Linking genetic diversity with phenotype for drought tolerance traits through molecular and physiological characterization of a diverse reference collection of chickpea

ICRISAT

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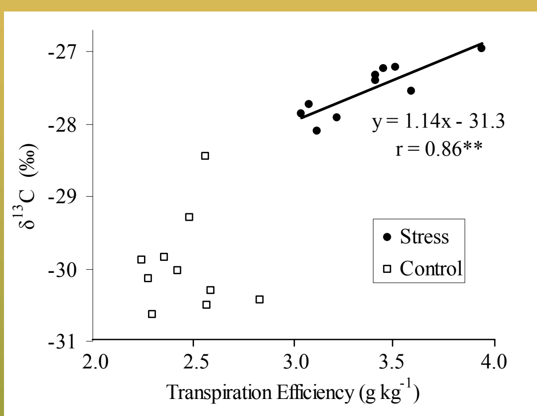
Rationale

- Grain yields of chickpea, the third most important grain legume, is constrained by terminal drought
- Adaptation to drought requires improvements of root system, transpiration efficiency (TE) and harvest index
- Breeding for component traits rather than drought yields are emphasized to minimize the G x E interaction
- Identification of diverse sources of variation for TE by $\Delta^{13}C$ and identification molecular markers for this trait to quicken the process of introgression while pyramiding beneficial genes in an acceptable genetic background.



Relationship between transpiration efficiency (g kg $^{-1}$) and $\Delta^{13}C$ in a few chickpea mapping population parents with contrasting root system. Source: Kashiwagi et al. 2006. ICPN 13: 19-21.

Objectives and outputs

Objectives

(a) characterization of target drought environments

(b) physiological characterization of the chickpea reference collection (n=300) aiming at improving the drought tolerance through trait-based breeding strategy, and

(c) identification of molecular markers using association genetics approach, to improve the drought tolerance in chickpea

Outputs

1. Target drought environments characterized (climatic and soil property)
2. Chickpea reference collection characterized for TE via $\Delta^{13}C$,
3. SPAD chlorophyll meter readings (SCMR),
4. Specific leaf area (SLA),
5. Genome wide DArT marker analysis, and
6. Identification of molecular markers with drought tolerance associated traits, viz., TE through $\Delta^{13}C$ (ii), photosynthetic capability through SCMR (iii), and leaf morphology through SLA .

Physiological traits measurement

- A field trial was conducted at ICRISAT, Patancheru with the reference set of chickpea germplasm in two soil moisture ([1] nonirrigated receding soil moisture and [2] optimally irrigated environments) with 3 replications in an alpha lattice design.
- Leaf samples that are required for $\Delta^{13}C$ analysis were collected at 35 DAS (Before the soil moisture treatment was applied) and 59 DAS (when drought stress was mid-way through).
- The harvests for yield and yield components estimation were carried out
- A delayed sowing of the field trial at UAS, Bangalore had lead to a poor growth necessitating a repeat of this trial

$\Delta^{13}C$ estimations

- $\Delta^{13}C$ estimations of the samples from ICRISAT are in progress at JIRCAS, Japan.
- Similar analysis planned for the samples from UAS, Bangalore from Mar 2010

Marker identification

- Existing DArT arrays developed at DArT Pty Ltd. (Australia) turned to be monomorphic in cultivated chickpea germplasms tested.
- Therefore an expanded DArT array of about 15,360 genomic clones from 96 diverse chickpea genotypes have been developed in collaboration with DArT Pty Ltd.
- This expanded DArT array includes 7,680 new clones and 7,680 earlier clones.
- The DNA of chickpea reference set has already been sent to DArT Pty Ltd (Australia) for genotyping.
- The genotyping results are expected soon.

Plans for 2010

- Conducting a field trial at UAS, Bangalore and at ICRISAT, Patancheru during postrainy season 2009- 2010. Repeating the sampling protocol at UAS, Bangalore and collection of data on SLA amd SCMR at both locations.
- Conducting a field trial at ICRISAT, Patancheru during postrainy season 2009- 2010 for collection of data on SLA and SCMR as well the yield and yield components.
- $\Delta^{13}C$ analysis of the samples from UAS, Bangalore at JIRCAS, Japan.
- Confirming the presence of polymorphism with DArT markers
- Association mapping and linking phenotypic data with the genotypic data