

RADseq techniques can be applied to DNAs derived from plant museum specimens

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Plant genomic studies are beginning to routinely include DNAs extracted from plant museum (herbarium) specimens. However, many researchers remain reluctant to employ restriction site-associated DNA techniques (RADseq) with these DNAs, since highly-degraded herbarium DNAs could include relatively few intact fragments flanked by appropriate cut sites. Here we apply a basic double-digest restriction-site associated DNA Sequencing (ddRADseq) protocol to multiplexed samples from four genera (*Boecheera*, *Draba*, *Ilex*, and *Solidago*). Herbarium-derived DNAs comprised 60% of the sample set, spanning collection dates from 1883-2014. We demonstrate that RADseq is effective in generating large phylogenetically informative datasets from herbarium specimens, and the relationship between specimen age, DNA degradation, and locus recovery is presented. RADseq therefore represents a cost-effective genomics option for labs working with sample sets comprising multiple lineages and tissue types.