**A platform for the rapid gene introgression of wild alleles into chickpea**

Maria Pazos Navarro[1]
Simone Wells[1], Judith Lichtenzveig[1] and Janine Croser[1]

[1] The University of Western Australia

Chickpea (*Cicer arietinum* L.) would benefit from access to a wider genetic variability than currently available within the species. The expansion of genebank entries of the wild chickpea progenitor, *Cicer reticulatum* L., offers new opportunities to identify and introgress traits of value into the domestic species.

To accelerate introgression of genes from wild *Cicer* relatives to domestic, we report the development of a platform for rapid gene introgression (RGI) between divergent taxa with distinctive phenology: *e.g.* chickpea flowers about two months earlier than *C. reticulatum* during the cropping season. The RGI platform (1) shortens the gap in time to flowering under controlled-environment conditions to allow interspecific crosses, (2) permits year-round crossing, (3) yields high numbers of F2 seed through cloning of F1 hybrid material and (4) utilises the chickpea accelerated single seed descent (aSSD) process to rapidly return interspecific progeny to homozygosity.

To shorten the time-to-flowering gap, we evaluated 20 *C. reticulatum* accessions and four chickpea cultivars. Plants were grown in two controlled-environments (CEs) at 24/20ºC day/night with 20 h photoperiod provided by AP67 LED arrays (Valoya, Finland). Growth under CEs compressed time to flower across all wild accessions and cultivars by 40-80% when compared to in-season growth. The flowering gap was reduced to one week i.e. PBA HatTrick 23 ± 1 days after imbibition (DAI) and *C. reticulatum* CudiB_022C 31.5±0.8 DAI. Artificial hybridisations between PBA HatTrick x *C. reticulatum* CudiB_022C were performed under CE. Putative F1 seeds were harvested at maturity. Confirmed F1's were grown in the glasshouse under natural light and cloned up to 10 x per hybrid to produce > 1000 F2 seeds.

To refine the growth conditions for SSD, we grew two sets of 110-F2 individuals in two environments. Environment 1 (E1) had a 20 h photoperiod supplied by natural light with supplementation with AP67 LED arrays (Valoya, Finland) and time to flowering of 22-47 d. Environment 2 = 20 h supplied by AP67 LED arrays and time to flower of 25-45 d. At 28 days after flowering (DAF) seed was harvested, nicked and imbibed prior to germination to the following generation. As time to flowering was faster in E1 ($P>0.01$), it was adopted to repeat this process until F6.

Using the RGI platform, the breath of genetic variation is maintained. This is evident from the range of time to flower at F6, 24-47 days (median= 25 days) and demonstrates late genotypes are not selected against. Generation turnover time ranged from 54-77 days (DAF + 28 d until pod maturity), with 89.4% of the population under 60 days from seed to seed.

We validated the effectiveness of the RGI platform by developing a F6 RIL population derived from a domestic x wild genotype in less than 18 months from crossing to F6. The platform represents a successful mechanism to rapidly harness traits from wild germplasm and has potential to be adapted to wild relatives from other species including lentil.

**Funding:** GRDC CUR24.

**Acknowledgements:** We thank Ms S. Tschirren for her assistance in performing crosses.