**A high-quality genome assembly of an Australian chickpea variety**

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We have generated a genome assembly for an inbred line (i4) of the Australian desi chickpea variety, PBA HatTrick. PBA HatTrick (Jimbour/ICC14903, released 2009) is adapted to Australian conditions. It has been used to generate bi-parental and mutant populations for research, and as a parent for newer varietal releases.

The assembly was developed using PacBio HiFi sequencing data for contig generation, and alignment to Bionano consensus maps. Employing the hifiasm algorithm [1], we generated two assemblies: the first by using all HiFi reads, and the second from chloroplast-free HiFi reads. The latter was aligned to Bionano maps, and the former was used to close gaps between scaffolds. Scaffolds were anchored to two genetic maps and assigned to chromosomes by sequence alignment to CDC Frontier genome assembly v3 [[CicerMine: Data Categories (legumeinfo.org)](https://mines.legumeinfo.org/cicermine/dataCategories.do)].

For six chromosomes we created pseudomolecules that contain only small gaps (regions with N bases). The other two chromosomes (3 and 5) remain fragmented as ordered scaffolds, due to the presence of large repetitive regions. Two scaffolds, containing mainly repetive DNA, could not be allocated to chromosomes. The total estimated genome size of 710.44 Mb is close to what has been published for CDC Frontier (738.09 Mb) [2].

Our PBA HatTrick assembly, which is a significant improvement over earlier genome assemblies, is a valuable new resource for chickpea research.  It is available for download or for BLASTing with sequences of interest, via the webpage [https://hatchiblap.adelaide.edu.au](https://hatchiblap.adelaide.edu.au/).

***References:***

 *[1] Cheng H. et al, ‘Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm’,* Nat Methods, *vol.* ***18****, 2021, p. 170.*

*[2] Varshney R. et al, ‘Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement’ Nat Biotechnol, vol. 31, 2013, p. 240.*