

Genetic control of drought avoidance root traits in chickpea (*Cicer arietinum* L.)

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Abstract

Improving the root systems is one of the important strategies to alleviate yield reduction under drought environments. In chickpea, the rooting profile influenced the seed yield under terminal drought environments. Especially, root length density (RLD) in 15-30 cm played an important role, and deeper root systems had positive effects when the drought was severer. A significant improvements in the research methodology for the chickpea root systems has allowed us to conduct large scale experiments, and a supreme genotype in terms of RLD and root depth, ICC S261, was identified from the chickpea mini-core collection (n = 211). A genotype, ICC 4958 also was confirmed as one of the most prolific and deep rooting. These progresses are leading us to develop robust breeding strategies for enhancing chickpea drought avoidance through the root system improvement.

Introduction

In chickpea, the terminal drought is one of the major abiotic constraints limiting the productivity. It is estimated that if the soil water stress is alleviated, chickpea production could be improved up to 50% increment that is equivalent with approximately U.S.\$ 900 million (Ryan, 1997). A lot of research efforts, therefore, have been made to reduce the yield loss of chickpea under terminal drought environments. However, a lot more issues related to drought are yet to be resolved since drought is a highly complex phenomenon. Considering the large quantitative and temporal variations in soil moisture availability in

chickpea growing areas and the $G \times E$ interactions for yield it becomes necessary to categorize the drought environments and to identify the relevant traits that could improve the adaptation of chickpea to its growing environment before developing the research strategies aimed at improving the chickpea production under drought environments. The drought that the chickpea faces is terminal drought with the soil moisture keeps depleting progressively under high evaporative demand with normally less or no precipitation during the crop season where the crop consequently suffers from progressively increasing soil moisture deficit with advancing growing time (Fig. 1). ICRISAT chickpea breeding team have been applying the drought escape breeding strategy to cope with the terminal drought, and released several popular chickpea genotypes that were early in maturity (Kumar *et al.*, 2001). However, the early maturing crop can not accumulate enough plant biomass due to reduced total photosynthetic period compared to the relatively late maturing genotypes. Alternative research strategies need to be developed to cope with this issue. Kashiwagi *et al.* (2005) reported that prolific root systems, especially in 15-70 cm in depth, had positive effects on the seed yield in chickpea under moderate drought intensity at ICRISAT, on the other hand deeper root systems had the advantage in severer drought conditions. This suggests that enhancing the root systems would be one of the promising approaches to improve the drought avoidance of chickpea under the terminal drought environments.

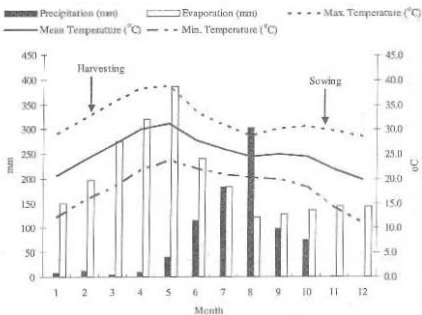


Fig. 1. Average climatic conditions for displaying the terminal drought environment at ICRISAT, Patancheru, Andhra Pradesh, India

Root Research

Conducting the research on root systems in a field is fairly laborious, expensive and time consuming. In ICRISAT, a systematic field root extraction method that is a modified monolith method has been established allowing us to have a root sampling done approximately 3.3 worker⁻¹ day⁻¹. Obviously, developing an alternative screening method for chickpea root research is necessary to simplify the research. Tall PVC cylinder systems were optimized to estimate the chickpea root growth since the rooting profile cannot be estimated in shallow pot grown plants. When the plants were grown in PVC cylinders with 18 cm in diameter and 120 cm height with sand-Vertisol mixture containing 70% field capacity, there was a significant relationship in the root biomass between the field and cylinder conditions ($r = 0.63$, $p < 0.05$). In addition, the sampling efficiency could be improved dramatically up to approx. 25 worker⁻¹ day⁻¹. In addition, by applying an image capturing and analysis system, we could convert the root samples to digitized images quickly (>150 samples day⁻¹) before they are decayed and also analyze more than 500 of the images in a day. These are fairly an important progress made towards establishing simpler root research systems, *viz.*, cylinder culture method plus image capturing and analysis system, because it would allow us to conduct larger scale root research in chickpea.

Variability and Gene Components

It is necessary to understand the range of genetic diversity of the target traits to identify the suitable research/breeding materials. ICRISAT genebank has developed a chickpea mini-core germplasm collection ($n = 211$) that maintains the genetic diversity of important agronomic traits of the entire chickpea collection (Upadhyaya *et al.*, 2001; Upadhyaya and Ortiz, 2001) but no information on any of the root traits. This mini-core germplasm collection would be the best suited material to investigate the variation of the root traits. In 2003, the genetic diversity of root traits among chickpea mini-core collection was investigated in two different seasons in the cylinder systems. Although a significant $G \times S$ interaction was observed, it was minor and not a cross-over type. Moreover, there was significantly large enough variability for all root traits such as root length density (RLD), root dry weight (RDW), rooting depth (RDp) and root to total plant weight ratio (R/T) (Kashiwagi *et al.*, 2005). An accession, ICC 4958, that has been previously used as the key donor parent and almost the only breeding material for drought avoidance improvement in chickpea was once again confirmed as one of the best accessions for most prolific and deepest root systems among the mini-core collection. In addition, an accession, ICC 8261 was also newly identified as the one with the most prolific and deeper root systems among the chickpea mini-core collection (Fig. 2). These would be important baseline information for further research on the root traits in different research area on chickpea.

It was felt necessary to estimate the gene effects so that a proper breeding strategy could be developed before initiating large scale breeding program on root traits. In this context, two crosses, *i.e.* one with parents ICC 283 (smaller roots) \times ICC 8261 (larger roots) and the other with ICC 4958 (larger roots) \times ICC 1882 (smaller roots), were made for the

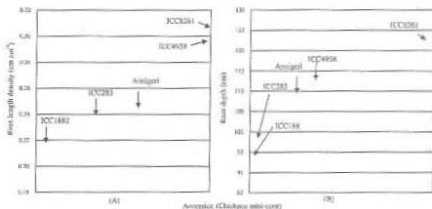


Fig. 2. Ranking distribution on the mean of 211 mini-core germplasm plus 5 cultivars on (A) root length density (RLD), (B) root depth (RDp) in 2 different seasons at 35 days after sowing. SEd of RLD = 0.022, and RDp = 12.95

estimation of gene effects through generation mean analysis. The results showed that the additive gene effect and the additive \times additive gene interaction did contribute to the variation in the root biomass, and the direction of the gene effect was consistently towards increasing RLD except for 30–60cm and 60–90cm depth in ICC 4958 \times ICC 1882. These results suggest that recurrent selection at later generations would be an appropriate method of breeding to achieve the desired improvements in the RLD since the presence of relatively large amounts of dominance and epistasis effects.

New Technology Applications

The vigorously developing molecular techniques can be used as a powerful tool to screen the genotypes with desirable traits. Especially for root traits, the marker assisted selection (MAS) is a promising screening method to reduce the difficulties inherent to the root research, e.g., the laborious and time-consuming research processes. However, MAS could be employed only when two critical hurdles have been cleared, that is, i) identification of adequate molecular markers that show polymorphism among the entries chosen for the genotyping, and ii) quick observation/measurement systems for the target traits to cope with the large scale phenotyping. In chickpea, there is >400 molecular markers available to-date, but still more need to be developed for the saturated marker maps such as the one rice has. On the other hand, enough quantities as well as qualities phenotyping data have proving through our cylinder systems. Although inadequacy exists in the number of molecular markers that are available and the suitability of parental lines that were chosen, we were able to identify a relatively powerful marker, Taa170 which could explain about 33% of the total variation of root biomass such as root length and root dry weight by using a RIL mapping population derived from cross between ICC 4958 (large roots) and Annigeri (intermediate

roots) (Chandra et al., 2004). Currently, two new RIL mapping populations (ICC 283 x ICC 8261, and ICC 4958 x ICC 1882) are being phenotyped for establishing the robust MAS.

Conclusions

In chickpea, adequate baseline information has already been generated in terms of suitable screening methodology and identification of contrasting parental material. However more need to be done to improve the methodology employed for screening and to increase the genetic diversity of the selections as contrasting genotypes or accessions. Genetic control of drought avoidance root traits has been established allowing further breeding towards increased drought adaptation. Further research, however, is needed to identify suitable regions where the technology of root avoidance can be applied to alleviate the yield reduction in chickpea due to the drought. One of the approaches that need to be pursued next is to conduct multi-locational evaluation of the newly-bred lines over several years and to conclude the agro-climatic regions and soil types where the improved root system can result in better drought yields.

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