Background
Grain legumes such as pigeonpea (Cajanus cajan (L.) Mill sp.) and chickpea (Cicer arietinum L.) are the primary sources of dietary protein especially for vegetarian human population worldwide. Genetic enhancement in these crops is not adequate due to their narrow genetic base. Further, the production and productivity of these crops is adversely affected by different biotic and abiotic stresses and high levels of resistance/tolerance for these stresses is not available in the cultivated genepool. This necessitates the utilization of new and diverse source of variations to broaden the genetic base of crop cultivars and to improve the genetic gain of these crops.

Chickpea
- Promising ILs having early-duration (23 ILs), medium-duration (19 ILs); early-duration + bold-seeded (15 ILs), medium-duration + bold-seeded (15 ILs); and early duration + erect + high yield (15 ILs) identified.
- Screening for ascochyta blight & botrytis gray mold resistance across hot-spot locations in progress.

Compressing pre-breeding timeframe
- Use of vernalization and extended-photoperiod treatments for inducing early flowering (20 - 85% reduction in number of days to first flowering) in cultivated and wild Cicer species.
- Use of immature seed germination for rapid generation turn-over in pigeonpea and chickpea pre-breeding.

Crop Wild Relatives (CWRs) as the sources of new variability
Crop Wild Relatives (CWRs) possess many useful genes/alleles including high levels of resistance/tolerance to multiple stresses and hold a great potential for genetic improvement of crop cultivars.

Accessing novel genes/alleles from CWRs for grain legume improvement

Cross | Populations | Traits to be addressed
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**Pigeonpea**
Complex cross | C. cajan × C. acutifolius × C. scarabaeoides | 2 populations (~400-500 ILs per population) Pod borer
Simple cross | C. cajan × C. acutifolius / C. scarabaeoides / C. reticulatum / C. scarabaeoides | 6 populations (~100-1100 ILs per population) Phytophthora blight, sterility mosaic disease + wilt, pod borer, yield-related traits
C. cajan × C. piliocarpus | 138 ILs Phytophthora blight, salinity, yield-related traits

**Chickpea**
Complex cross | C. arietinum × C. reticulatum × C. echinospermum | 2 populations (~1500-2000 ILs per population) Ascochyta blight, botrytis grey mold, heat, drought
Simple cross | C. arietinum × C. reticulatum / C. echinospermum | AB-QTL mapping populations Botrytis grey mold, dry root rot

Development and utilization of trait-specific genepools for crop improvement

**Pigeonpea**
- Promising ILs having mid-early duration + high yield (25 ILs), bold-seeded (>15 g 100-seed weight) (22 ILs), medium-duration + high yield (25 ILs); early-duration + determinate dwarf plant type (17 ILs); early-duration + indeterminate (10 ILs); salinity tolerant (23 ILs); SMD + wilt resistant (323 ILs) identified.
- Screening for Phytophthora blight and pod borer tolerance/resistance in progress.
- Promising ILs being tested for restorer ability in hybrid pigeonpea breeding programs in India.

**Chickpea**
- Promising ILs having early-duration (23 ILs), medium-duration (19 ILs); early-duration + bold-seeded (15 ILs), medium-duration + bold-seeded (15 ILs); and early duration + erect + high yield (15 ILs) identified.
- Screening for ascochyta blight & botrytis gray mold resistance across hot-spot locations in progress.

Sharing pre-breeding populations
- High-yielding (12 ILs), salinity tolerant (23 ILs) and disease-resistant (20 ILs) ILs shared with NARS in India and Myanmar; bold-seeded (22 ILs) ILs shared with breeders in Kenya.

Developing and utilizing pre-breeding methods

- C. arietinum × C. yamashitae, C. cajan × C. pinnatifidum, C. yamashitae C. arietinum

Over 5000 Prebreeding lines shared across globe