

Drought Management in Pulse Crops

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Abstract

In the context of the rainfed production systems of the Semi-Arid Tropics (SAT), crop drought resistance is defined in terms of yield stability in a specific target environment. Chickpea and pigeonpea are known for their adaptation to SAT regions and their relative ability to produce grain and biomass under water-limited conditions. However, the current challenge is to reduce the yield gaps under rainfed conditions, and sustain food security for the benefit of resource poor farmers across the SAT. Efforts are currently being made at ICRISAT to implement a holistic approach for drought resistance improvement, with the objective to enhance crop performance under water-limited conditions. The component traits currently considered for marker assisted selection of drought resistance in legumes include drought-avoidance root traits in chickpea. The identification and mapping of quantitative trait loci (QTLs) for specific drought-resistance component traits can also be used to dissect the genetic and physiological mechanisms involved in drought performance. If validated with accurate phenotyping and properly integrated into marker-assisted breeding programmes, this approach will allow pyramiding of drought resistance mechanisms and accelerate the development of locally adapted pulse genotypes.

1. Introduction

Chickpea (*Cicer arietinum*) and pigeonpea (*Cajanus cajan*), which are the mandate crops of ICRISAT, are known for their relative ability to withstand periods of water-deficits and still produce grain and biomass under these conditions. However, the constant challenge is to reduce yield gaps observed between research plots and farmers' fields under rainfed conditions of semi-arid tropics (SAT), to assure sustained food security for the benefit of resource poor farmers.

Drought stress is a complex syndrome involving several climatic, edaphic and agronomic factors, and characterized by three major varying parameters, i.e., timing of occurrence, duration, and intensity. The general complexity of drought problems is often aggravated under the SAT conditions, by erratic and unpredictable rainfall, and by the occurrence of high temperatures, high levels of solar radiation, and poor soil characteristics of the target environments. The high variability in the nature of drought and the insufficient understanding of its complexity have made it generally difficult to characterize the physiological traits required for improved crop performance under drought, consequently, limiting the plant breeding efforts to enhance crop drought resistance.

In the agricultural context of SAT and the current global water challenges, it is critical that both agronomic and genetic management strategies focus on maximum extraction of available soil moisture and its efficient use in crop establishment, growth, and maximum biomass and seed yield. Recent research breakthroughs in biotechnology have revived interest in targeted drought resistance breeding and use of new genomics tools to enhance crop water productivity (Crouch and Serraj, 2002). However, with the fast progress in genomics a better understanding of the gene functions and drought physiological mechanisms will also be crucial for the progress of genetic enhancement of crop drought tolerance (Serraj, 2003).

Characterizing drought in post-rainy season crops such as chickpea is simpler, compared to the intermittent drought experienced by the rainy season crops. The reason being much of the rainfall is received before planting of the crop, which is, therefore, grown almost entirely on stored soil moisture, and exposed mostly to progressively increasing (terminal) water deficit. Therefore, the factors governing crop growth and water use in the post rainy season, *i.e.*, radiation, temperature, vapor pressure and potential evaporation, are relatively stable and predictable, so that simulation modeling of both crop growth and the effects of various crop traits is eminently feasible.

Pigeonpea is grown mainly by resource-poor farmers in India and to a varying extent throughout the tropics, usually under rainfed conditions. Traditionally, medium to long duration landraces have been cultivated, with crop duration of 150-300 days. Pigeonpea can be exposed to intermittent drought stress during dry periods of the rainy season and to terminal drought stress in the post-rainy season. However, over the last two decades, shorter duration genotypes have been developed, with some genotypes able to reach maturity within 90 days (Nam *et al.*, 1993). The introduction of such genotypes has enlarged the scope for pigeonpea cultivation in various, non-traditional cropping systems. However, the developed short-duration genotypes are usually sensitive to intermittent drought (Chauhan *et al.*, 1992).

It is now well accepted that the complexity of the drought syndrome can only be tackled with a holistic approach integrating physiological dissection of the resistance traits and molecular genetic tools together with agronomical practices that lead to better conservation and utilization of soil moisture and matching crop genotypes with the environment (Serraj *et al.*, 2003).

The agronomic and management options for increasing the productivity and conserving the natural resources adopted by ICRISAT for the integrated watershed management have been recently reviewed (Wani *et al.*, 2003). This paper reports the recent progress made at ICRISAT in deciphering the complexity of crop water deficits problems and developing drought tolerant varieties of the pulse mandate crops.

2. Development of Short-Duration Genotypes

Since a strong relationship between the yield potential and the sensitivity of genotypes to end-of-season drought was observed for all legume mandate crops, the first approach to minimize yield losses due to terminal drought has been to breed for earliness. But in the case of mid-season drought such relationship does not hold, which requires specific genetic enhancement programmes for drought resistance, mainly focusing on avoidance mechanisms. The appropriate crop duration is a compromise of various factors, including season length, yield potential and the timing of occurrence of drought stress.

2.1 Chickpea

Short duration varieties that mature before the onset of severe terminal drought have proved successful in increasing yield under drought-prone conditions in chickpea (Kumar *et al.*, 1996). However, since seed yield is generally correlated with the length of crop duration under favourable crop growing conditions, any reduction of crop duration below the optimum would have a penalty in terms of yield (Saxena, 1987). Depending upon the water availability, optimum crop duration for maximum yield would vary. Thus, selection of varieties needs to be matched with the maximum length of growing period (LGP). Significant progress has been made in developing improved chickpea varieties of short duration that mature in 85-90 days in mild winter chickpea growing conditions, as prevailing in peninsular India (Kumar *et al.*, 1996). Even extra-short duration chickpea varieties, termed super-early have now been developed (Kumar and van Rheenen, 2000). Development of these new varieties has expanded options to include chickpea as a crop in many prevailing- and evolving new-production systems, such as rice fallows.

2.2 Pigeonpea

Traditional long and medium duration pigeonpea landraces have evolved under, and have apparently adapted to, terminal drought stress conditions. However, studies in which irrigation has been supplied during the reproductive phase indicate that terminal drought usually reduces grain yield of landraces growing in their typical environment (Chauhan *et al.*, 1992). This is more apparent in the shorter duration environments closer to the equator where evapotranspiration is high during the postrainy season. Thus, in terms of maximizing grain yield, the duration of these landraces seems too long for the common period of soil moisture availability. However, a large spectrum of genotype duration is now available (Gupta *et al.*, 1989), and matching genotype duration with likely period of soil water availability is the first line of defense against terminal drought stress. Further, opting for a shorter duration cultivar than

those traditionally used in a region does not necessarily mean a sacrifice in yield potential as even extra-short duration varieties can produce yields above 2.5 tons ha⁻¹ (Nam *et al.*, 1993).

3. Drought Avoidance Root Traits in Chickpea

Research efforts have been made at ICRISAT to identify sources of genetic variation for large and deep root systems among the cultivated varieties of chickpea and also within the mini-core germplasm collection available in the ICRISAT gene bank.

Rooting depth, extent and timing of root growth are expected to play a major role in the adaptation of chickpea to terminal drought stress. In 2000-02, the genetic variation available among the recombinant inbred lines (RILs) derived from a cross between a large root parent (ICC 4958) and a well adapted, best yielding variety (Annigeri), was evaluated and their suitability to identify QTLs for root traits was assessed. The RIL mapping population showed large variations for rooting depth and root biomass at 35 day after sowing (DAS), shoot biomass and seed yield at maturity, and for the rate of partitioning (Serraj *et al.*, 2004). But there were no direct relationship between the seed yield and the root depth or the root biomass. The root trait benefits on the yield were previously shown to be visible in environments with a productivity level of <1.0 tons ha⁻¹ (Saxena, 1987). However, the drought intensity experienced in the study was moderate and, therefore, further studies are needed to confirm the results obtained under low residual soil moisture conditions.

In 2000-01 and 2001-02 post-rainy seasons, root growth parameters were evaluated in field trials using 12 contrasting types of cultivated chickpea genotypes for duration, growth habit, rooting extent in terms of root mass, rooting depth, and yield under terminal drought. The results showed a clear positive relationship between root biomass extracted from the 15-30 cm soil depth at 35 DAS and the seed yield at maturity in both the trials (Table 1). In 2001-02, a severe drought year, rooting depth and total root biomass also exhibited positive relationship with seed yield. Although significant G x E interaction was detected, the broad sense heritability of total root biomass (67.4%), and shoot biomass (72.0%) was relatively high. These results indicate that root traits such as the root depth, total root biomass as well as profile-wise root distribution need to be paid more research attention for the improvement of yield stability in chickpea.

The agronomic evaluation and phenotyping of root traits of the mapping population derived out of ICC 4958 and Annigeri, were recently carried out in multilocation trials (Krishnamurthy *et al.*, 2004; Serraj *et al.*, 2004). Based on these studies, it was concluded that the relative closeness of the two parents (Annigeri and ICC 4958) and

Table 1: Correlation coefficients of agronomic traits to seed yield in field trials of chickpea grown in progressively receding soil water conditions in a Vertisol at ICRISAT during 2000-01 and 2001-02 post-rainy seasons

Stage	Characteristics	2000-01	2001-02
35 days after sowing	Root dry weight (g)		
	0-15cm	0.277	0.442
	15-30cm	0.637 *	0.726 **
	30-45cm	0.402	0.792 **
	45-60cm	0.340	0.593
	60-75cm	0.375	-
	Whole profile	0.553	0.628 *
	Potential rooting depth [#]	0.260	0.746 **
	Shoot dry weight (g)	0.241	0.665 *
	Root/total plant dry weight ratio	0.849**	0.402
Maturity	Shoot biomass	0.352	0.592 *
	Harvest index	0.895**	0.857 **
	100 seed weight (g)	-	0.431
	Duration of vegetative stage	--	-0.605 *
	Duration of reproductive stage	--	-0.515
	CGR during vegetative stage	--	0.648 *

*, ** indicates significance at 0.05, and 0.01 probability levels respectively

— indicates non-availability of data

[#]Potential rooting depth was estimated by an exponentially declining model.

the low level of polymorphism available between them made these parents not suitable for the mapping purpose. Therefore, a series of new experiments were carried out in 2002-2003 to develop a new set of mapping populations, based on germplasm screening for root traits.

The screening of chickpea minicore collection for root traits was recently carried out with the double objective of characterizing the genetic variability of drought-avoidance root traits and selecting suitable mapping population parents for molecular mapping. The whole mini-core germplasm collection of *C. arietinum* (211 accessions) along with 12 popular cultivars as references and 10 accessions of wild annual species

were evaluated in PVC cylinders. The statistical differences of entries were highly significant ($p < 0.001$) for both root and shoot traits (Krishnamurthy *et al.*, 2003) (Table 2). The root and shoot growth of the wild species was relatively poor compared to *C. arietinum* lines. The maximum root depth of ICCV 2, ICC 4958, and Annigeri was relatively high. Some of the accessions with a deep root system were ICCs 1431, 8350, 15697, 3512, and 11498. The germplasm accession ICC 4958 was previously used as the only source for deep and large root system parent or control in most of the drought avoidance related studies. The new genotypes identified could be utilized as valuable alternative sources for diversification of mapping populations with varying growth duration and to obtain the required polymorphism for successfully mapping root traits in chickpea.

Table 2: Means and range of root and shoot traits at 35 days after sowing among chickpea accessions at ICRISAT

Trait	Mean	Range	LSD (0.05)
Maximum root length (cm)	110.9	62 – 124	24.6
Root dry weight (g cylinder ⁻¹)	0.922	0.293 – 1.381	0.360
Shoot dry weight (g cylinder ⁻¹)	1.168	0.294 – 1.662	0.393
Root/total plant ratio	0.433	0.276 – 0.504	0.070

The development of new mapping populations was recently initiated with the evaluation of 21 candidate parental lines, showing extreme contrasts for root traits (depth, mass and RLD). After maturity matching, two genotypes with large root systems (ICC8261, ICC4958) and two other lines with similar maturity and smaller roots (ICC283, ICC1882) were selected for the development of new mapping populations. The four parental lines were crossed and the resulting F1, F2, BC1 and BC2 are now being analyzed for the estimation of genetic components, and evaluated for root traits and field agronomic performance.

Two chickpea dry-down experiments were recently carried out in the glasshouse for the analysis of plant water relations response to water-deficits, and for comparing putative drought-avoidance physiological traits (Serraj *et al.*, Unpublished). The response curves of plant transpiration (T) to fraction of transpirable soil water (FTSW) showed the existence of genetic variability among 11 cultivars and potential mapping population parents, which was related to plant water use and leaf gas exchange. A significant negative correlation was observed between the threshold for T response to FTSW and transpiration efficiency (TE). These results indicated a causal relationship between TE and the stomatal regulation under drought, which opens new possibilities of understanding

the physiological responses to drought and for mapping new putative drought avoidance QTLs in chickpea.

4. QTLs and MAS

Marker-assisted breeding has revolutionized the improvement of temperate field crops (Spangenberg *et al.*, 2001; Toenniessen *et al.*, 2003) and will have similar impacts on plant breeding of tropical crops, particularly for traits where phenotyping is only possible late in the season, or is difficult or prohibitively expensive (Dwivedi *et al.*, 2003). In the longer term, comparative genomics and bioinformatics will allow the intensive advances in model systems to be rapidly and effectively applied to a wide range of related crops.

Large-scale development of microsatellite markers has been initiated for chickpea and pigeonpea (Burns *et al.*, 2001). A traditional size fractionation approach was followed in chickpea using 4 different restriction enzymes. The genomic libraries were screened with various di- and tri-nucleotide repeat motifs, resulting in 174 microsatellite markers. In the case of pigeonpea, two enriched libraries were created using the method of Edwards *et al.* (1996) resulting in low recovery rate of only 10 useful microsatellite markers. Due to the substantial amount of time and cost incurred, there is considerable interest in establishing a more cost effective and labor-saving alternative in generating additional markers.

ICRISAT is combining empirical lab-based approaches with bioinformatic strategies in order to develop an efficient system for screening the vast public domain sequence databases of soybean and *Medicago* to identify those sequences of most value for molecular breeding of chickpea and pigeonpea. Information on conserved gene sequences among these genera will also facilitate prediction of gene location in the crop of interest based on its location in other genera. This approach may be particularly useful in tagging agronomic traits that have already been intensively studied in pea, soybean and *Medicago*.

5. Conclusion

A strong relationship was observed between yield potential and the sensitivity of genotypes to end-of-season drought for pulse crops, which makes breeding for earliness the first priority approach to minimize yield losses due to terminal drought. However, in the case of mid-season drought such relationship does not hold, which requires specific genetic enhancement programmes for drought resistance, mainly focusing on avoidance mechanisms. Despite the methodological difficulties, genetic enhancement of root systems for more effective water extraction is a high-priority effort for rainfed

chickpea and extra-short duration pigeonpea. Dissection of root traits and development of a screening system relevant to field conditions have been attempted at ICRISAT, in parallel with extensive genotyping and search for molecular markers. There seems to be much scope for improving such characters, using QTLs and molecular breeding techniques, aided by physiological characterization and conventional breeding to significantly improve the ability of the mandate crops to withstand drought stress in defined target environments.

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