Marker Assisted Selection

Biotechnology in Action

Traditional Tree Breeding

◆ The selection of trees is based on visible traits (phenotypes).

◆ Grafts or seeds are taken from selected trees.

◆ Tree breeders or scientists then crossbreed the selected trees and grow them in test plantations.

◆ Then they perform progeny testing. Trees are evaluated for how well they meet the growers objectives such as yield, adaptation to particular conditions, pest-resistance, etc.

◆ Growers then select the best and repeat the whole process. It is time consuming and results are sporadic.

Marker Assisted Selection (MAS)

Marker assisted selection (MAS) is an indirect selection process where a trait of interest is selected not based on the trait itself but on a marker linked to it. For example if MAS is being used to select a tree with a disease, the level of disease is not quantified but rather a marker allele that is linked with disease is used to determine disease presence. The assumption is that the linked allele associates with the gene of interest. MAS can be useful for traits that are difficult to measure, exhibit low heritability, and/or are expressed late in development. Scientists and breeders use this process for breeding trees.

Genetic markers

Genetic markers are sequences of DNA that have been traced to specific locations on the chromosomes and associated with particular traits. They demonstrate polymorphism, which means that the genetic markers in different organisms of the same species are different. An example of a genetic marker is the area of the DNA which codes for blood type in humans: all humans have and need blood, but the blood of individual humans can be very different as a result of polymorphism in the area of the genome which codes for blood.

Genetic markers

Some genetic markers are whole genes, while others are snippets of DNA which do not necessarily serve a function. They can appear at one point in the genome, or in multiple areas, sometimes on different chromosomes. Genetic markers can also consist of strands of repeating DNA .

Identifying new markers is a painstaking process which includes processing DNA from related individuals to find commonalities which could be used to pinpoint particular traits. Especially when markers appear at multiple points in the genome and interact with each other, tracking them down can be very challenging.

Utilizing MAS

- Many traits are genetically complex and involve many genes.

- Selecting individuals from a population based solely on phenotype would not produce desired offspring.

- Markers have been found that are always associated with the desirable phenotype.

- Example: Frost resistance in trees is a genetically complex trait.

- Markers have been used to identify offspring of parent trees with frost resistance.

MAS and frost resistance

- DNA is extracted from selected trees.

- Electrophoresis is used to identify individuals with the desired marker.

- Marker indicates presence of frost resistance.

MAS analysis

Marker for frost resistance

Individuals 1, 3, 4 and 6 have the marker for frost resistance in their genotype. Individuals 2, 5 and 7 do not have the frost resistance marker.

Future of MAS

- Has the potential to reduce the time it takes to create new seed plantations.

- Could produce a "better" tree in years instead of decades.

- Only major species of trees will be utilized.

- Not enough studies to determine if the process is cost effective on a commercial basis.

- May be utilized to save trees such as the American chestnut.