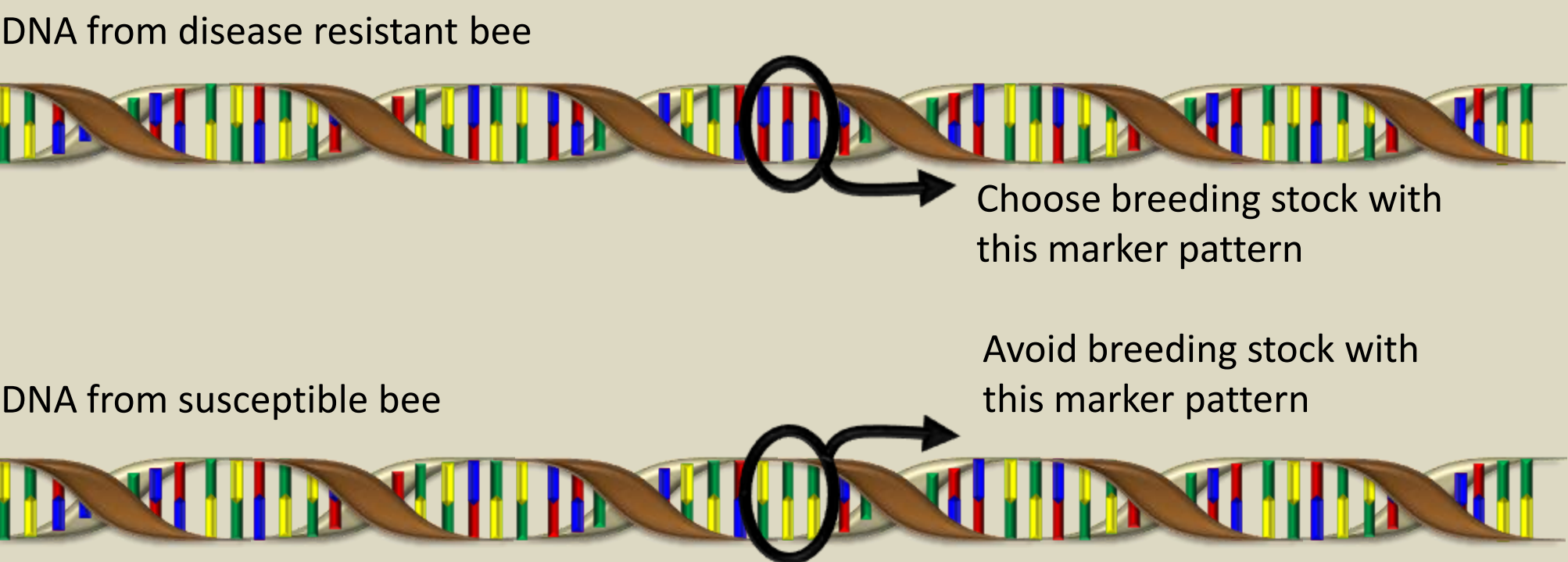


Marker-assisted selection in the honey bee

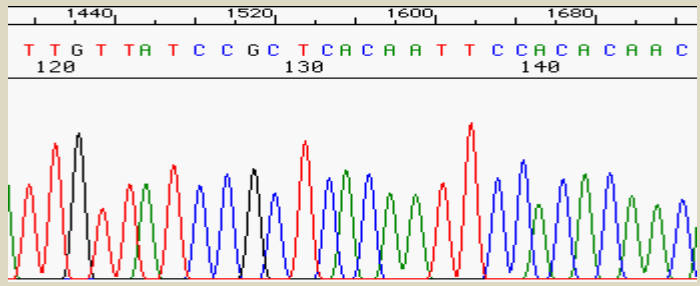
What is marker-assisted selection?

Using unique genomic sequences that associate with a trait of interest to chose which individuals to breed in order to keep the trait in the next generation.

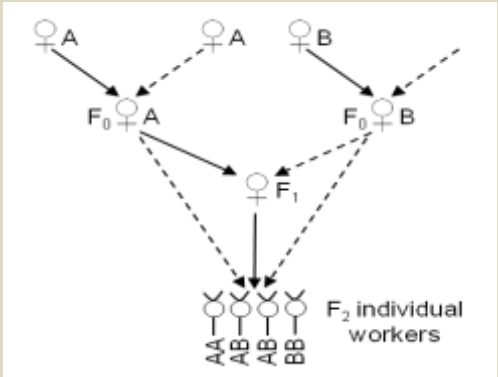


How do you find markers for marker-assisted selection?

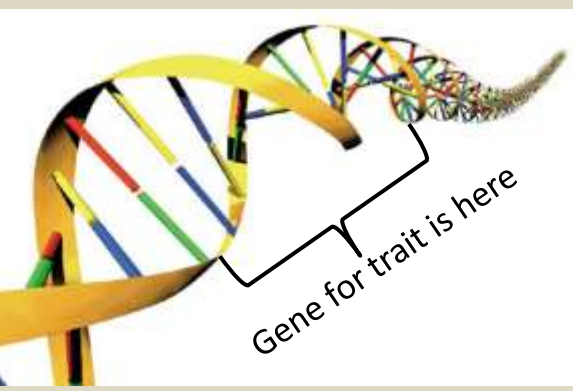
•The honey bee genome sequencing project¹ identified millions of unique genomic patterns that can be used as “markers” for mapping of traits to the genome.



•Develop a backcrossed population of bees that show variability in the trait.



•Screen each bee for the trait then screen markers throughout the genome to find which markers associate with the trait. Those that associate are in or near the gene that controls the trait.



How do you use the markers for breeding?

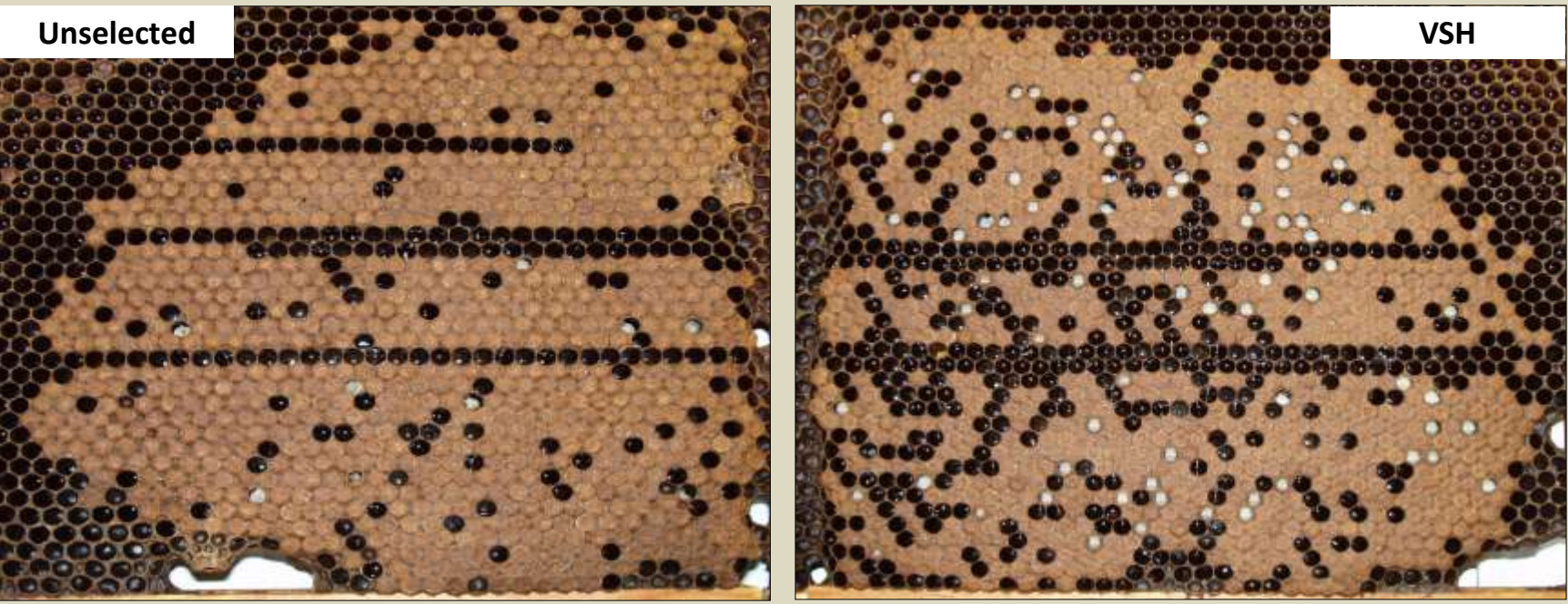
•Laboratory tests identify the genomic sequence by amplifying the DNA surrounding the marker, then treating the amplified DNA with special enzymes that differentiate which pattern each bee has.

•Potential breeding stock is evaluated for the marker in a lab.

•Compatible stocks are bred by instrumental insemination for tightly controlled traits, or by natural mating for less stringent breeding.

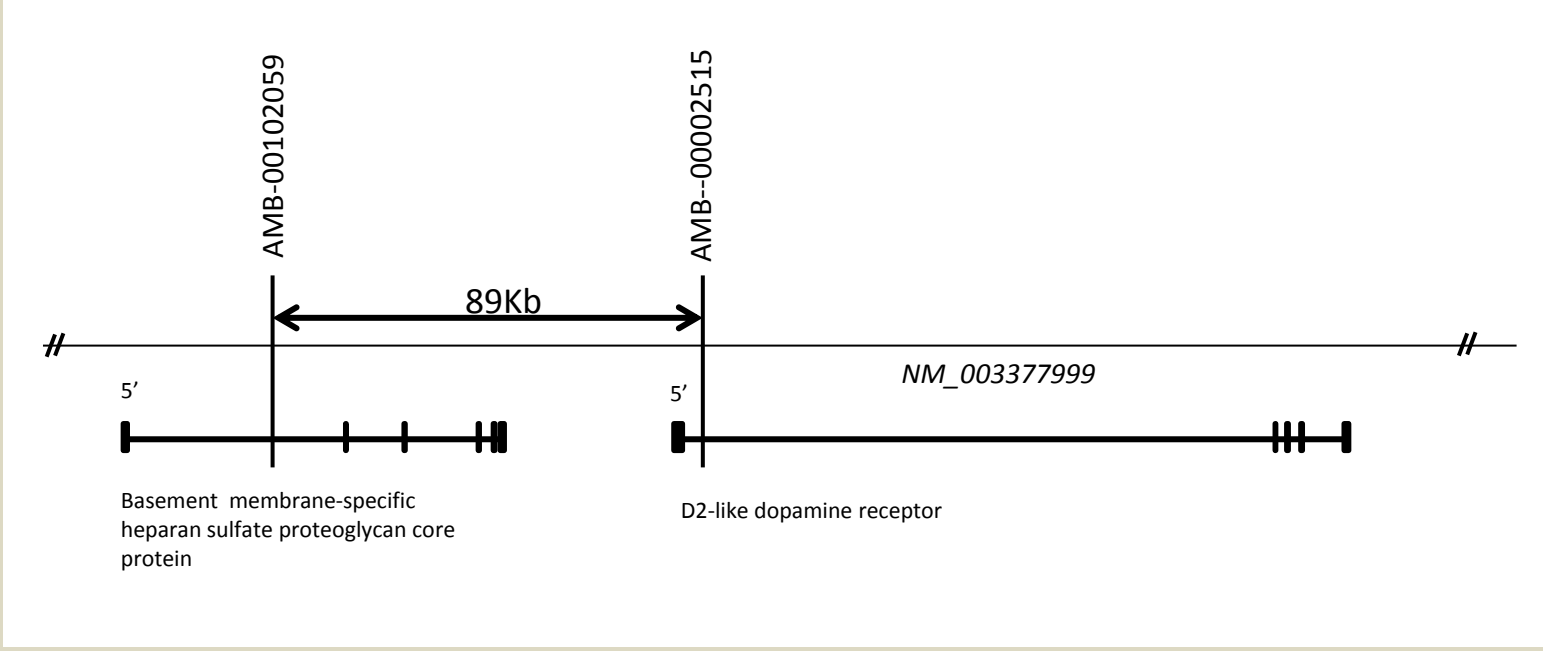
	Resistant	Resistant	Resistant	Susceptible	Susceptible	Susceptible
	---	---	---	==	==	==
Drone source 1	✓					
Drone source 2		✗				
Drone source 3			✓			
Drone source 4				✓		
Drone source 5					✗	
Drone source 6						✗

Varroa Sensitive Hygiene

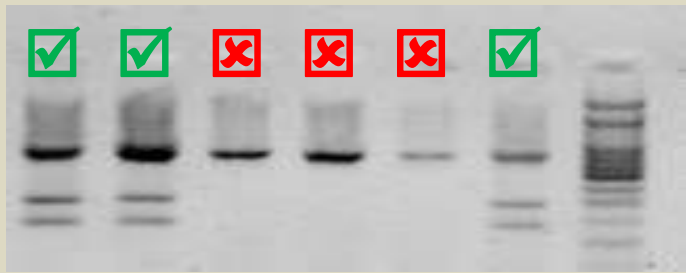


•What is VSH?
A behavior exhibited by adult bees where capped brood that are infested by *Varroa* are preferentially uncapped, inspected, cleaned or removed.

•Current status of mapping
Quantitative trait loci mapping has found a region on chromosome 9 that has strong control over the behavior, and a region on chromosome 1 that has minor control². Fine mapping has narrowed the region on chromosome 9 to an interval of 89kb containing segments of 2 genes.

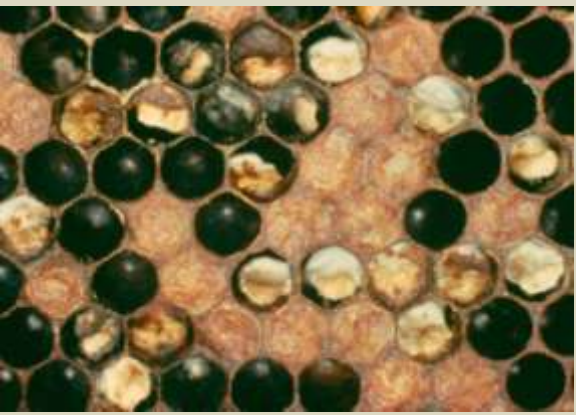


•Markers for the interval
The interval is defined by flanking markers that are easily discernible by laboratory testing.



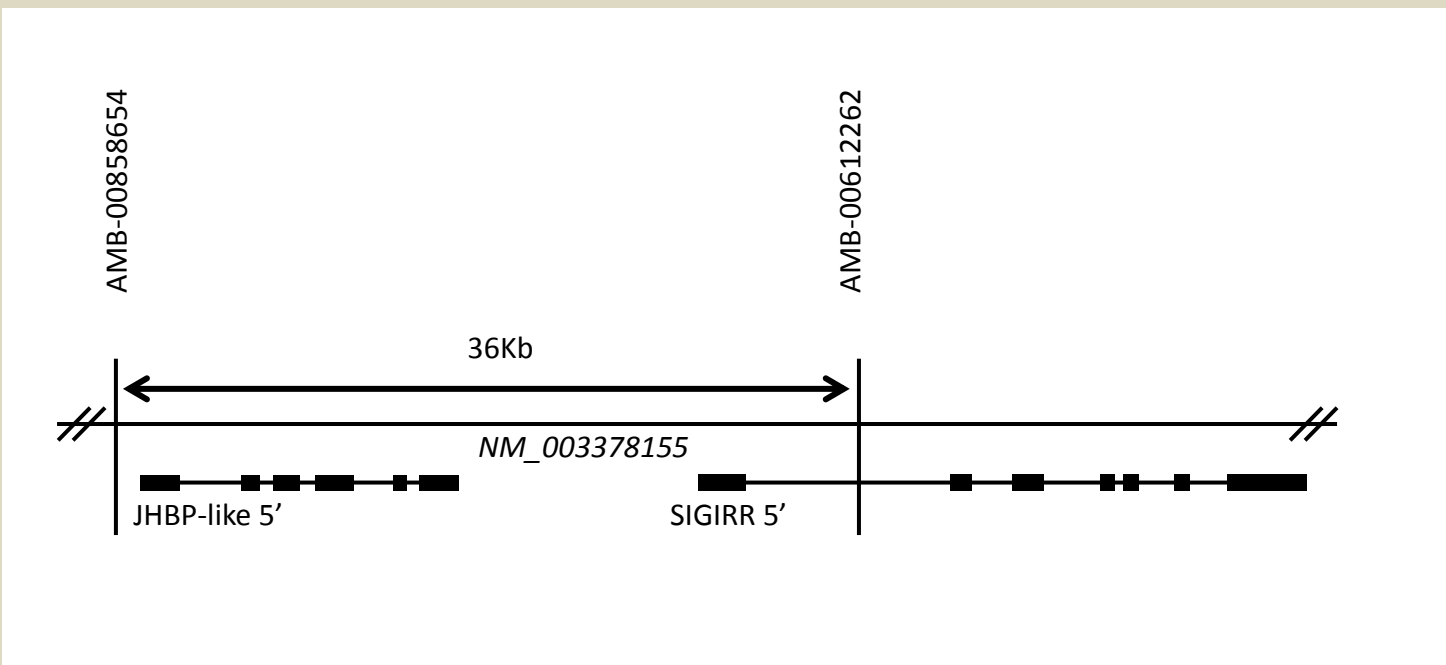
•Current research
Markers are being used to predict the hygienic abilities of VSH colonies, as well as being screened in non-related bee stocks to determine if the markers associate to the trait in non-selected honey bees.

Chalkbrood Resistance



•What is Chalkbrood resistance?
Resistance that is observed in inoculated honey bee larvae where the resistant individuals survive the infection whereas the susceptible larvae form the classical chalkbrood disease symptoms of fungal hyphae formation at the posterior.

•Current status of mapping
Quantitative trait loci mapping has found a region on chromosome 11 that has strong control over the trait. Fine mapping has narrowed the region on chromosome 9 to an interval of 36kb containing 2 genes or gene segments³.



•Markers for the interval
The interval is defined by flanking markers that are easily discernible by laboratory testing.



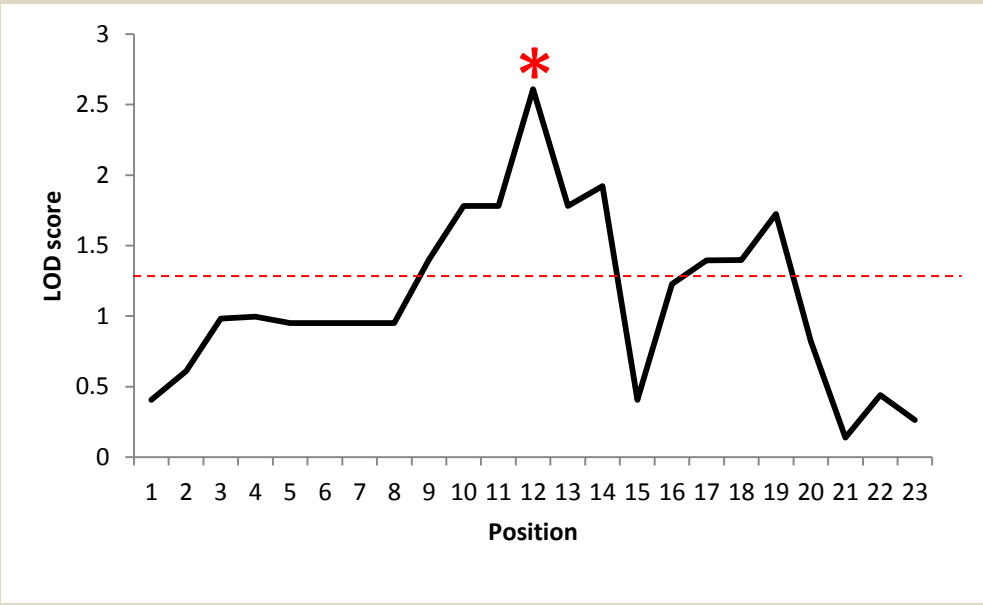
•Current research
Markers are being used to evaluate larvae that are examined in a lab-based bioassay to understand how different strains of the chalkbrood fungus (*Ascosphaera apis*) affect the honey bee. Different mechanisms of resistance may affect the infection process of many strains of fungus.

Tracheal Mite Resistance



•What is tracheal mite resistance?
Resistance that is observed in adult honey bees where either through physiological or behavioral mechanisms the infestation of tracheal mites is reduced or inhibited.

•Current status of mapping
Quantitative trait loci mapping has found a region on chromosome 7 that has moderate control over the trait.



•Markers for the interval
Markers were evaluated and found to not validate in a related and selected population⁴.

•Current research
Additional populations of honey bees are being bred for the resistance trait. While the markers have not proven successful so far, they will be evaluated in subsequent populations.

References

- ¹ The Honeybee Genome Sequencing Consortium et al. (2006) *Nature* 443, 931-949
- ² Tsuruda, J.M., Harris, J.W., Bourgeois, A.L., Danka, R.G., Hunt, G. (2012) High-resolution linkage analyses to identify genes that influence Varroa Sensitive Hygiene behavior in honey bees. *PLoS ONE*
- ³ Holloway, B.A., Tarver, M.R., Rinderer, T. (2013) Fine mapping identifies significantly associating markers for resistance to the honey bee brood fungal disease, Chalkbrood. *Journal of Apicultural Research* 52(3)
- ⁴ Bourgeois, A.L., Villa, J., Holloway, B.A., Danka, R.G., Rinderer, T.E. Molecular genetic analysis of tracheal mite resistance of colonies and individual honey bees. *Submitted to Journal of Apicultural Research*