



## Can we use DArT sequencing to identify our herbarium collections?

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The opportunities to extract better value out of herbarium collections are increasing with the improved DNA extraction success and genomic approaches increasing in affordability and efficiency. We present a collections-based workflow that outlines a comprehensive instructional toolkit for sampling herbarium specimens following an earlier protocol developed in the early sampling strategy stage by Genomics for Australia Plants (GAP). Our methodology provides a versatile module of solutions for effective controls over sampling, annotating and tracking data of herbarium specimens that are used for genomic study. Its design ensures a priority of care while at the same time improves access to the incredible biological research resource that herbarium collections provide for answering fundamental questions associated with identification, systematics and taxonomy, and evolutionary change through time. As a proof of concept we describe our pilot study using SNP-based genomic scans of 94 *Indigofera australis* Willd. herbarium collections.

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