

GeneChip® Medicago Genome Array

The GeneChip® Medicago Genome Array is designed specifically to monitor gene expression in *Medicago truncatula*, *Medicago sativa*, and the symbiotic organism *Sinorhizobium meliloti*. The Medicago Genome Array is particularly useful for agricultural researchers studying legume genomics and symbiotic relationships between nitrogen-fixing bacteria and plants.

This array was created in collaboration with leading Medicago researchers through the Affymetrix GeneChip® Consortia Program and was designed based on content from The Institute for Genomic Research (TIGR) *M. truncatula* gene index, gene predictions from International Medicago Genome Annotation Group (IMGAG), gene predictions from the *S. meliloti* genome, and *M. sativa* expressed sequence tag (EST) information made available by TIGR.

Applications

M. truncatula is an important model organism for plant biology. In addition to its tractable genetic characteristics (small diploid genome and relatively short lifecycle), *M. truncatula* provides opportunities to investigate plant processes that are unique to legumes, such as the interaction with the rhizosphere and formation of symbiotic relationships with nitrogen-fixing soil bacteria and colonizing arbuscular mycorrhizal fungi.

The Medicago Genome Array is useful for genomic approaches to identify the underlying genetic mechanisms that are important for high crop yield, resistance to diseases and insects, and response to environmental factors.

Array profile

The Medicago Genome Array is a 49-format, 11 µm array design that contains 11 probe pairs per probe set. The sequence information for this array was selected from data sources including the TIGR *M. truncatula* gene index, gene predictions from IMGAG, gene predictions from the

Specifications

Number of probe sets, <i>M. truncatula</i>	50,902 + 14 controls
Number of probe sets, <i>M. sativa</i>	1,896
Number of probe sets, <i>S. meliloti</i>	8,305 (gene prediction)
Number of transcripts, <i>M. truncatula</i>	48,116
Number of transcripts, <i>M. sativa</i>	1,850
Number of transcripts, <i>S. meliloti</i>	8,226 (gene prediction)
Number of arrays in set	One
Array format	49
Feature size	11 µm
Oligonucleotide probe length	25-mer
Probe pairs per sequence	11
Hybridization controls	<i>bioB</i> , <i>bioC</i> , <i>bioD</i> from <i>Escherichia coli</i> and <i>cre</i> from P1 bacteriophage
Poly-A controls	<i>dap</i> , <i>lys</i> , <i>phe</i> , <i>thr</i> , <i>trp</i> from <i>Bacillus subtilis</i>
Housekeeping/control genes	beta-actin, GAPDH, glutathione S-transferase, ubiquitin for <i>M. truncatula</i> and <i>M. sativa</i>
Detection sensitivity	1:100,000*

*As measured by detection in comparative analysis between a complex target containing spiked control transcriptions and a complex target with no spikes.

S. meliloti genome, and *M. sativa* EST information made available by TIGR. The array contains more than 61,200 probe sets: 32,167 *M. truncatula* EST/mRNA-based and chloroplast gene-based probe sets; 18,733 *M. truncatula* IMGAG and phase 2/3 BAC prediction-based probe sets; 1,896 *M. sativa* EST/mRNA-based probe sets; and 8,305 *S. meliloti* gene prediction-based probe sets.

Instrument/software requirements

- GeneChip® Scanner 3000
- Affymetrix® GeneChip® Command Console® Software (AGCC)

Ordering information

Part number	Description
GeneChip® Medicago Genome Array	
900734	Contains 2 arrays
900735	Contains 6 arrays
900736	Contains 30 arrays

Supporting products

Part number	Description
GeneChip® 3' IVT Express Kit	
901228	10 reactions
901229	30 reactions

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