Genomic tools for *Pongamia pinnata* enable comparisons of nuclear and organellar genomes, diversity assessments, and potentially point to historical seed movements.

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*Pongamia pinnata* (syn. *Millettia pinnata*) is an economically important sub-tropical arboreal legume producing a bean with many uses similar to those of soybean (e.g. oil and meal). Proprietary methods now also allow production of human food. Further, as a tree, pongamia provides additional ecological benefits such as carbon sequestration.

To explore the genomic biology of pongamia, we assembled a high-quality reference genome comprising ∼999.3 Mb across 11 chromosomes. Completeness of the genome assembly was assessed with a Fabales BUSCO dataset of 5,366 genes. Comparative mapping of the BUSCO dataset with three other species within the Millettioid clade (*Phaseolus vulgaris*, *Vigna radiata* and *Cajanus cajun*) revealed chromosomes with highly conserved structures, and other chromosomes with various rearrangements.

Organellar genome sequence as well as transcriptomic data of *P. pinnata*, *Lotus japonicus* and P*. vulgaris* were also compared (Kazakoff et al., 2012) showing extremely high sequence and structural homology (range 1.6 to 9.0%).

To compare relationships among diverse seed sources, we genotyped 199 accessions from Asia, Australia, and the United States using 1,089 single-nucleotide polymorphisms. Principal component analysis revealed several related clusters amongst Australian and U.S. collections, possibly indicative of historical seed movements.

As shown here, genomic resources from nuclear and organellar genomes can facilitate a better understanding of Millettioid evolution, while likewise illustrating genetic relationships among pongamia seed sources to facilitate germplasm improvements.

*Reference:*

*[1] Kazakoff et al., 2012, PLoS ONE:e51687, 7(12)* [*https://doi.org/10.1371/journal.pone.0051687*](https://doi.org/10.1371/journal.pone.0051687)