Using sequence capture datasets to clarify phylogenetic relationships in Lasiopetaleae (Malvaceae)

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The Genomics for Australian Plants (GAP) Phylogenomics Stage 2 involves the generation of sequence capture datasets for denser sampling of several Australian angiosperm genera. Bioinformatic tools for assembling and processing these datasets have been developed and made available to Australian researchers, including the pipeline HybPiper 2 and paralogy resolution methods from Yang & Smith. These fantastic tools enable substantial automation and accessibility, and as researchers apply them to more groups, there is a need to evaluate their effectiveness in diverse biological systems. Some questions that may be asked include: How do researchers critically evaluate output? How can these tools be best adjusted for variable diversity and gene duplication? Are there other complementary approaches for the same data? Here we show results of ongoing explorations of these and other techniques within the tribe Lasiopetaleae (Malvaceae). The tribe consists of eight genera, with generic boundaries particularly problematic between four of them (*Guichenotia*, *Lasiopetalum*, *Lysiosepalum*, and *Thomasia*). We sequenced 144 samples from the group using two bait sets: Angiosperms353 and OzBaits. Our preliminary results showed congruence between the two bait sets and better resolution of generic relationships, including a paraphyletic *Lasiopetalum*. We continue to evaluate methods to extract phylogenetic signal and handle discordance, and will present what we have found so far.