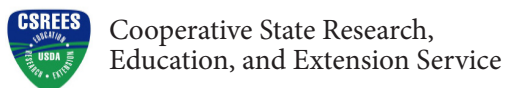




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Honey Bee Genome Sequencing Consortium. 2006. Insights into Social Insects from the Genome of the Honeybee, *Apis mellifera*. *Nature* 443: 931-949.

The newly sequenced genome for honey bee, *Apis mellifera*, remains incomplete and may contain some errors. One way to verify the accuracy of the sequence is by testing how many of the 'predicted genes' are actually active, or transcribed. In this project, the researchers created a genome-wide map, obtained by a custom designed microarray, to assist in validating the sequence. This map confirmed a surprising observation. Unlike the human genome that contains large 'gene deserts' rich in nucleotides Adenine and Thymine, the honey bee genome is rich in the nucleotides Guanine and Cytosine. Results using the new microarray express a 67 percent confidence that the predicted genes were valid. Thus, these genes will be used for the "official gene set" for annotation and analysis by the Honey Bee Genome Sequencing Consortium. This work demonstrates an efficient approach for rapidly developing an unbiased empirical annotation of a new genome. This process substantially reduced the time-lag between sequencing and annotation. As a result, researchers can quickly identify the genes that are relevant to key traits that may lead to improved honey bee pollination of the world's crops.

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