Phenotyping reference set of chickpea (Cicer arietinum L.) for agronomic traits including resistance to legume pod borer (Helicoverpa armigera)\(^1\)

About the chickpea crop

- Second in area and third in production among pulses, grown over 45 countries; annual production 9.3 mt from 11.7 mha (http://apps.fao.org)
- Originated in an area of present day southeastern Turkey and adjoining Syria, around the upper regions of the Tigris and Euphrates rivers
- A cool season highly self-pollinated crop with \(2n=16\) and genome size 732Mb
- Grains, the primary source of dietary protein for rural people, are rich in carbohydrate, protein, minerals and vitamins
- Several biotic and abiotic stresses, in addition to narrow genetic base and lack of adapted varieties, contribute to variation in yield across regions
- ICRISAT genebank contains 19,916 cultivated accessions from 60 countries and 224 wild Cicer accessions from 18 species.

Developing genotype-based reference set

A composite collection consisting of 3000 accessions developed, molecularly profiled using 48 SSRs, and a reference set of 300 accessions representing 78% (1315 of 1683 alleles) allelic diversity of the composite collection extracted (http://www.generationcp.org). Both biological and geographical diversity adequately represented in this reference set.

Identifying trait-specific germplasm

Reference set with five control cultivars (Annigeri, G130, ICCV10, L550 and KAK 2) evaluated for agronomic, quality traits and resistance to pod borer.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Accession Identity</th>
<th>Y:15,000 and seed size</th>
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</thead>
<tbody>
<tr>
<td>Yield and seed size</td>
<td>ICC 1880, 2263, 8802, 13892, 15868 (3.1 to 3.7 t ha(^{-1}))</td>
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<tr>
<td>Eartiness</td>
<td>ICC 8155, 12328, 16654, IG 6905 (2.4 to 3.5 t ha(^{-1}) and 39 to 44 g 100-seed weight)</td>
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<tr>
<td>High Protein</td>
<td>ICC 12654, 11903, 9418, IG 69974 (26% to 27%)</td>
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<tr>
<td>Pod borer tolerance</td>
<td>ICC 3218, 15294; IG# 6067, 6905, 73074</td>
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1. 2.0 to 2.5 score on 1 to 9 scale (G 130, 5); larval survival 35% to 65% (Annigeri, 76%), larval weight 0.61-2.04 mg larva\(^{-1}\) (G 130, 3.85)

Association mapping for allelic variation with beneficial traits

- Genotyping with additional 100 SSRs to buildup 150 SSR loci data in reference set
- Using fluorescent-based multiplex genotyping system - multiplexes each with four SSRs and high throughput platform (ABI3130)
- Phenotyping reference set for agronomic traits and stress tolerance (Helicoverpa, drought and salinity)