Molecular Markers for Allele Mining

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International Plant Genetic Resources Institute, Generation Challenge Programme

IPGRI is
a Future Harvest Centre
supported by the
Consultative Group on
International Agricultural
Research (CGIAR)

The International Plant Genetic Resources Institute (IPGRI) is an autonomous international scientific organization, supported by the Consultative Group on International Agricultural Research (CGIAR). IPGRI's mandate is to advance the conservation and use of genetic diversity for the well-being of present and future generations. IPGRI's headquarters is based in Maccarese, near Rome, Italy, with offices in another 19 countries worldwide. The Institute operates through three programmes: (1) the Plant Genetic Resources Programme, (2) the CGIAR Genetic Resources Support Programme and (3) the International Network for the Improvement of Banana and Plantain (INIBAP).

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The Generation Challenge Programme (GCP) is a research and capacity building network that uses plant genetic diversity, advanced genomic science, and comparative biology to develop tools and technologies that enable plant breeders in the developing world to produce better crop varieties for resource-poor farmers.

The GCP is one of four Challenge Programmes established by the CGIAR to make high impacts in the short term through thematic approaches involving a multitude of research, development, health, and delivery organizations.

The Generation Challenge Programme brings together three sets of partners—the centres of the Consultative Group on International Agricultural Research (CGIAR), advanced research institutes (ARIs), and national agricultural research systems (NARS) in developing countries—to deliver the fruits of the Genomics Revolution to resource-poor farmers.

The Generation Challenge Programme has five subprogrammes that span the spectrum of research in germplasm, genomics, bioinformatics, and molecular breeding for agricultural development:

Genetic Diversity of Global Genetic Resources
Comparative Genomics for Gene Discovery
Trait Capture for Crop Improvement
Genetic Resources, Genomic, and Crop Information Systems
Capacity Building and Enabling Delivery

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Mining the chickpea composite collection for allelic variation

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Chickpea, *Cicer arietinum* L., is believed to have originated in south-east Turkey. However, at present, the major chickpea-growing countries are India, Pakistan, Iran, Turkey, Australia, Ethiopia, and Mexico. Chickpea is a leguminous food crop, self-pollinating, and diploid. Its gene pool consists of 43 species: one annual cultivated (i.e. chickpea), eight annual wild, and 34 perennial wild species. Two types of chickpea are known: desi types with coloured flowers, and angular-shaped and dark-coloured seeds, primarily grown in South Asia and Africa; and kabuli types with white flowers, owl's head-shaped and beige-coloured seeds, and grown mostly in Mediterranean countries. To study the allelic richness and diversity associated with beneficial traits, a composite set of 3000 chickpea germplasm accessions was constituted. This set included the chickpea core collection, old and new cultivars and trait-specific germplasm accessions from ICRISAT and accessions representing the ICARDA collection.

Some progress on genotyping chickpea accessions has already been achieved. In 2004, a set of 288 chickpea accessions that included 211 minicore subset accessions (75% desi type), 57 accessions of kabuli type, and 20 accessions of wild *Cicer* species were genotyped, using 35 SSR markers at ICRISAT and 15 at ICARDA. Preliminary analysis revealed a broad allelic diversity in this set, detecting 873 alleles, with an average of 25 alleles per locus.

A smaller number of alleles (averaging 11 alleles) was detected for dinucleotide motifs than for trinucleotide motifs (averaging 27 alleles). Similarly, gene diversity was lower for the dinucleotide motif (average 0.723) than for the trinucleotide motif (0.898). The mean gene diversity of all the SSR markers was 0.873. The dendrogram constructed as per shared allele distance, using the unweighted pair-group mean average (UPGMA) method, indicated two main groups: one consisting mainly of accessions from the Indian subcontinent, and the other from the Mediterranean Region, Middle East, and Ethiopia. The wild species (*C. reticulatum* Ladiz. and *C. echinospermum* P. H. Davis) were split into two groups, flanking two ends of the group of chickpea accessions.

Discriminant function analysis (DFA) was used to determine the extent to which the genotypic data supported the 28 clusters from which the chickpea minicore was selected based on phenotypic data. For DFA, 40 SSR markers data on 210 minicore accessions were used. Overall, most individuals were assigned to the original phenotypic clusters. Only 27% of the individuals were re-assigned into new clusters according to data from markers, identified mainly within clusters 4, 6, and 7 of the minicore.