

Plant Genomics

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Reaping the benefits of genome sequence and re-sequence information for chickpea improvement

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Chickpea (*Cicer arietinum* L.) is one of the most important annual pulse crops cultivated by resource poor farmers across the globe. Besides being the rich source of human dietary proteins, it improves the soil health through symbiotic nitrogen fixation. Globally it is cultivated on over 13.2 Mha with an annual production of 13.1 million tons and productivity is less than 1 ton per ha much less than estimated potential of 6 t/ha under optimum growing conditions. In order to understand the impact of breeding on genetic diversity and gain insights into temporal trends in diversity in chickpea, a set of 100 chickpea varieties released in 14 countries between 1948 and 2012 were re-sequenced. For analysis, the re-sequencing data for 29 varieties available from an earlier study was combined and genome analysis was conducted for 129 genotypes. Linkage disequilibrium decay was higher in landraces than in breeding lines. Re-sequencing of a large number of varieties has provided opportunities to inspect the genetic and genomic changes reflecting the history of breeding, which we consider as breeding signatures and the selected loci may provide targets for crop improvement. In addition, the analysis provided insights into population structure, genetic diversity, gene loss, domestication and selection sweeps in this crop that is important for global food security in developing countries.

Biography

Mahendar Thudi has obtained his PhD in Plant Sciences from University of Hyderabad, India. His seminal contribution includes genome sequences of chickpea, molecular breeding products in chickpea, genetic resources like TILLING populations (in chickpea and pearl millet) and genomic resources like SSR markers, genetic maps (in chickpea and pearl millet) and high-throughput DNA fingerprinting, genome diversity analysis, marker-trait associations and chickpea physical map. His research articles (>40) are published in high-impact factor journals including, *Nature Biotechnology*, *Scientific Reports*, *PLoS ONE*, *Theoretical and Applied Genetics*, etc. that are widely read and cited.

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