

Genetic origins of macadamia cultivars: What we know so far

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Macadamia as a crop is almost wild. Modern cultivars are very few generations removed from undomesticated forebears: typically their great-grandparents were (and perhaps still are) wild trees in natural populations. Native stands exist in a narrow strip of eastern Australia's subtropical rainforest, fragmented and highly threatened by habitat clearing and degradation. Perhaps a few thousand mature specimens remain for each of the two main crop species, *M. integrifolia* and *M. tetraphylla*.

Most of macadamia's available genetic diversity is horticulturally untapped. Around the turn of the millennium, nuclear DNA marker research compared genetic diversity in a germplasm collection from wild populations with that among a large set of cultivars from Australia, Hawaii, and South Africa. The DNA markers were also used to confirm parentages and deduce wild origins of each cultivar. Key findings were strong intraspecific provenance structure across the several sampled geographic regions, varying degrees of genetic diversity within each region, most commercial cultivars being derived from the lowest-diversity region of *M. integrifolia*, and few to no cultivars appearing to have arisen from the region of highest intraspecific diversity of *M. integrifolia* – right where the large city of Brisbane now sits. Recent chloroplast sequence analyses have corroborated those conclusions. Both sources of evidence suggest there is a large reservoir of *M. integrifolia* diversity that is yet to be explored. The earlier research also calculated species compositions for wild trees and cultivars. While natural hybrid zones were characterized at regions of multiple species sympatry, hybrid cultivars, common especially in the Australian industry, appear to have derived from more recent crosses in cultivation. Contributions to the commercial nut production industry is almost non-existent from the other species within the genus, *M. ternifolia* and *M. jansonii*.

An exciting opportunity beckons to establish a baseline for all subsequent understanding and exploiting of macadamia's genetics. Whole-genome DNA profiling, by SNP arrays or resequencing, of all mature wild trees and cultivars would reveal the critical information: patterns of diversity and recombination as represented by each individual's parental haplotypes. Haplotype patterns among trees would reveal precisely how and where cultivar genomes arose, loci favored by historical selection, and geographical regions harboring unique alleles. Systematic investigations of the genetic contribution of each allele could then ensue. The sooner that this whole-crop genetic diversity is databased the better, before further valuable alleles are lost.