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Use of Biotechnology in Apiculture

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SUMMARY

The genome sequence of the honey bee, Apis mellifera, has been known since 2006. The bee genome lets bee biologists understand how to tick, and has also produced insights. The genome is rich in odor-related genes, but has comparatively fewer genes associated with taste and immune function, suggesting evolutionary adaptations associated with their unusual lifestyle. This article evolving the facts and roles of biotechnology for honey bees.

INTRODUCTION

Genetically-Modified Honey Bees: A Key Technology for Honey Bee Research

Schulte *et al*. reported the creation of a honey bee containing a "foreign" gene -in this case, one that made some of the cells in the bee glow. This is a first bee research. These researchers did not establish a colony of genetically- modified bees; they only showed that genetically manipulated queens could produced genetically modified drones in the lab. Using genetic technologies in the laboratory to actually manipulate the bee genome in living bees will lead to deeper insights, such as how they fight infections like foulbrood disease or parasites like Varroa mites, as well as the genetic basis for bee behaviour. Today there are many technologies that enable scientists to insert genes into chromosomes. This is because insect-genome-modification technologies requires physically injecting these technologies (usually bits of DNA) into honey bee egg; having the eggs hatch and develop into fertile queens, and then getting the queens to reproduce. However, bees do not like having their eggs injected. The key to Schulte et al success was their innovative approaches to manipulating and controlling bee reproduction and behaviour in the laboratory so they could successfully inject their eggs.

Molecular Marker Approach in Honey Bee

Molecular markers analysis and genetic mapping are valuable tools for identifying chromosomal region affecting behavioural traits. DNS markers have contributed significantly for understanding genetic basis of diversity, mapping medically and agriculturally important genes and quantitative trait loci (QTLs) in honey bee. Molecular markers are used to infer phylogeny and biogeography of insect population and to understand modes of evolution and evolutionary trajectories. DNA markers such as mtDNA, RAPD, AFLP, microsatellite and ESTs are used as popular marker systems in honey bee genetic research.

Genetic Linkage Mapping:

In honey bee, RAPD markers have been extensively used to generate genetic maps for honey bee genome. A saturated linkage map of the honey bee facilitates the characterization of complex social behavioural traits. The higher recombination rates effectively increase the accuracy of linkage mapping and high recombination rate and the low incidence of repetitive DNA should facilitate map-based cloning of genes in the honey bee. Detailed linkage mapping of the honey bee genome has been constructed for use in behavioural genetic studies and for sex determination.

Quantitative Trait Loci Analysis

Quantitative trait loci (QTLs) that influence colony level behavioural traits in bees have been mapped and most of these QTL have been confirmed in independent crosses. QTLs that influence learning performance have been mapped based on the performance of the individual drones. In honey bee, social behaviours are polygenic traits and are influenced by more than one gene referred to as QTL. The two major QTLs that determine the foraging behaviour in honey bee have been identified by employing RAPD markers in backcross population between bees collecting nectar and those collecting pollen .AFLP marker study was conducted to detect binary

trait loci (BTLs) that influence guarding behaviour of individual honey bee *Apis mellifera* L. and to locate genetic markers that are associated with BTLs on genetic maps Two genetic maps were generated ,one for each type colony.

Behaviour Analysis:

Exploiting similar procedure with molecular markers in colony. In honey bee, colony- level behaviours such as stinging behaviour, body size, pheromones alarm level, traits for reversal learning and hygienic behaviour have also been dissected at the level of specific genomic regions. AFLP markers and microsatellites have been used in dissecting the guarding and stinging behaviours in honey bee. In bumblebees AFLP markers employed to study genetic basis of ecological implications of foraging range and nest density behaviours. The genetic regulations of defensive behaviours is now better understood from the mapping of quantitative trait loci (QTLs) associated with the variation in defensiveness. uses of microsatellite markers successfully used specifically in honey bees and bumblebees to identify genes responsible for the diversity in foraging range and mating behaviours host parasitisation and colonization.

Mitochondrial DNA Markers and Phylogenetic Analysis

Phylogenetic studies utilizing mitochondrial RFLP and sequences have largely supported the 3-4 major dispersal lineages postulated by morphometric analysis. Cornute and Garnery et.al explaining the evolutionary pathway of the mtDNA region sequenced by Garnery et.al, explaining the evolutionary change through DNA duplication, elongation, and regression. They extended the sequence data 185 bp into the region of the large ribosomal unit yielding a total of 61 informative sites. Based on both a neighbour-joining and a parsimony analysis (PAUP 3.0 software package) they obtained phylogenetic trees. Cornute and Garnery suggested that both cave-breeding species *A. mellifera* and *A. cerana* diverged about 5.9 million years from common ancestor. Willis et.al also presented a phylogenetic tree on tree on the basis of mtDNA variability. They analysed the CO-II sequence of the wasp (Excristes roborator) as an outgroup.

RAPD Study

The RAPD markers reported here are specific to groups of honey bee subspecies (east European or African), and their representation in populations coincides with the findings of RFLP markers. RAPD have been proved to be a valuable tool especially for further interpopulation studies of *Varroa Jacobsoni* collected from *Apis mellifera* L colonies in California, Texas and Germany, and specimens collected from *Apis cerena* Fab colonies in Malaysia were compared by means of RAPD. Cross section study of larva and pupa pattern of some RAPD products and homology of some developmentally regulated genes in *Apis mellifera and Apis cerena*have been reported and the comparison was performed at the DAN level. In conclusion, the difference between two species at the DNA level is more obvious than that the tissue level.

Genetic Variation and Population Study:

The genetic variation of any species shows undergoing genetic differentiation, a process which can be driven by ecological, evolutionary or historical factors. Honey bee DNA probes have proved to be very useful in a study focusing on Intracolonial variability. Various techniques have been tested and have shown the great potential of the function of the honey bee colony as a whole.

CONCLUSION

Molecular marker data help to distinguish between different species, when there is no other comprehensive way available to do so. In insect, DNA markers are used to provide raw information based on which an ecologist makes estimates of genetic diversity and gene flow between species, identified haplotypes and lineages or predicts migration and colonization history. Honey bee plays and important role in our society and exhibit significant genetic diversity due to geographical and environmental variations. So,it's needed to highlight the recent trends of applications of molecular marker in honey bee studies and explores the technological

advancement in molecular marker tools that may be applied in entomological researches for better understanding of social insect ecology at molecular level.

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