



## **Dealing with allopolyploidy in the genomic age: a pragmatic approach using amplicon sequencing of COS markers in Australasian *Lepidium*.**

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New Zealand is home to 16 endemic species of *Lepidium* (Brassicaceae) including two species considered to have become extinct since European colonisation, and one species shared with Australia (with c. 26 endemic species). Previous meiotic chromosome counts suggest at least some are high polyploids. A hybrid origin has been proposed for some of them, with African and American species implicated as parents. We generated amplicon sequence data for 15 Conserved Orthologous Sequence derived markers from a selection of New Zealand endemic species and species of African and American and Australian origin naturalised in New Zealand. These were analysed along with publicly available genomic data from other *Lepidium* species. Our results are consistent with earlier work in supporting two main groups of endemic New Zealand *Lepidium* corresponding with different dominant nrDNA sequences. Our data suggest these two groups differ in ploidy (octoploid or decaploid). The octoploid species combine four distinguishable subgenomes and the decaploid species are the products of allopolyploidisation between octoploid species and a diploid species closely related to, if not, *L. africanum*. Previously proposed links to American *Lepidium* are also supported with at least two New Zealand *Lepidium* subgenomes related to subgenomes present in American polyploid species.

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