

Backyard macadamias in Brisbane as a reservoir of genetic diversity for breeding

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Introduction

Macadamia F. muell is an iconic Australian plant genus. It is the only international food crop domesticated from the Australian flora, and trees of *M. integrifolia* and *M. tetraphylla* produced highly valued kernel. The genus is endemic to the lowland rainforest of south-eastern Queensland and North-east New South Wales (Hardner et al 2009).

It is likely a tree planted by Walter Hill tree in the Brisbane Botanical gardens in 1858 (Figure 1) was the first domesticated macadamia. Macadamias were also planted throughout the backyards of sub-tropical Australia (Figure 2). The commercial potential of the plant was initially developed in Hawai'i from several small introductions of germplasm in the late 19th Century (Hardner 2015), possibly sourced from the Gold Coast Hinterland in Queensland (Hardner 2015). Hawai'i cultivars are estimated to produce around 70% of current world production of macadamia.

As only a few initial plants contributed to the development of macadamia in Hawai'i (Hardner 2015), it is likely the genetic diversity in the wild is greatly under-represented in current commercial cultivars and, there is great potential to produce elite cultivars by harnessing this diversity.



Figure 1. Existing Walter Hill tree in Brisbane botanical gardens. National Trust (<http://www.trusttrees.org.au/>)

Results

- 516 chloroplast genome SNPs were detected across the 79 individuals, 38% of SNPs were located in the coding regions, 38 SNPs were located in the *ycf1* gene
- There was a strong geographic trend to the distribution of variation among chloroplast genomes from remnant wild populations
- Expect for the cultivar H.791 and a sample from the Nutridge seed orchard (H.Nut14), the genomes of all Hawai'i samples (i.e. cultivars 246, 294, 333, 334, 425, 508, 660, 814 and Honokaa Special, 5 from Nutridge and 1 from Waipio Valley seedling orchards, 4 individuals believed to be remnants of original 19th century introductions) were identical to reference genome (REF)
- The reference genome (REF) was identical to samples from remnant populations at Mooloo (M08.Mo3, M08.M04) and Mt Bauple (M04.MB1), was clustered with other populations from the Gympie region (Figs 3 and 4), and not the Willowvale population where the Hawaiian introductions were believed to have been originally sampled.
- Samples from the Walter Hill tree (A.WH), a tree planted in the early 1880s at University of California Berkeley (C.UCB), and a backyard tree in Brisbane (A.CH) were not associated with any cluster of the wild populations.



Figure 2. Old macadamia in backyard of property at Yeronga, Queensland

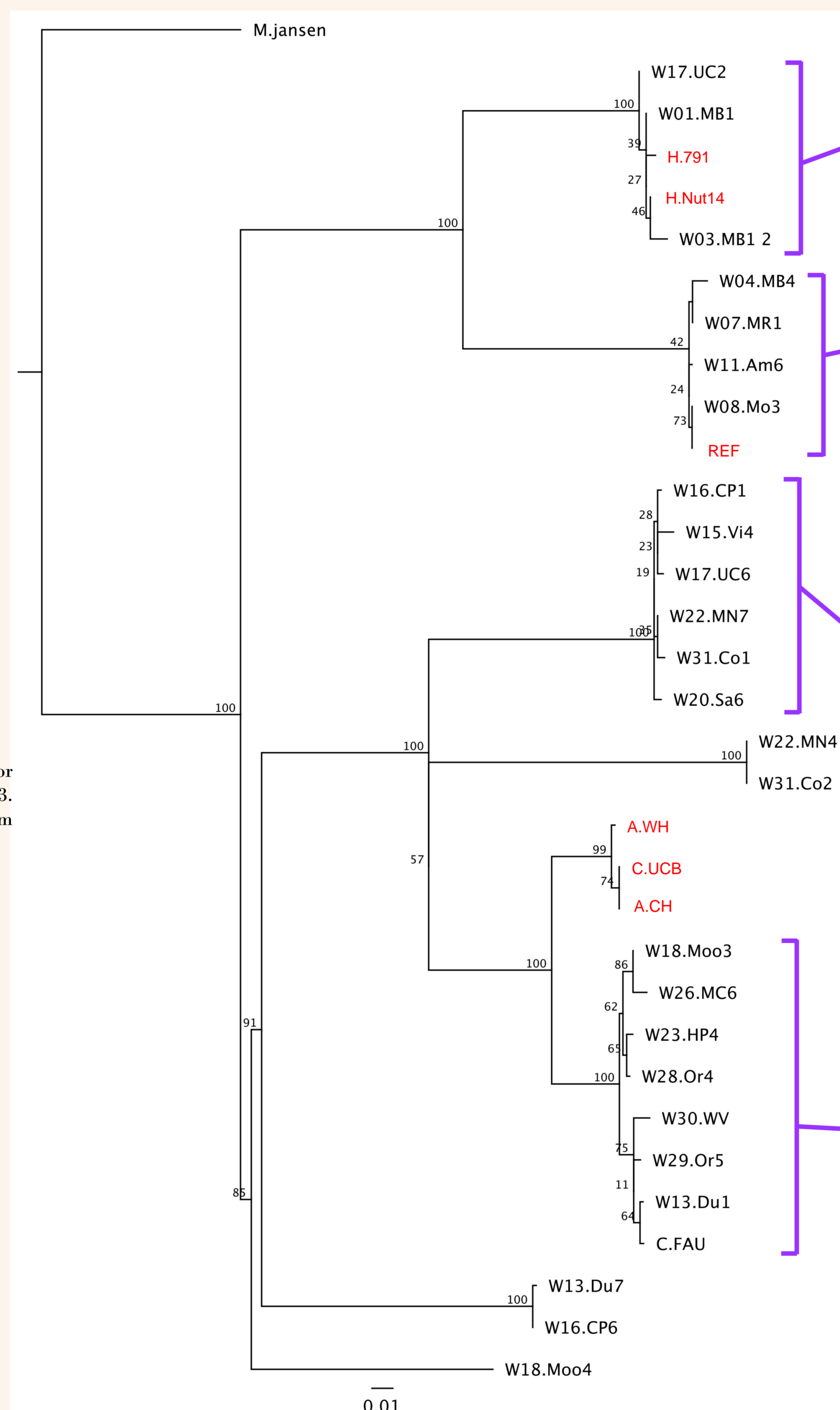


Figure 3. Phylogenetic tree based on chloroplast sequence variation of sub-sample of 25 individuals from 18 wild populations (Table 1), the Walter Hill tree (A.WH, Figure 1), a backyard tree in Yeronga Brisbane (A.CH, Figure 2), the Hawaiian cultivar H.791, a sample from a remnant Hawaiian seedling orchard (H.Nut14), a tree planted at the University of California Berkeley (C.UCB), an early Californian cultivar (C.FAU), and the reference genome (REF).

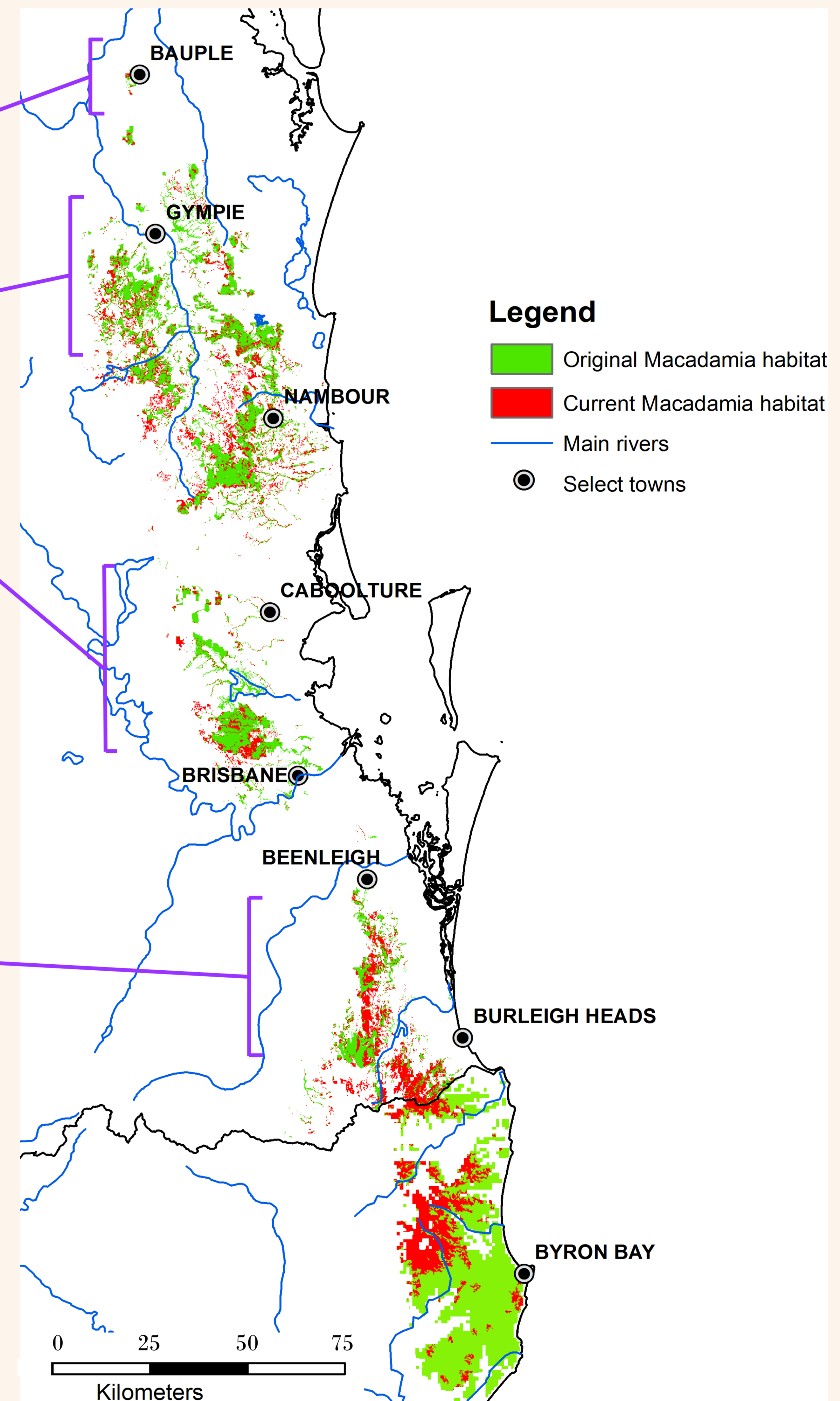


Figure 4. Predicted distribution of pre-colonisation and current remnant habitat suitable for wild populations of *M. integrifolia*, *M. tetraphylla* and *M. ternifolia*. Extracted from: Powell MN et al 2014

Method

DNA samples collected from:

- 50 individuals sampled from 31 wild populations across the range of *Macadamia integrifolia* (Figure 4, Table 3)
- Walter Hill Tree (Figure 1) and tree planted in south Brisbane backyard (Figure 2)
- Tree planted in the early 1880s at UC Berkeley, and early Californian variety Faulkner
- Hawai'i cultivars and selections, and remnants of Hawai'i seedling orchards from which original cultivars were selected and trees believed from original 19th Century introductions
- Macadamia janseni* used as out-group

Chloroplasts sequenced with Illumina Hi-Seq 2500

Illumina paired end reads mapped to reference sequence (Nock et al 2015) using SAPalinger

SNP calling undertaken using SAMTOOLS

Phylogenetic tree constructed using Genious

References

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Discussion

- Evidence of strong geographic pattern in *Macadamia* chloroplast sequence supports using chloroplast variation to identify likely origins of domesticated germplasm
- Strong evidence that cultivars selected in Hawai'i are derived from introductions of only a few individuals
- The Mooloo valley north of Gympie is the likely wild origin of the most of the germplasm domesticated in Hawai'i, not Willowvale on the Gold Coast hinterland, as previously thought
- The distinct clustering of the Australian and Californian domesticated germplasm suggests:
 - some genetic variation present prior to colonisation has been lost
 - effort should be made to conserve existing remnant wild populations
 - backyard trees may provide an addition genetic resource for breeding

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