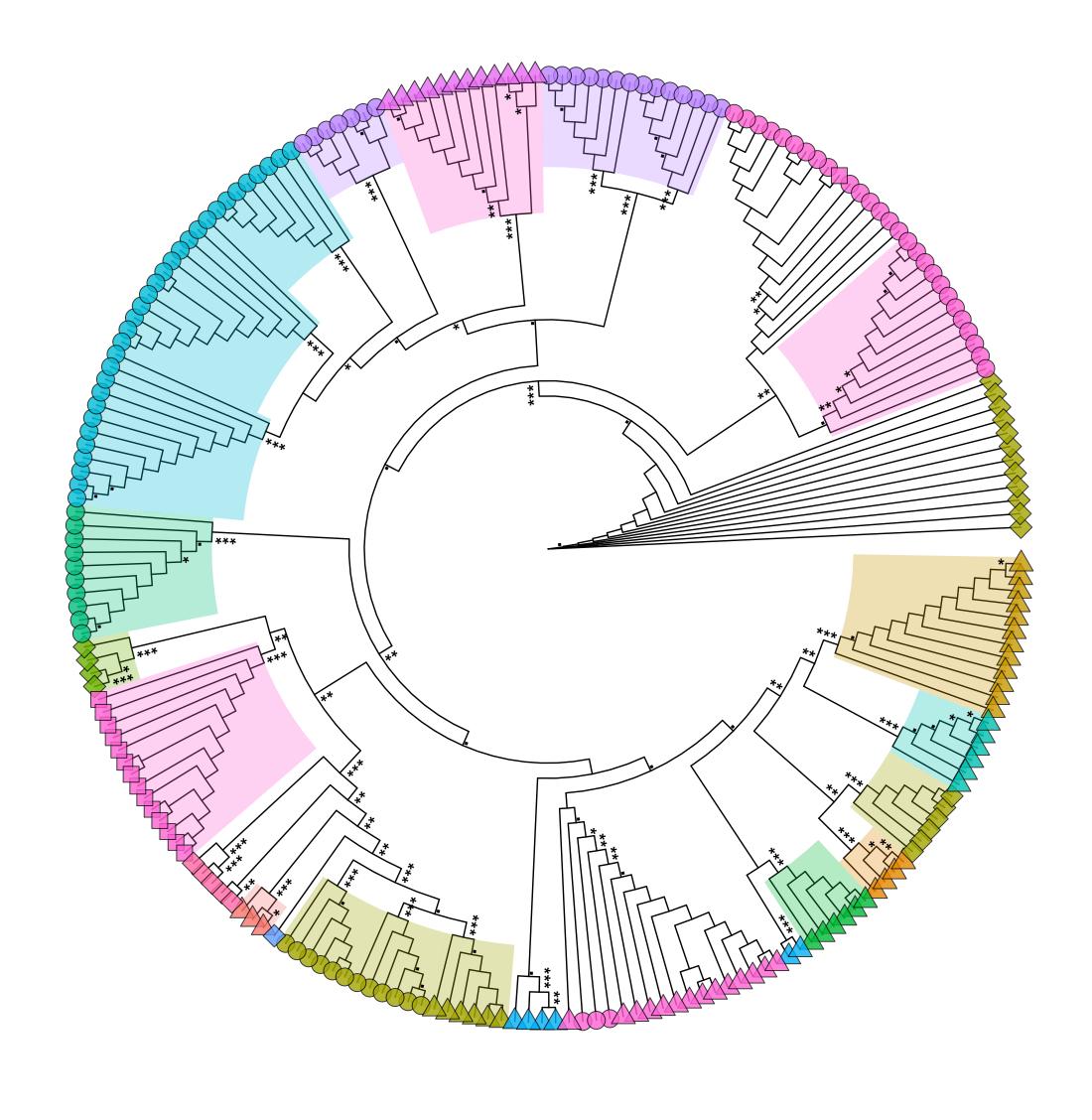
## Maximum likelihood phylotranscriptomic tree cladogram (7,688 SNPs)



## Study **Species** Vidal–Dupiol2014 Poquita–Du2019 acuta Zhou2019 Yuan2017 damicornis Zhou2017 Buitrago-Lopez2020 sp8 Chuang–Mitarai2020 Brener–Raffali2018 verrucosa Delgadillo–Nuno2018Li2020 ConnellyEAPSI Tang2018 Grupstrá2022 Wecker2018 Zhou2018