

## Cicer inter-specific barriers (and gates)

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The primary gene pool of chickpea (*Cicer arietinum* L., Ca), including closely related wild species, was once a single interbreeding population. About 95-127 thousand years ago [1], a series of barriers to genetic exchange arose resulting in the partial isolation of two populations and subsequent speciation into *C. reticulatum* Ladiz. (Cr, the wild chickpea ancestor) and *C. echinospermum* Davis (Ce) [2]. Ca\*Ce and Cr\*Ce hybrids are partially sterile [2]. Evidence indicates chromosomal rearrangements are primary contributors to hybrids' fertility [2]. A recent report hypothesised about an incompatibility locus underlying pollen viability in Ca\*Ce hybrids [3]. Through cross-pollination, only some of the genetic information is transferable from Ce to chickpea. Considering the Ce germplasm bears several traits of interest and benefit to breeders, we aim to identify and map transferrable loci in wild accessions.

The extended collection of wild material by Cook and colleagues [1] provides new opportunities. We generated 46 hybrids for 14 combinations between cultivars PBA Hattrick or PBA Slasher and representative Ce accessions from six different sites in Turkey described in [1]. Another 72 crosses, 18 Ca\*Cr combinations, were done for comparison and research into complex traits. Hybrids were assessed for pollen viability and frequency of seed formation in reproductive nodes. F2 populations were evaluated for plant fertility and genotyped to identify chromosomal rearrangements in linkage maps. The loci will be further evaluated using *in-situ* hybridisation.

The success rate in crossing cultivars to wild germplasm was higher than reported so far, 0.07-0.92 and 0.22-0.50 for Ca\*Cr and Ca\*Ce, respectively. As expected, Ca\*Ce hybrids had lower percentage of fully developed pollen grains with differences depending on the Ce accession (range 0.00-33.98%) compared to Ca\*Cr ones (99.00- 97.00%). Plant fertility was also genotype specific for Ca\*Ce hybrids (<0.001-0.154). Our observations point to intra-specific karyotype diversity; the existence of incompatibility loci is yet to be evaluated. The identification and validation of loci associated with the chromosomal rearrangement(s), (*i.e.* difficult to introduce into cultivars) are underway. All F2 populations are being advanced to F5:6 recombinant inbred lines (RILs); seeds will be released through the AGG as soon as ready and genotypes will be available upon request.

This project is co-funded by GRDC and UWA (UWA00175-var2). The project's expected outputs are (i) characterisation of a diverse range of Ce germplasm and gene introgression into locally adapted cultivated backgrounds, (ii) determination of Ce's genetic potential in conventional chickpea breeding and production of a catalogue of transferable (gates) and non-transferable loci (barriers), (iii) genotyped RILs and near isogenic line (NIL) to determine the genetic basis of traits affecting yield. The significance of this project is broader; it contributes to our understanding of the crop's evolution and our ability to expand its adaptation to a range of changing climates.

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1-von Wettberg et al., 2018 Nature Communications

2- Ladizinsky & Adler, 1976 Euphytica

3- Kahraman et al., 2017 Crop Science