SurePrint Microarray Design for Chickpea (*Cicer arietinum*) Genomics

Microarray provides a high-throughput means to study the gene expression of thousands of transcripts simultaneously. We have developed, tested and validated a 60-mer oligonucleotide based microarray design with 60,000 carefully validated probes for chickpea, a very important legume crop plant, based on the transcriptome sequence. The chickpea transcripts were re-annotated, orientation reconfirmed by hybridization with RNA, validated and then tested experimentally for genomic DNA and RNA hybridizations. This is an endeavor towards development of genomic resources for chickpea. We believe the platform developed will be very useful for high-throughput gene expression analysis in chickpea for various functional genomics studies.

Microarrays have increasingly become a powerful tool for high-throughput gene expression studies and discovery of novel biomarker genes. Microarrays have been developed for a large number of organisms including plants. However, still the microarray resource is limited for several important plant species.

Chickpea is a very important food legume crop. However, the genomic resources are very limited. Recently, the complete transcriptome of chickpea has been sequenced using next generation sequencing technologies [1,2] at the National Institute of Plant Genome Research under the Next Generation Challenge Program on Chickpea Genomics funded by the Department of Biotechnology, Government of India.

The availability of transcriptome sequence in public domain has provided the opportunity to develop a high-throughput resource for studying the expression of all the transcripts in different biological contexts.

The design of custom oligonucleotide probes have varied applications such as, performing gene expression analysis, miRNA profiling, comparative genomic hybridization (CGH), ChIP-on-chip and SNP analysis. In order to understand the function of different transcripts that would help functional genomics and breeding programs, a validated microarray design was developed jointly by the Genotypic Technology Pvt. Ltd. and the National Institute of Plant Genome Research.

Oligonucleotide probes (both sense and antisense) were designed from chickpea transcriptome using Agilent eArray Tool. Multiple probes were designed for longer transcripts. The best probes for each transcript sequence were selected for designing test arrays with about 400,000 spots.

The 2 X 400K chip was hybridized with DNA and RNA samples of chickpea and microarray analysis was carried out. A total of 73,922 probes were found to be specific. Best probes were filtered from the analyzed data and a total of 61,659 probes were selected to develop the microarray design. Finally, a 8 X 60K gene expression slide was designed. The probes represented 51,444 non-redundant transcripts. The probes were annotated based on their corresponding chickpea transcript and similarity with other plants species. This microarray, in addition to gene expression analysis, can also be used for gene copy number and development of functional molecular markers studies. This product represents a valuable genomics resource for chickpea.

Specifications

Platform	:	Agilent
Part No.	:	G4102A
Design ID	:	037094
Slide Format	:	8 x 60 K
Oligo Length	:	60-mer
Number of Probes	:	61,659
Number of genes covered	:	51,444
Number of Agilent control probes	:	1319
Detection	:	One or two color
Application	:	Gene expression, CNV, CGH

References

Garg R, Patel RK, Tyagi AK, Jain M (2011) De novo assembly of chickpea transcriptome using short reads for gene discovery and marker identification. DNA Res 18, 53-63.

Garg R, Patel RK, Jhanwar S, Priya P, Bhattacharjee A, Yadav G, Bhatia S, Chattopadhyay D, Tyagi AK, Jain M (2011) Gene discovery and tissue-specific transcriptome analysis in chickpea with massively parallel pyrosequencing and web resource development. Plant Physiol 156, 1661-1678.

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