

Supplementary Materials

Discovering the Repeatome of Five Species Belonging to the Asteraceae Family: A Computational Study

Maria Ventimiglia †, Marco Castellacci †, Gabriele Usai, Alberto Vangelisti, Samuel Simoni, Lucia Natali, Andrea Cavallini, Flavia Mascagni * and Tommaso Giordani

Department of Agriculture, Food and Environment (DAFE), University of Pisa, Via del Borghetto, 80-56124 Pisa, Italy

* Correspondence: flavia.mascagni@unipi.it

† These authors contributed equally to this work.

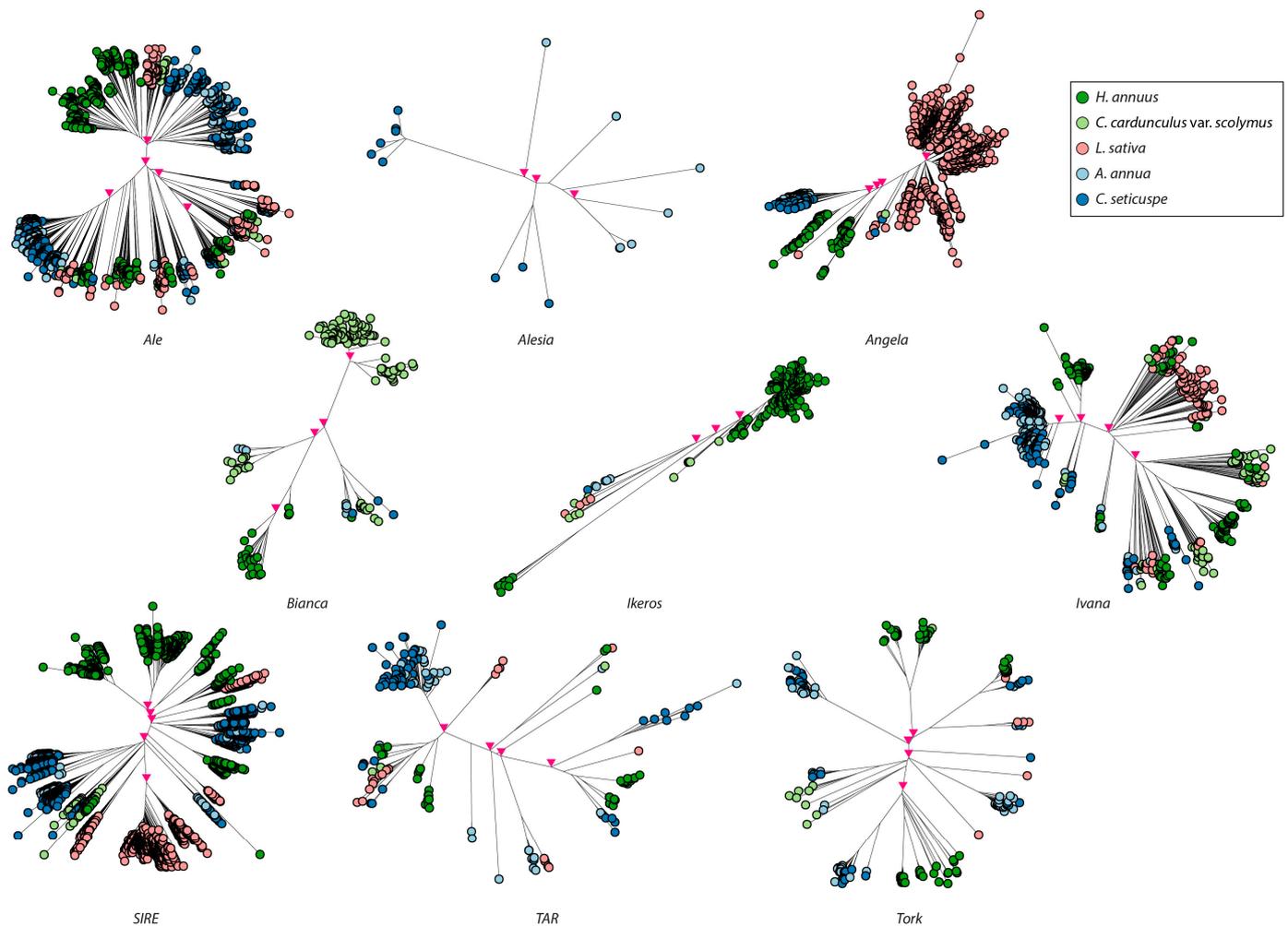


Figure S1. Phylogenetic trees of all RT sequences of *Copia* elements retrieved in the five Asteraceae species, separated according to the lineage. The main nodes (bootstrap values > 0.6) are marked with pink triangles. RT = reverse transcriptase.

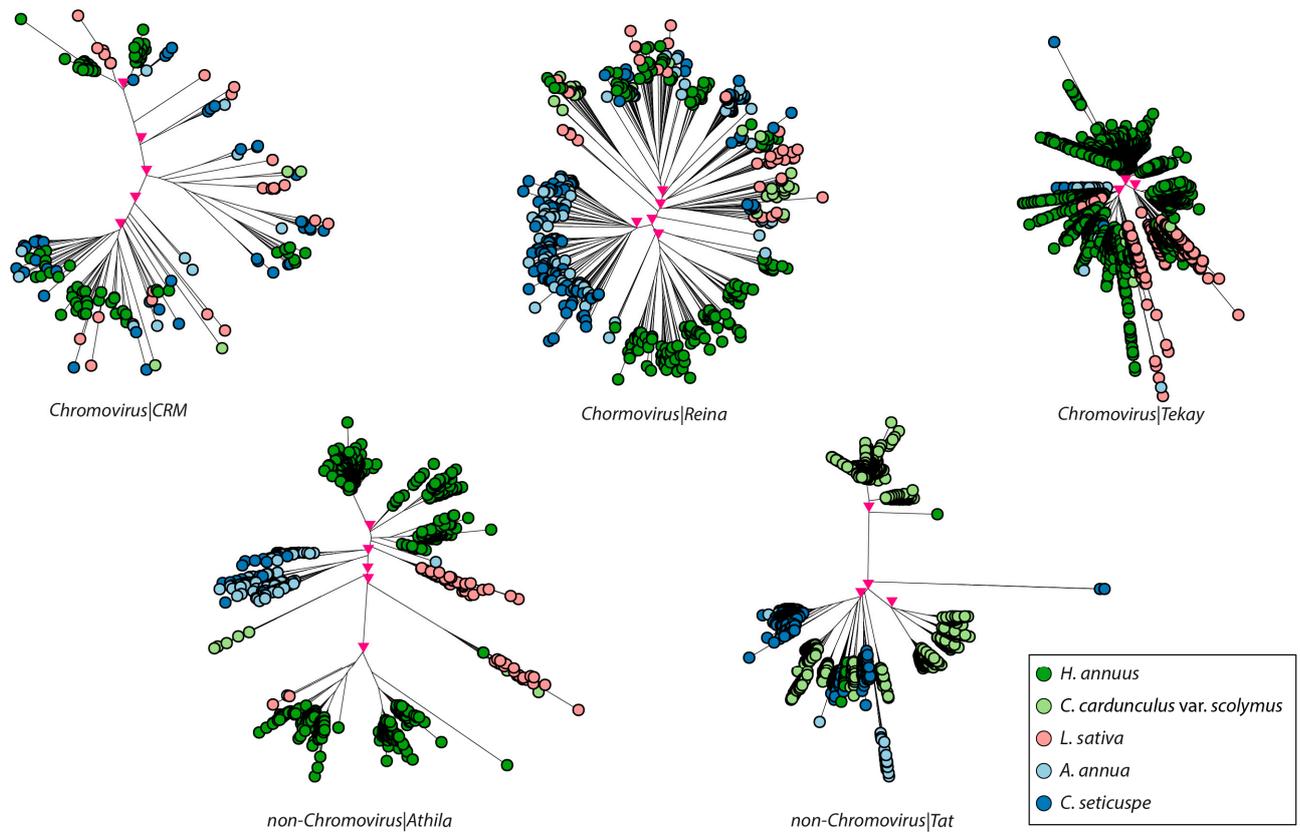


Figure S2. Phylogenetic trees of all RT sequences of *Gypsy* elements retrieved in the five Asteraceae species, separated according to the lineage. The main nodes (bootstrap values > 0.6) are marked with pink triangles. RT = reverse transcriptase.