

## **Germplasm**

### **A validated chickpea germplasm reference collection**

The Chickpea Reference Set is composed of a core set of 300 accessions representing the genetic diversity of ICRISAT's genebank collection.

<http://www.icrisat.org/chickpea-genebank-reference-set.htm>

### **A validated groundnut germplasm reference collection**

The reference set is composed of a core set of 300 accessions representing the genetic diversity of ICRISAT's genebank collection.

<http://www.icrisat.org/crop-groundnut-genebank-Referenceset.htm>

### **Sources of resistance to groundnut Rosette virus**

From 300 genotypes screened from the Generation Challenge Programme (GCP) reference collection, four sources of resistance to Groundnut Rosette Virus were identified.

### **Sources of resistance to groundnut Early Leaf Spot**

From 300 genotypes screened from the GCP reference collection, six sources of resistance to Early Leaf Spot were identified.

### **Sources of resistance to groundnut rust**

From 300 genotypes screened from the GCP reference collection, five sources of resistance to Groundnut Rust were identified

### **Sources of drought tolerance in groundnut**

Highly contrasting drought-tolerant germplasm identified from 300 genotypes screened for the GCP reference collection

### **A pigeonpea germplasm reference collection**

This reference set is composed of a core set of 298 accessions representing the genetic diversity of ICRISAT's entire genebank collection.

### **Finger millet germplasm reference set**

This is a collection of 300 accessions the genetic composition of which is representative of the genetic diversity ICRISAT's composite genebank collection.

<http://www.icrisat.org/gene-bank-home.htm>

### **Validated foxtail millet germplasm reference set**

The foxtail millet reference set is a collection of 203 accessions whose genetic composition represents the diversity ICRISAT's genebank collection.

<http://www.icrisat.org/gene-bank-home.htm>

### **A validated germplasm reference set for pearl millet**

The pearl millet reference set is a collection of 300 accessions whose genetic composition represents the diversity ICRISAT's genebank collection.

<http://www.icrisat.org/gene-bank-home.htm>

### **A set of domestic x wild groundnut chromosomal segment substitution lines (CSSL)**

This comprises about 80 CSSLs developed from crosses with the domestic variety Fleur 11 amphidiploid (A. ipaenesis x A. duranensis).

<http://www.genesys-pgr.org/>

#### **For details, contact**

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### **Recombinant inbred line (RIL) sets for pearl millet**

This comprises 14 recombinant inbred line sets derived from pearl millet biparental crosses: F<sub>7</sub> seed for eight RIL populations, F<sub>6</sub> seed for two RIL populations, F<sub>5</sub> seed for three RIL populations and F<sub>4</sub> seed for a single RIL population.

#### **For details, contact**

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### **MAGIC lines for trait mapping**

A total of 1200 MAGIC lines were developed by using eight desi chickpea elite lines/cultivars (ICC 4958, ICCV 10, JAKI 9218, JG 11, JG 130, JG 16, ICCV 97105 and ICCV 00108) from Ethiopia, Kenya and India.

#### **For details, contact**

Dr Pooran Gaur  
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### **Root QTL introgressed drought tolerant chickpea breeding lines**

A genomic region from Linkage Group 4 that affects root traits and several other drought tolerance traits was introgressed into three well-adapted cultivars (JG 11 and KAK 2 from India and Chefe from Ethiopia) using 3 cycles of marker-assisted backcrossing (both foreground and background selection). The genomic region from ICC 4958 was introgressed in JG 11 and from ICC 8261 in KAK 2 and Chefe.

#### **For details, contact**

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### **Sorghum breeding lines and landraces with AltSB gene**

This comprises 17 lines with AltSB, not all of them confirmed in field condition, adapted to southern Mali, Burkina.

#### **For details, contact**

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### **Random Mating Sorghum Population (ms3) with segregation for AltSB and PSTOL1 for use in Africa**

This comprises 11 West African breeding lines and landraces crossed with a diversified guinea population source of male sterility with two random mating.

#### **For details, contact**

Dr Eva Weltzien  
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### **Drought tolerant chickpea breeding lines**

Promising drought tolerant chickpea breeding lines selected based on the yield performance under terminal moisture stress conditions.

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**Genomic resources****A validated Sorghum germplasm reference collection**

The reference set is composed of a core set of 384 accessions representing the genetic diversity of a composite set of 3384 accessions germplasm from the ICRISAT genebank collection genotyped with 48 SSR markers.

<http://www.icrisat.org/crop-sorghum-genebank-reference.htm>

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**A microsatellite kit for the GCP chickpea reference germplasm set**

This is a reference kit of 35 SSRs, with sequence list and protocol, germplasm checks, and allele sizes of microsats for those checks.

<http://www.icrisat.org/bt-genomics-chickpea.htm>

**A SNP dataset for chickpea**

This comprises a set of 2,005 SNPs validated and optimized by KASPar assays.

**SSR markers for chickpea**

A total of 1655 SSR markers were developed from enriched libraries and BAC-end sequences.

**A reference genetic map for chickpea**

A comprehensive genetic map comprising 1,291 marker loci including SSRs, DArTs and SNPs on eight linkage groups (LGs) spanning a total of 845.56 cM distance was developed. The number of markers per linkage group ranged from 68 (LG 8) to 218 (LG 3) with an average inter-marker distance of 0.65 cM.

### **Drought and salinity responsive ESTs in the chickpea genome**

A total of 20,162 (18,435 high quality) drought- and salinity- responsive ESTs were generated from ten different root tissue cDNA libraries of chickpea. Sequence editing, clustering and assembly analysis resulted in 6,404 unigenes (1,590 contigs and 4,814 singletons).

<http://www.biomedcentral.com/1471-2164/10/523>

#### **For details, contact**

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### **A pigeonpea germplasm reference collection**

This reference set is composed of a core set of 298 accessions whose genetic composition represents the diversity ICRISAT's genebank collection.

#### **For details, contact**

Dr H D Upadhyaya  
h(dot)Upadhyaya(at)cgiar.org

### **Validated SSR marker kit for diversity analysis of sorghum germplasm collections**

This comprises a reference kit of 48 SSRs with primer sequence list used to define the Sorghum Germplasm Reference Set composed of a core set of 384 accessions representing the genetic diversity of a composite set of 3384 accessions.

<http://www.icrisat.org/bt-genomics-sorghum.htm>

### **A transcriptome assembly and SNP dataset for chickpea**

A total of 103,215 tentative unique sequences (TUSs) have been produced from 435 018 Roche/454 reads and 21,491 Sanger expressed sequence tags (ESTs). Alignment of ~37 million Illumina/Solexa tags generated from drought-challenged root tissues of two chickpea genotypes against the TUSs identified 44,639 differentially expressed TUSs. The TUSs were also used to identify a diverse set of markers, including 728 simple sequence repeats (SSRs), 495 single nucleotide polymorphisms (SNPs), 387 conserved orthologous sequence (COS) markers, and 2088 intron-spanning region (ISR) markers.

#### **For details, contact**

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## **The chickpea genome sequence**

The draft genome sequence of chickpea (CDC Frontier, a kabuli chickpea variety) adds to the genomic resources available for legume research.

doi:10.1038/nbt.2491

## **Informative markers**

### **Markers for major drought tolerance QTL in chickpea**

Predictive markers for QTL associated with a 'hotspot' harbouring several root-related traits for drought tolerance contributing about 30% of phenotypic variation as well as for CID (60% phenotypic variation) including four other minor effect QTL.

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## **Informatics Application/Tool**

### **Laboratory Information Management System (LIMS) for high-throughput molecular genotyping**

A LIMS developed by ICRISAT to meet the needs of a moderately high-throughput molecular genotyping facility.

<http://www.icrisat.org/bt-bioinformatics-lims.htm>

### **Next Generation Sequencing (NGS) Data Analysis Pipe Line**

A data analysis pipeline capable of identifying the SNPs between parental genotypes using different algorithms.

<http://hpc.icrisat.cgiar.org/ngs/>

### **iMAS, an integrated decision support system for marker assisted selection**

The Integrated Marker-Assisted Selection System (iMAS) is an integrated molecular breeding analysis platform to facilitate an integrated system, based on freely available software.

<http://www.icrisat.org/bt-software-imas.htm>