



## **Cost-effective target sequence capture through drastically miniaturised DNA libraries and automatisation – a head-to-head test.**

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Targeted enrichment of DNA libraries using target sequence capture is increasingly becoming an indispensable part of the molecular genetics toolkit, being used to recover genome-wide orthologous loci across highly divergent taxa and from difficult specimens. However, for many applications, this method remains prohibitively expensive, especially in a high-throughput context. One cost-effective solution may be to drastically scale down reactions, automate labour, and increase sample multiplexing, but tests are required to demonstrate no loss of data integrity. Here, we prepared libraries from 96 plant specimens spanning 15 families with both a newly-developed miniaturised workflow and a standard workflow, and compared target recovery post-enrichment with the myBaits Angiosperms353 kit. We found that while the amount of target data obtained from the miniaturised workflow was overall lower than the standard workflow, the phylogenetic tree generated was comparable in both topology and support to that generated from the standard workflow. This shows that adequate genome-wide genetic data suitable for phylogenetic analysis can be obtained from a wide variety of taxa and specimens using a miniaturised workflow, and at a fraction of the cost of alternative workflows. Thus, our high-throughput target sequence capture pipeline shows promise for future adoption by large-scale genomics initiatives.

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