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Transcriptome sequencing of chickpea for discovery of novel genes and genetic variations

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Chickpea is an important food legume because of its high nutritional value and ability to fix atmospheric nitrogen. Very low levels of genetic diversity within cultivated chickpea species has been an important constraint in chickpea improvement. The importance of wild species having important agronomic traits in improvement of chickpea has been realized. Thus, sequencing the transcriptome of wild species will lead to the identification of genetic variations of agronomic use. We sequenced the transcriptomes of cultivated desi (Cicer arietinum) and wild (Cicer reticulatum) chickpea using next generation sequencing technologies. Various softwares and approaches were used to obtain the best optimized assembly. A total of 34,760 and 37,265 transcripts were generated for desi and wild chickpea, respectively. The comprehensive functional annotation identified transcripts involved in various cellular processes. We studied the global gene expression to identify genes exhibiting tissue-specific expression. In addition, we identified several genetic variations (simple sequence repeats and single nucleotide polymorphisms) among the cultivated and wild chickpea. Many of these SSRs and SNPs were found to be present in the tissue-specific and transcription factor encoding transcripts. The experimental validation of few polymorphic SSRs and SNPs showed very good correlation with in silico prediction. The results of this study will help to accelerate research in various areas of genomics and provide a rich resource for exploiting genetic variations for breeding programmes in chickpea.