



# Mining Allelic Diversity Associated with Drought and Salinity Tolerance in the Reference Subset of Chickpea Germplasm Collections



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Chickpea is the 4<sup>th</sup> largest grain legume crop, predominantly grown in Asia. Drought, salinity, and variations in temperature are the major abiotic constraints. CGIAR genebanks maintain a large collection of chickpea germplasm. For enhancing the utilization of chickpea germplasm in breeding and genomics applications, a global composite collection (Upadhyaya et al. 2006) and reference subset have been developed (<http://www.generationcp.org>).

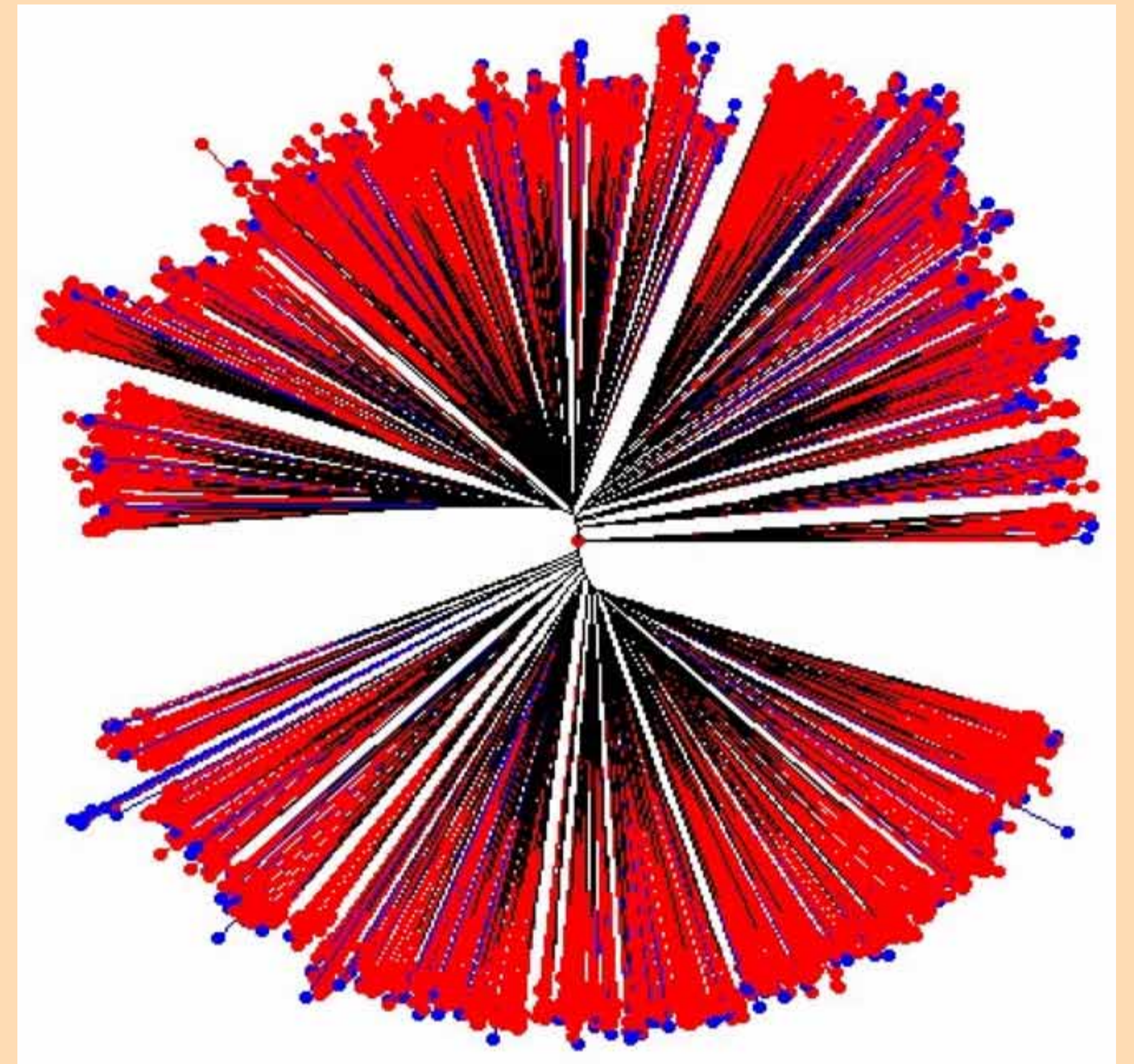
## A Historical Perspective of Composite Collection and Reference Subset in Chickpea

### Genetic structure of composite collection

Allelic richness	1791 alleles (994 rare and 797 common) Range 14-67; Average 36 alleles/locus
Marker polymorphism (PIC) and gene diversity (GD)	PIC: 0.468 to 0.974 GD: 0.534 to 0.975
Seed type-specific alleles	Kabuli 117, desi 310, pea-shaped 5
Region-specific alleles	Mediterranean (M) 122 West Asia (WA) 121 South and Southeast Asia (SSEA) 123
Common alleles	Kabuli and desi 458 SSEA and WA 77 M and SSEA 33 M and WA 39
Wild <i>Cicer</i> specific alleles	74

### Genetic structure of reference subset (300 accessions)

Allelic richness	78% (1403 alleles) of the 1791 alleles of the composite collection
Allelic range	8 to 56 alleles, 28 alleles per locus
Marker polymorphism (PIC) and gene diversity (GD)	PIC: 0.488 to 0.964; GD: 0.540 to 0.965



• 300 accessions representing reference set

• Remaining 2615 accessions of the composite collection (2915 accessions)

Figure 1. Tree diagram of the chickpea reference subset showing allelic diversity in composite collection

## Phenotypic Screens for Drought Tolerance

- A PVC cylinder (18 cm diameter and 120 cm tall) technique developed to screen for drought-avoidance root traits (Kashiwagi et al. 2006)



Figure 2. PVC-based screening technique for drought tolerance in chickpea

## Phenotypic Screens for Salinity Tolerance

- A pot (27 cm diameter) screening technique for salt tolerance (80mM to 100mM NaCl) developed (Vadez et al. 2007)

### Future Perspective to the Utilization of Reference Subset in Chickpea Genomics and Breeding

- Saturate with more number of SSRs and DArT markers
- Evaluate for drought and salinity tolerance
- Evaluate for agronomic and seed quality traits
- Detect allelic variation associated with drought and salinity using association genetics
- Identify accessions with contrasting response for diverse uses

## References

- Kashiwagi J, Krishnamurthy L, Crouch JH and Serraj R. 2006. Variability for root characteristics and their contributions to seed yield in chickpea (*Cicer arietinum* L.) under terminal drought stress. *Field Crops Res.* 95:171-181.
- Kashiwagi J, Krishnamurthy L, Upadhyaya HD, Krishna H, Chandra S, Vadez V and Serraj R. 2005. Genetic variability of drought-avoidance root traits in the mini core germplasm collection of chickpea (*Cicer arietinum* L.). *Euphytica* 146:213-222.
- Upadhyaya HD, Furman BJ, Dwivedi SL, Udupa SM, Gowda CLL, Baum M, Crouch JH, Buhariwalla HK and Singh S. 2006. Development of a composite collection for mining germplasm possessing allelic variation for beneficial traits in chickpea. *Plant Genet. Resour.* 4:13-19.
- Vadez V, Krishnamurthy L, Serraj R, Gaur PM, Upadhyaya HD, Hoisington DA, Varshney RK, Turner NC and Siddique KHM. 2007. Large variation in salinity tolerance in chickpea is explained by differences in sensitivity at the reproductive stage. *Field Crops Res.* (in print).

## Assessing Genetic Variation in Chickpea Mini Core for Drought and Salinity Tolerance

### Variability for drought and salinity tolerance traits

#### Drought (Kashiwagi et al. 2005)

- Largest variation for root length density (RLD) and plant dry weight to RLD (PDW/RLD) ratio
- Several accessions with high RLD and PDW/RLD ratio identified
- ICC 8261 with largest RLD and deepest root while ICC 4958 with prolific and deep roots
- Landraces from central Asia showed relatively larger RLD

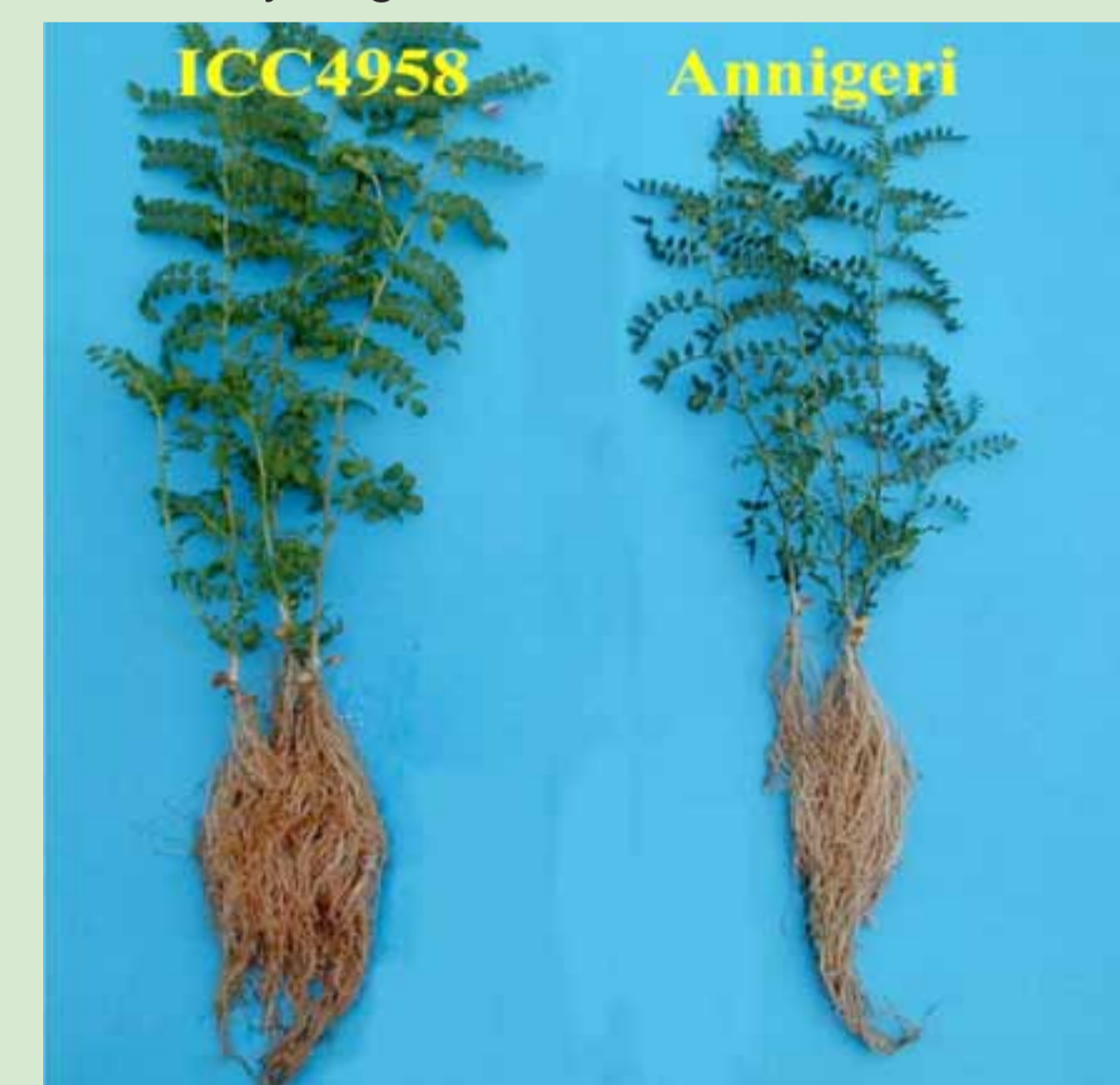


Figure 3. Genotypic variation for root mass in chickpea germplasm

#### Salinity (Vadez et al. 2007)

- Six-fold variation for seed yield under salinity (80mM NaCl)
- Desi's had higher salinity tolerance than Kabuli's
- Number of filled pods the major salinity tolerance trait
- Tolerance not related to the shoot Na<sup>+</sup> or K<sup>+</sup> concentrations
- Several tolerant accessions identified

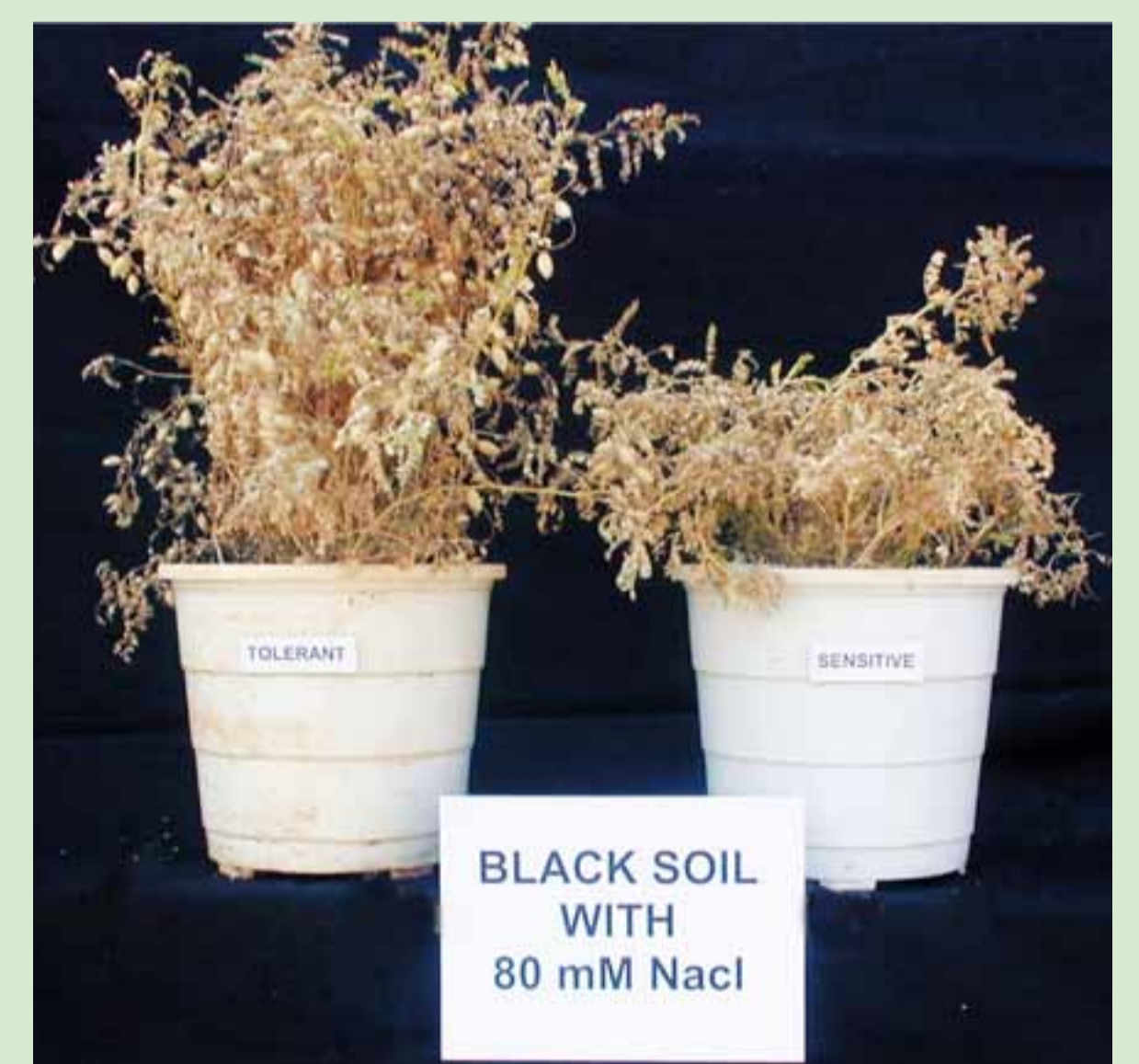


Figure 4. Genotypic variation for salinity tolerance in chickpea germplasm