Observations of Transposable Element Richness and Diversity in Embryophytes

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Outline

- What are transposable elements (TEs)? Why are they important?
- Analysis of existing libraries, and methods of discovery
- Diversity of transposon content across green plants
- Comparison of *Arabidopsis thaliana* individuals
- Conclusions
- Future Research

What are transposons?

Transposons are:

- **Mobile genetic elements**
- **Often able to replicate during transposition**
- **Able to affect the genetic make-up of the host**

Where did they come from?

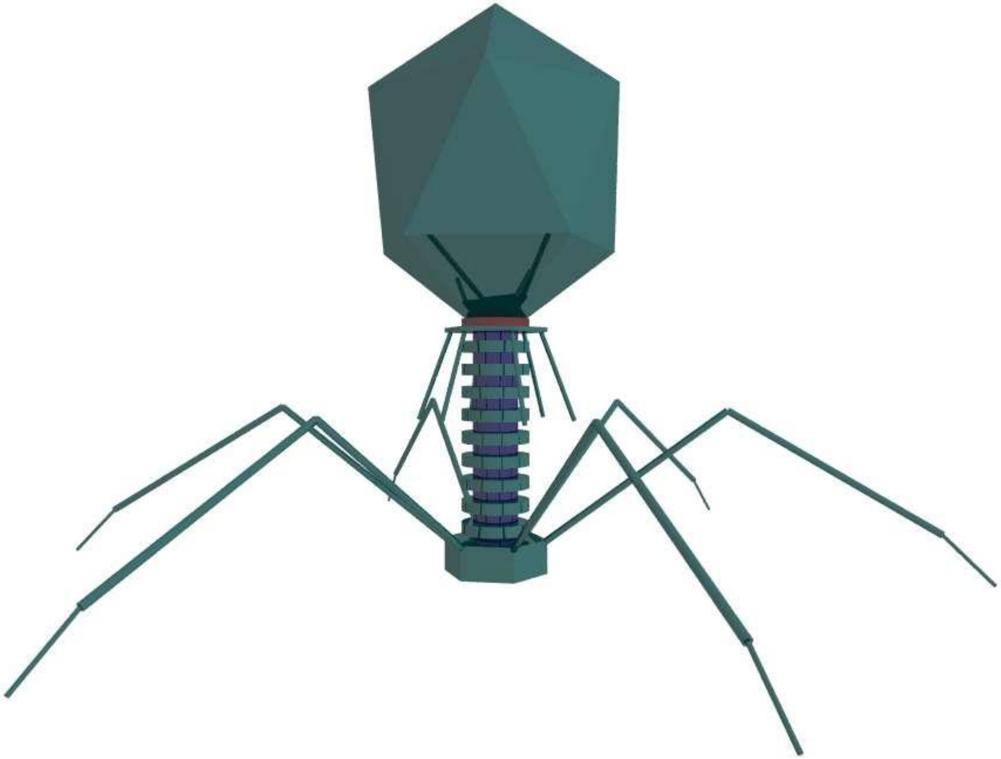


Figure 1. Bacteriaphage (http://cronodon.com, 2008)

How abundant are they?

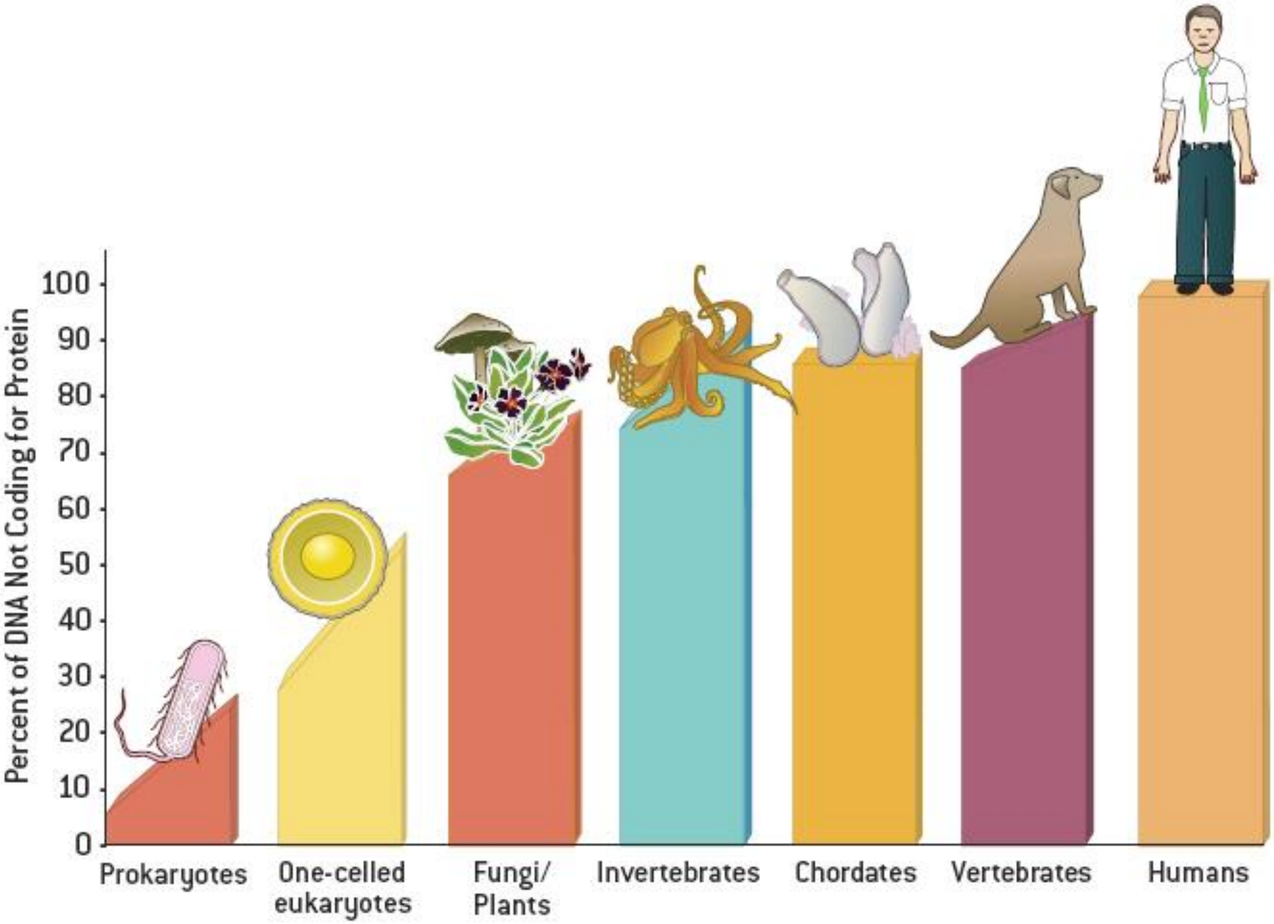


Figure 2. Non-coding DNA content species (Gregory, 2008)

What is their structure?

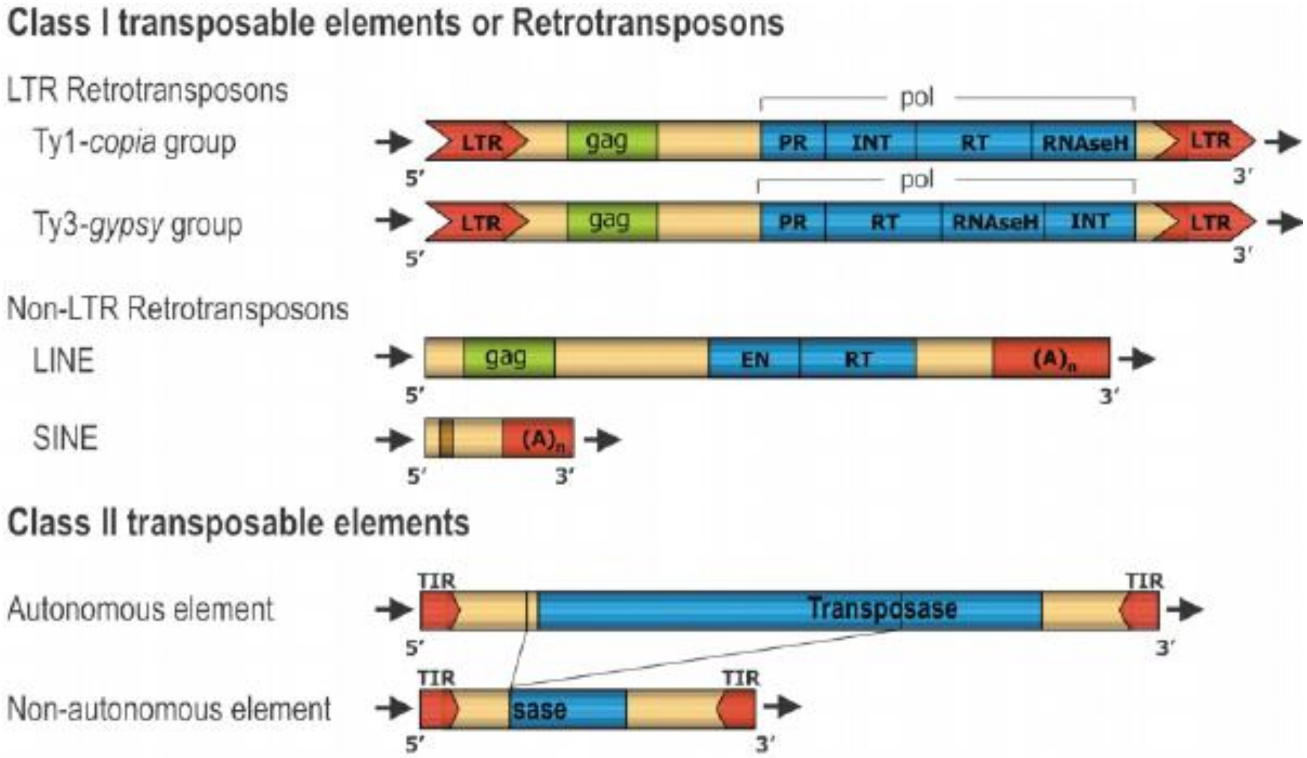
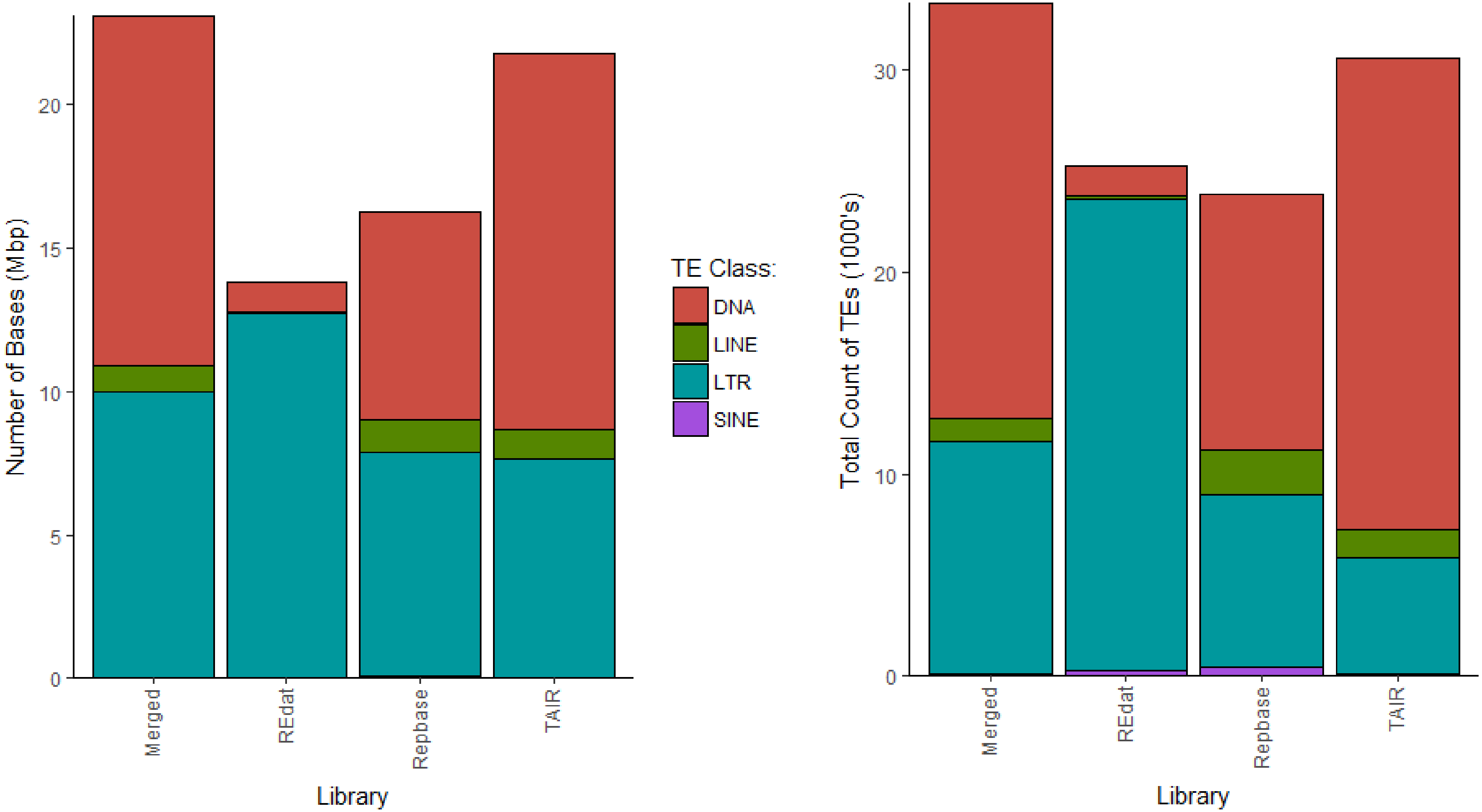


Figure 3. Structure of the different types of plant transposable elements (Casacuberta & Santiago, 2013).

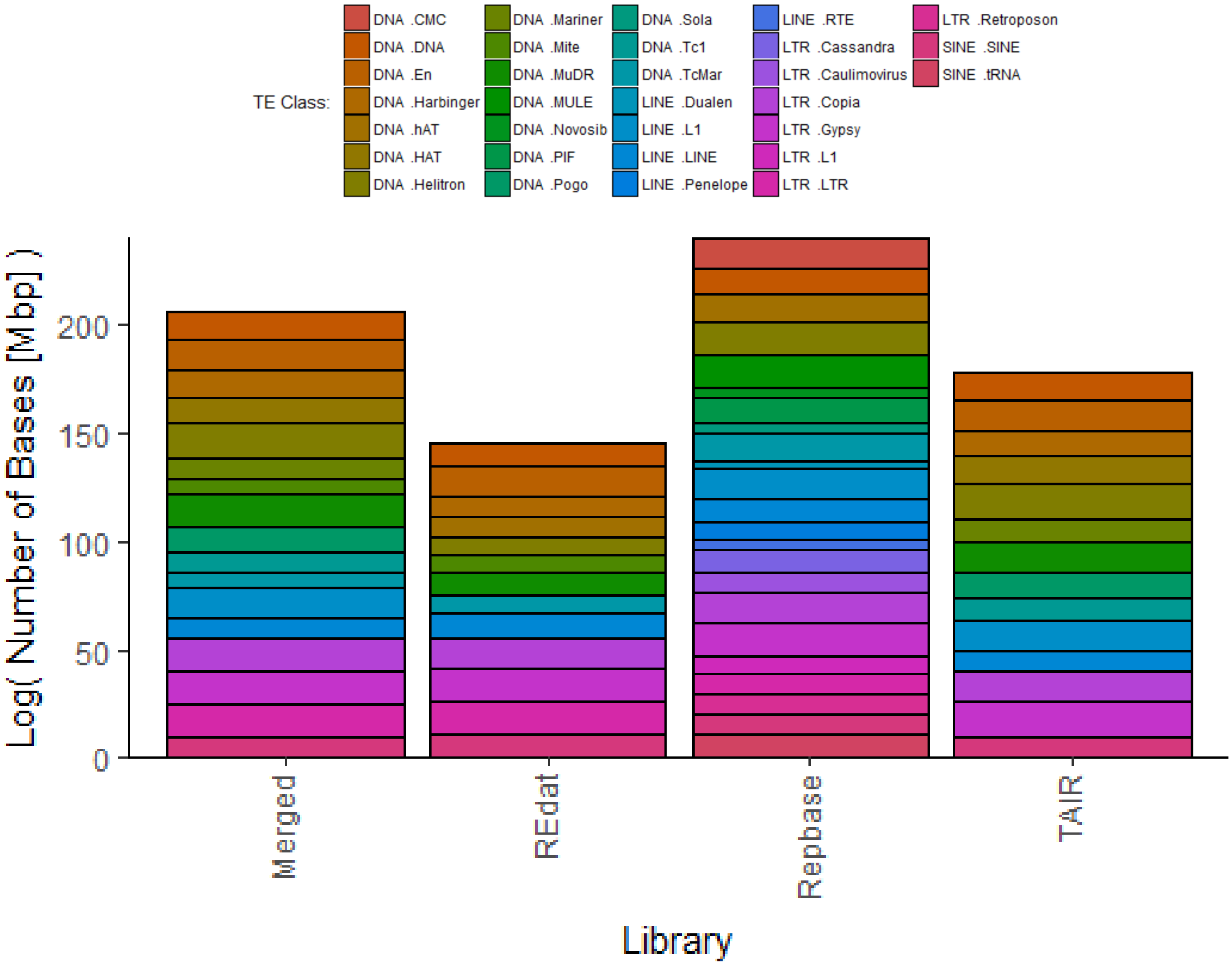
Comparison of TE Libraries

- **REdat (Plant Genome and System Biology Group, Germany)**
  - **Combination of TREP, TIGR repeats, PlantSat and Genbank libraries**
  - **450 Mbp, 61K sequences**
- **Repbase (Genetic Information Resource Institute, USA)**
  - **36 Mbp, 12k sequences**
- **TAIR (The Arabidopsis Information Resource, USA)**
  - **23 Mbp, 31k sequences**
- **Merged Library**
  - **Contains all above sequences**

Comparison of TE Libraries

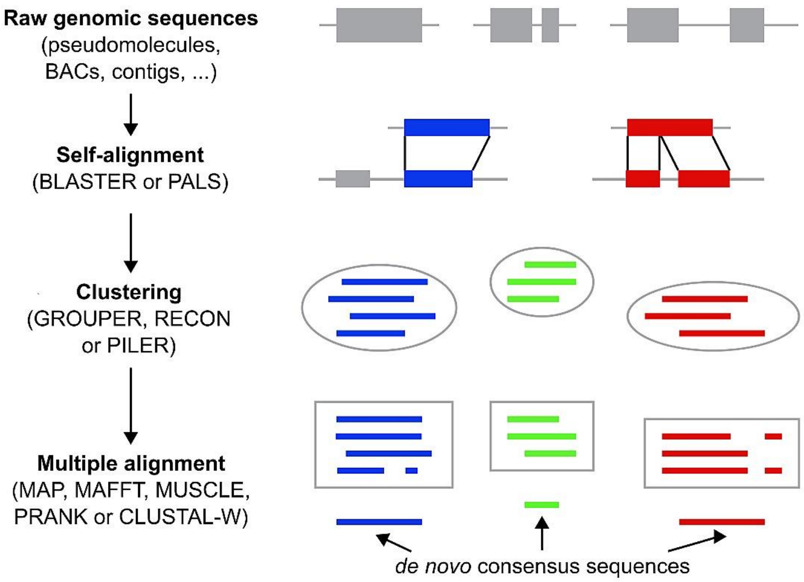


Comparison of TE Libraries



Discovery of Novel TEs

- **RepeatModeler**



Raw genomic sequences
(pseudomolecules,
BACs, contigs, ...)

Self-alignment
(BLASTER or PALS)

Clustering
(GROUPER, RECON
or PILER)

Multiple alignment
(MAP, MAFFT, MUSCLE,
PRANK or CLUSTAL-W)

de novo consensus sequences

- **Red (REpeat Detector)**
  - **Uses a machine learning algorithm to find repeats**

Discovery of Novel TEs

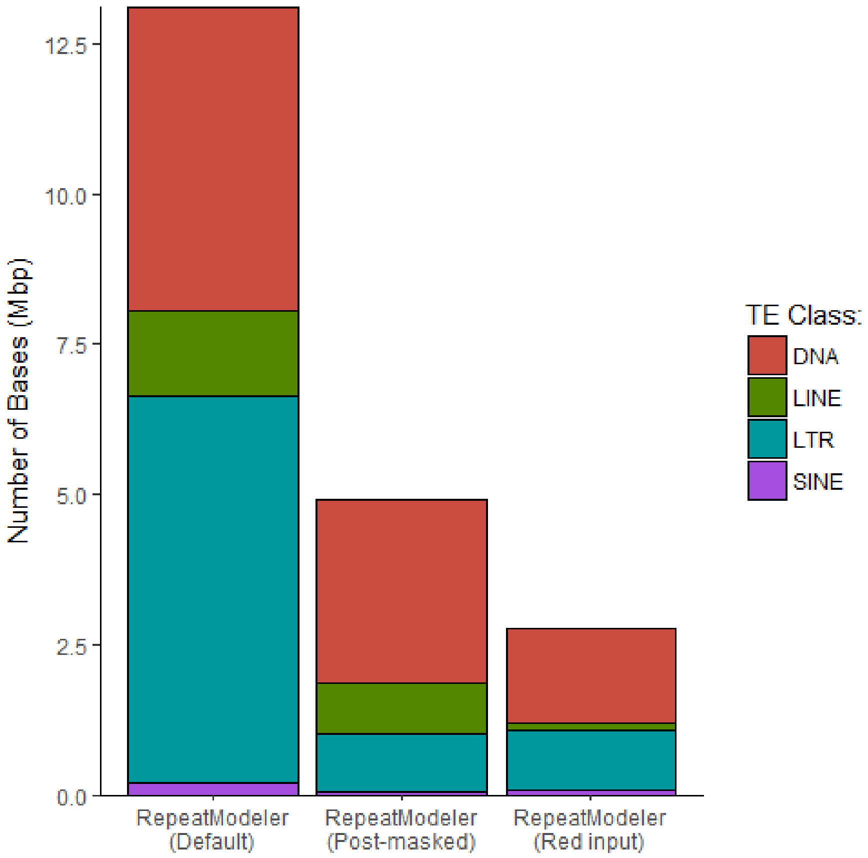
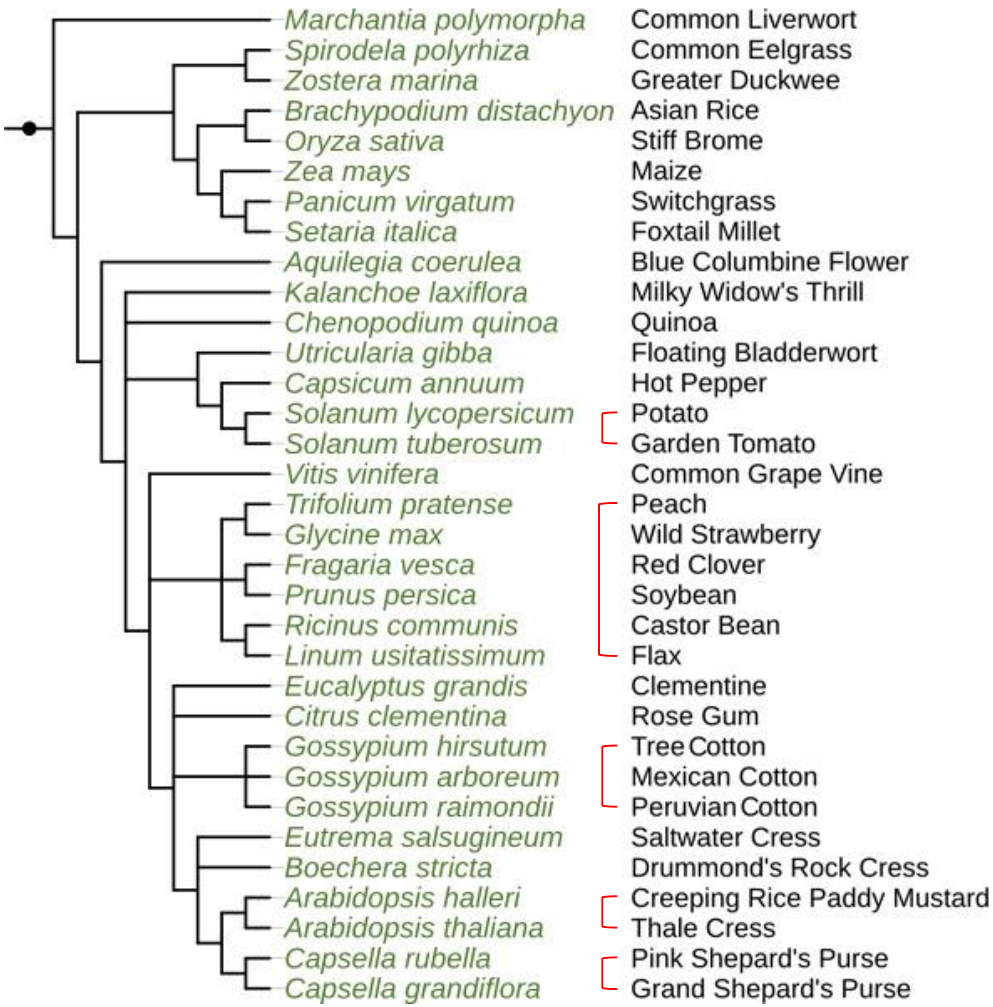


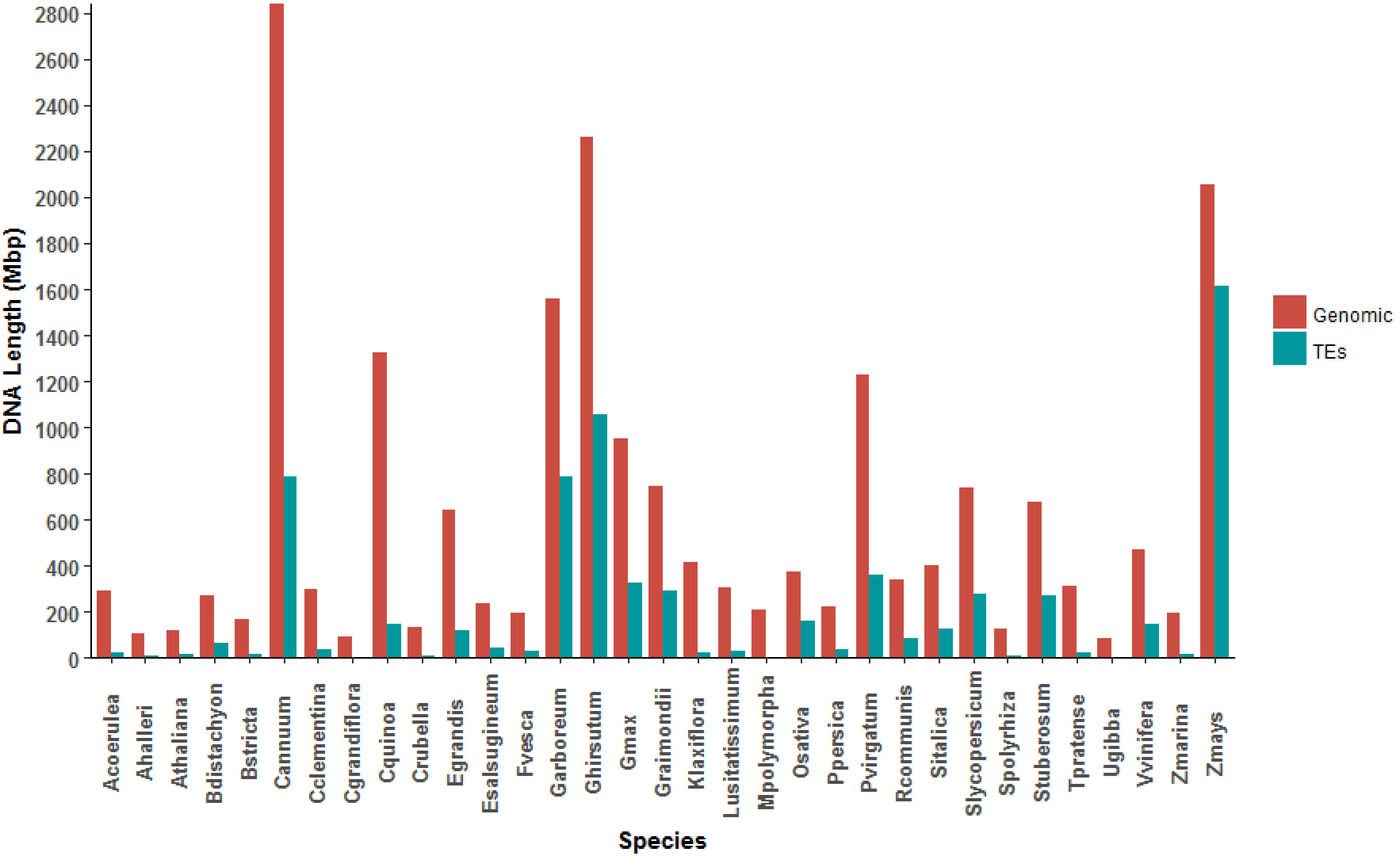
Table 1. Run-time for RepeatModeler with Embryophyte genomes

Species	Genome Size (Mbp)	Run-time (HHH:MM)
A.thaliana	117	198:16
A.thaliana	38	154:52
O.sativa	374	306:32
U.gibba	68	76:38
S.italica	407	314:28

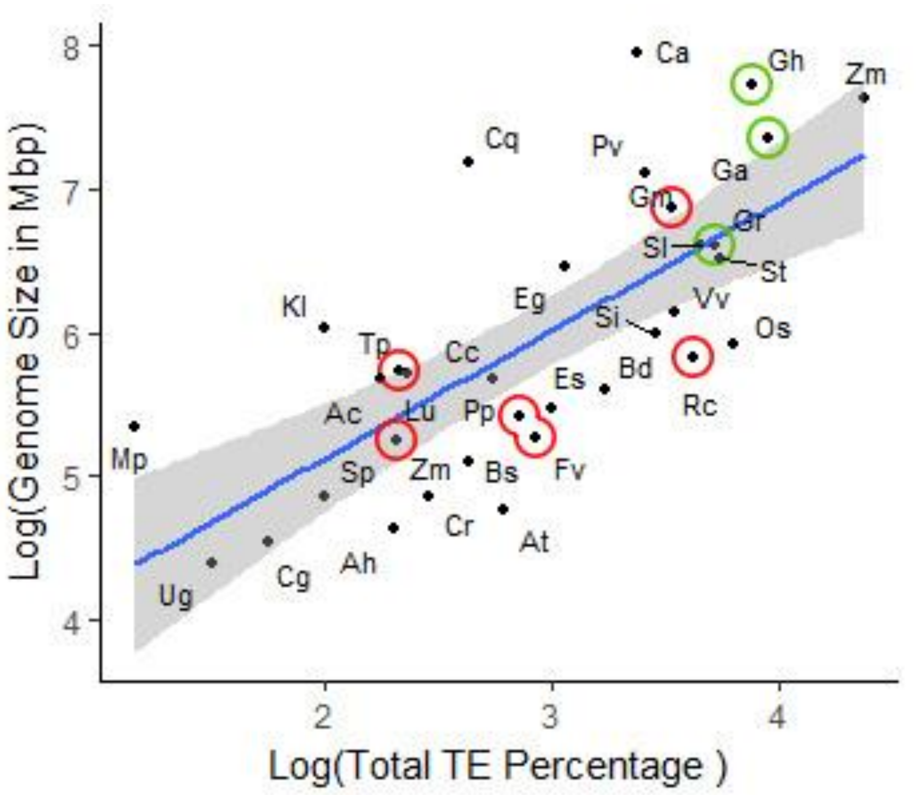
Transposons in Green Plants



Transposons in Green Plants



Transposons in Green Plants



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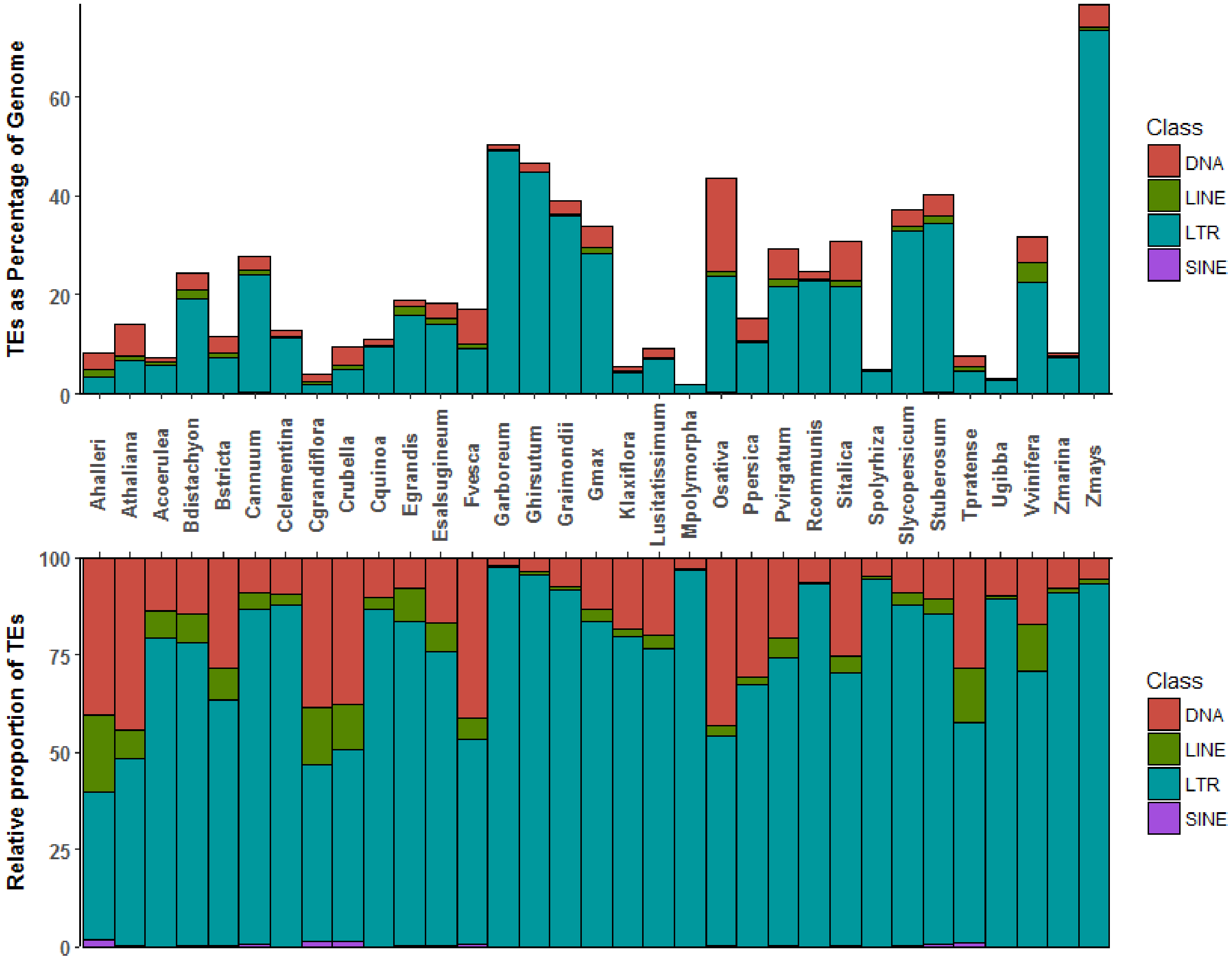
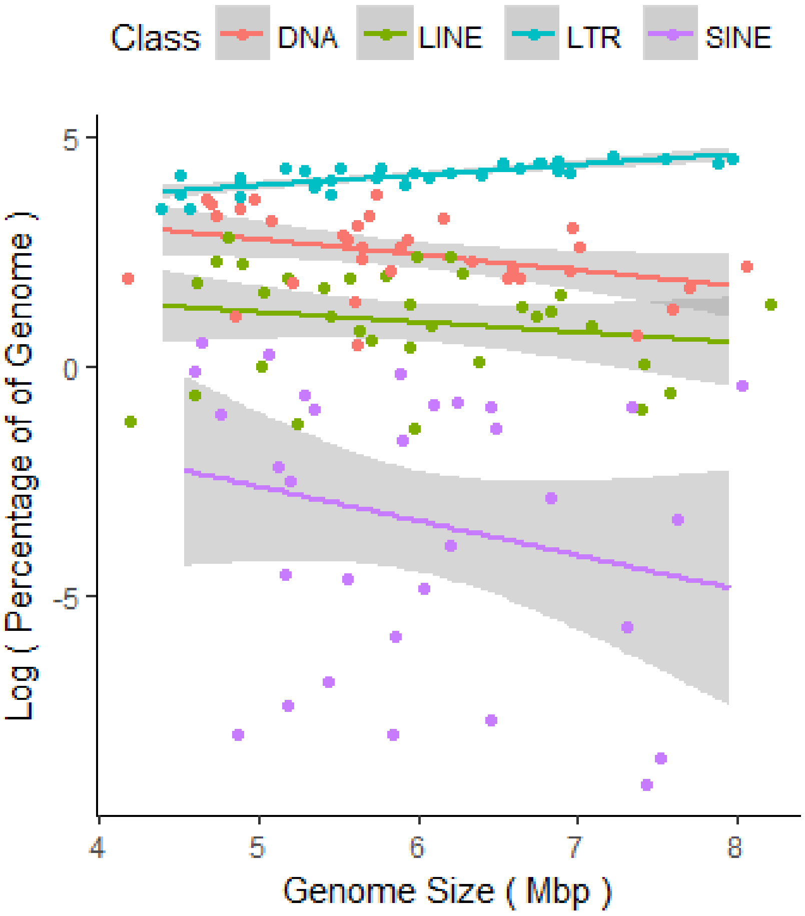


Transposons in Green Plants



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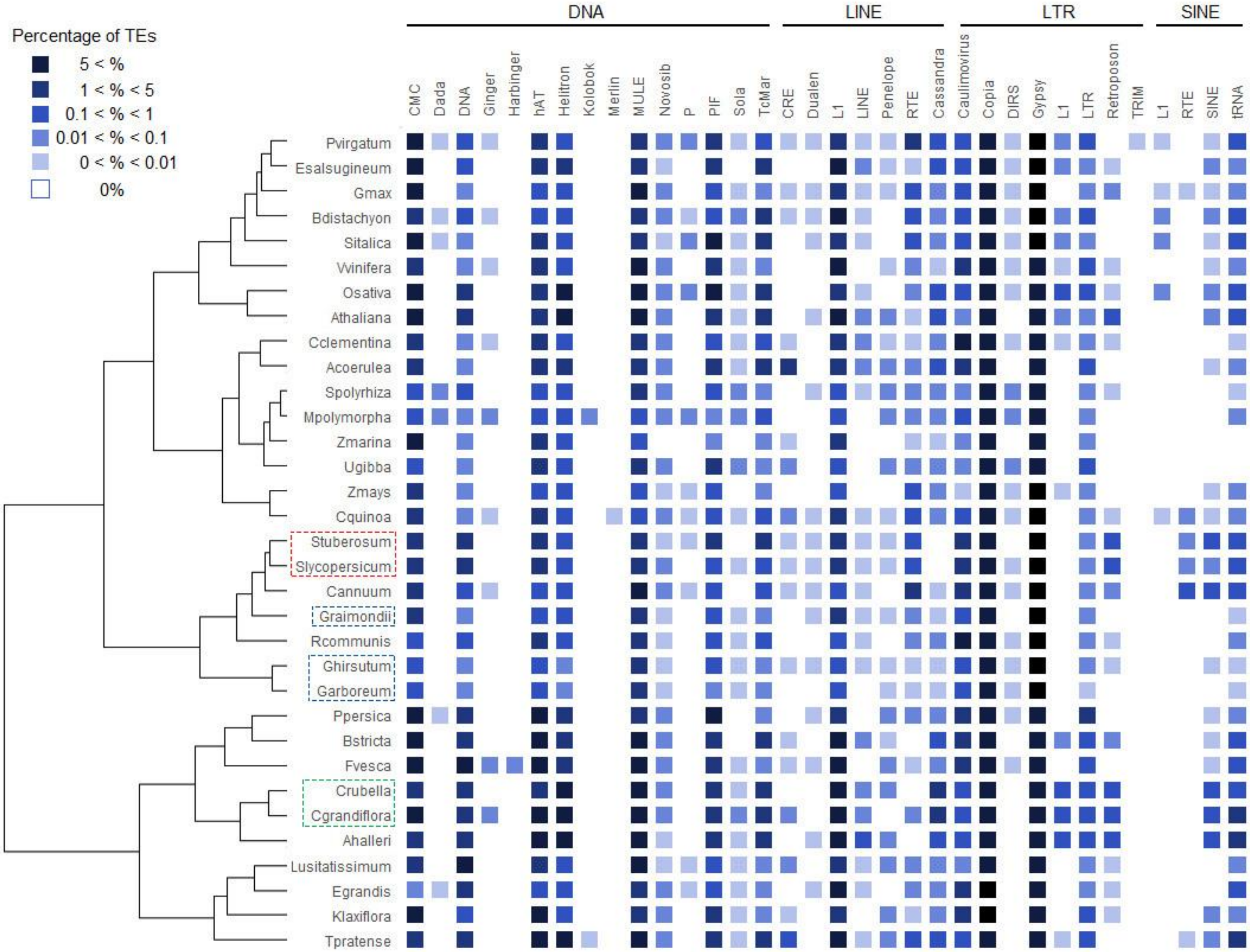
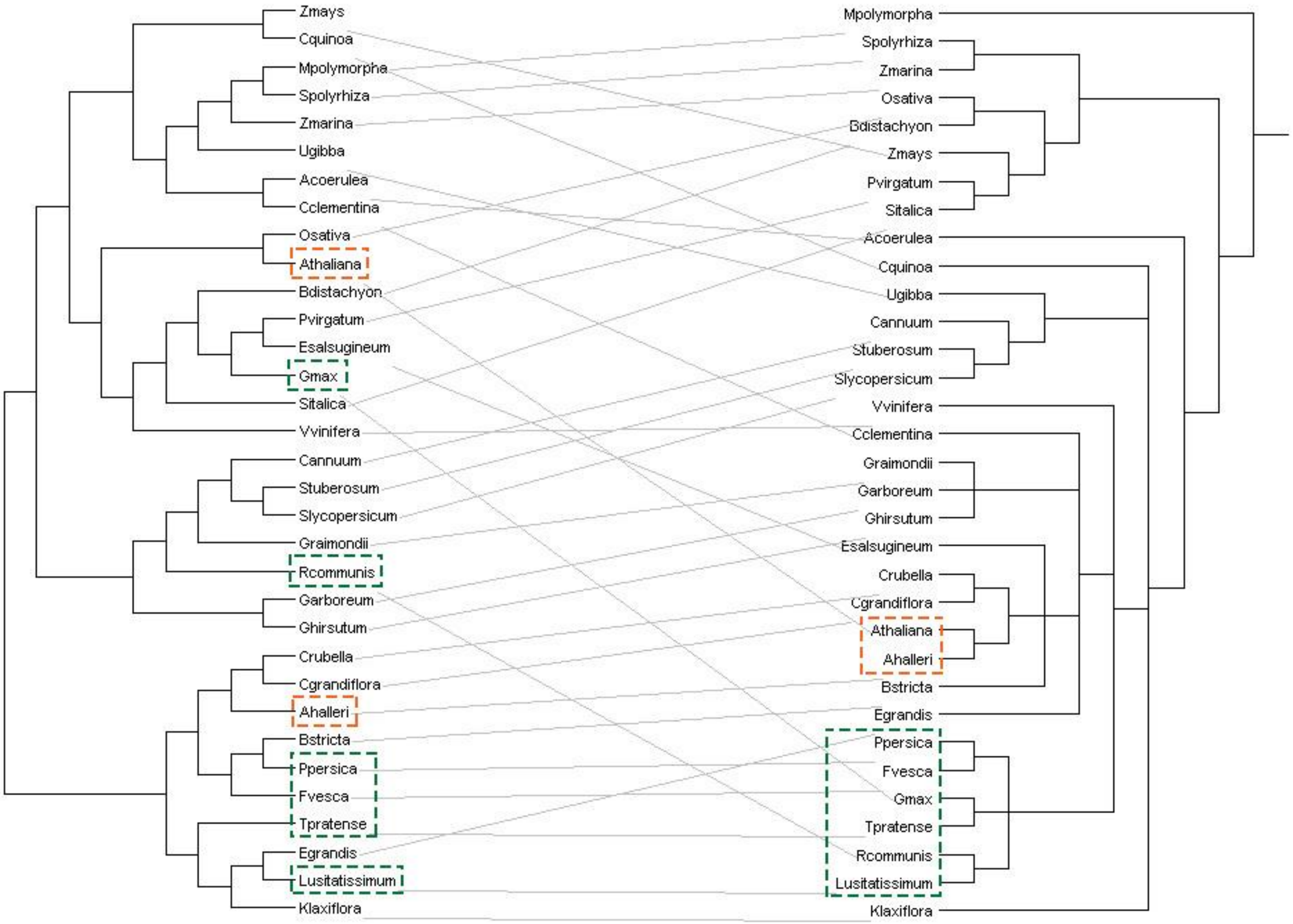


Transposons in Green Plants



Transposons in Arabidopsis

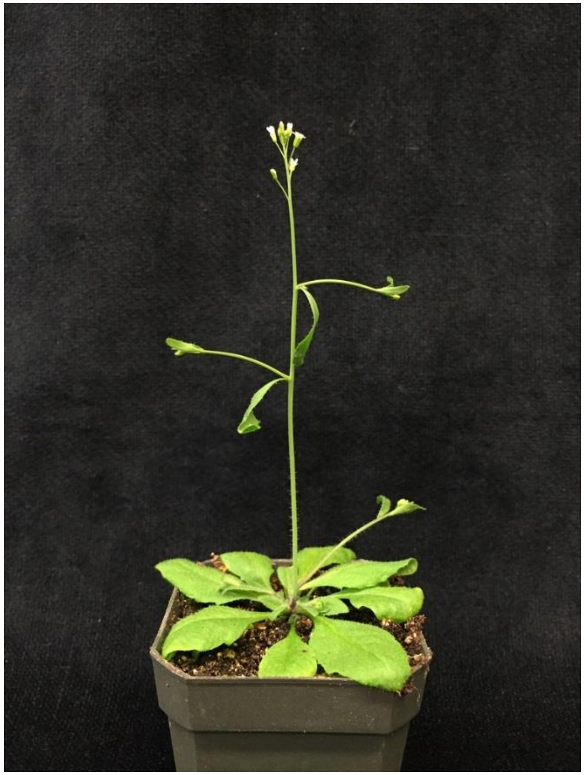
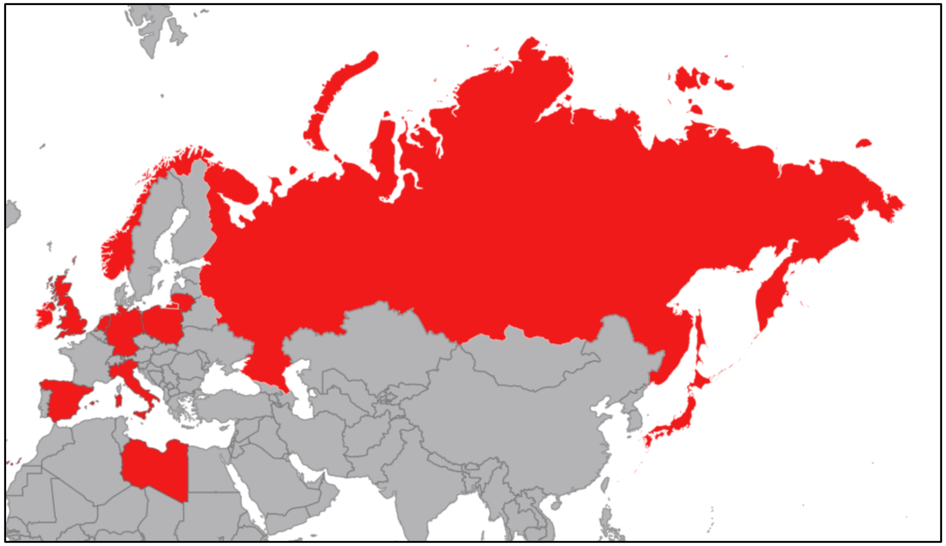
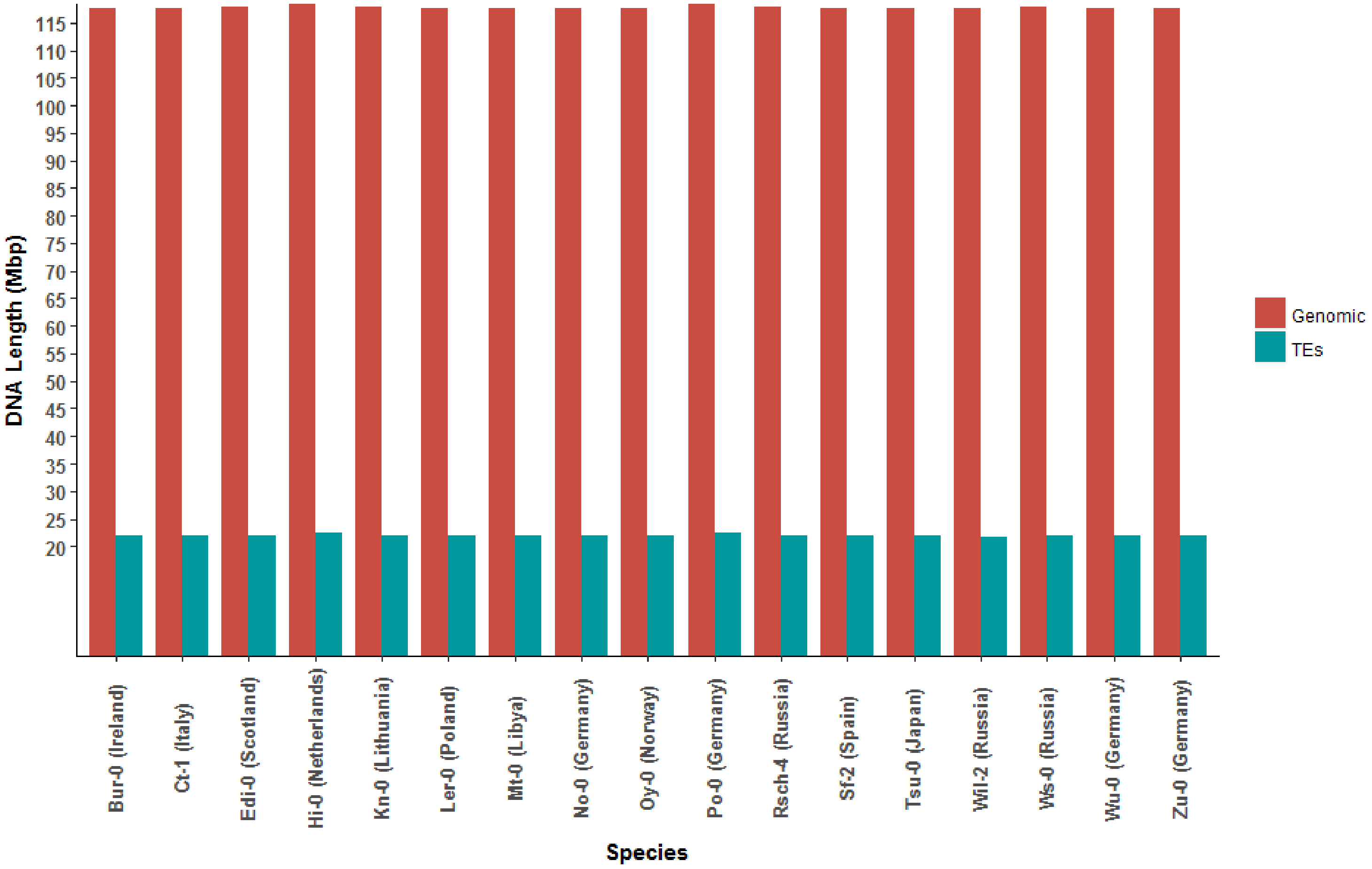


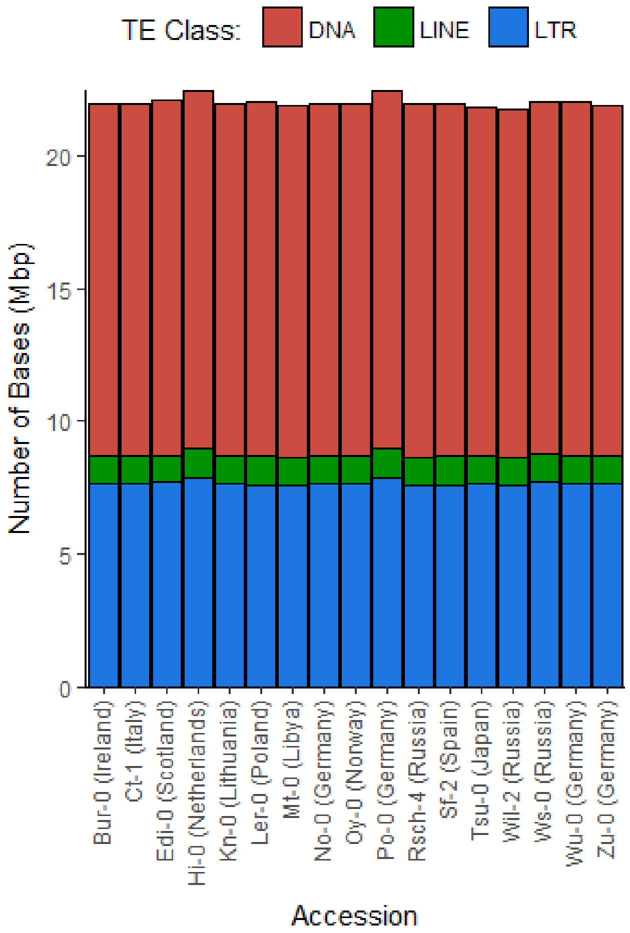
Figure 3. Arabidopsis thaliana (Roepers, 2004)



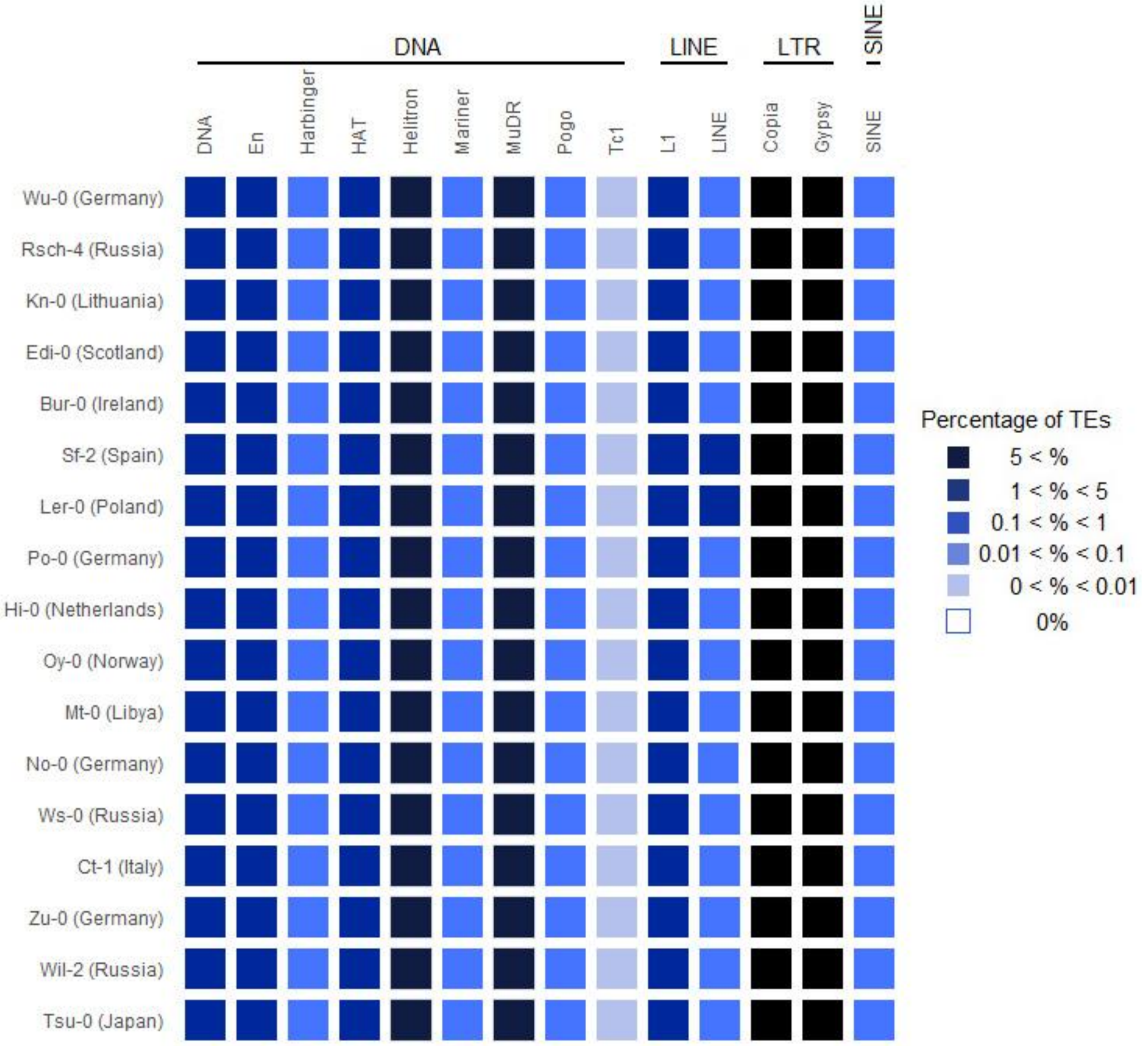
Transposons in Arabidopsis



Transposons in Arabidopsis



Transposons in Arabidopsis



Transposons in Arabidopsis

Kimura Distance:

$$K = -\frac{1}{2}\ln(1-2p-q)\sqrt{1-2q}$$

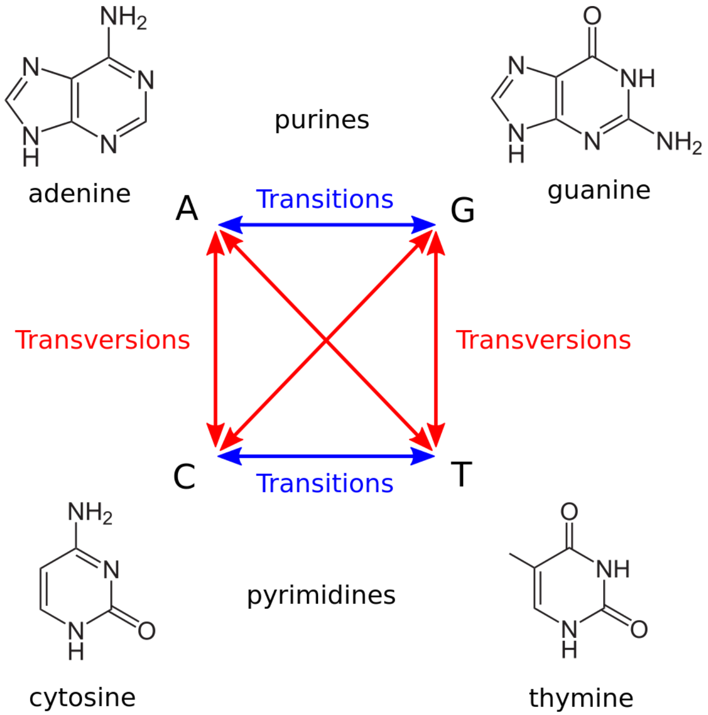
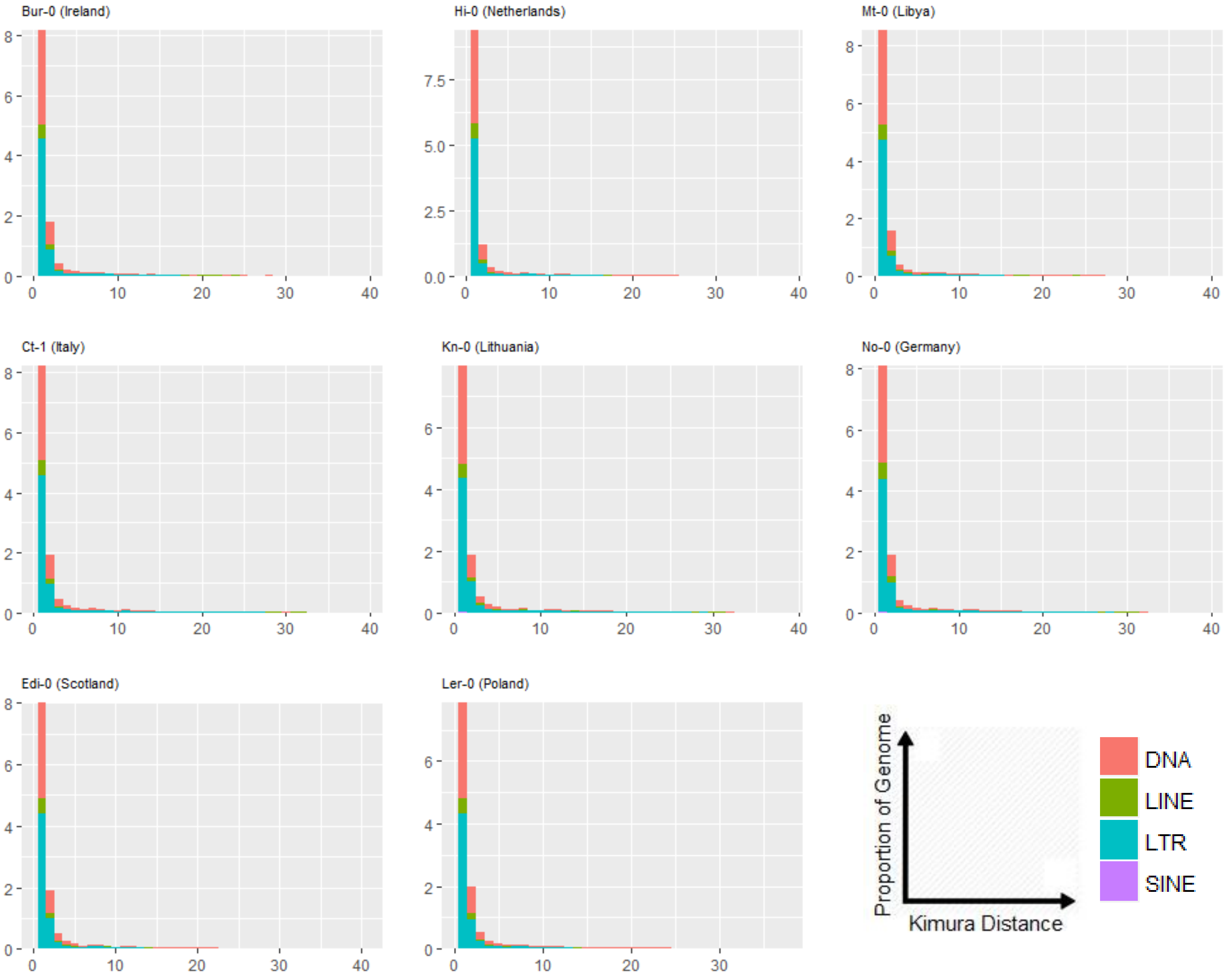
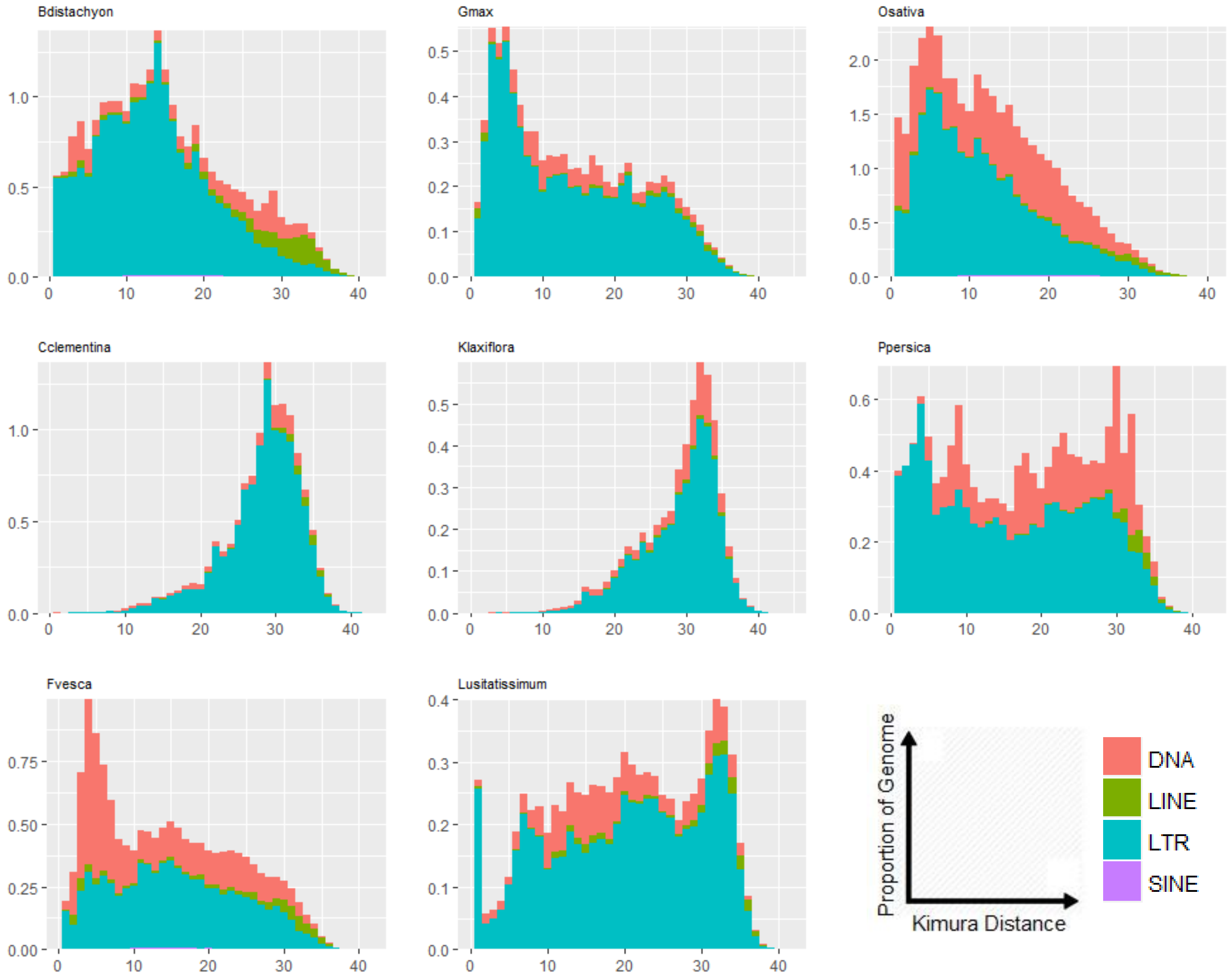


Figure 3. Transitions-transversions (Petulda, 2008)

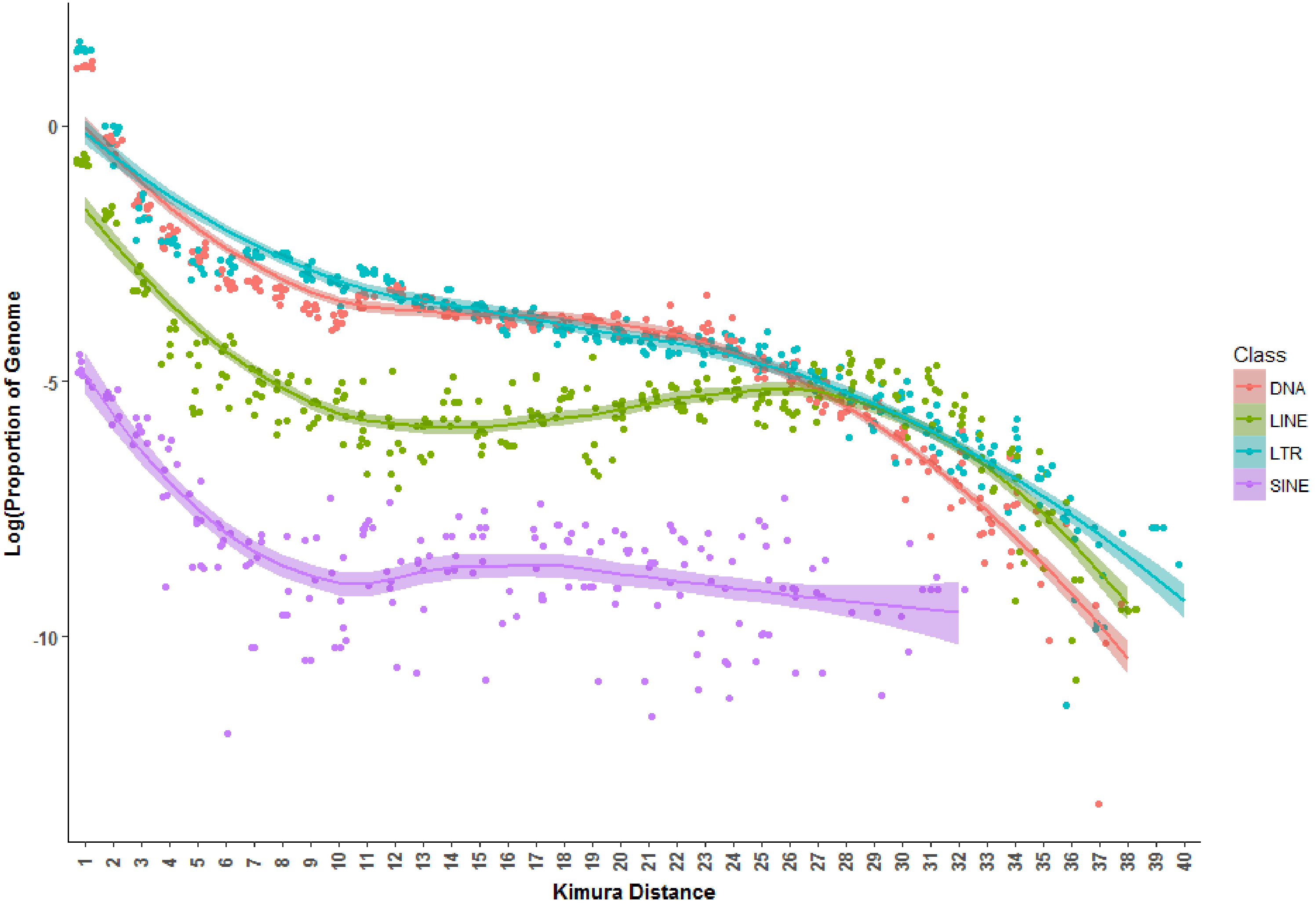
Transposons in Arabidopsis



Transposons in Green Plants



Transposons in Arabidopsis



Conclusions

Repbase has the widest library of TE subfamilies

- 23 found in A.thaliana, < 15 found in others

REdat has strong LTR content

- By copy number, REdat LTR > All Repbase

High amount of overlap is existing TE libraries

- 22% on merged; 19%, 15%, 14% on others

Conclusions

Correlation between genome size and TE content

- Pearson’s Test (*t* = 10.389, P << 0.005)

Correlation between genome size and LTR content

- Pearson’s Test (*t* = 5.18, P < 0.005)

Evidence for TE transfer

- *DNA/Kolobok* in *M. polymorpha*, *DNA/Merlin* in *C. quinoa*

Evidence for TE extinction

- *LINE/Cassandra* in *S. tuberosum*, *S. lycopersicum*

TE content is not reflective of phylogeny

- *G.max, R.communis* removed from other Fabids

Conclusions

Map distances may not reflect genomic differences

- Japan and Libya show minimal separation

Arabidopsis has recent common ancestor

- Equal genome sizes, minimal divergence for TEs

Cited mutation rates may be incorrect

- 10^{4} -10^{6} rate not reflected in Arabidopsis

Future Work

Develop TE discovery pipeline with Red

- Use existing libraries as training data

Analyze RepeatModeler TEs

- Compare against known sequences (TE, coding, ncDNA)

Create a tool to generate non-overlapping libraries

- Combine and cluster sequences to maximize efficiency

Future Work

Expand search for TE transfer mechanisms

- Search for individual subfamilies across unrelated species

Investigate TE contribution to speciation

- Detect bursts of transposons

Analyze extremely large genomes for trends

- *Paris japonica* (130 Gbp)

Future Work

Expand Arabidopsis data

- Find relict individuals (pre-1700’s)

Compare other equations for evolutionary change

- Include for insertions and deletions

Detect transposon activity

- Search parent/offspring for increased copy numbers