

Gil Yardeni, Michael H. J. Barfuss, Walter Till, Matthew R. Thornton, Clara Groot Crego, Christian Lexer, Thibault Leroy and Ovidiu Paun. 2025. "The Explosive Radiation of the Neotropical *Tillandsia* Subgenus *Tillandsia* (Bromeliaceae) Has Been Accompanied by Pervasive Hybridization" *Systematic Biology* doi.org/10.1093/sysbio/syaf039



M. Nabil



BotBln

Class focus area:
Networks

EEB603: Brian O'Meara

All quotes and images from the above paper unless otherwise noted

"I heard you liked *Tillandsia*, so I put subgenus *Tillandsia* inside genus *Tillandsia*"

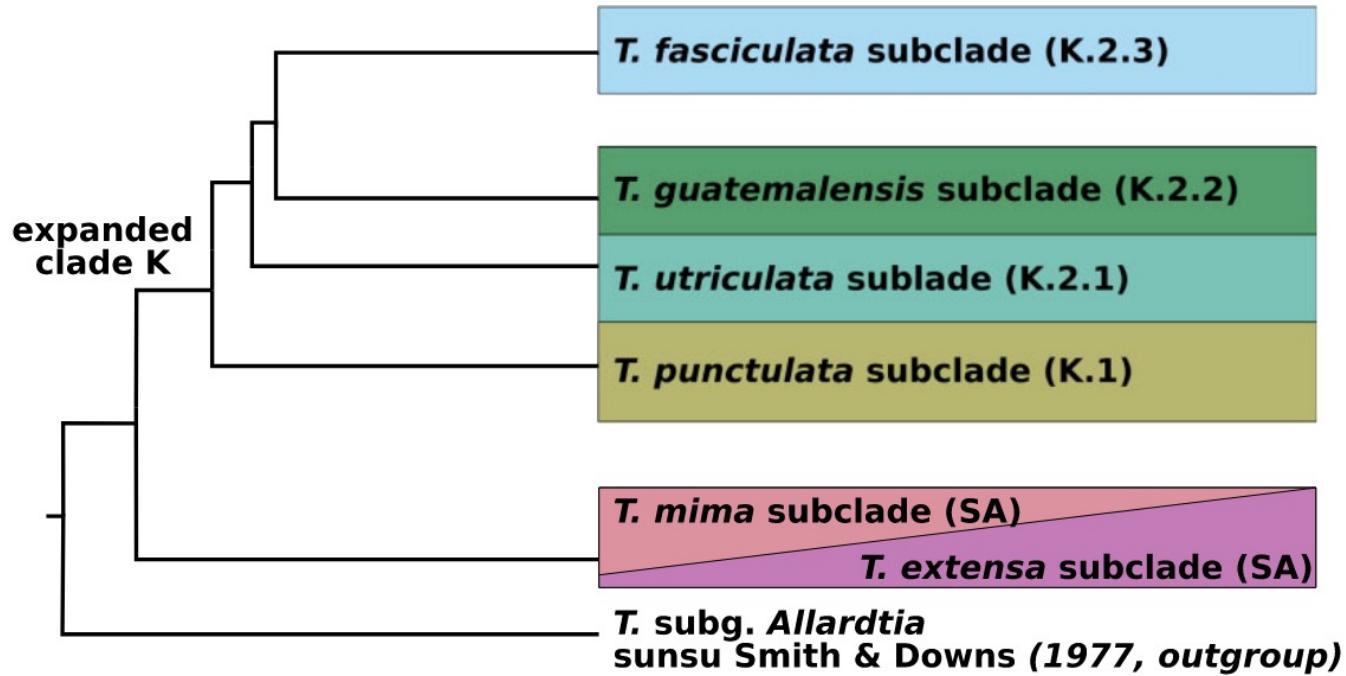


FIGURE 1. A simplified phylogeny of the subclades sampled in this study, as generally hypothesized in previously published studies (Barfuss et al. 2016; Pinzón et al. 2016; Vera-Paz et al. 2023). The shared grouping of the South American (SA) subclades denotes disagreements in the literature. Subclade names correspond to naming in this study, following previously proposed names.

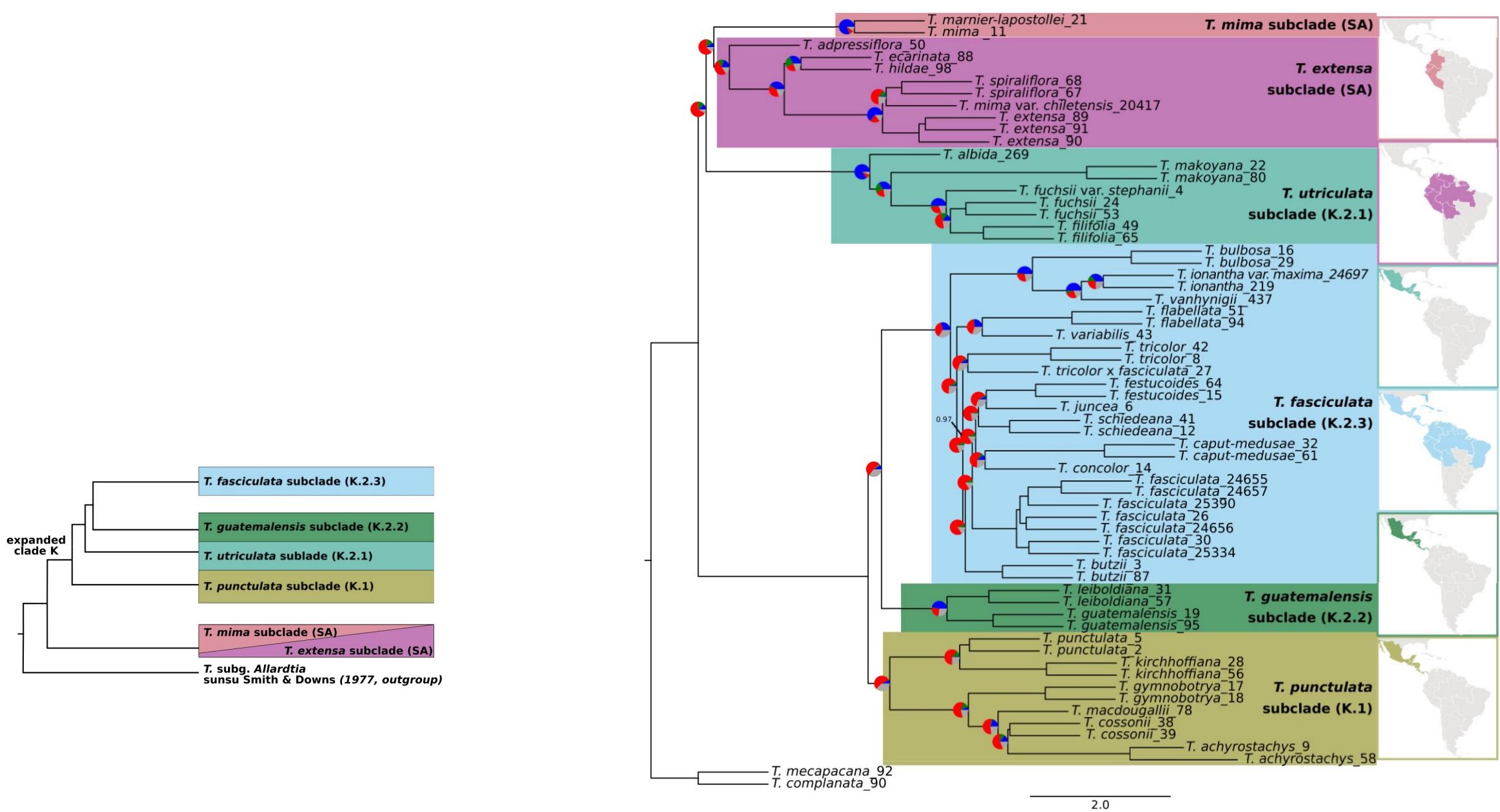
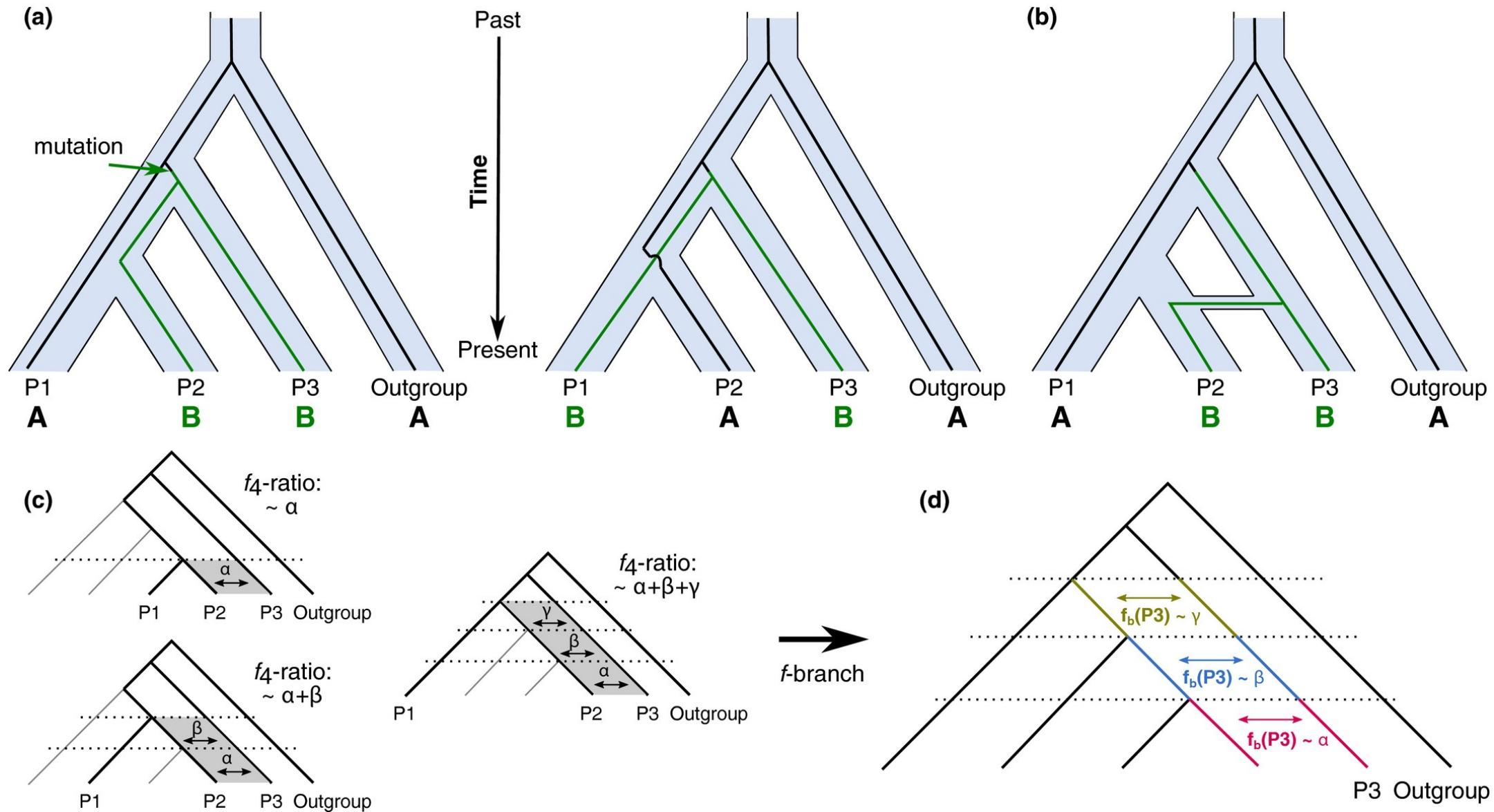


FIGURE 2. A coalescent-based species tree generated on 15,791 genomic windows with ASTRAL-III for 64 individuals representing 33 species of *Tillandsia* subgenus *Tillandsia*, plus 2 outgroups of subgenus *Allardtia* sensu Smith and Downs (1977). Branch lengths are given in coalescent units. Node values represent local posterior probabilities for the main topology and are equal to 1 unless noted otherwise. Pie charts at the nodes show levels of gene-tree discordance: the percentages of concordant gene trees (blue), the top alternative bipartition (green), other conflicting topologies (red), and uninformative gene trees (gray). Clade terminology follows previously proposed names (e.g., Barfuss et al. 2016; Pinzón et al. 2016).



Basic principles behind the *D* and *f*-branch statistics. (a) Example genealogies showing the sharing of derived alleles, denoted as 'B' between populations P2 and P3 (the ABBA pattern) and between P1 and P3 (the BABA pattern) as a result of incomplete lineage sorting. In a scenario without gene flow, both patterns are assumed to be equally likely (but see (Eriksson & Manica, 2012) for exceptions). (b) Gene flow between P2 and P3 introduces additional loci with ABBA patterns, which would lead to a positive *D* statistic. (c) An example illustrating interdependences between different f_4 -ratio scores, which can be informative about the timing of introgression. In this example, different choices for the P1 population provide constraints on when the gene flow could have happened. (d) Based on relationships between the f_4 -ratio results from different four taxon tests, the *f*-branch, or f_b statistic, distinguishes between admixture at different time periods, assigning signals to different (possibly internal) branches in the population/species tree.

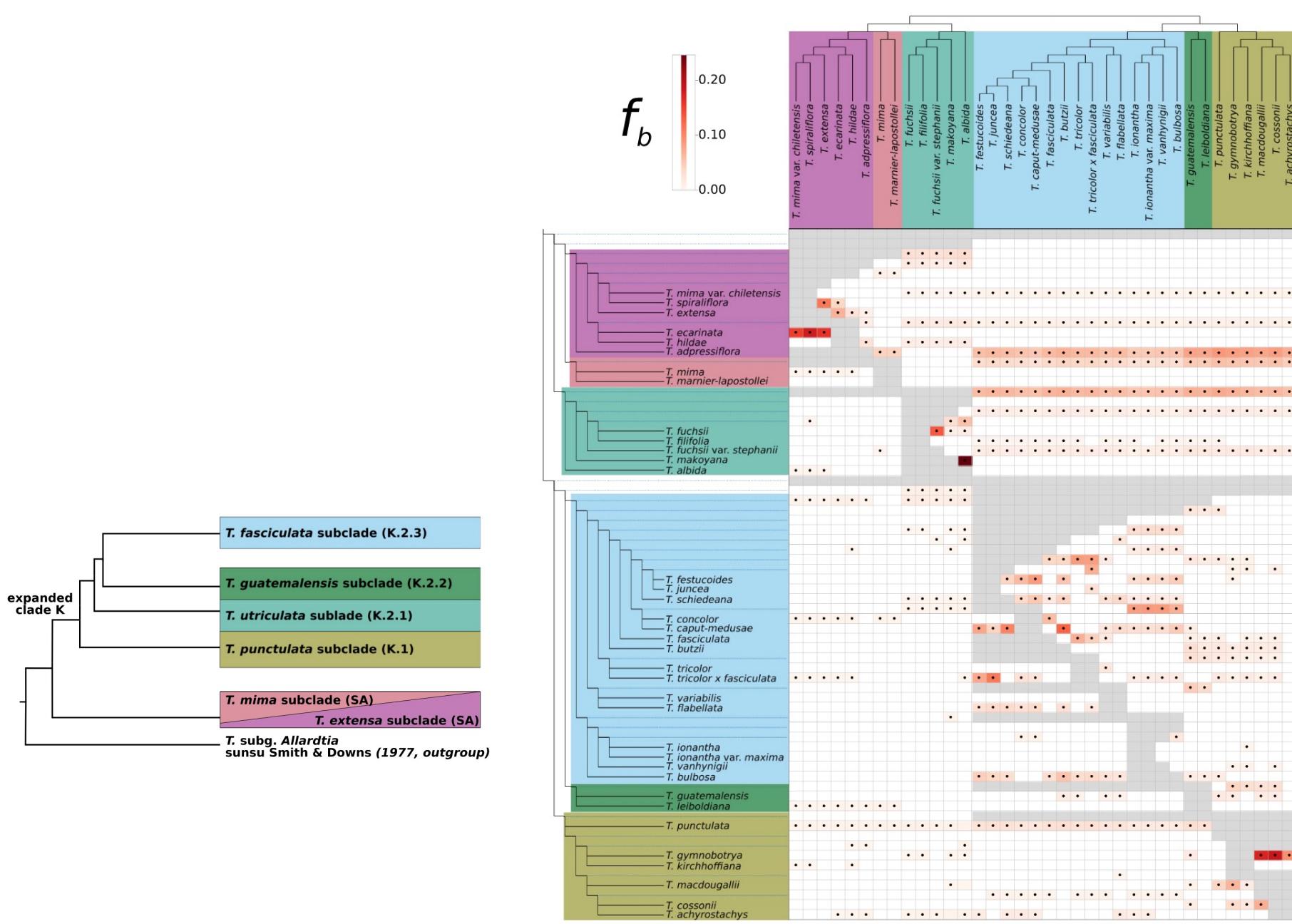


FIGURE 3. Heatmap summarizing the statistic $f_b(C)$, where excess sharing of derived alleles is inferred between the branch of the tree on the y-axis and the species C on the x-axis. The ASTRAL species tree was used as input topology for the branch statistic. The matrix is colored according to $f_b(C)$ values and gray squares correspond to tests that are inconsistent with the ASTRAL phylogeny. Dots within the matrix denote a significant P-value, estimated using a block jackknife procedure and corrected for family-wise error rate. Colors correspond to the clades in Fig. 1.

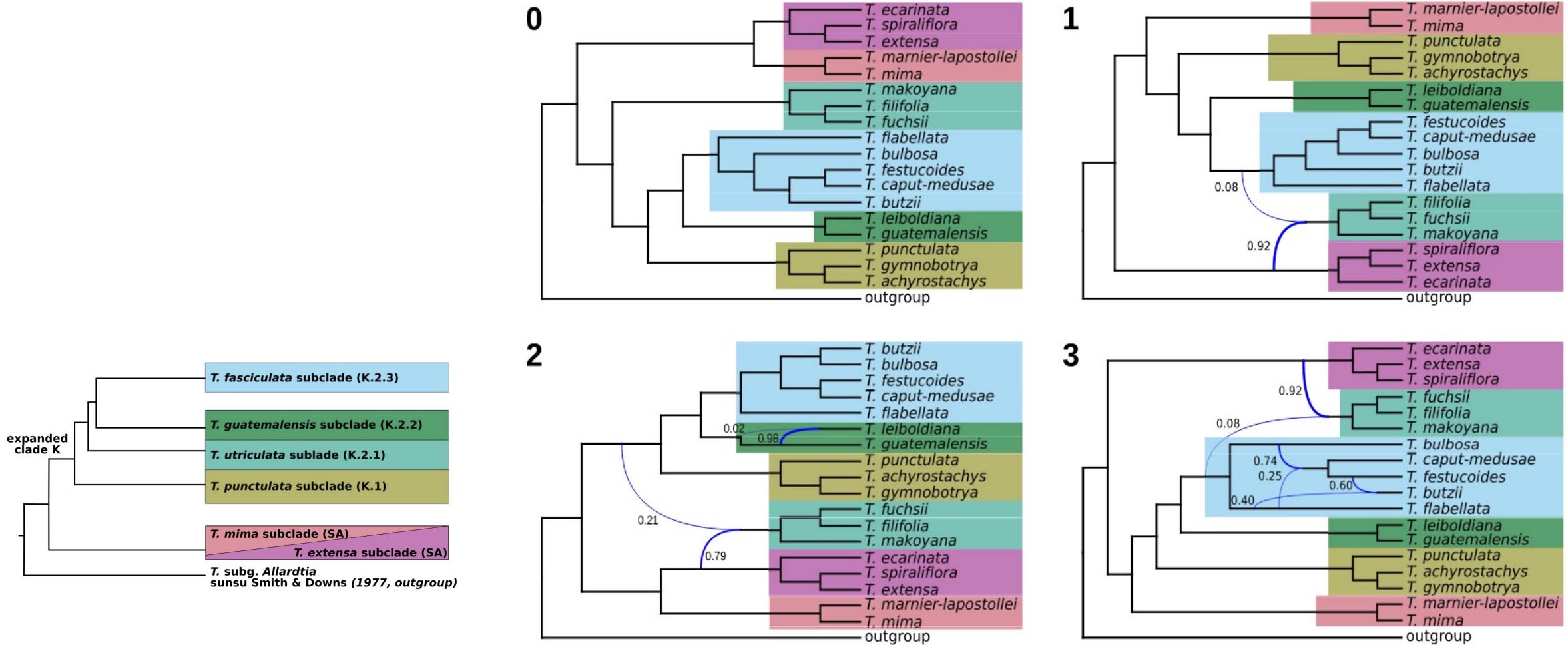


FIGURE 4. Pseudo-likelihood species networks inferred with PhyloNet for 0–3 reticulations (network presented was scored with the highest log probability). Curved branches indicate reticulation events. Numbers next to curved branches indicate inheritance probabilities for each event. Colors correspond to the clades in Fig. 1.

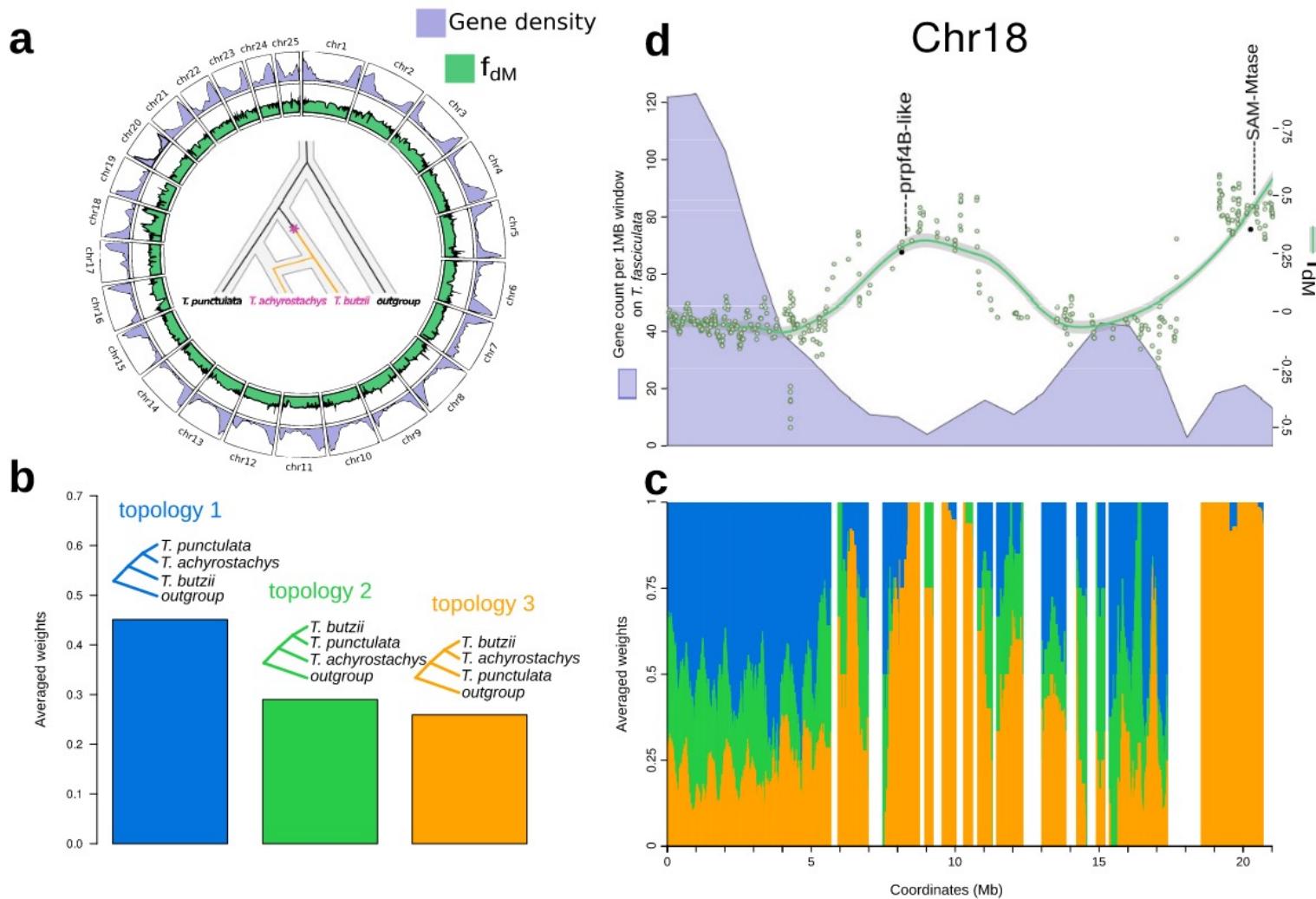


FIGURE 5. Signature of introgression and topology weighting on chromosome 18 between *T. punctulata*, *T. butzii*, and *T. achyrostachys* (P1, P2, and P3; *T. complanata* was used as the outgroup). (a) Values of f_{dM} -statistic and gene content for each chromosome calculated between *T. punctulata*, *T. butzii*, and *T. achyrostachys*. (b) Topology weighting by iterative sampling of subtrees in genomic windows of 50 SNPs using *Twisst*. Colors represent the frequency of each topology in (c) along the chromosomal position in chromosome 18: White gaps indicate regions excluded due to high levels of missing data. (d) f_{dM} -statistic (green dots and smoothed green line, scale on the right) calculated in genomic windows. Analysis was performed on windows of 50 SNPs with a step size of 10. Shared variation is quantified in positive values when shared between P2 and P3 and as negative values when shared between P3 and P1. Gene content as the number of predicted genes per 1 MB window is in lavender with scale on the left.

- What is a window?
- What is introgression?
- What is reticulation?
- ABBA-BABA
- ILS vs reticulation?

