Chickpea’s large domestication bottleneck as a constraint to agricultural innovation

Wild species → Modern elite varieties

26 representative wilds

29 modern elite varieties

6.7M variants

0.172 M variants

Wild Relatives

Domestication

Regional diversification

Modern breeding

~95% loss of variation
Evaluation Strategies

**In situ association genetics for candidate gene nomination**

Association genetics with phenology-normalized NAMs

Advanced backcross introgression lines

Breeding

Ecology and population genomics

Phenotyping

Trait discovery

Genomics-driven Introgression
Reverse introgression
26 wilds x 5 elites = 100 pops

Normalize for cultivated phenology and growth habit

Quasi-domesticated wild RILs

Forward introgression
Segmental introgression of wild genome intervals in

Breeding-ready wild introgression lines

5,000 normalized NAM-RILS

20 diverse wilds

5 adapted elites
Developing genetic resources: pre-breeding, trait and gene discovery

270 accessions in the multi-lateral system.

469 additional accessions under curation at partner institutions in Turkey

>26 wild accessions x 5 elite cultivars in pre-breeding pipeline (NAMs and ABIs).

~15,000 Segregating F3 families
Mobilize the genetic capacity of wild relatives

~15,000 unique lineages entering into field trials and breeding

- Engage international networks of breeders.
- Combine developing world needs with developed world capacities.
- Massively leverage new funding sources.
Traits

Genes

Crops in farmers' fields
ICC96029 x wilds as system for phenotype-genotype exploration
Screening for heat tolerance at ICRISAT