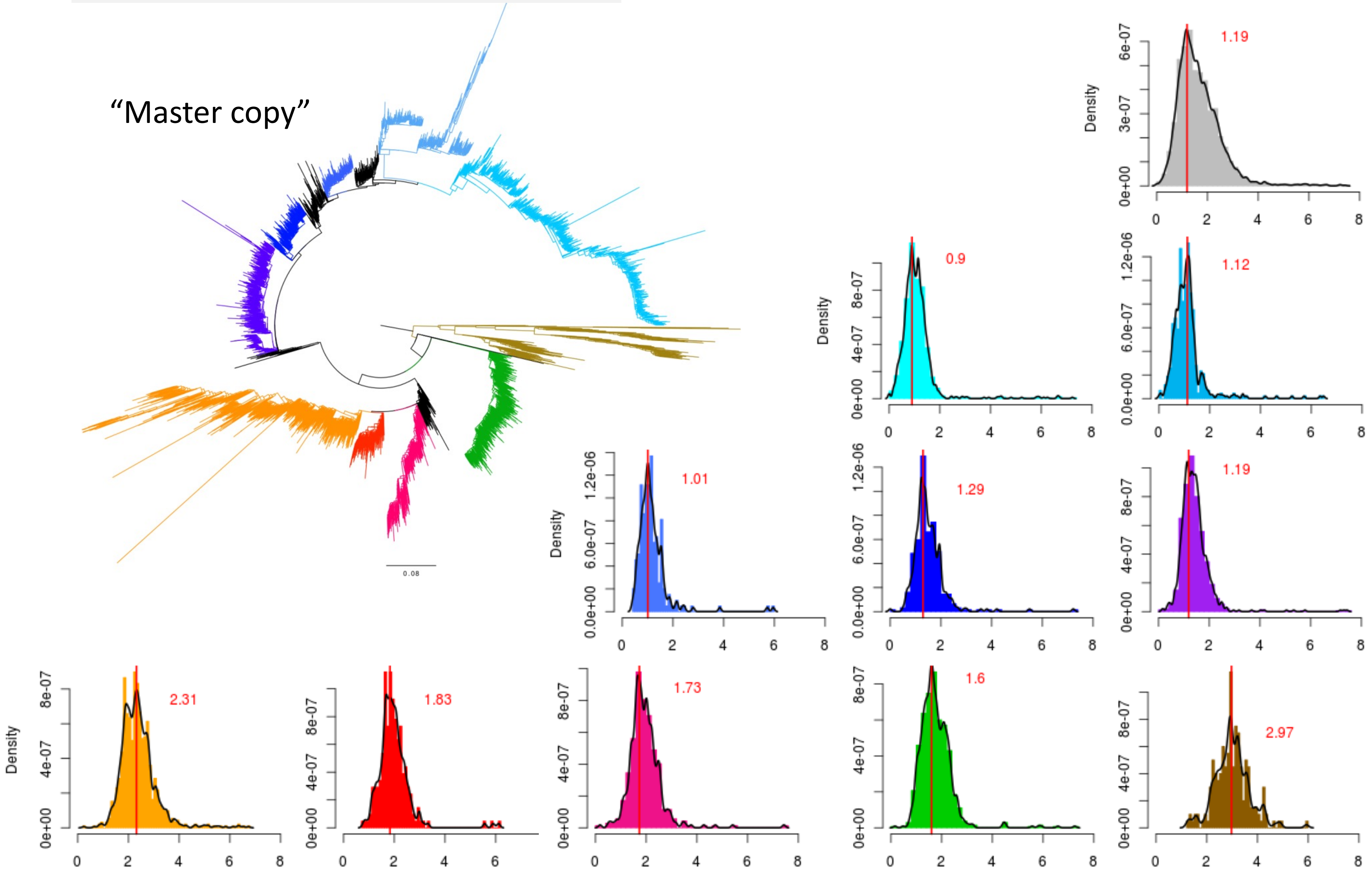






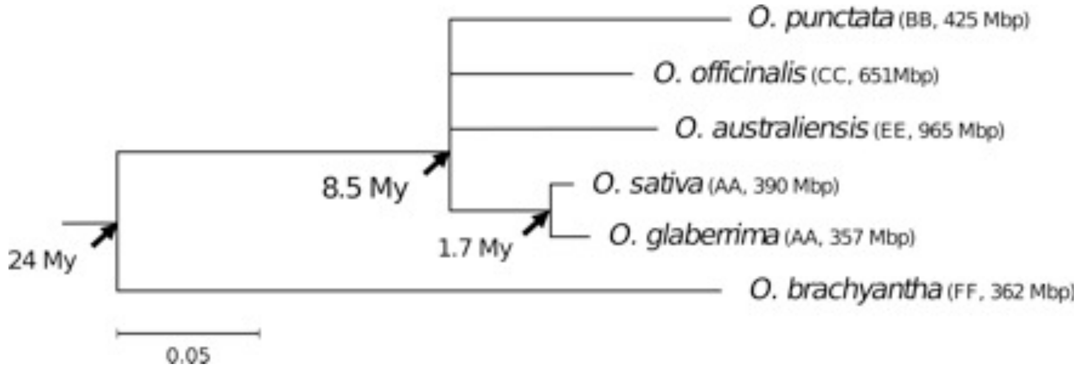
Daron et al., 2014

Burst of transposition



Daron et al., 2014

Burst of transposition



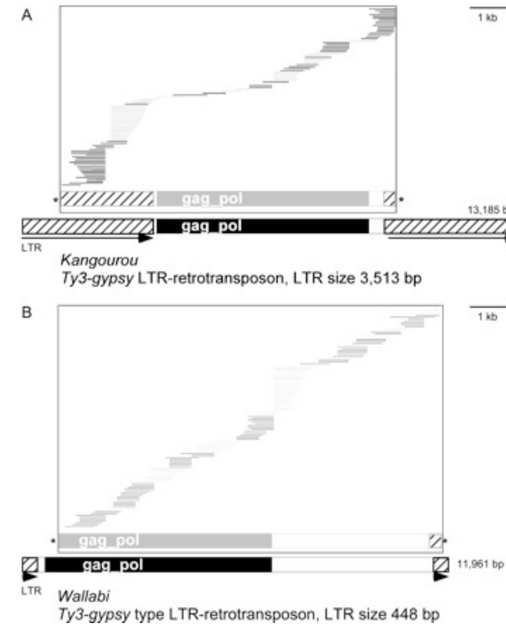


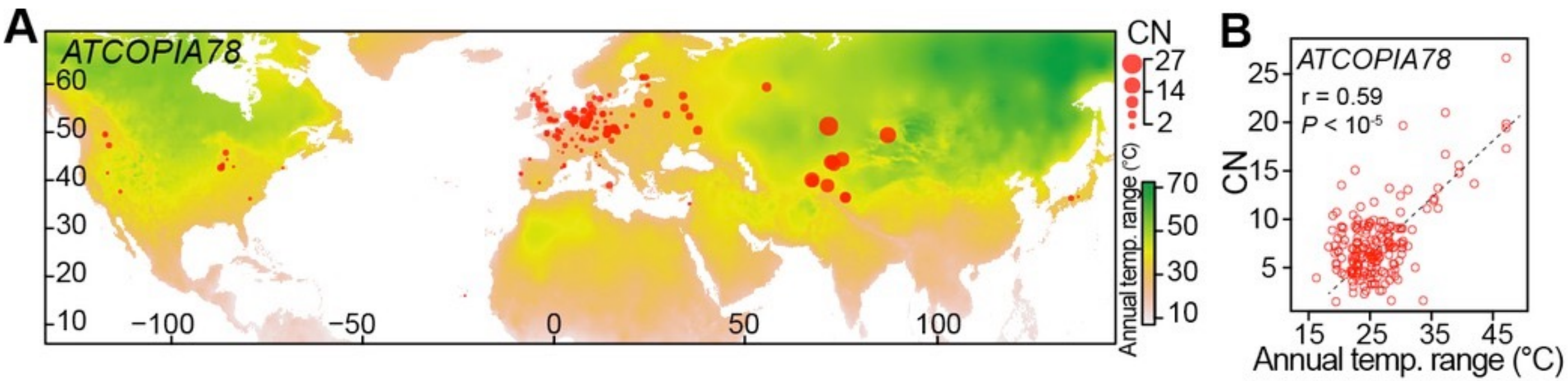
Table 1. Description of the three retrotransposons, *RIRE1*, *Kangourou*, and *Wallabi*, in the genome of *O. australiensis*

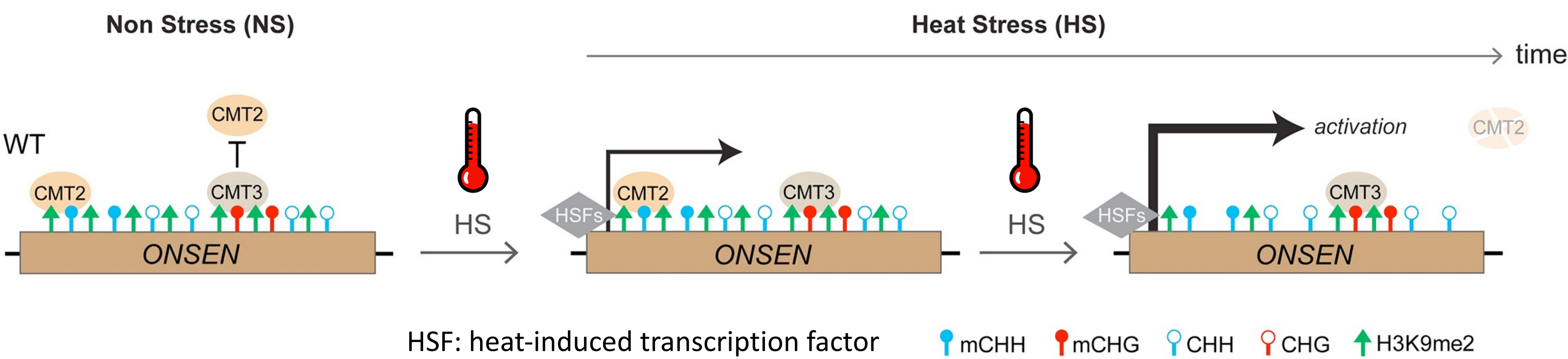
		Size in bp	Number of copies	Size in the genome	Total
RIRE1	Full element	8300	30,000 ± 3000	250 ± 25 Mbp	265 ± 26.5 Mbp
	Apparent single LTR	1500	10,000 ± 1000	15 ± 1.5 Mbp	
Kangourou	Full element	9200	9500 ± 1000	87 ± 9 Mbp	90 ± 9 Mbp
	Apparent single LTR	3500	1000 ± 100	3.5 ± 0.5 Mbp	
Wallabi	Full element	9000	27,000 ± 3000	240 ± 24 Mbp	250 ± 25 Mbp
	Apparent single LTR	500	12,000 ± 1000	6 ± 0.5 Mbp	
					605 ± 60 Mbp

The number of copies is estimated based on dot-blot hybridizations. Mean and standard deviation (based on eight repetitions, see Supplemental data #1) are given for each element (either for the full element or for the apparent single LTR).

Piegu et al., 2006

Geo-climatic variation



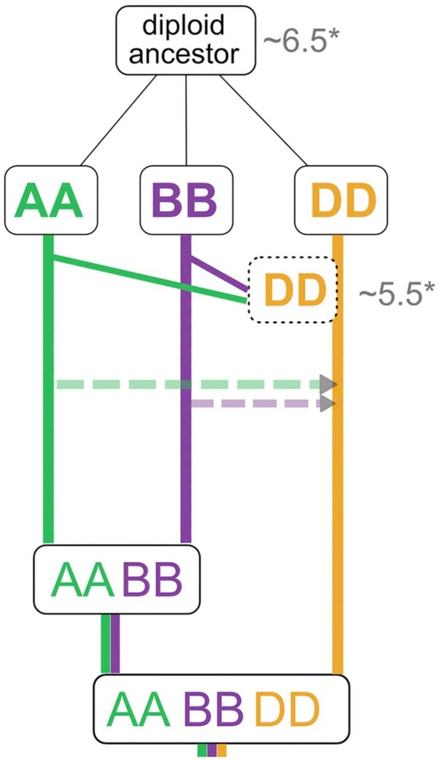


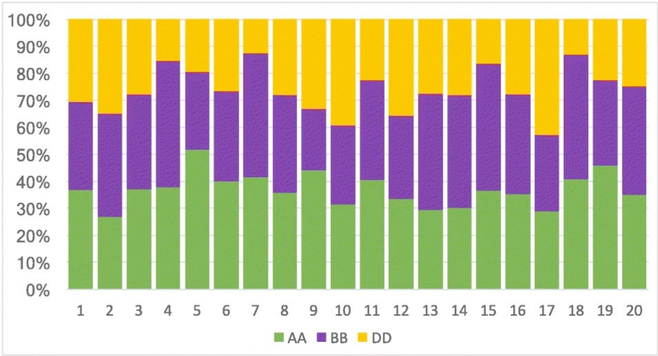
HSF: heat-induced transcription factor

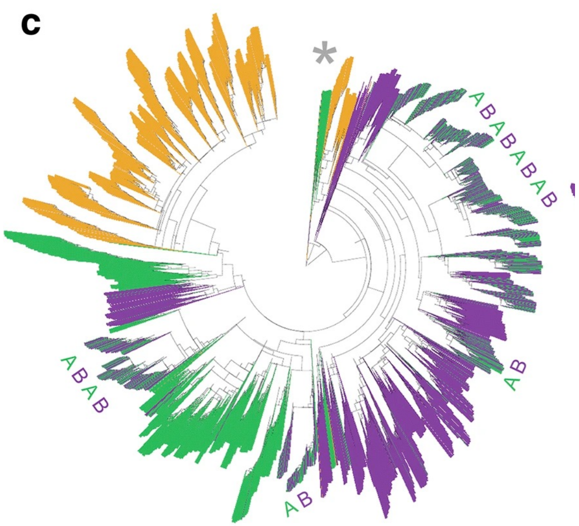
Quadrana et al., 2016

Nozawa et al., 2021

Latent level of transposition

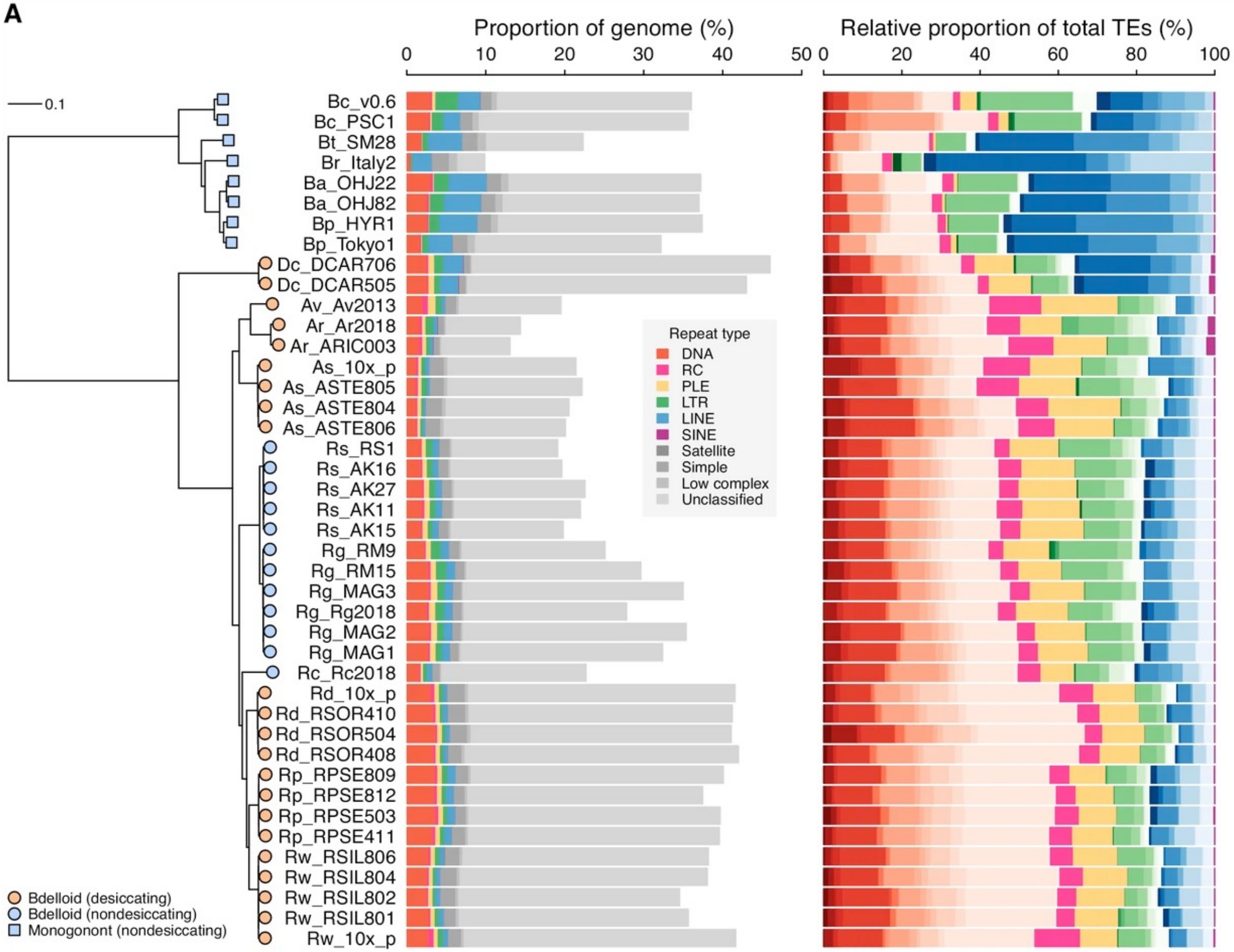






Wicker et al., 2018

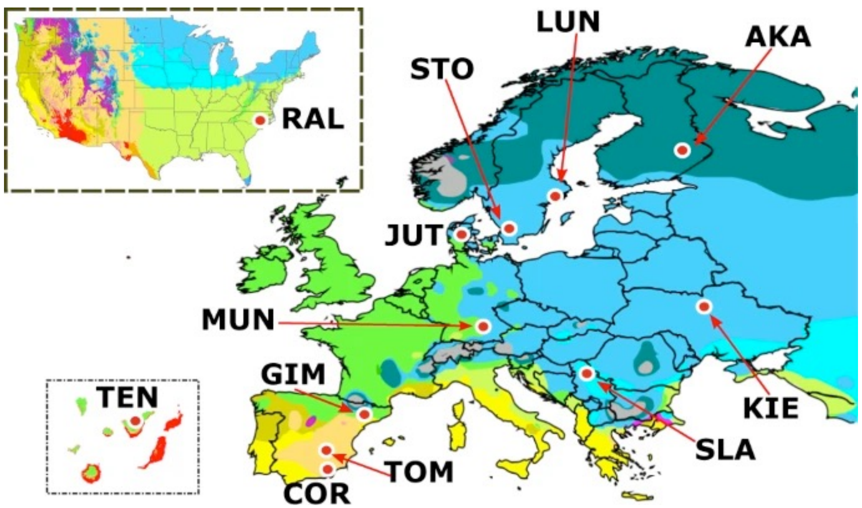
Latent level of transposition

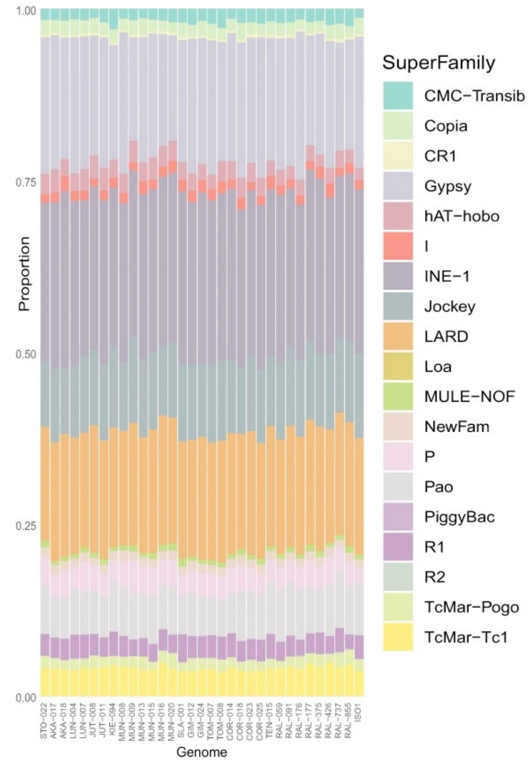


bdelloid rotifers

Nowell et al., 2021

Latent level of transposition

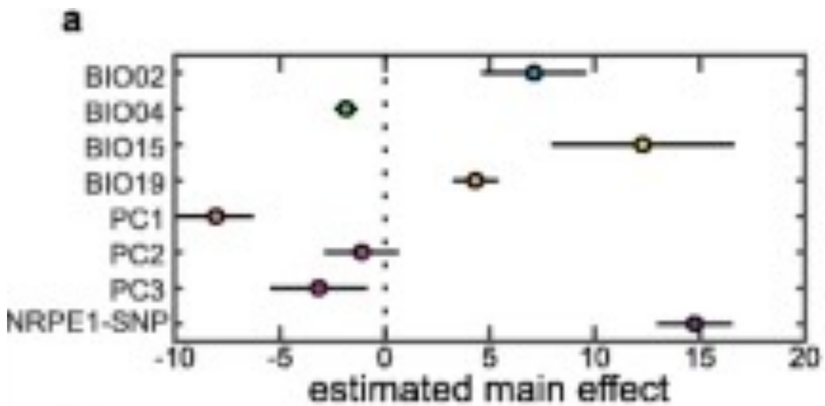




Average number of TE copies = 2016 (+/-69.6)

Rech et al., 2022

Latent level of transposition



diurnal temperature range

seasonality of precipitation

NRPE1 polymophism

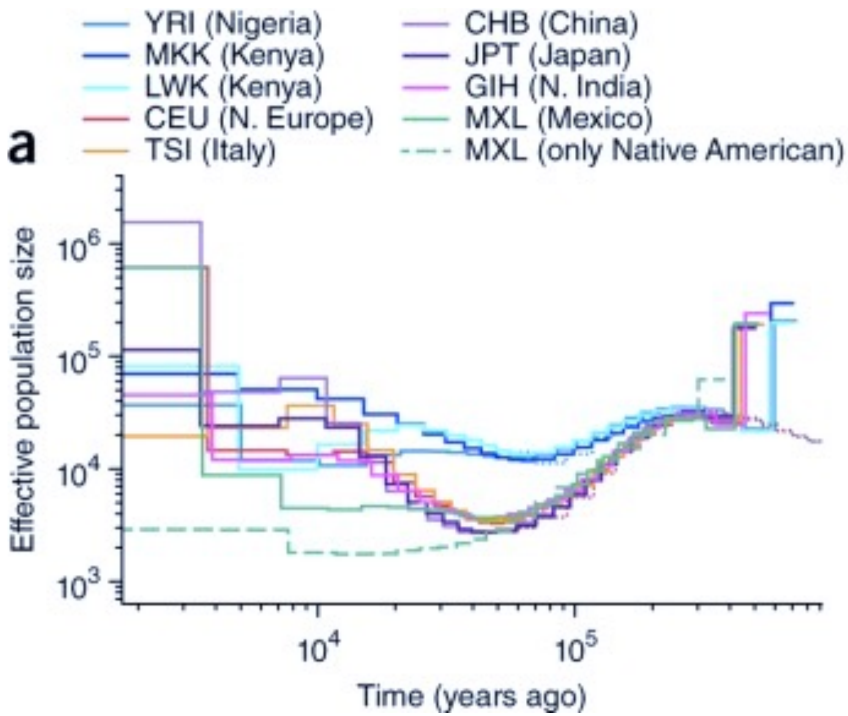
- ONSEN is one out of thousand TE families present in the genome, what’s the rules what’s the exception?

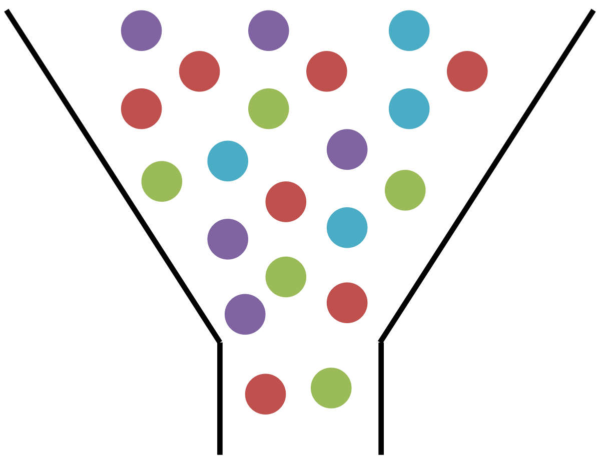
Baduel et al., 2021

Role of demography in TEs accumulation

Demographic history

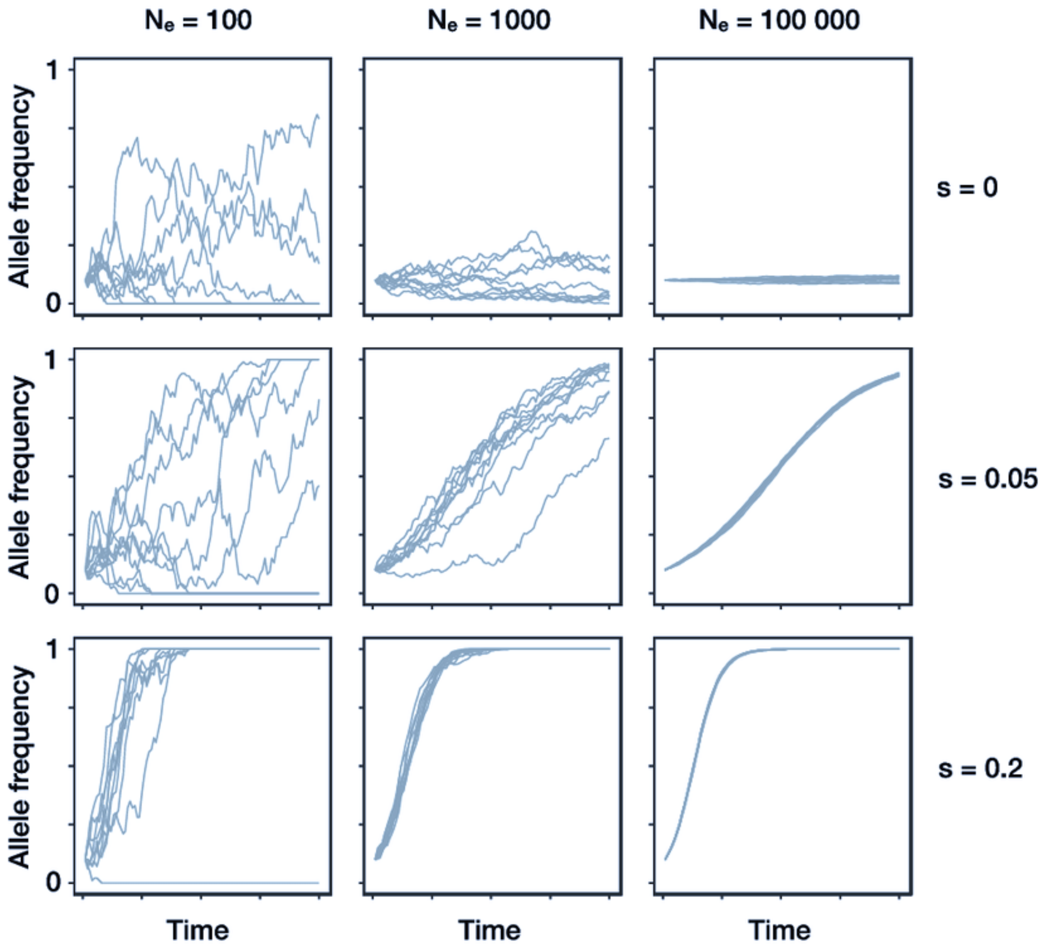
effective population size (Ne) = number of breeding individuals in a (idealised) population





Schiffels et al., 2014

Demographic history (genetic drift)

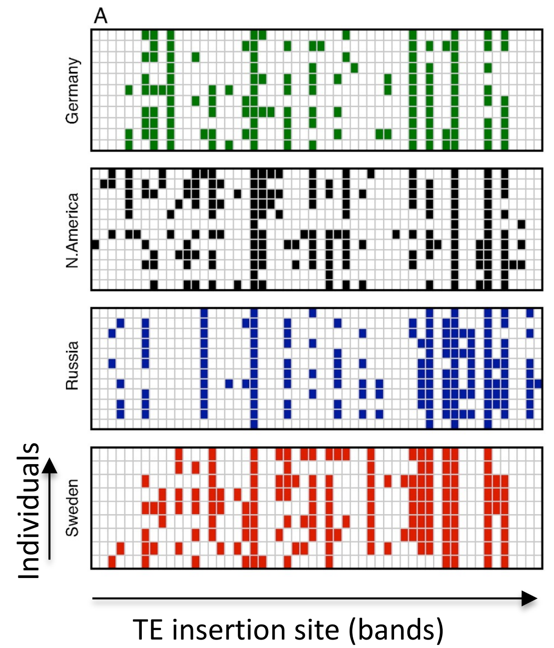


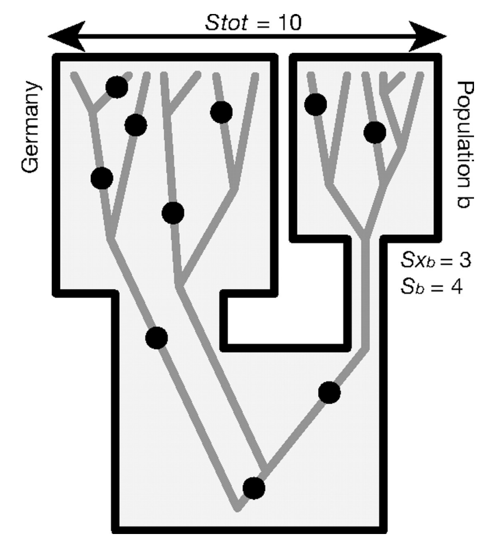
Retel et al., 2019

Demographic history

Stot = the total number of bands in the two populations
Sxb = the number of unique bands in the bottlenecked population
Sb = the total number of bands in the bottlenecked population

To assess the relative contributions of demography on patterns of TE diversity ?





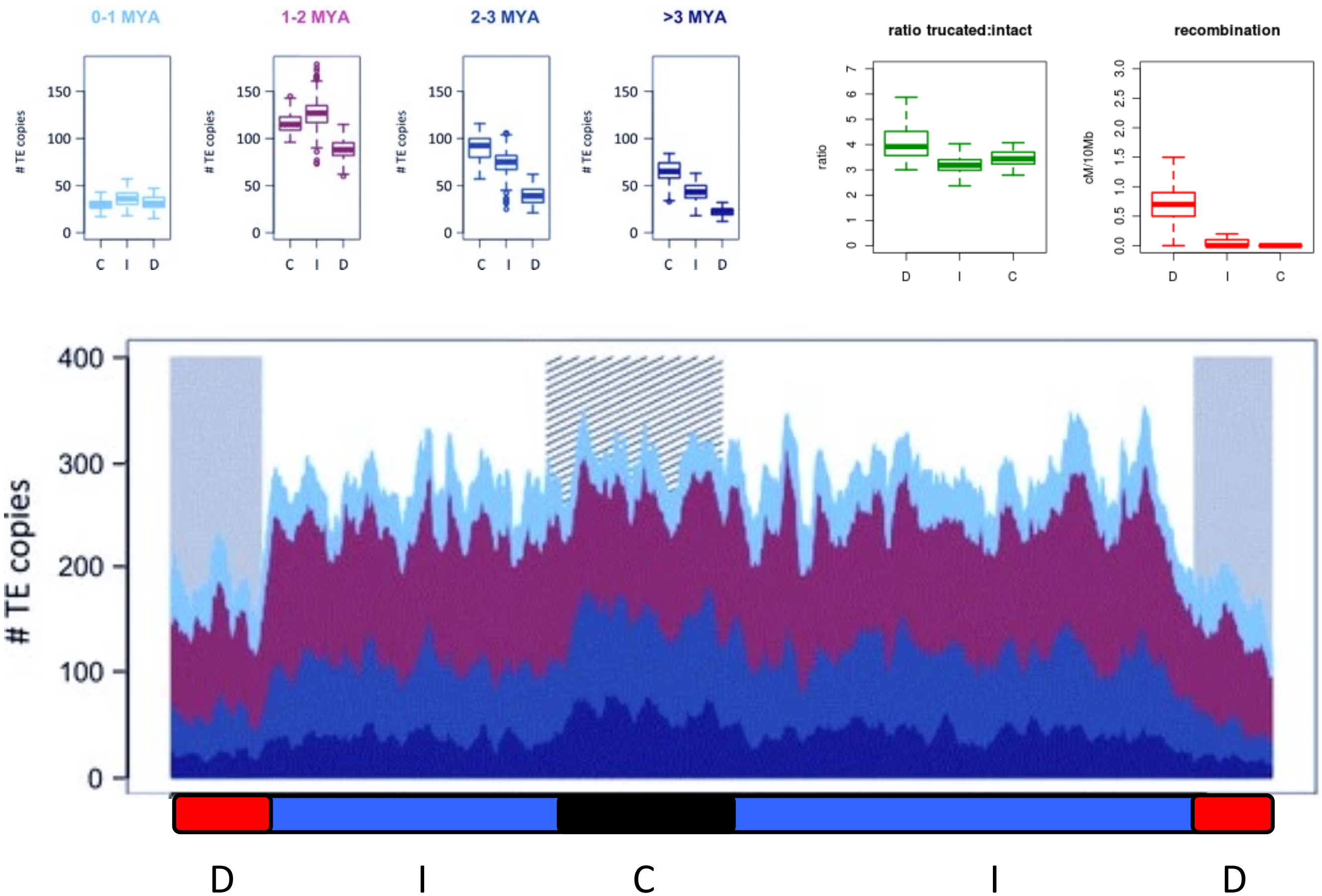
- Significantly higher pairwise Sx_b than expected (North America: *Ac*, CACTA, LINE; Russia: LINE; Sweden: *Ac*; $P < 0.05$)
- Most likely explaination: an excess of Sx_b could be explained by purifying selection removing TEs in the German population, thus increasing the number of TEs appearing as unique to other populations.

Lockton et al., 2008

Evolutionary forces driving TE distribution

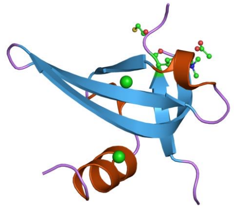
Preferential loss

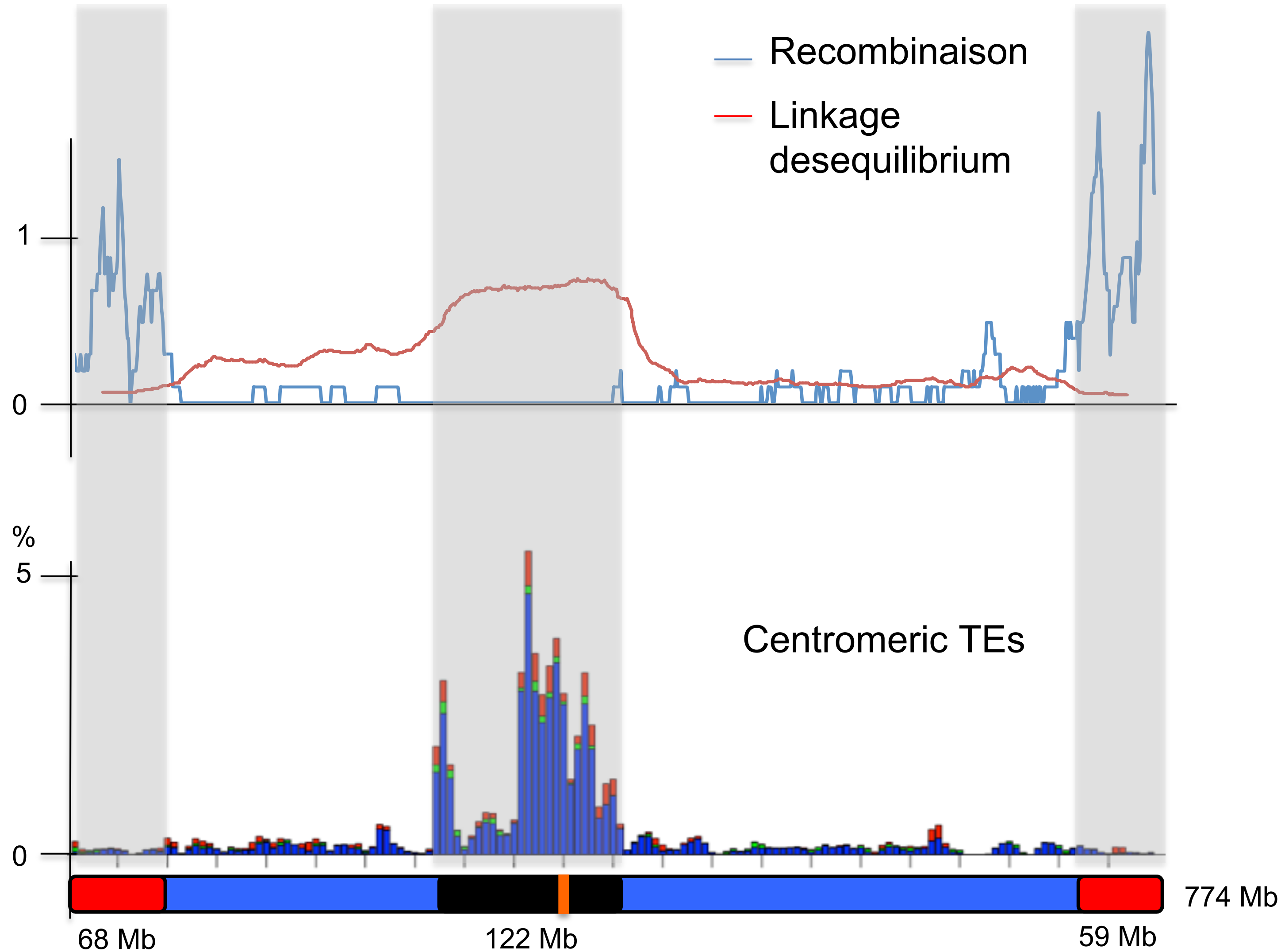
Ectopic recombinaison



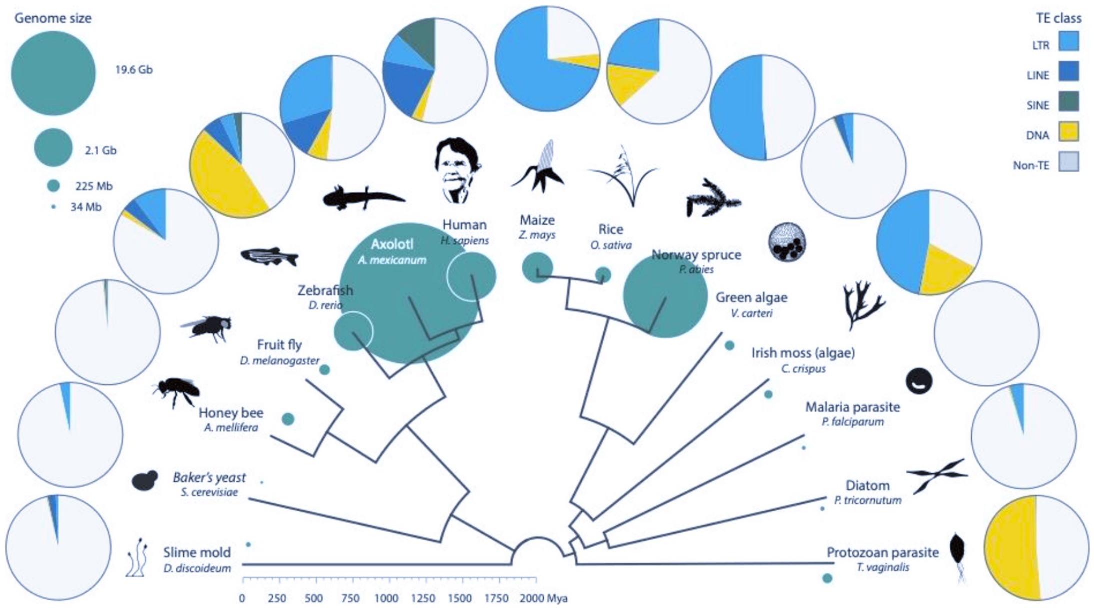
Daron et al., 2014

Preferential insertion





Choulet et al., 2014



Transposition rate

Demography

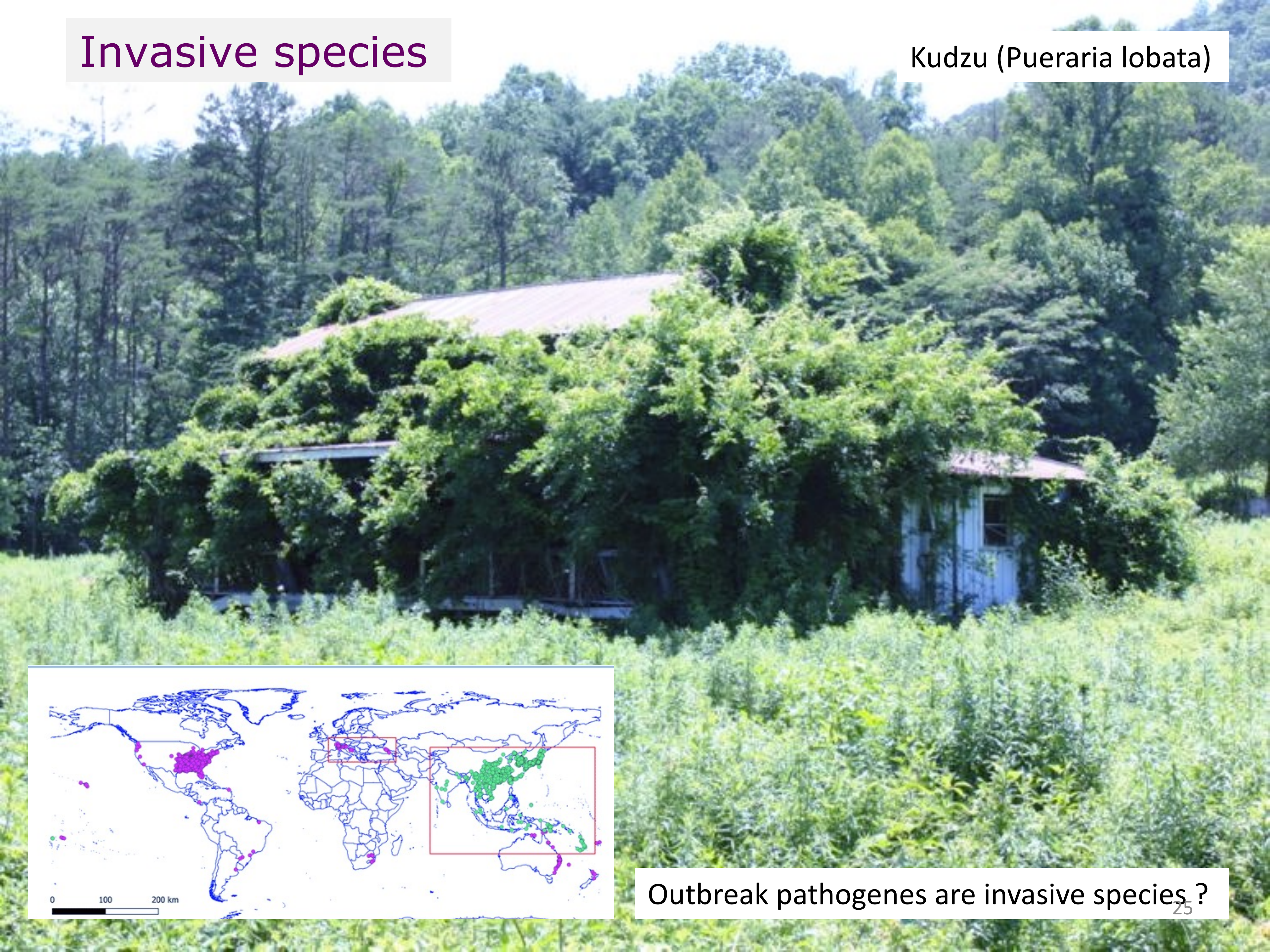
Insertion/loss

What is the relative contribution of each of those factor in TEs content/diversity ?

TEs activity through the prism of invasive species

Invasive species

Kudzu (Pueraria lobata)



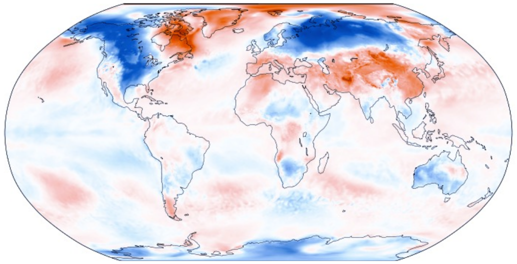
Outbreak pathogenes are invasive species ?

Why invasive species are a good 'model' to look for TEs activity ?

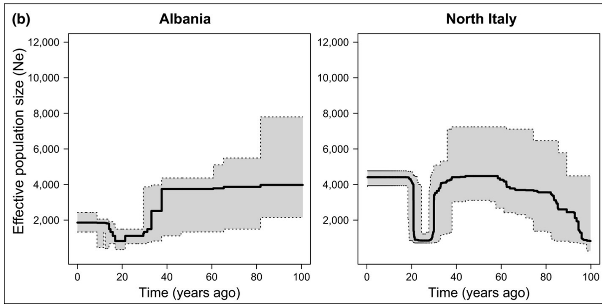
- Invasive species have critical ability to **rapidly adapt** to new environments

- Classic evolutionary theory states that **constantly and randomly emerging genetic mutations** generate mild phenotypic differences in a population, thus providing the substrate for **gradual evolutionary progress** through selection and adaptation.

- The narrative of "evolution through gradual change" **fails to explain episodes of rapid adaptation** and organismal diversification (Gould, 1980).



Climatic niche changes



Demographic variation

FYI: Niche changes

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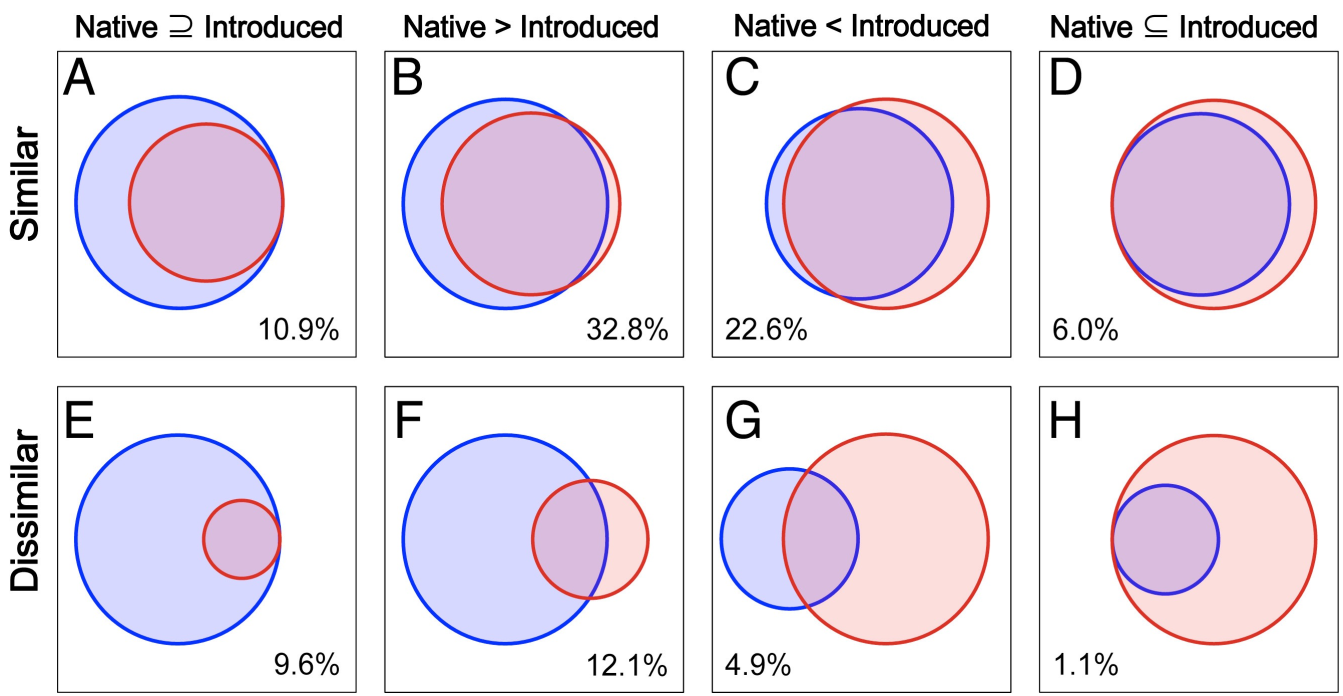
Most invasive species largely conserve their climatic niche

Chunlong Liu, Christian Wolter, Weiwei Xian, and Jonathan M. Jeschke Authors Info & Affiliations

Edited by Susan P. Harrison, University of California, Davis, CA, and approved August 6, 2020 (received for review March 6, 2020)

September 3, 2020 | 117 (38) 23643-23651 | https://doi.org/10.1073/pnas.2004289117

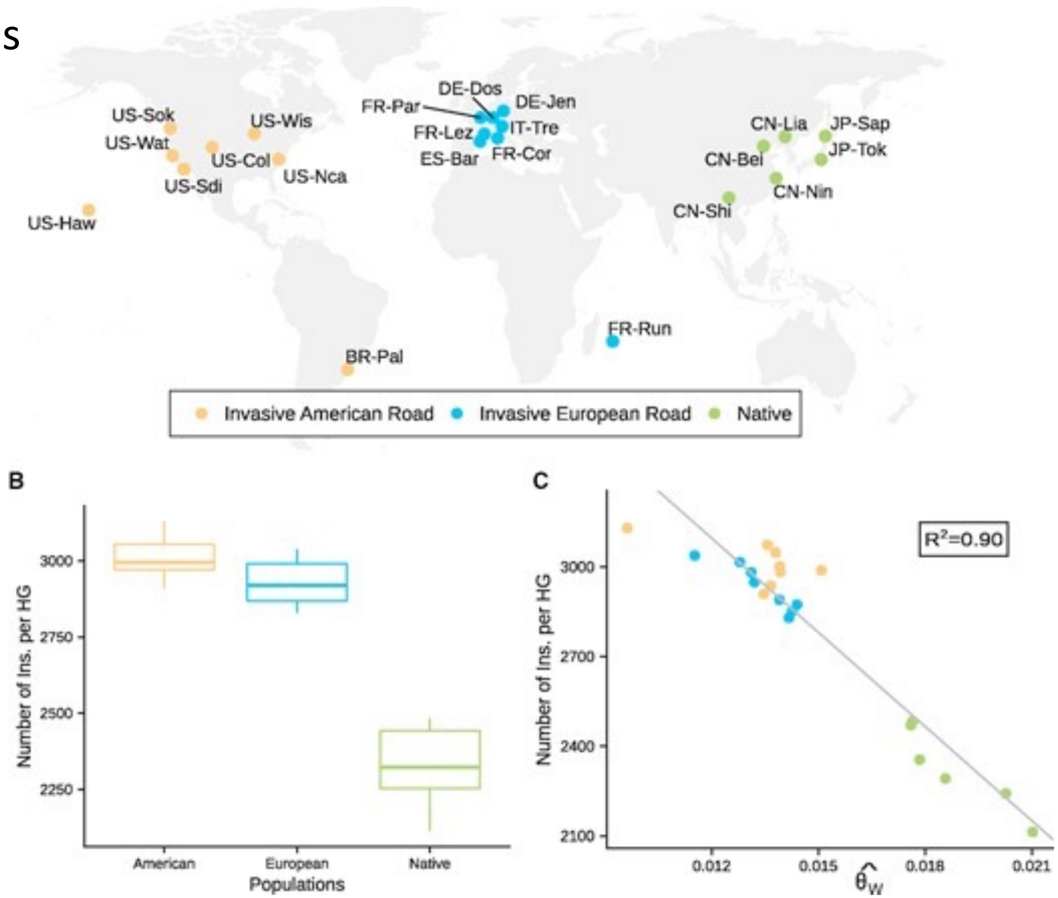


Native Introduced

Liu et al., 2020

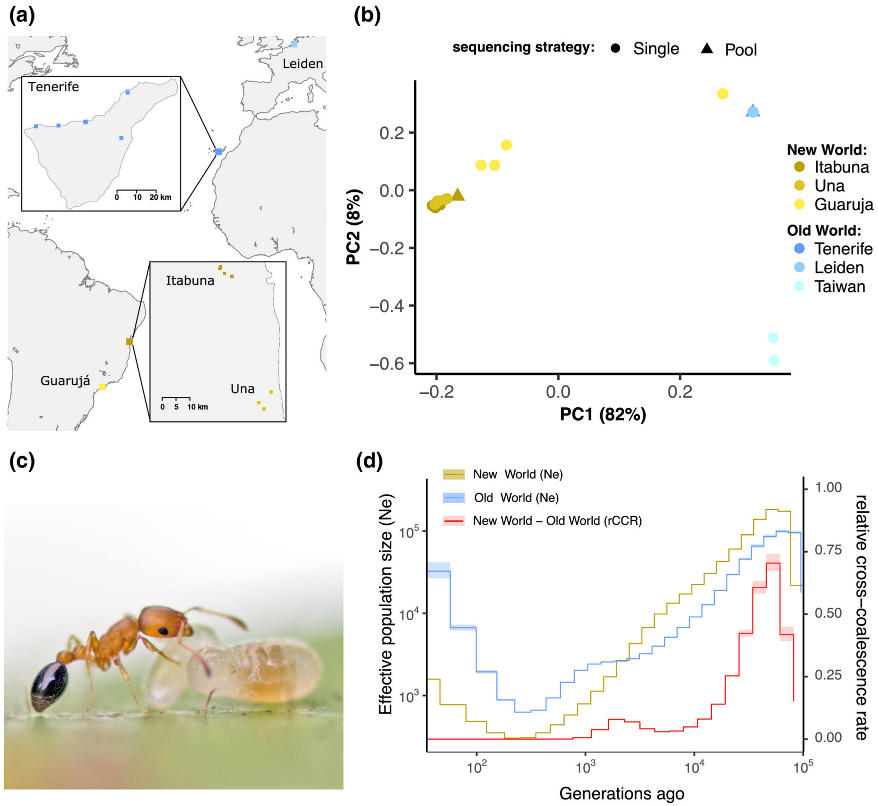
Demography as Driver of TE Contents in *D. suzukii* Populations

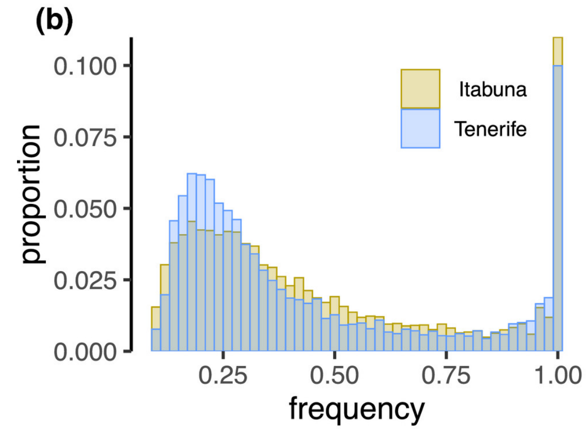
11,751 insertions

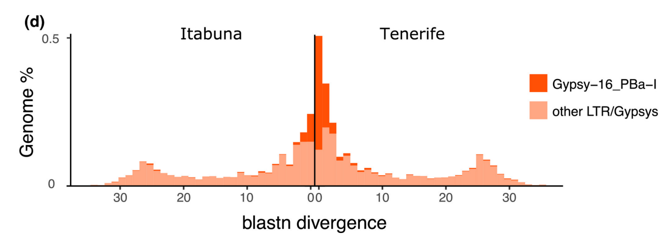


No significaive correlation between 19 bioclimatic variables and TE family abundance

Mérel et al., 2021







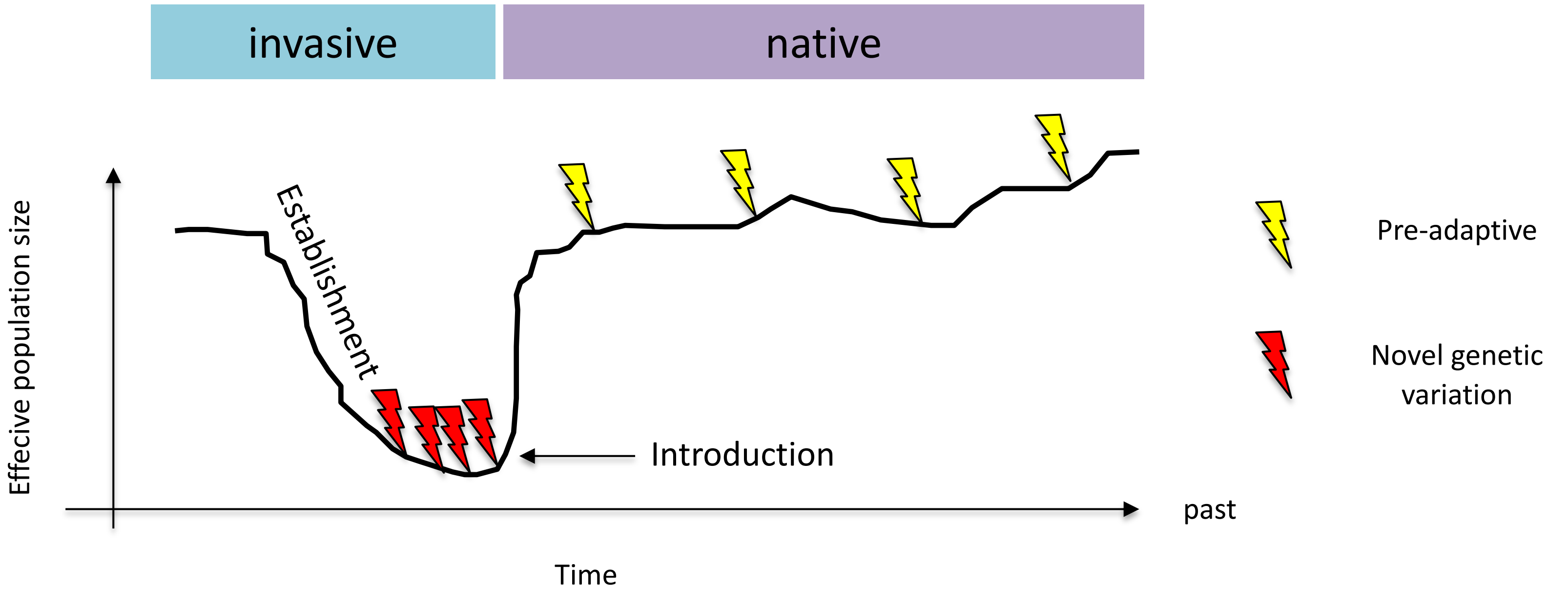
New World lineage: 30 workers

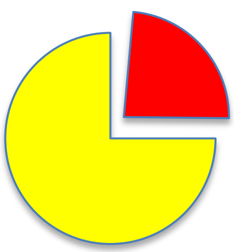
Old World lineage: 16 workers

Mérel et al., 2021

Role of TEs throughout the invasion

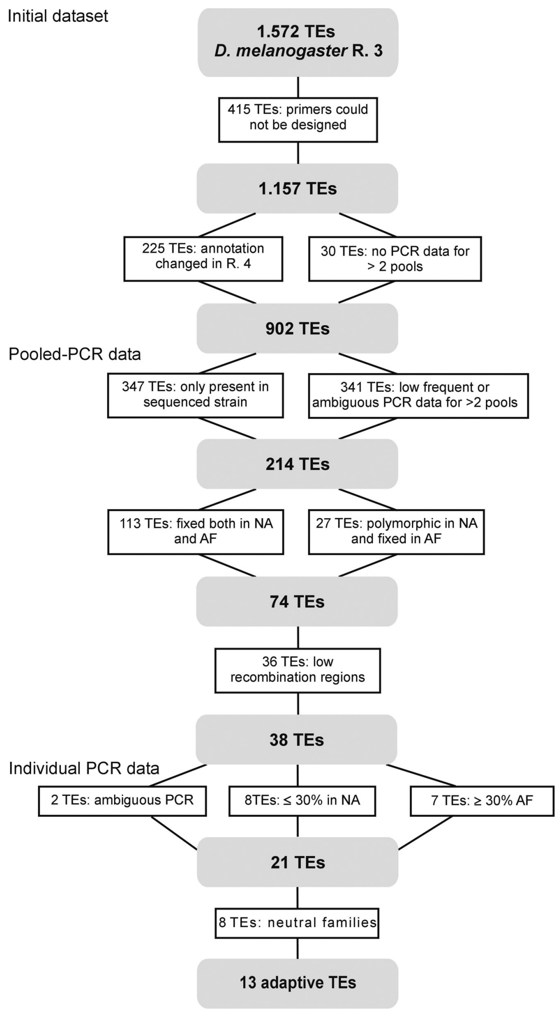
Standing genetic variation or de novo adaptation ?

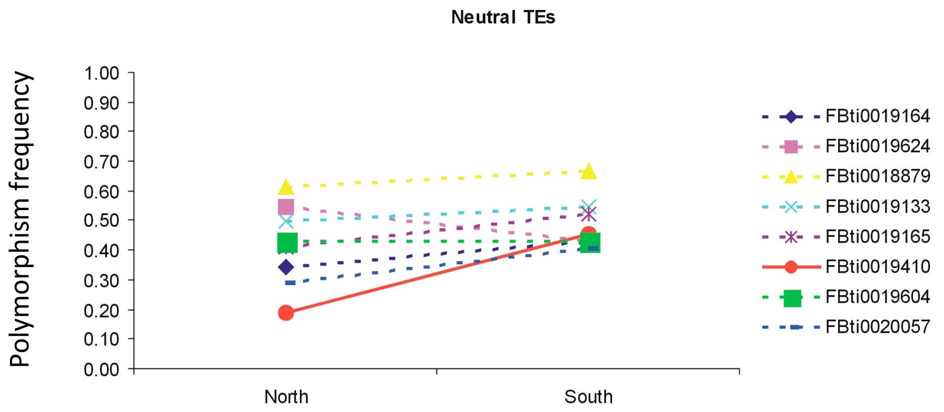


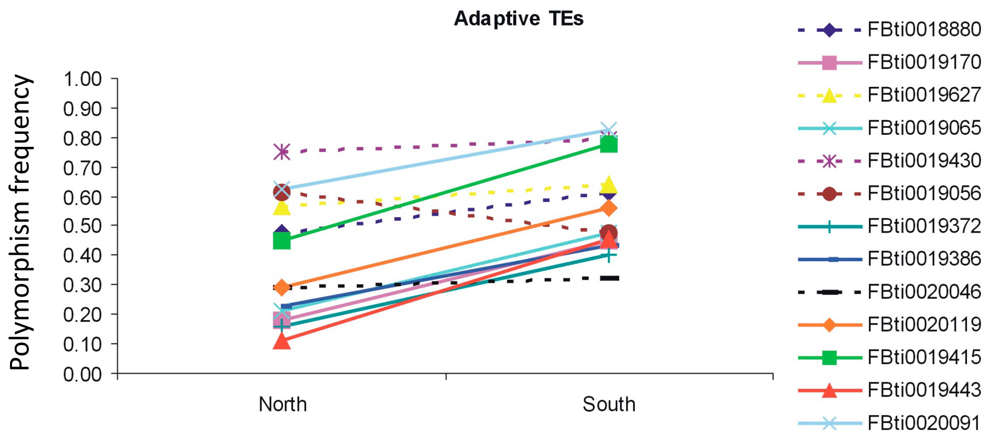


Bibliography ?

Adaptive TEs are already present in native population

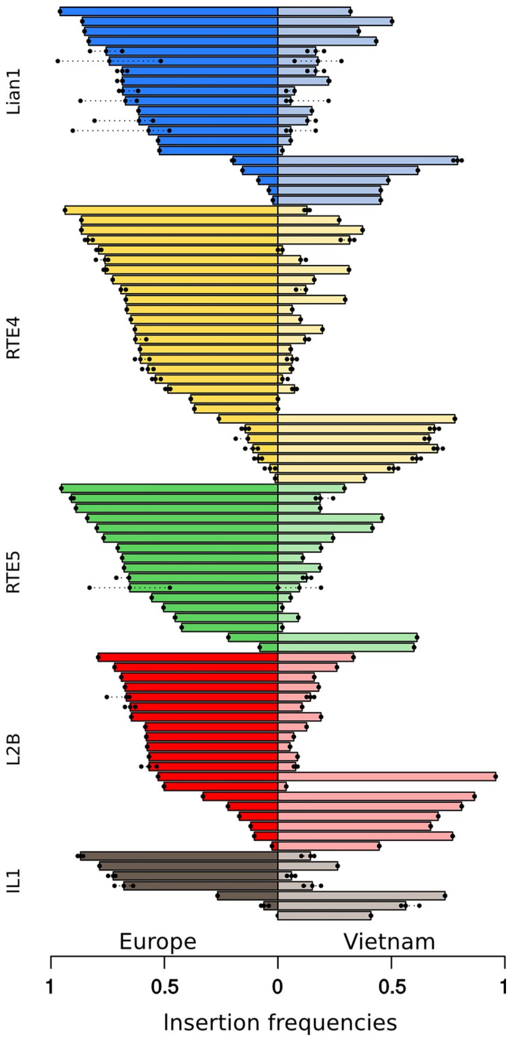


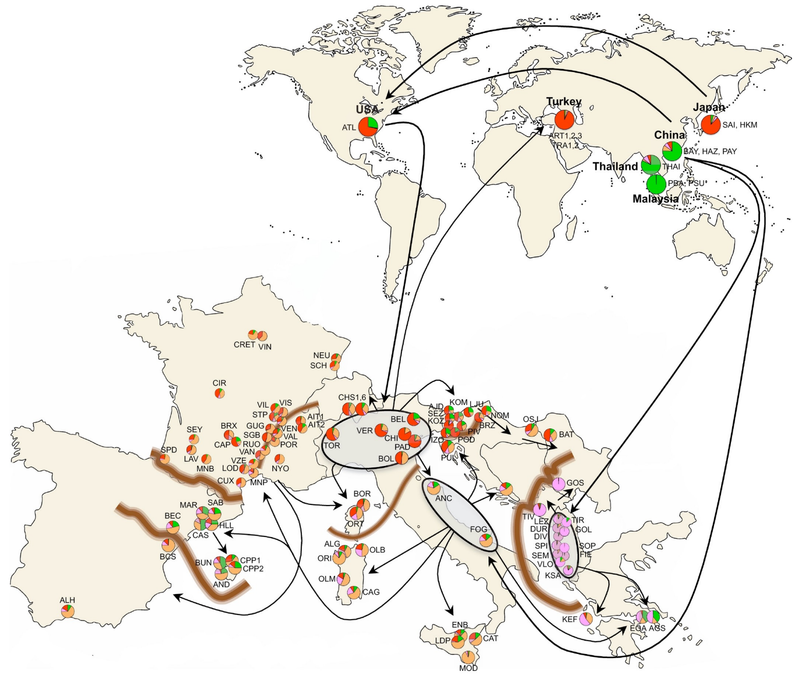


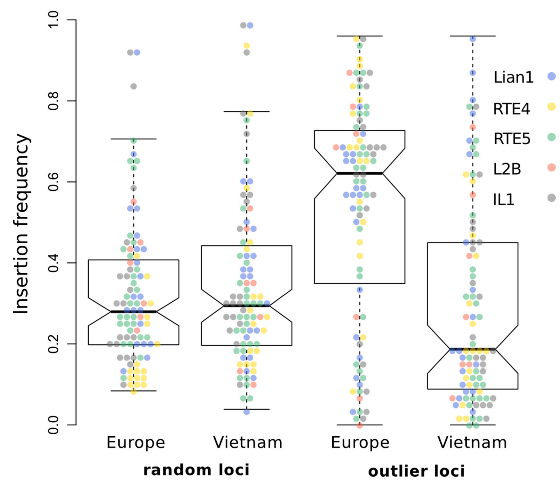


González et al., 2008

Adaptive TEs are already present in native population

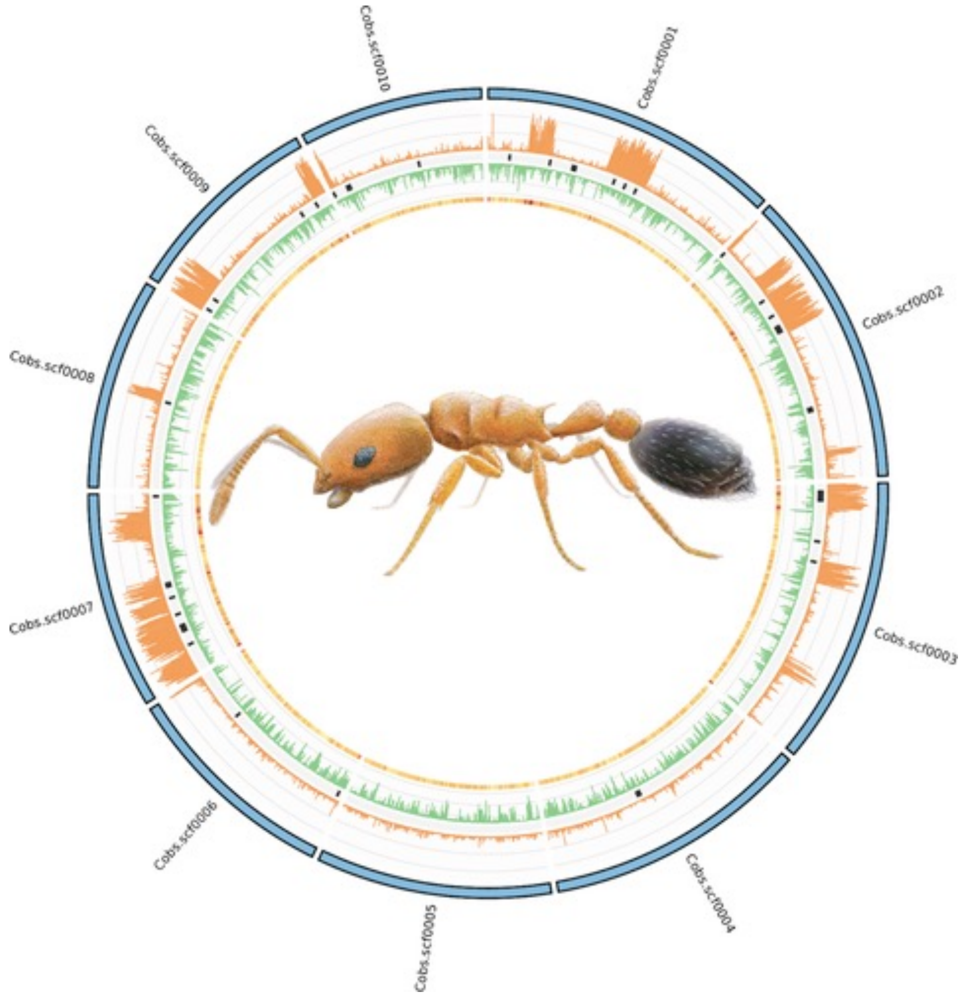






Goubert et al., 2017

Sherpa et al., 2019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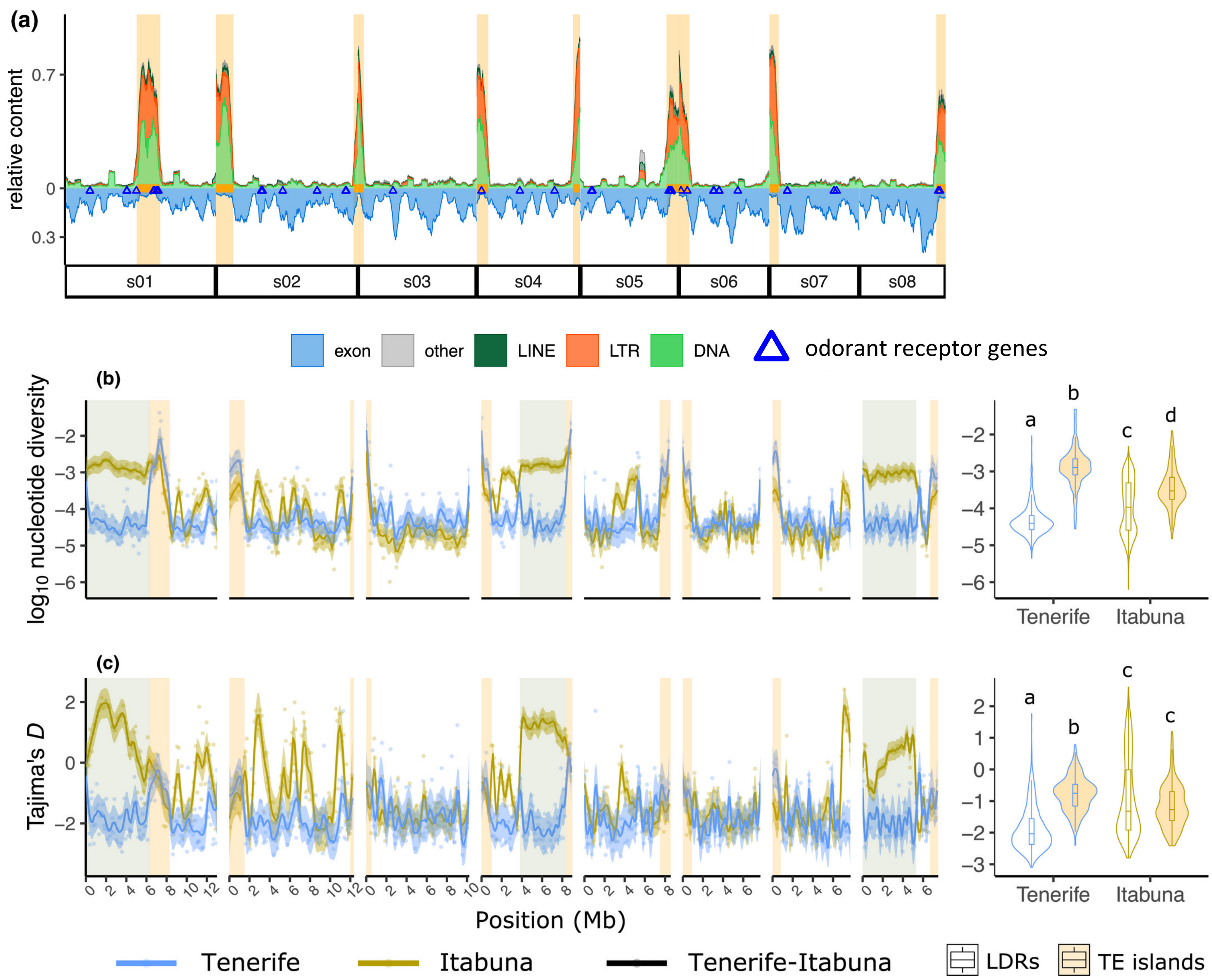
TE islands evolve more dynamically than the remainder of the genome



Open Access Review

On the Population Dynamics of Junk: A Review on the Population Genomics of Transposable Elements

by Yann Bourgeois and Stéphane Boissinot *

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Genes **2019**, *10*(6), 419; https://doi.org/10.3390/genes10060419

Received: 4 April 2019 / Revised: 5 May 2019 / Accepted: 21 May 2019 / Published: 30 May 2019

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Transposable elements as agents of rapid adaptation may explain the genetic paradox of invasive species

Jessica Stapley, Anna W. Santure, Stuart R. Dennis

First published: 21 January 2015 | https://doi.org/10.1111/mec.13089 | Citations: 119

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Adaptation

FLC, which encodes a key transcription regulator that repress expression of flowering factors

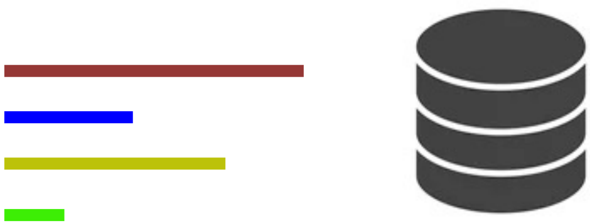
https://www.tandfonline.com/doi/full/10.1080/21541264.2020.1803031

From one to a 1000 genomes

1. understand what kind of standard in term of annotation, structure and evolutionary dynamics of TEs have been set up by other model organism

introduced populations usually face novel environmental conditions that require an adaptive response despite the reduced adaptive capability of small, genetically homogeneous populations.

TEs Annotation

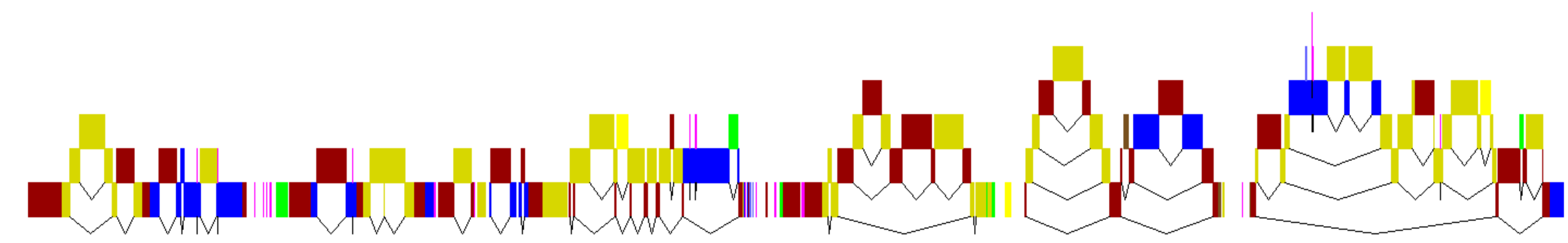


TE library

Dfam

https://www.dfam.org/home

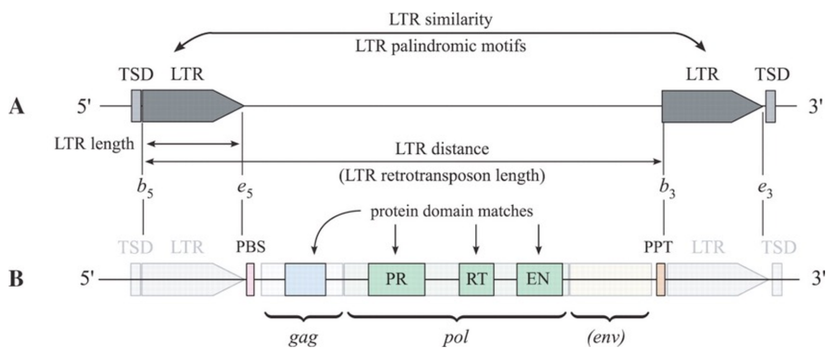
Homology search programs
(RepeatMasker)



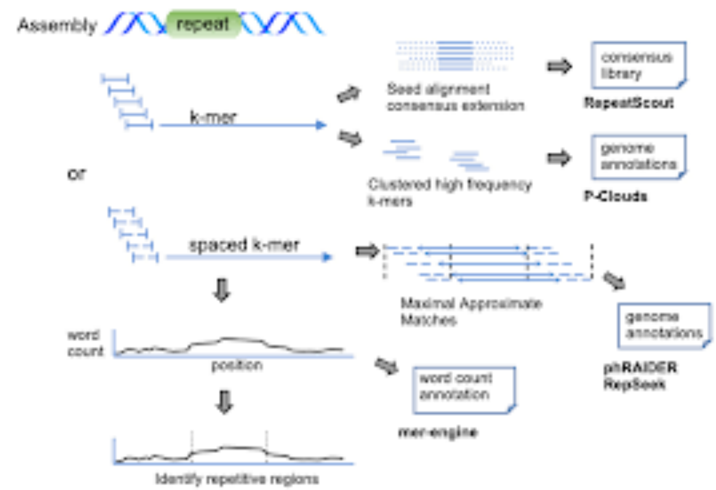
TEs Annotation

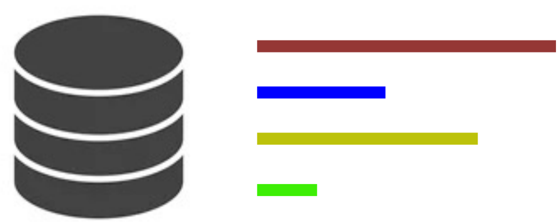
Step #1: generate a library of TEs

Structural Annotation

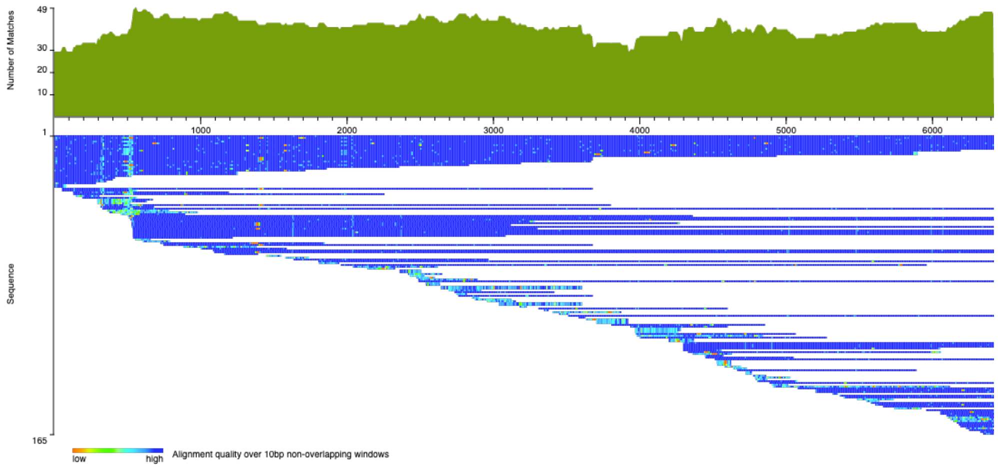


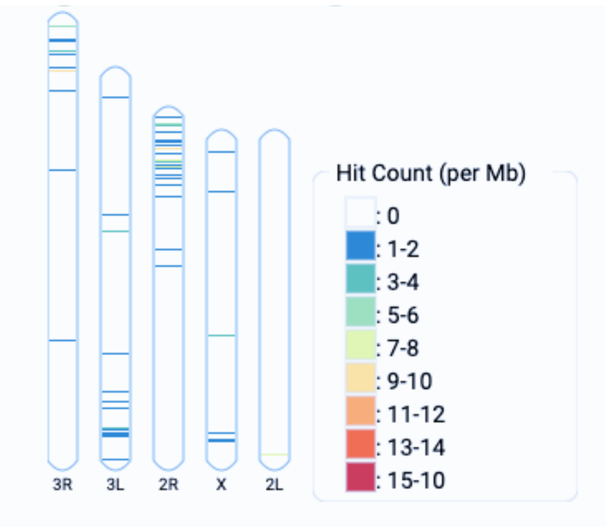
De novo approch



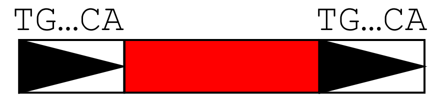


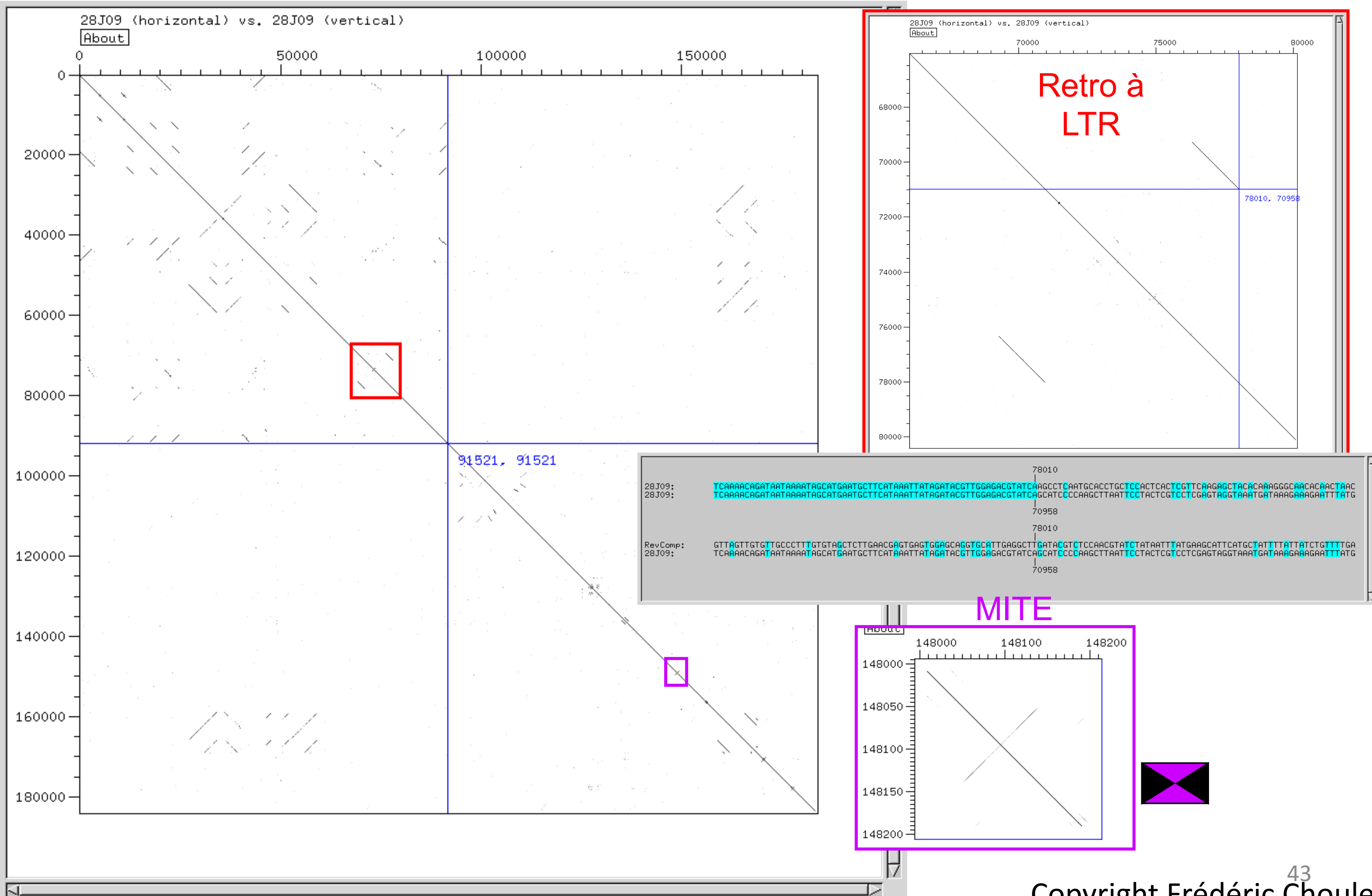
TE library

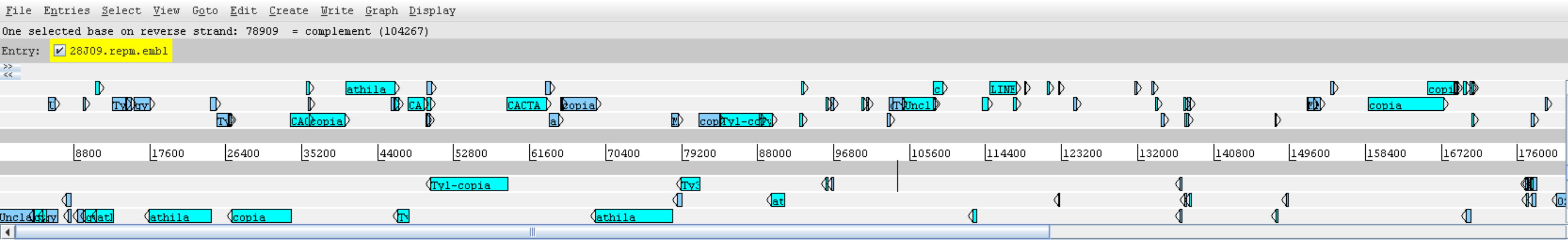

Number of Matches
49
30
20
10
1000
2000
3000
4000
5000
6000
1
Sequence
165
low
high
Alignment quality over 10bp non-overlapping windows


3R
3L
2R
X
2L
Hit Count (per Mb)
: 0
: 1-2
: 3-4
: 5-6
: 7-8
: 9-10
: 11-12
: 13-14
: 15-10

Dotter representation of structural TEs features



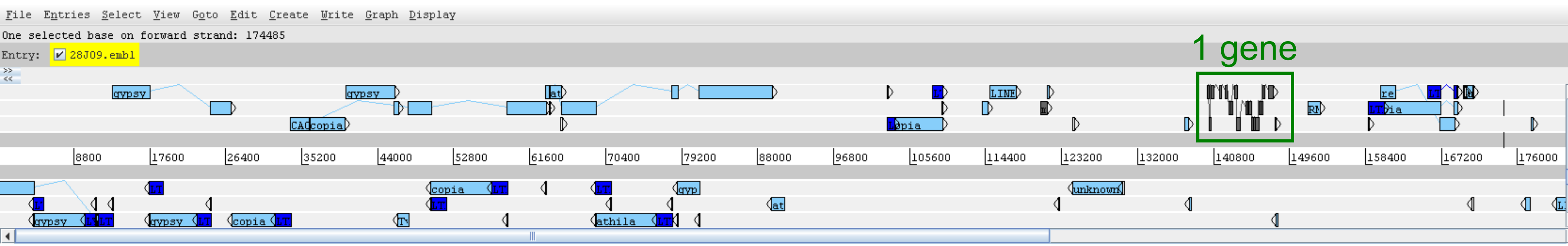




105 TE fragments (raw results)
→ TE content: 63%

Polished annotation

1 gene



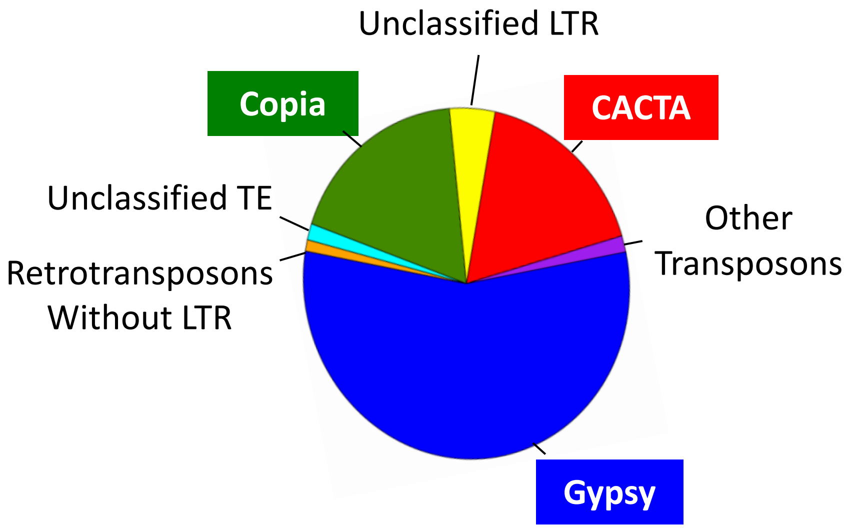
32 TE (complets and fragmented)
→ TE content: 66%

- 7 pairs of LTR identified
- 4 pairsTIR identified

From high quality TEs annotation

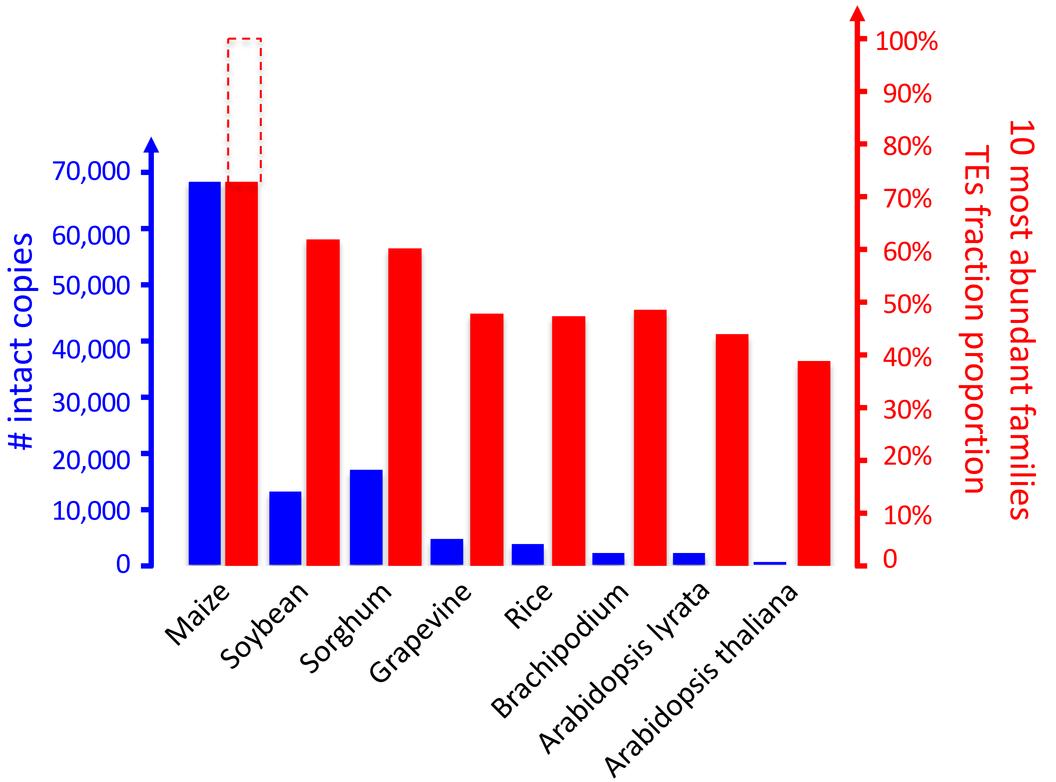
- TE content
- TE dynamics
- TE organization

TE content



Unclassified LTR
Copia
CACTA
Unclassified TE
Other Transposons
Retrotransposons Without LTR
Gypsy

TE content



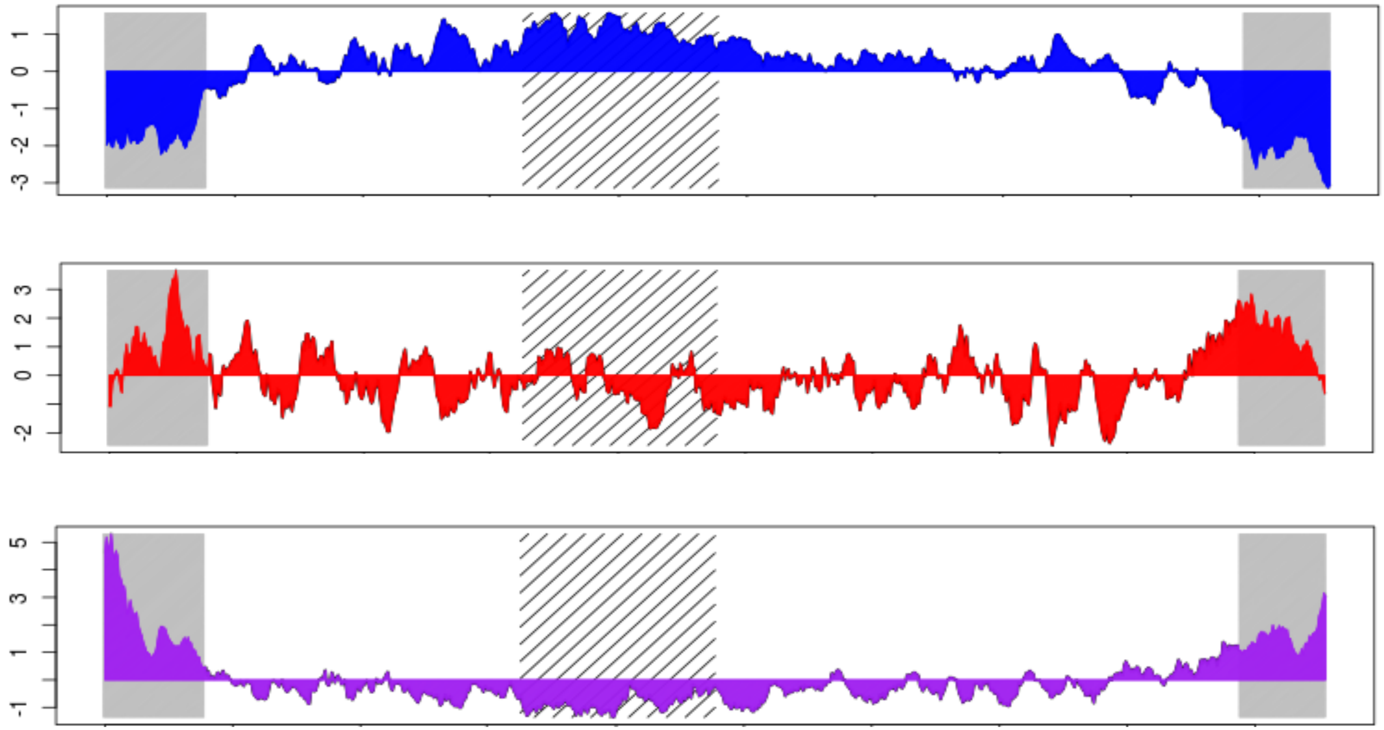
El Badouri et al., 2013

TE organization

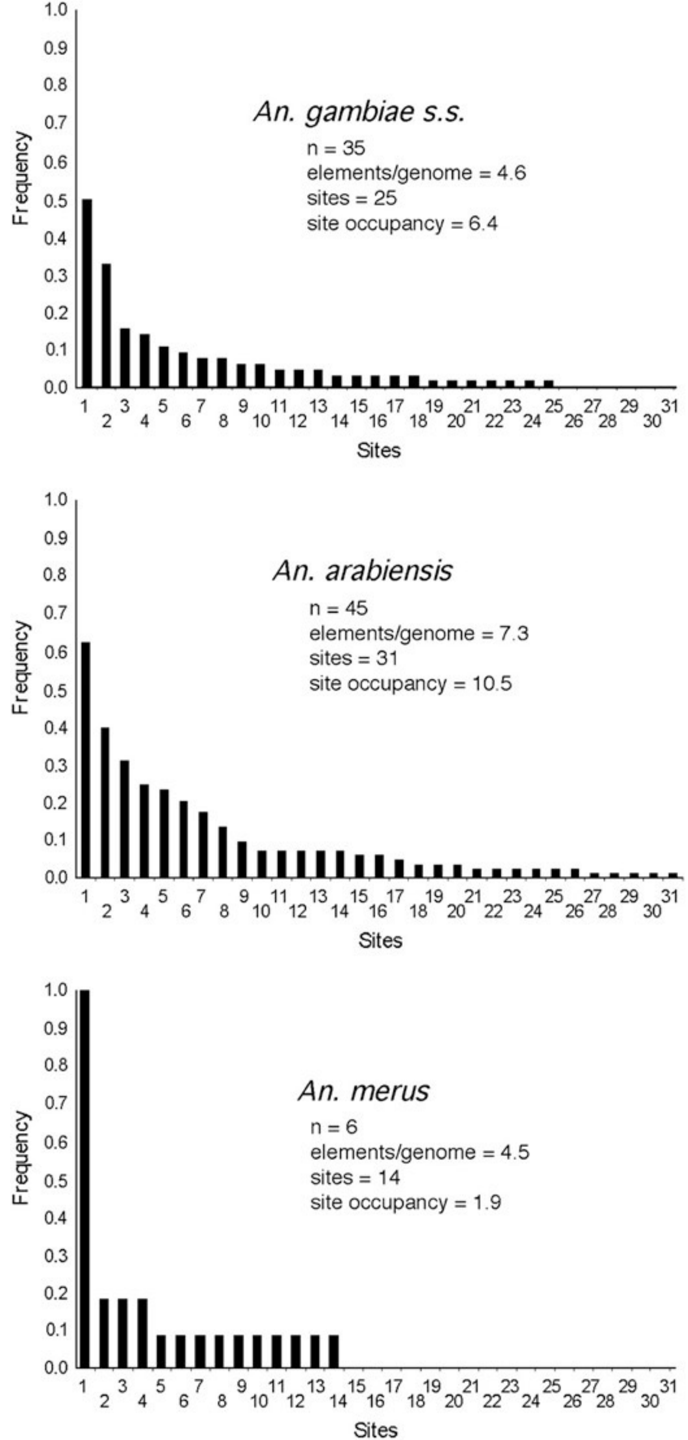
GYPSY

CACTA

Other Class II



class II element of the hAT element superfamily, called Herves



TEs have been successful in plant genomes

Arabidopsis thaliana	*Brachypodium distachyon*	*Oryza sativa*	*Glycine max*	*Hevea braisiliensis*	*Zea mays*	*Hordeum vulgare*	*Triticum aestivum*
125 Mb	272 Mb	389 Mb	1 115 Mb	2 150 Mb	2 300 Mb	5 100 Mb	17 000 Mb

2,400-fold angiosperms