

Master Beekeeper Certification Course: Category #3

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Name: Genetic Control of Colony Traits

Subject: A look at the recently published Honey Bee Genome (*Apis mellifera*), it's uses and potential ramification for the Beekeeping Industry and Human Health.

PROPOSAL

1. What is the Honey Bee Genome?
2. The present uses of the Honey Bee Genome
3. The potential uses and ramifications of the Honey Bee Genome on the Beekeeping Industry and Human Health.

REFERENCES

Detecting and controlling honey bee brood mites (*Varroa jacobsoni* Oudemans) Royce, L. A., L. A. Ibay, D. M. Burgett & G. C. Fisher, 1988.. Extension circular - Oregon State University, Extension Service No. 1272: 1-3.

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ABSTRACT

Honey Bee Genetics: A look at the recently published Honey Bee Genome, it's uses, and potential ramifications for the beekeeping industry

In October 2006, Nature Magazine announced and published the completion of the Honey Bee DNA Genome Project. This means that the entire genetic code of the honeybee is known. From it we can determine the conserved areas of DNA which do not change within species of honeybees and those areas which are not conserved. These consterved areas of DNA can tell us many things about *Apis mellifera* and what is common among all the species. The non-conserved areas can tell us a lot about the differences not only between physical characteristics of honeybees but also the differences in behavior. Using specific DNA markers and techniques, scientists can determine whether a bee from a particular colony is an African bee or European bee, as well as many other differences. There are many ongoing and potential research studies, which will determine what areas of the genome determine particular physical characteristics, biochemical processes, and behavioral patterns. Once these are determined and further studied, we can obtain more information on better management and breeding techniques. Beneficial physical features and behaviors of the honeybee can be promoted while unwanted properties can be eliminated.

Although the ramifications of the Honey Bee Genome are virtually unlimited, I hope to give a brief overview of some of the present and potential uses derived from the publishing of this genome.

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A look at the recently published Honey Bee Genome (*Apis mellifera*), it's uses and potential ramification for the Beekeeping Industry and in the study of human behavior

What is the Honey Bee Genome (*Apis mellifera*)

The Honey Bee Genome Consortium and it's History

The Honey Bee Genome Consortium is a group of researchers who were dedicated to the completion of the draft genome sequence of the Honey Bee. This consortium was led by Richard Gibbs, Ph.D. and George Weinstock, Ph.D., co-directors of the Human Genome Sequencing Center at Baylor College of Medicine in Houston, Tx. Their efforts were supported by the National Institute of Health's (NIH) National Human Genome Research Institute (NHGRI) along with the U.S. Department of Agriculture and other NIH components. The analysis team involved consisted of more than 170 investigators representing nearly 100 research groups from 13 different countries. Dr. Steve Sheppard, a WSU entomologist, was a member of this sequencing team. Baylor College began the sequencing in 2003 with the assistance from Texas A&M, Australian National University and other universities. Dan Weaver of Navasota, Texas, with the help of Dr. Spencer Johnston, entomologist with the Texas Agricultural Experimental Station, initiated in 2001 interest in the need for and potential benefits of sequencing the genome. Their "white paper" to the National Institute of Health (NIH) was accepted and provided funding to Baylor College for research. Dan Weaver (Bee Weaver Apiaries) also provided the honeybee queen for the research. Drones from this queen, being genetically identical, gave enough DNA to complete sequencing the entire honeybee genome. After much DNA sequencing, the entire genome was completed in March 2006 and published in Nature Magazine in October 2006. This Bee Genome information is housed at Texas A&M University.

The honeybee is only the 4th insect whose complete genome was been sequenced. The other 3 are the silkworm, the malaria-carrying mosquito (*Anopheles gambiae*), completed in 2002 and fruit fly (*Drosophila melanogaster*), completed in 2000. "This research puts the honey bee center stage as the first agricultural animal that's been fully sequenced," said Joseph Jen, USDA Undersecretary for Research, Education and Economics.

Weaver said: "Once you have an assembled sequence, then you have to make sense of it. You have to identify which are genes, where are they located, what are the regulatory elements that control the genes, how are these genes are turned on and off, what are the genes they lie adjacent to, how they compare to similar organization of common functionality in the mouse or human or fruit fly."

What is the Honey Bee Genome?

Every living plant or animal cell contains long strands of DNA (genetic code). DNA contains all the information to create, maintain and control each cell in the organism. The molecules of DNA

resemble a long spiral ladder called a helix, and the rungs of the helix are made up of chemical units called nucleotide bases. There are only 4 different nucleotide bases, which make up the entire DNA of all living organisms. Sequencing all of this genetic information consists of identifying the bases and determining their order out of millions of bases present in the genome. Genes are organized clusters or working subunits of DNA, which contain particular sets of instructions, usually coding for a particular protein or you can say that genes dictate the physical and behavioral traits of an organism. Genes are located on chromosomes, which are larger compact spools or packages of DNA which allow these long strands of DNA to fit within each cell. The object of mapping the honeybee genome is to show where genes are located on the chromosomes.

The honeybee genome consists of about 270 million base pairs of nucleotides making up the entire genetic code. This is only 9% as many as the 3 billion base pairs found in the human genome. Even with only 9% of the number of base pairs, the honeybee genome contains 10,157 genes, which is nearly half as many genes, 20,000, contained in the human genome. This is a significant discovery. The honeybee genome is twice as large as the fruit fly but contains about the same number of genes. Again, the object of mapping the genome is to find where the genes are located on the bee chromosomes so we can study physiological and behavioral similarities and differences within all honeybees and with other organisms.

What are the present uses of the Honey Bee Genome

Honeybees are very valuable to scientists as model research organisms. Knowing and analyzing the honeybee genome and which areas or genes which correspond to certain inherent physical and behavioral traits, researchers have been able to come up with DNA markers to use to study different bees. DNA markers are small sections of DNA specific to a certain area in the entire genome which correspond to particular traits. These areas may be present in the genome of all honeybees (conserved DNA), such as number of legs, wings, etc. or these areas of DNA may be present or absent between honeybees depending on differences within honeybees (non-conserved DNA), such as color, or various behaviors. Using markers as primers, scientists determine whether honeybee DNA has come from a Carniolian or Italian bee (Genotyping honeybees). They can compare bees that have better hygiene with bees who do not. A number of these markers have already been discovered and continue to be discovered and are being used to study the honeybee for various differences on many physical, behavioral and metabolic levels. For example: It was found from studying the honeybee genome and using markers that the African, Asian and European Honey Bee had a common origin in Africa. The genome contains information about the many similarities and differences of these subspecies of honeybees.

According to Dr. Steve Sheppard of WSU, scientists have developed new techniques for tracing honeybee relationships by analyzing “single-nucleotide polymorphisms” (SNP’s), which are single base changes within the DNA code. He says by analyzing 1000’s of these SNP’s researchers have tracked the invasion of Africanized bees in the United States.

Even though the honey bee genome contains a similar number of genes as other insects, it has been found that bees contains fewer genes involved with innate immunity, detoxification enzymes and taste receptors while containing more genes for olfactory receptors and novel genes for nectar and pollen utilization. These scientists found that the honeybee genome is more similar to vertebrates than other insects for genes involved with rhythm and biological processes involved with turning genes on and off.

As stated in Nature Magazine, it was discovered that the honeybee genome contains 9 genes involved in the “royal jelly protein family”, not present in the mosquito genome. Genes involved with development are similar to other insects but this is not so for genes that influence sex determination, brain function and behavior.

At the North Carolina Honey Bee Research Consortium (NCHBRC), they are using microarray technology to determine candidate genes that are involved in foraging behavior and the regulation of

reproduction (nursing, feeding and caring for brood). Microarray technology allows these scientists to use thousands of different markers or primers simultaneously on one sample of DNA to determine the presence or absence of specific sequences of DNA involves with a thousands of different traits. These scientists can compare the presence or absence of non-conserved regions on genes responsible for better or worse foraging behavior and/or with better or worse regulation of reproduction. They are also using Quencher-Tether-Ligand (QTL) analysis to determine the genetic architecture of colony-level foraging behavior.

Gene Robinson, professor of entomology at the University of Illinois and his team are using microarray technology to look at how American Foulbrood is effecting bees, which genes are involved in the process, and more importantly, what kinds of immune responses the bee can mount.

The map of the honey bee genome has, in addition to helping understand the foraging behavior of the honey bee, also helped in uncovering the genes that control the very important and accurate thermoregulation of the nest allowing the honey bee to withstand winters well below freezing. It has helped and will further help understand the dance language, hygienic behavior, and the allocation of different workers tasks corresponding to different stresses on colonies.

One of the things discovered from sequencing of the honeybee genome is that the honeybee has the highest rate of genetic recombination of all known animal. Recombination is the process by which genetic material is physically mixed during sexual reproduction. According to research team headed by Dr. Martin Beye the honeybee had an average of 5.7 chiasmata (crossovers) per chromosome as opposed to an average of only 1.6 were found in bumble bees, parasitic wasps, fruit flies, worms and humans. This is because the queen is the only reproductive female in the colony. This high recombination rate boosts the genetic diversity of the population. This in turn helps speed changes in selectively advantageous traits including the slowdown of the spread of parasites and task specialization leading to social complexity, colony performance and fitness.

The potential uses and ramifications of the Honey bee Genome on the Beekeeping Industry and Human Health.

Any scientist interested in a particular physical, biological or behavioral trait of the honeybee, would want to know what gene or genes are involved with these traits. Some of these genes are turned on or off due to changes in colony needs or normal or abnormal environmental changes. Dr. Christine Elsik, an expert in genomics at Texas A&M University said, "Honeybee biologists would have to go to a lot of trouble to sequence in their labs every single gene they are interested in."

The map of the honeybee genome has stimulated much new collaboration between researchers involved in many areas of comparative genomics.

The newly published honeybee genome opens up a new branch of the insect world since it will have implications not only for agriculture, but also honeybee and human health and behavioral research. As stated earlier, genetic markers pertaining to certain areas of the genome are being discovered to analyze certain characteristics of the bees.

Once more of these markers are determined, more studies can be done to discover new knowledge about how some bees react to certain stimuli, how some bees have better hygiene, why (and where on the genome, which genes) some bees are black and others yellow, why some bees swarm more than others, why some bees have better resistance to disease than others, and almost any unlimited number of other attributes to be studied.

One of the discoveries from the genome is that the innate immune system of the honeybee is relatively simple. This means that there is a great deal of room to improve the bee's resistance and with more study, manipulation and research of the honeybee genome, pathogens such as varroa mites and viruses can be better controlled. There are a number of researchers whose primary interest is defining the responses of bees to a range of diseases. They want to characterize genes that are key in the honeybee immune response and then use this information to improve bee breeding and management. Specific genes code for the production of specific proteins; scientists are discovering new genes responsible for an array of these protein and how they are involved with keeping bees healthy.

It was also found that there is a reduced number of genes for insecticide resistance which means that there is a lot of room for improvement in the bees ability to resist certain insecticides. This is potentially allow beekeepers to have fewer losses from unwarranted use of insecticides.

Studying the honeybee genome will also help in the analysis of different disease resistant pathways and metabolic adaptations to various diets. Also, it will gives insights into the longevity of queen honey bees and the sperm stored in the spermatheca.

Honeybees contribute an estimated \$15 billion per year in agricultural value through pollination of fruit, nut and vegetable crops, Weaver said. "It's also estimated that one out of three bites on your table is a direct consequence of honeybee pollination," he said. With this information, you can see that using the knowledge of the honeybee genome, even with small improvements in pollination or foraging behavior, the bee potentially could make a definite difference in increasing food production.

A technique in molecular biology known a RNA interference (RNAi) can potentially change genes (and the corresponding action the gene is specific for) with a population of honeybees. This would make a significant advance in agriculture. RNA (Ribonucleic Acid), similar to DNA, is a molecule used by DNA as a template to translate genetic (Transcription) information into proteins (Translation). RNAi, recently discovered, and for which two scientists (Craig Mello and Andrew Fire) won the Nobel Prize, effectively silences certain genes by administering or injecting into certain regions of the honeybee short double-stranded RNA (dsRNA) complementary to the gene a scientist wants to turn off. This can be used to study honeybee behavioral changes when certain genes are turned off. Better bees can be bred, using RNAi associated with knowledge of the genes discovered within the genome. Bees can be changed by eliminating unwanted attributes or improving more desired attributes, such as, more efficient pollination, increased honey production, decreased swarming behavior, increased hygienic behavior, decreased defensive behavior or a number of similar attributes. Weaver says: "Ultimately, it's about more and better food on your table, easier and better ways to control Africanized honeybees, improving human health and providing new tools for medicine." If scientists can develop techniques to improve the honeybee without the use of potentially dangerous or toxic chemicals to prevent pathogens from destroying colonies, not only would this protect beekeepers but also the environment.

The honeybee is a insect with an incredibly complex social behavior. This makes it an important model for understanding how genes regulate behavior. Studying the genes responsible for different aspects of this social behavior, may lead to knowledge about common mental and brain disorders, such as depression, schizophrenia or Alzheimer's disease. Other honeybee genes can be studied to help understand the mechanisms of their ability to communicate and this may help us better understand human communication, aging, social dysfunction and even infectious diseases.

One of the most interesting things about honeybees is that each bee has a specific function in the hive based on age or needs of the colony. When stressed is placed on the hive, these functions change to maximize the survival of the hive. Job transition involved changes in thousands of genes in the honeybee brain. Some genes turn on and other turn off. This involves particular molecules called transcription factors. Study of these changes in genes and transcription factor binding can help in the study of stress not only in the honeybee but also in humans.

There are many many present uses of the honeybee genome and I couldn't even begin to cover all the things scientists are discovering from it since it was published, let alone all the potential discoveries the genome will help bring about. There are many diverse areas including allergic diseases, gerontology, neuroscience, social behavior and venom toxicology which can be added to the list of areas the honeybees genome will hopefully be of great value.