



Current status and future prospects of genomic resources in legumes

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Grain legumes (primary)

| Scientific name | Common name | Regions of diversity |
|---|-------------|--------------------------|
| <i>Arachis hypogaea</i> L. | Groundnut | South America |
| <i>Cajanus cajan</i> (L.) Millsp. | Pigeon pea | India |
| <i>Cicer arietinum</i> L. | Chickpea | SW Asia, Ethiopia, India |
| <i>Glycine max</i> (L.) Merr. | Soybean | East Asia |
| <i>Lens culinaris</i> Medic. | Lentil | SW Asia, Mediterranean |
| <i>Phaseolus lunatus</i> L. | Lima bean | Peru |
| <i>Phaseolus vulgaris</i> L. | Common bean | Mexico, Guatemala |
| <i>Pisum sativum</i> L. | Pea | SW Asia, Mediterranean |
| <i>Vicia faba</i> L. | Faba bean | Asia, Mediterranean |
| <i>Vigna angularis</i> (Willd.) Ohwi & Ohashi | Adzuki bean | Japan, China |
| <i>Vigna radiate</i> (L.) Wilczek | Mung bean | India, SE Asia |
| <i>Vigna unguiculata</i> (L.) Walp. | Cowpea | W. Africa, India |

Legume production: small-scale, marginal & resource-poor



Regional yield of some legumes

Average yield (t ha⁻¹)

| Region | Soybean | Beans | Peas | Chick-pea | Broad bean | Lentil | Cowpea | Pigeon-Pea |
|--------|---------|-------|------|-----------|------------|--------|--------|------------|
| World | 2.27 | 0.68 | 1.70 | 0.79 | 1.52 | 0.81 | 0.37 | 0.72 |
| Africa | 0.91 | 0.67 | 0.55 | 0.72 | 1.36 | 0.58 | 0.35 | 0.76 |
| Asia | 1.38 | 0.54 | 1.18 | 0.78 | 1.58 | 0.77 | 0.93 | 0.72 |
| Europe | 1.88 | 1.48 | 2.99 | 0.83 | 2.39 | 0.86 | 2.95 | - |
| North | 2.54 | 1.07 | 1.32 | 1.30 | 0.79 | 0.92 | 0.78 | - |

- Limited/no genomic resources
- Low level of genetic diversity
- Limited financial resources in crop legumes
- Significant investments in Medicago, Lotus and soybean in US, Europe and Japan

Current status of genomic resources

| Resources | Medicago | Lotus | Soybean | Groundnut | Cowpea | Common bean | Chickpea | Pigeon-pea | Lentil |
|-----------------------------|----------|-------|---------|-----------|--------|-------------|----------|------------|--------|
| SSR | ++++ | ++++ | ++++ | ++ | +++ | +++ | +++ | +++ | + |
| SNPs | ++++ | ++++ | ++++ | ++ | +++ | + | ++ | ++ | - |
| Genetic maps | ++++ | ++++ | ++++ | + | ++ | ++ | ++ | + | + |
| Physical map | ++++ | ++++ | ++++ | + | ++ | + | - | - | - |
| Genome sequences | ++++ | ++++ | ++++ | - | - | - | - | + | - |
| Functional genomics | ++++ | ++++ | ++++ | + | + | ++ | + | - | - |
| Trait linked markers | + | + | +++ | + | + | ++ | + | - | - |
| Mol Breed | - | - | ++ | - | - | ++ | + | - | - |

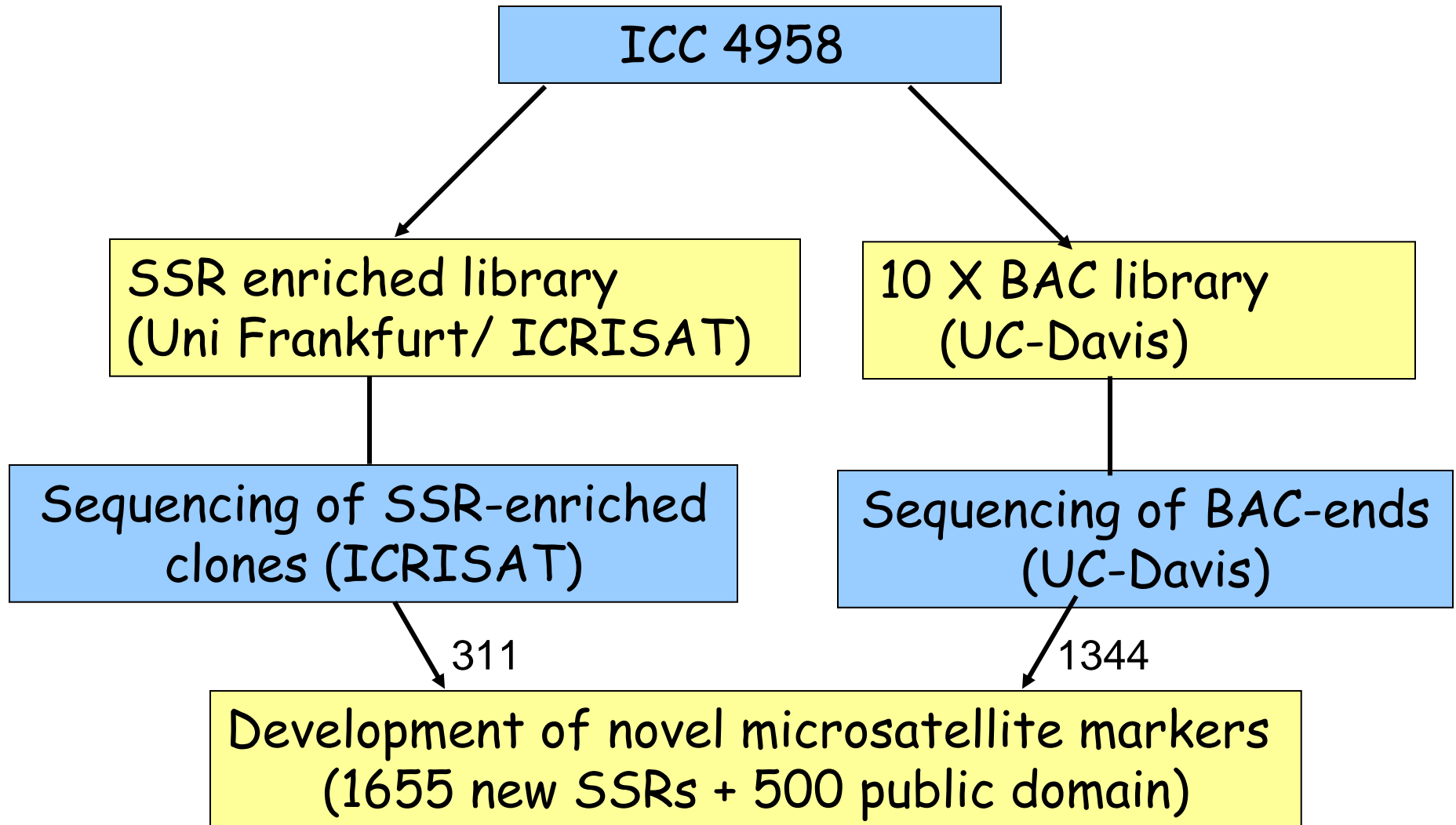
Success story, as an example, chickpea:

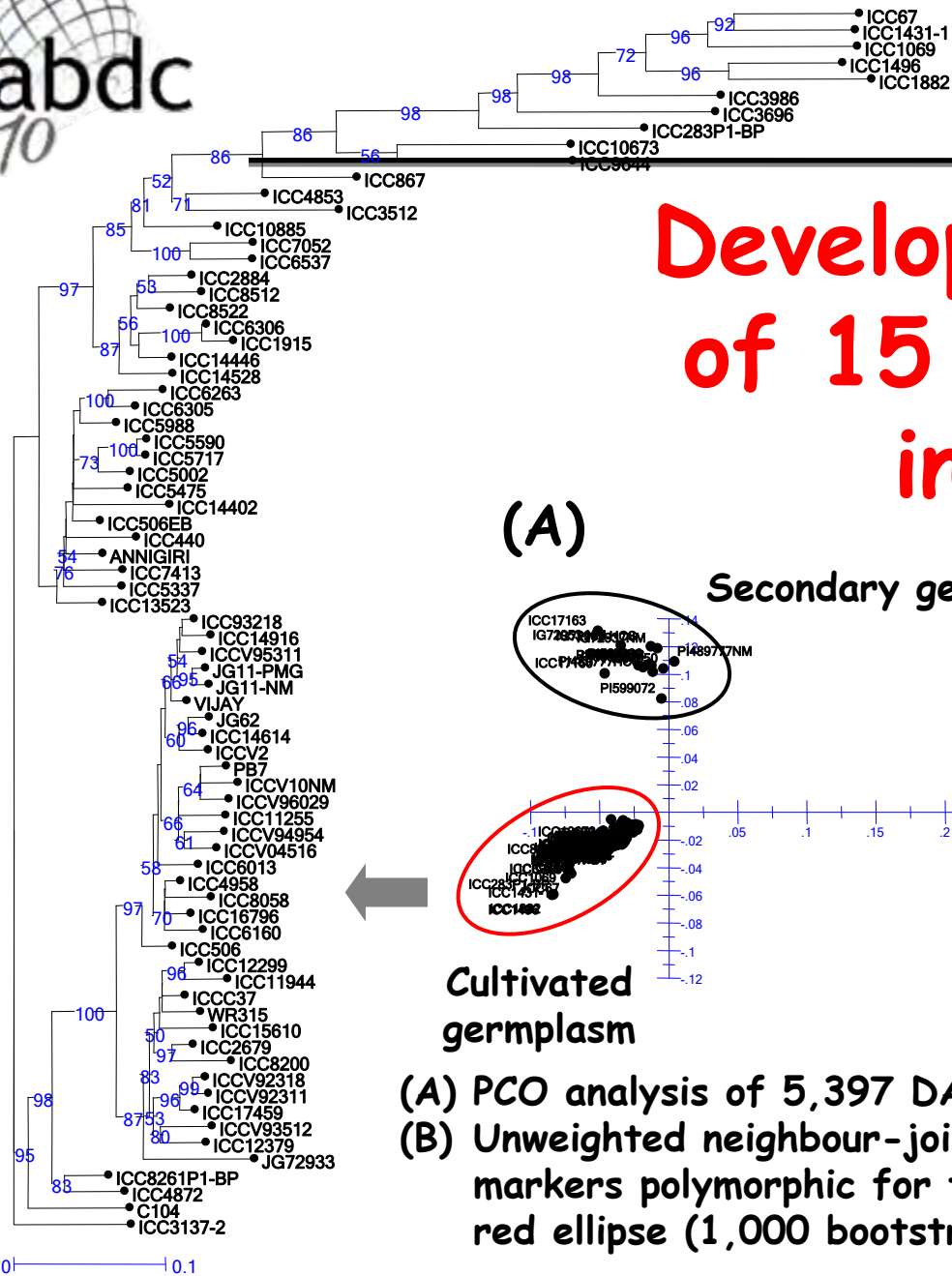




Large scale SSR isolation

(GCP/TLI, ICRISAT, Fra Uni, JCVI, Macrogen)





Development and use of 15 K DArT array in chickpea

(A)

Secondary gene pool

Tertiary gene pool

Cultivated germplasm

(A) PCO analysis of 5,397 DArT markers

(B) Unweighted neighbour-joining dendrogram based on 901 DArT markers polymorphic for the set of 75 cultivated lines in the red ellipse (1,000 bootstrap replicates)



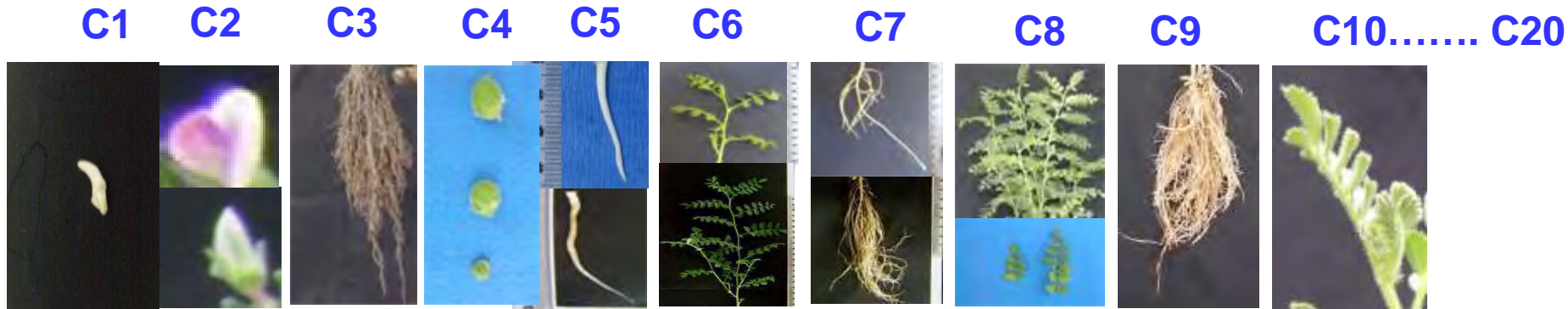
>20,000 Sanger ESTs

(NF-India, ICRISAT, JCVI, NRCRPB)

| Trait/Genotype | Total ESTs | High quality ESTs | Unigenes |
|---|------------|-------------------|----------|
| Drought : | | | |
| ICC 4958 | 5,982 | 5,461 | 2,656 |
| ICC 1882 | 5,919 | 5,535 | 2,392 |
| Total Drought responsive (ICC 4958 + ICC 1882) | 11,901 | 10,996 | 4,558 |
| Salinity: | | | |
| JG 11 | 3,798 | 3,132 | 1,707 |
| ICCV 2 | 4,460 | 4,307 | 1,251 |
| Total Salinity responsive (JG 11 + ICCV 2) | 8,258 | 7,439 | 2,595 |
| ESTs from public domain | 7,097 | | 4,059 |
| Total Chickpea ESTs | 27,257 | 25,532 | 9,569 |

Cataloguing chickpea genes !

(GCP, ICRISAT, JCVI, NCGR, Everogen)



Pooled RNA from different developmental stages used to generate normalized cDNA library and subjected to FLX- 454

FLX- 454 Reads

Total numbers of FLX ESTs : 435,018
 Average read length : 216 bp
 Number of ESTs with >200 bp: 379,039

Sanger + FLX 454 ESTs

Number of Tentative Unique Sequences (TUs) : 103,215
 Number of Contigs : 46,740
 Number of Singletons : 56,475



Large-scale SNP identification

(GCP, ICRISAT, NCGR, UC-Davis)

- 100 million Illumina reads generated,
- >40,000 SNPs identified

| Sample | ICC 4958 | | ICC 1882 | | ICC 506 | | ICCC 37 | |
|--------------------------------------|----------|--|----------|--|----------|-----|---------|------|
| | | | | | C | S | C | S |
| Number of reads (in million) | 22.1 | | 15.6 | | 17.9 | 5.2 | 31.3 | 26.8 |
| Average read length | 36 | | 36 | | 36 | 36 | 36 | 36 |
| Average read quality | 23 | | 27 | | 28 | 27 | 29 | 28 |
| Total number of SNPs | 26, 082 | | | | 1,08,942 | | | |
| Total number of Indels | 2,405 | | | | 12,972 | | | |
| Transition/ Transversions | 23, 677 | | | | 95,970 | | | |
| High quality SNPs (≥5 read depth) | 9,237 | | | | 43,471 | | | |

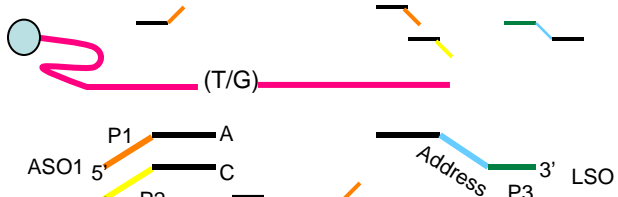


Illumina GoldenGate assay

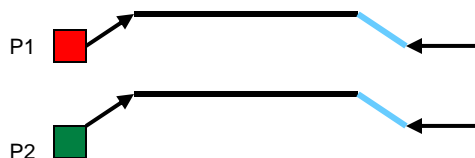
1. Make activated DNA



2. Hybridize Oligos to Activated DNA1



5. Bind PCR product, elute dye-labeled strand, prepare for hybridization



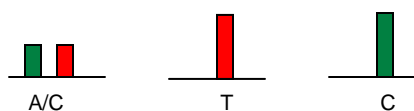
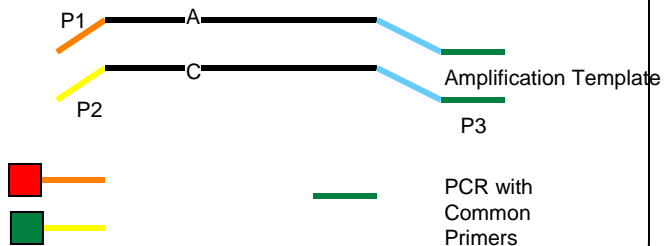
6. Assay Hybridization to Universal IllumiCode Array

7. Wash and dry Array Matrix or Bead chip



8. Image Array Matrix or Bead Chip

4. Assay Amplification



ASO = Allele-Specific Oligo
 LSO = Locus-Specific Oligo
 P1,P2,P3 = Universal PCR primers
 Address = Sequence unique targeting a particular bead type

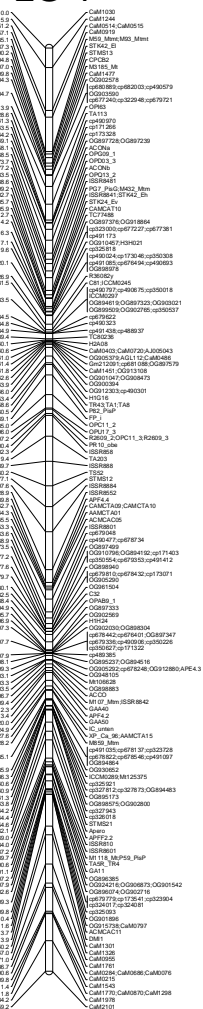


- GoldenGate assay for 768 SNPs
- Development of extended assay (1536 additional SNPs) is in progress

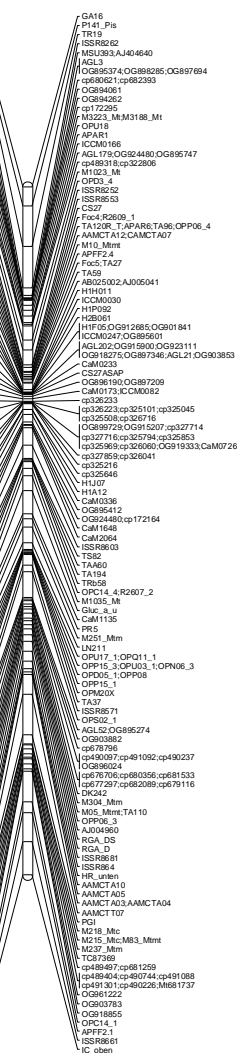


1,533 loci chickpea genetic map (ICRISAT, GCP, UC-Davis, Uni-Fra)

LG 1



LG 2



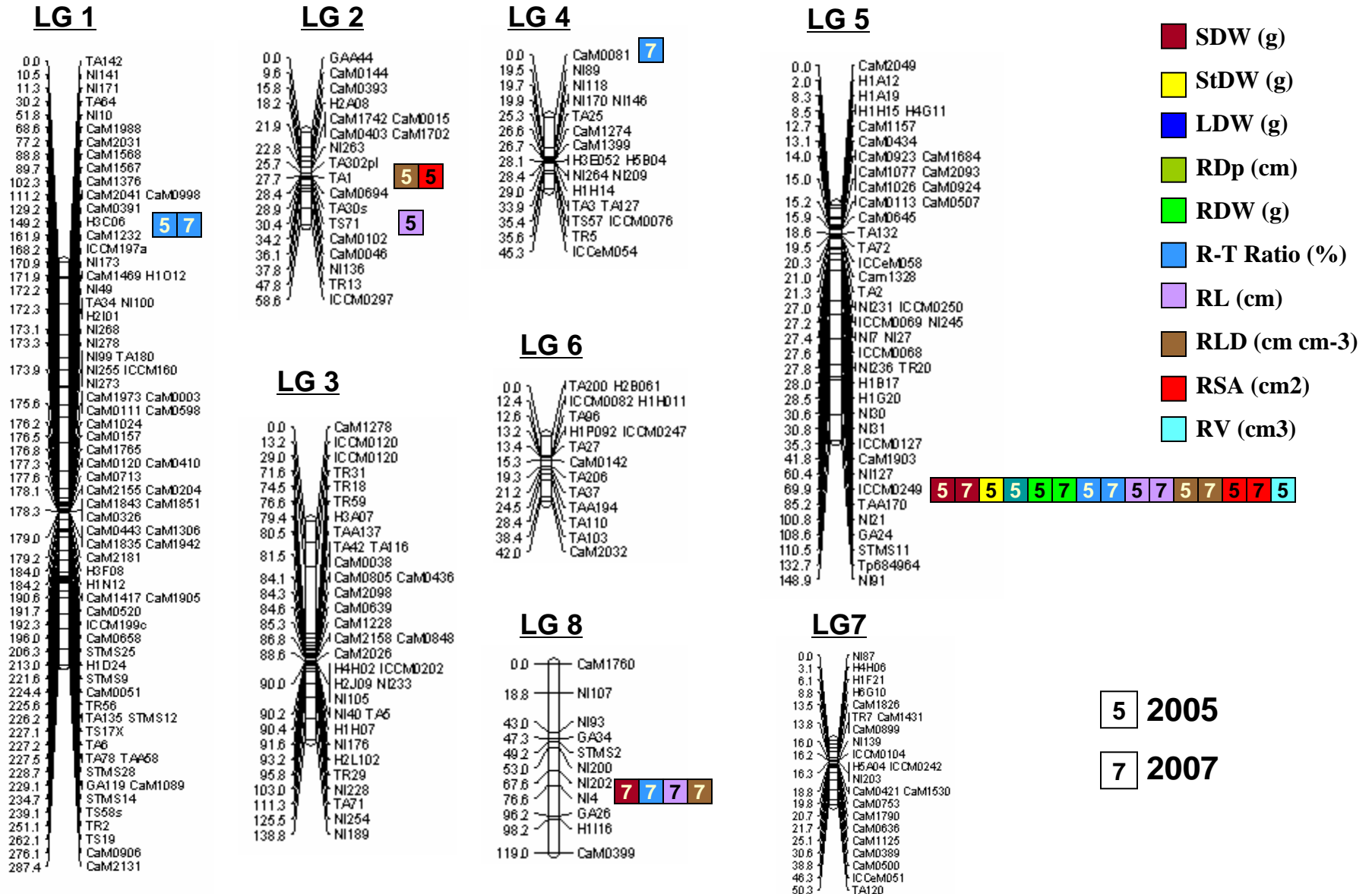
LG 3



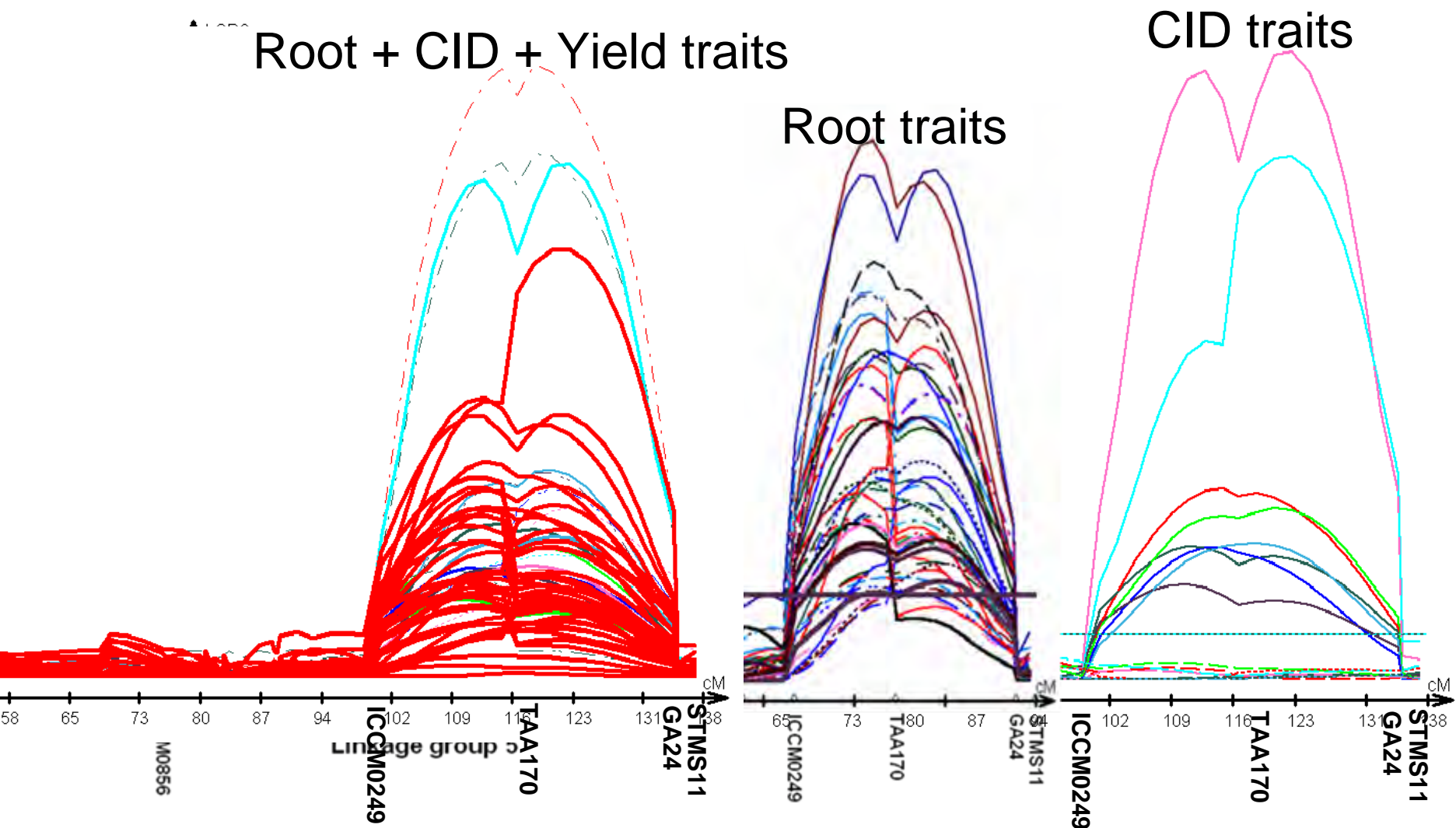
LG 4



Root trait- QTL map (ICRISAT, GCP, UAS-D, IIPR, NIPGR)



Hot spot for QTL -LG 5 (ICC 4958 × ICC 1882 map)



Marker-assisted selection (MAS) for improving drought tolerance

(ICRISAT, GCP, EIAR, EU, IIPR)

Crosses:

Elite cultivar x Donor genotype for root traits

BC1:

Cultivar x F1

BC1F1

BC2:

Cultivar x BC1F1

BC2F1

Subjected to foreground and background selection

BC3:

Cultivar x BC2F1

As in BC 2

BC3F1

Selected heterozygous plants for QTL-linked markers
and over 90% genome of the recurrent parent

BC3F2

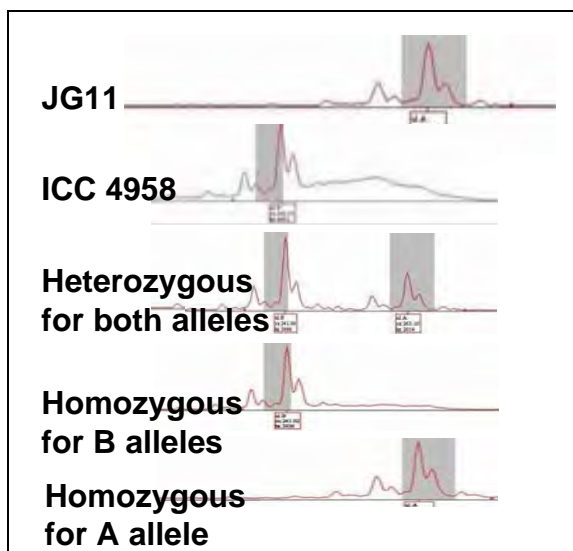
Select homozygous plants for QTL-linked markers

BC3F3

Seed multiplication

Multilocation evaluation BC3F4 lines

Being Done



D
O
N
E



International Chickpea Genetics and Genomics Consortium (ICGGC)



Coordination Areas

[Genetic Resources](#)

[Genomic Resources](#)

[Recombinational Analysis](#)

[Trait Mapping](#)

[Transcriptomics](#)

[Functional Analysis](#)

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Welcome to ICGGC

At the recent International Conference on Grain Legumes (ICGL-2009) held at Indian Institute of Pulse Research (IIPR), Kanpur in India during February 14 – 16, 2009, leading chickpea researchers from India, USA, Australia, Canada as well as from two CGIAR (Consultative Group of International Agricultural Research) Centers (ICRISAT, India and ICARDA, Syria) during an interactive chickpea genomics and breeding session decided to establish an international platform for facilitating the chickpea research in the area of genetics and genomics to understand genome architecture and dynamics and to assist chickpea improvement. As a result, International Chickpea Genetics and Genomics Consortium (ICGGC) was floated.

Chickpea is one of the major legume crops in the world and a staple food in many developing countries especially in South Asia and Sub Saharan Africa where it is grown for protein and carbohydrate supply. In developed countries like Canada and Australia it is grown for export, constitutes an important trade commodity.

[More Info....](#)

Cooperators :



[More Info....](#)

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Factors responsible...

- ❖ Strategic partnership and coordinated efforts (CGIAR, ARIIs, NARS, Private companies-service providers)
- ❖ Involvement of partners from the beginning
- ❖ Genomics initiative at national and international level
- ❖ Data access and sharing



...and several others



National Science Foundation
WHERE DISCOVERIES BEGIN



भारत अन्न
ICAR