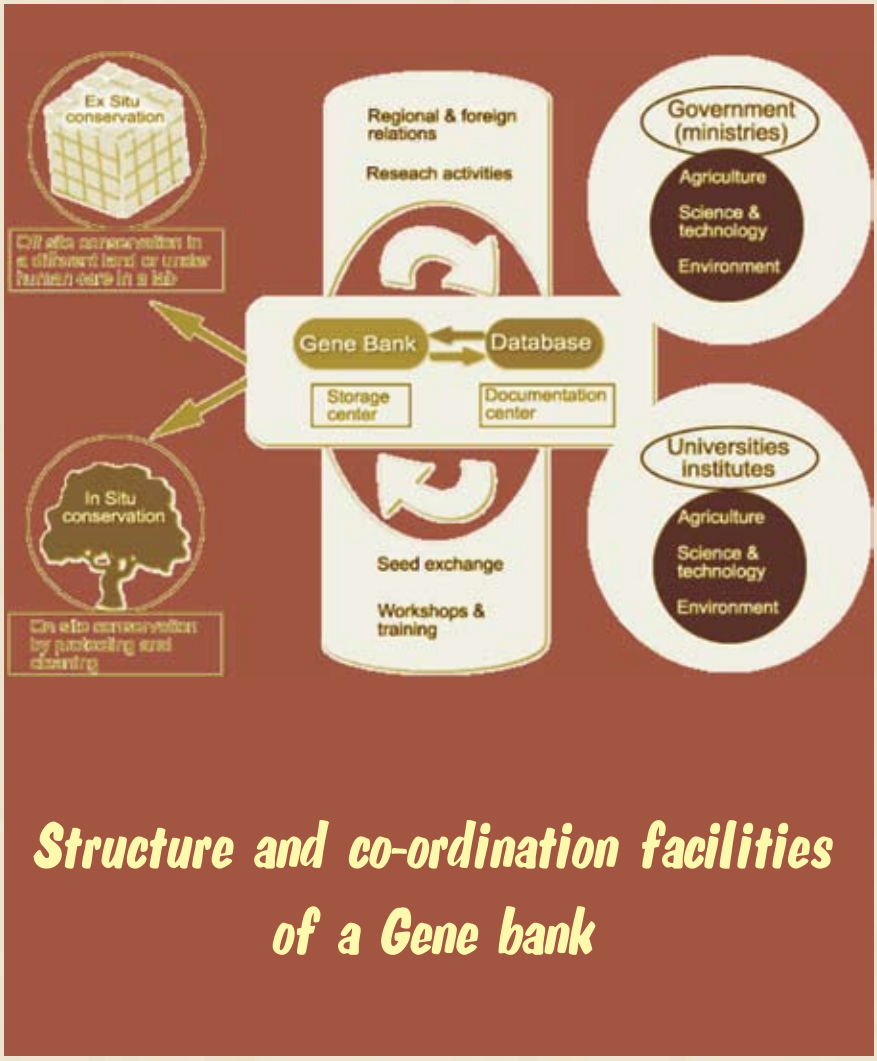
Scene Twelve



Structure and co-ordination facilities of a Gene bank

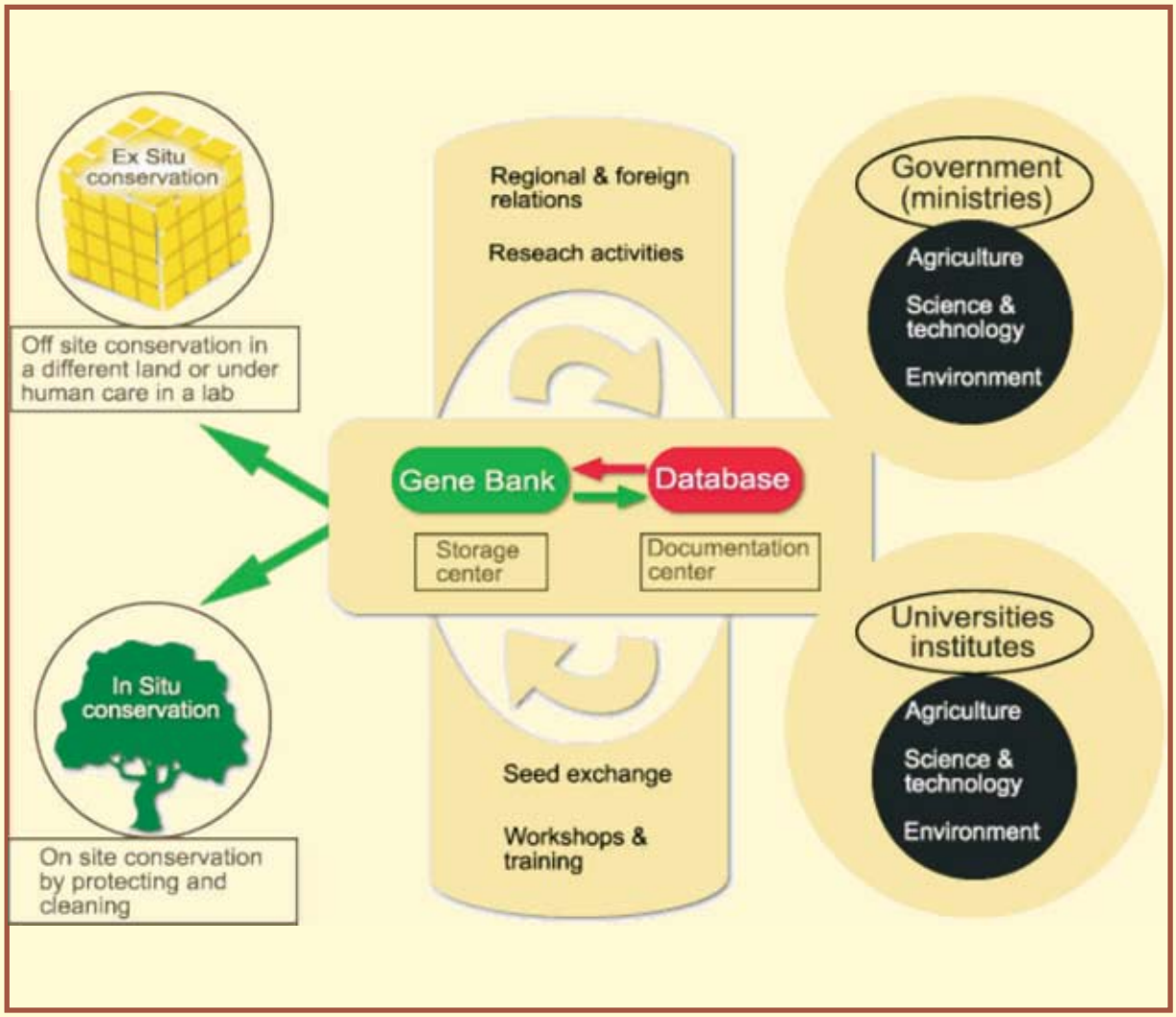
Monday afternoon

Scene Twelve: Monday afternoon

Place: Classroom

Characters: Efia, Ekow, all other students and the biology teacher

Situation: Biology class: discussion about gene banks, DNA and MAS



Structure and co-ordination facilities of a Gene bank

Various activities involved in Gene bank maintenance

Scene Twelve: Monday afternoon

Place: Classroom

Characters: Efia, Ekow, all other students and the biology teacher

Situation: Biology class: discussion about gene banks, DNA and MAS

Teacher:

Good morning everyone. Do you recall where we stopped in our last class?

Ekow:

Yes. Last Friday we discussed tissue culture and micropropagation and how they help in PGR conservation. But, I would like to know more about gene banks.

Teacher:

Yes. But first, let me ask you a question to see how much you know about gene banks and then I will decide what to talk about in today's class. Can someone tell me what gene banks are?

Dhakiya:

A gene bank is a place where genetic information is stored.
(***Ekow butts in***.)

Ekow:

No, it is a facility for *ex situ* conservation, where seeds, tissues or reproductive cells of plants are kept.

Teacher:

Ekow, the strict definition for gene bank is "a place where genetic information is stored". *In situ* conservation of plants in the fields are also considered as gene banks when plants are conserved for the purpose of propagation, storage and distribution. Any other definitions?

Efia:

A gene bank is a place where a collection of germplasm in the form of seeds, pollen, DNA and even whole plantlets is collected and maintained. If you need a specific sample, you can get it from there. That is why it is called a bank.

Lab workers at a gene bank at one of the Consultative Group of International Agricultural Research centers in Mexico, sorting through seeds and selecting high-protein corn kernels for preservation in cold storage units.

This gene bank in Ethiopia stores the seeds of hundreds of wild varieties of crops at sub-zero temperatures for up to 50 years. Every five years the collection is tested for its germination ability.

Various ways of storing seeds in gene banks:
individual varieties of seeds are packed and labeled (1&4) in bottles, (2,5&6)in packets and (3) in sacks in a room at a cold temperature.


Sabola

Sabola:

Aren't genes from animals also stored in gene banks.


Teacher

Teacher:

Yes. You are all correct! In simple words, a gene bank is a place where you can go in search of genetic resources. Can anyone tell me about plant gene banks?

Daila:

A plant gene bank stores material from plants of interest for future use in agriculture. It also stores information on the species in question and maintains a database on the PGR conserved within a country.


Pepukayi

Pepukayi:

Are cassava varieties stored in gene banks?


Teacher

Teacher:

Yes, Pepukayi. Many cassava varieties are also stored in gene banks.

Sabola:

Do all gene banks have a similar structure inside?


Sabola

Teacher:

Gene banks can be *in vitro* or *in situ* gene banks. Can anyone tell me what *in vitro* means?


Sabola

Sabola:

Yes! We discussed this when we talked about tissue culture. It means the process happens in an artificial environment.

Teacher:

Very good. An *in situ* gene bank means conservation of adult plants, in the field or in greenhouses.


Teacher

Gamba:

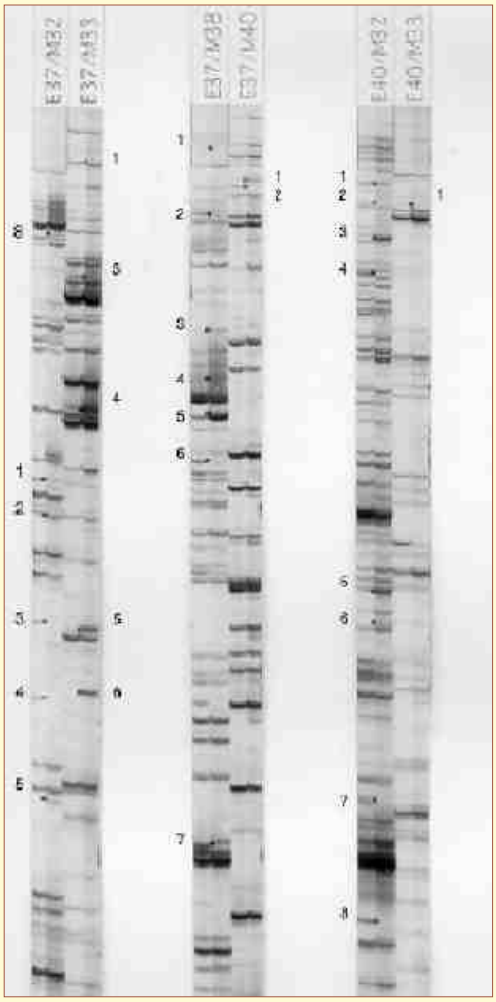
So, *in vitro* gene banks conserve parts of plants, cells and tissues in artificial conditions while *in situ* gene banks conserve complete plants under natural conditions.


Gamba

Teacher:

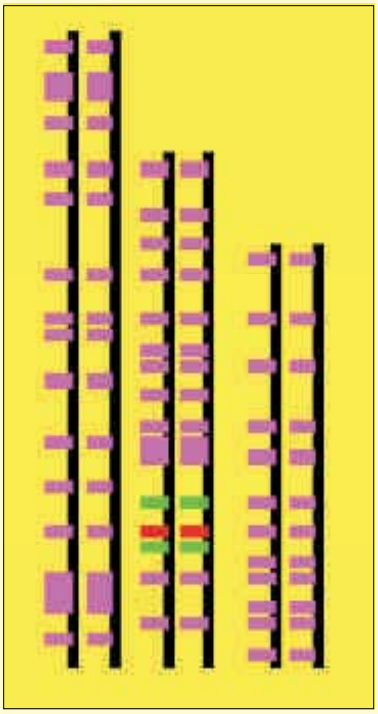
Yes. Originally, gene banks maintained information on the name of the crop variety and on some basic characteristics. But today, new techniques enable us to create gene maps and discover precise information on the roles that specific genes play. As a result, new varieties with desired traits can now be bred much faster. Does this make sense Gamba?


Teacher



The "DNA fingerprint" on the right shows typical results of Polymerase Chain Reactions (PCR) from plant DNA. In each pair of adjacent lanes in this gel image, DNA from barley cultivars Proctor (left lane) and Nudinka (right lane) are amplified. The results using six different primer sets (indicating the markers) are shown, for a total of 12 lanes. DNA differences (polymorphisms) between Proctor and Nudinka, marked with numbers, appear as a presence or an absence of bands on the gel. For example, the band labeled 1 for a specific (primer) marker is present in cultivar Proctor (left) but absent in cultivar Nudinka (right). This band represents a genetic locus at which the DNA sequence is different between the two cultivars. Between bands 1 and 2 is an unmarked band that is shared in common between Proctor and Nudinka. This band represents a different chromosomal locus that is identical between the two cultivars.

Source: University of Manitoba, Canada



Reconstituted elite cultivar:

A selection of plants in a given generation of backcross generation is done by scoring dozens of markers using DNA from individual plants. Each band on a gel can be scored as coming from one parent (presence of a band) or the other parent (absence of a band). In the figure (left), the map locations of markers from the elite cultivar are shown in magenta, and those from the wild parent are shown in green. If we screen enough plants, we can find those plants that maximize the number of markers derived from the elite parent, while retaining the important gene of interest. In this map, a marker located very close to that gene is indicated in red. The majority of the time, if we have the marker, we have the gene.

A cultivar is a cultivated plant that has received a name under the International Code of Nomenclature for Cultivated Plants


Gamba

Gamba:

I think so. But what is a gene map?


Teacher

Teacher:

A gene map is a graphic representation of the arrangement of genes or DNA sequences on a chromosome. It is also called a genetic map. New technologies help crop scientists to catalogue the gene bank samples through identifying the traits of each variety and identifying and marking the genes responsible for key traits.


Dhakiya

Dhakiya:

A trait is a specific characteristic of a plant, right?


Teacher

Teacher:

Yes, Dhakiya. Traditionally farmers select the best plants in their fields and grow them again. This is called selection and it can take years to get a new variety. Now crop scientists can select a variety known to hold a specific trait, "mark" the gene responsible for that trait and cross it with another known variety. The offspring of these plants are then tested to determine if they hold the marked gene. Those that have it are selected for further tests and eventual field planting.


Efia

Efia:

So the marker gene is the one that marks a specific trait in a plant and that trait can be identified from the plant's genetic map. But, how does a gene map help conserve PGR?


Teacher

Teacher:

A gene map on its own does not conserve PGR, Efia. But when you have a gene map of a plant, the knowledge you get from it, helps you to conserve a plant and to use its traits for breeding. The techniques that are generally used for accurate rapid detection are:

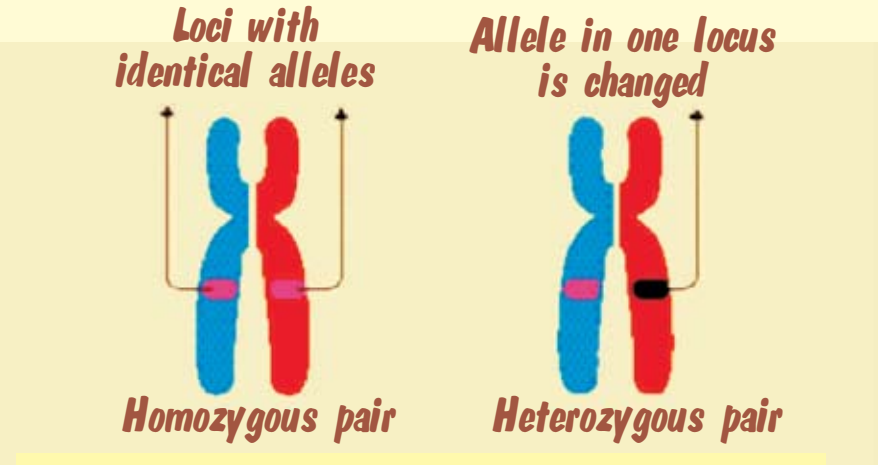
1. **DNA fingerprinting**: to find the degree of relationship between plant populations and also to measure the genetic distance between plant populations.
2. **Gene mapping**: to develop a map of markers using standard reference plant DNA.
3. **Identification of genetic markers:** to provide information on the presence or absence in an individual plant of specific genes, that are associated with plant traits.


Dhakiya

Dhakiya:

Genetic markers are responsible for identifying the genes that code for specific traits of a plant, right?

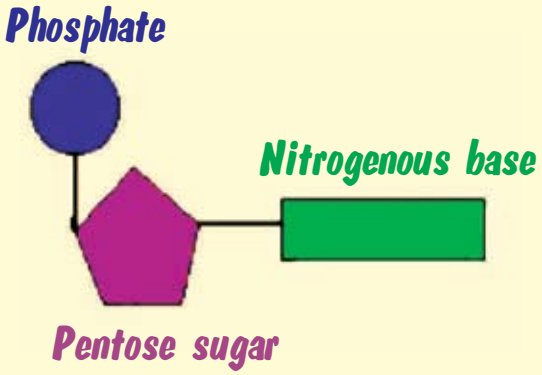
Chromosomes and Loci



A drawing of an homologous chromosome under conditions of homozygosity and heterozygosity

Homologous chromosomes are those that pair during meiosis, have the same morphology, and contain genes governing the same characteristics.

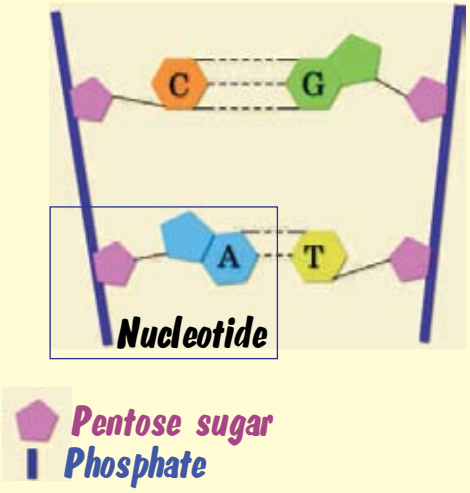
Nucleotide



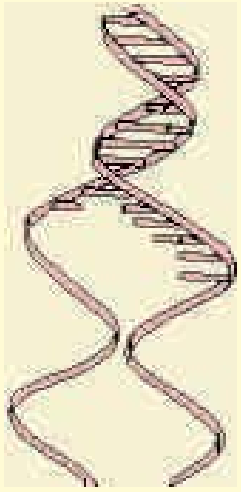
Nitrogenous bases

- A Adenine
- G Guanine
- C Cytosine
- T Thymine

Nucleotides bound by hydrogen bonds to form a double strand



DNA double helix



Teacher:


Teacher

Yes, Dhakiya. Most such traits are influenced by multiple genes. The identification of DNA markers associated with specific loci will allow their use in marker-assisted selection or MAS.

Ekow:


Ekow

What is a "loci" and how does a marker assist in selection?

Teacher:

Ekow, the word "loci" is plural and the singular is locus. Locus is the specific site of a particular gene on its chromosome. Before we discuss MAS, I would like to know more about your knowledge of DNA.

Ekow:


Ekow

But, must we know about DNA to understand MAS?

Teacher:


Teacher

Oh yes, you need to, because knowing DNA structure is essential in order to study anything related to biotechnology tools. The genes in the DNA "code" for various "proteins". Proteins are very important and there are thousands of proteins in a plant encoded by hundreds of genes. Only a small fraction of the DNA sequence carries genes that code for proteins, while the remaining DNA represents non-coding sequences

Sabola:


Sabola

In that case, please tell us more about DNA. I do not remember much about it.

Teacher:


Teacher

Yes, of course. All living things are made up of cells that contain the genetic material called deoxyribonucleic acid or DNA. DNA transmits genetic information. You can say that genes are made up of DNA. The DNA is packaged into chromosomes which are located within the nucleus of all cells. Every cell in the body contains all the chromosomes that collectively make up the genome of that organism.

Efia:


Efia

Is a plant genome then, a collection of all the chromosomes of that plant cell? Could you tell us a little bit more about DNA structure, please?

Teacher:


Teacher

A single DNA molecule is made up of nucleotides. There are four of them called the adenine, thymine, cytosine and guanine. There is a basic rule regarding the way in which each of these nucleotides pairs with another using hydrogen bonds. Adenine will bind only to thymine with two bonds, and cytosine will bind only to guanine with three bonds. Two strands of the DNA are shaped like a double helix.

Phenotype

The phenotype of an individual organism is either its total physical appearance or a specific manifestation of a trait, such as size, color, or behavior that varies between individuals.

White skin | Red skin | Thin and long | Round and short

Phenotype *is determined to a large extent by genotype, or by the identity of the alleles that an individual carries at one or more positions on the chromosomes. Many phenotypes are determined by multiple genes and influenced by environmental factors. Thus, the identity of one or a few known alleles does not always enable prediction of the phenotype.*

Genotype

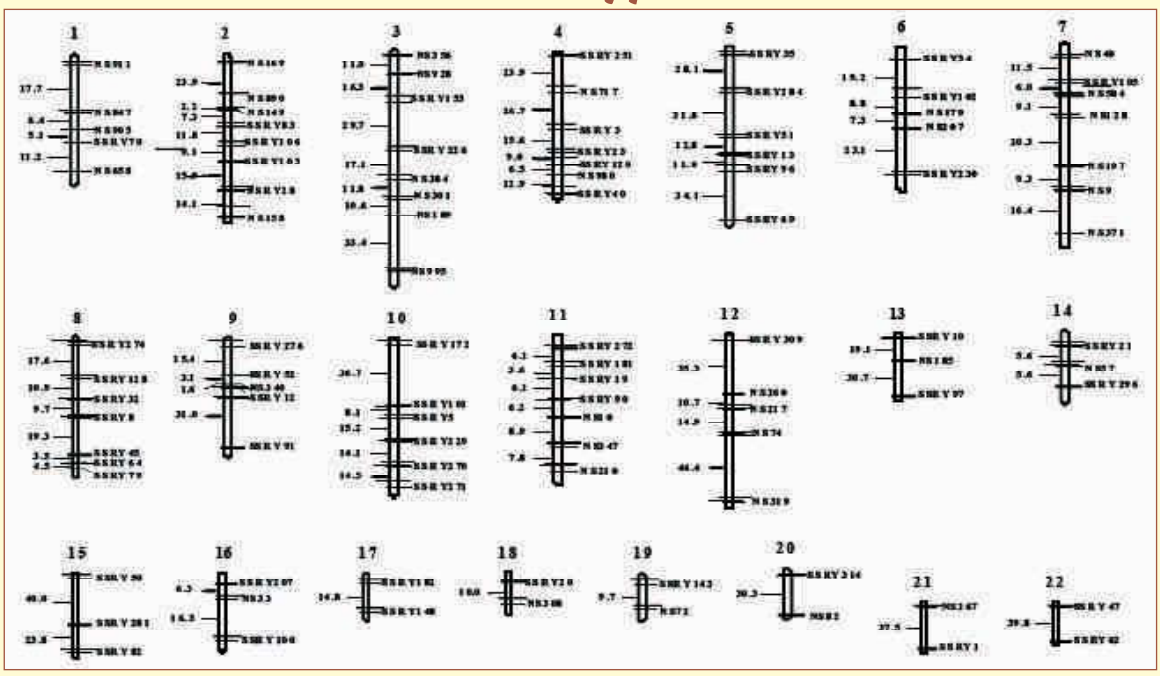


Figure above: A genetic linkage map of casava based upon a F2 cross and SSR markers.
Source: E. Okogbenin, J. Marin & M. Fregene; International Center for Tropical Agriculture, CIAT, ,Cali, Colombia

The genotype of an organism represents its exact genetic makeup, that is, the particular set of genes it possesses. The term "genotype" refers, then, to the full hereditary information of an organism. A gene map is a graphic representation showing the relative locations of each known gene on a particular chromosome. A gene map can also include DNA sequences on a chromosome. A gene map is used to locate and identify the gene or group of genes that determine a particular inherited trait. The mapping of a set of genotypes with a set of phenotypes is sometimes referred to as the genotype-phenotype map.

Efia:

The DNA carries the code for the appearance and the behaviour of the plant?

Teacher:

Yes, the genetic material of an organism is organized into sets of chromosomes. In addition to this, every gene has two copies which are called "alleles". The sexually produced new plant receives one allele of each gene from its mother, and one of each from its father. The visible characteristics or phenotype of the plant and the genetic make-up or the 'genotype' of the plant is determined by its DNA.

Dhakiya:

So, it is easy to see the phenotype by just looking at the plant but to know the genotype we have to study the DNA of the plant.

Teacher:

Yes, Dhakiya. But genotype and phenotype are not always directly correlated. Some genes express only a given phenotype under certain environmental conditions. Therefore, expression of phenotype is a result of interaction between the genes and the environment.

Ekow:

Very confusing. Could you explain how a phenotype can be the result of multiple genotypes?

Dafina:

Wait. But what about the genotype of a plant? When does the genotype express a specific phenotype due to environmental conditions?

Ekow:

Dafina, that is a brilliant question! Teacher, can you give us an example?

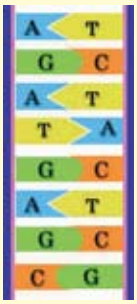
Teacher:

OK, I will give you a very simple example. We can actually do this experiment in the class. We can plant two bean seeds from the same plant in two different pots and let them grow into small plantlets. Then we, place one in a dark room and the other in bright sunlight. Will we see any difference in the appearance of these two plants?

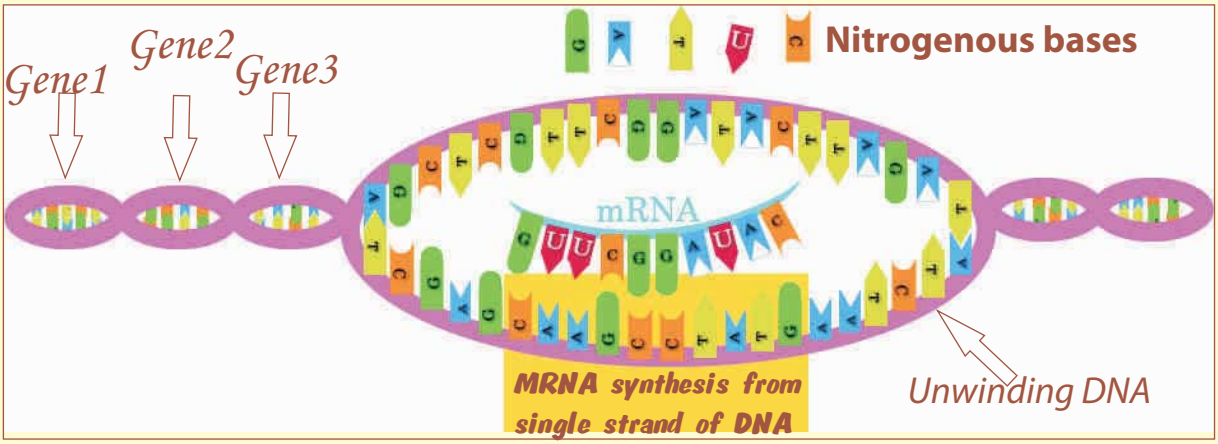
Gene expression

Nitrogenous bases

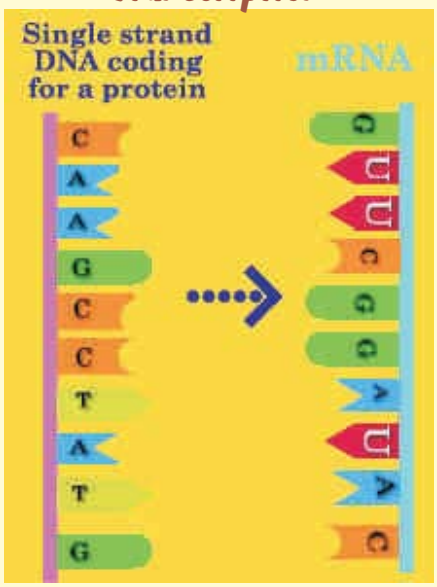
Double stranded DNA



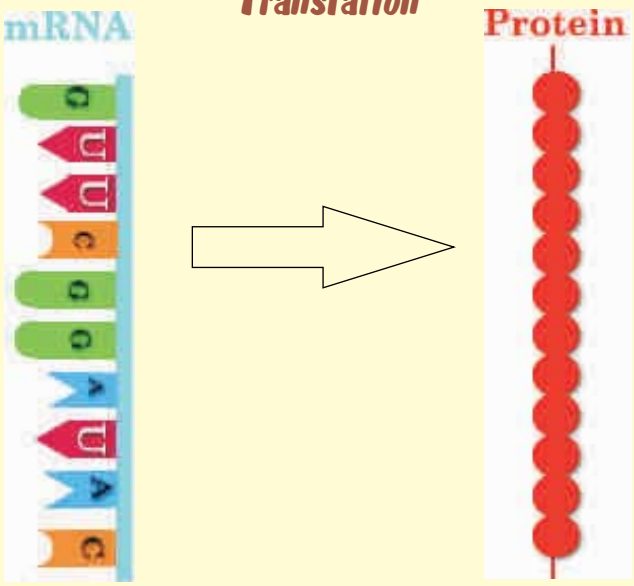
Message coded in a "gene" in DNA is first re-written (transcribed) into mRNA. In mRNA, Adenine binds with Uracil(U) instead of Thymine. MRNA is a single strand molecule.



Transcription



Translation



Dhakiya


Dhakiya

Yes. The plant in the dark room will grow taller than the one in bright light and will make less chlorophyll. Wow, so the gene expression is affected by the changed environmental condition and we can see it in the plant with our own eyes!

Thandiwe:


Thandiwe

In this case, the environment determines the phenotypic pattern of the expression which we can see. This process must involve expression of genes under certain environmental conditions. Can you give us an example?

Teacher:


Teacher

Thandiwe, do you remember that DNA is made up of four different nucleotides that code for proteins and may also even be responsible for regulating protein production? DNA sequences that encode a gene can differ between individual plants. These differences lead to genetic variation.

Ekow:


Ekow

Does this variation also affect the proteins?

Teacher:


Teacher

Yes, Ekow. The difference in the nucleotide sequence can affect the encoded proteins. A change in the DNA nucleotide sequence can also change the production of proteins. These have an effect on the phenotype.

Dhakiya:


Dhakiya

Does this mean that it is easy to know which gene is responsible for which characteristic of a plant?

Teacher:


Teacher

Well, yes and no. Scientists still do not know the full picture. Genetic variation is phenotypic variance in a population that is due to genetic heterogeneity. The interesting point is that genetic variants can differ from each other by the sequence of a "single" base pair. When there is a single base pair difference, it is called single nucleotide polymorphisms or SNPs, and is pronounced "snips". SNPs are a type of marker used in marker-assisted selection. They are commonly the basis of genotyping tests and are precise.

Dene:


Dene

Are they called markers because they help identify a trait?

Ayalew examines plant tissue regeneration from leaf discs transformed with the plant marker gene. Photo by R. Maxey, The University of Tennessee Institute of Agriculture
Source: Seed Quest News

On the DNA double helix, the "marker" (the green coloured area) acts as a red flag to indicate the presence of the gene of interest

Quantitative Trait Locus (QTL) is a polymorphic locus which contains alleles that differentially affect the expression of a continuously distributed phenotypic trait. Usually it is a marker described by statistical association to quantitative variation in the particular phenotypic trait that is thought to be controlled by the cumulative action of alleles at multiple loci.

QTL example in cassava breeding

In recognition of the importance of cassava improvement for dry areas and to develop cassava breeding for drought tolerance, molecular markers were studied. This study was funded by the **CGIAR challenge program**

This project planned *to develop single nucleotide polymorphism (SNP) markers throughout the genome to identify favorable alleles related to drought tolerance in these mapping populations. In order to achieve this goal, a physical map of the cassava genome was generated that allowed the development of SNP markers that were uniformly distributed around the genome. This facilitated the identification of quantitative trait loci (QTL) associated with drought tolerance in a high-throughput manner. These markers were used for marker-assisted selection of favorable traits.*

Quantitative trait loci (QTL) associated with drought tolerance were to *be identified by high-throughput genotyping of validated SNPs in two of the mapping populations. Additional SNP markers* were to *be developed around the "hot spots" identified after QTL mapping to allow marker-assisted selection of desirable QTL alleles for molecular breeding* of *drought resistance in cassava.*

Teacher:

Yes! Marker-assisted selection is a biotechnology tool that helps to select the economically important characteristics of trees and crops for breeding. It has the potential to allow rapid, reliable and effective selection. The efficiency and effectiveness of using molecular markers, associated with the selection of useful characteristics, greatly help breeding programs.

Ekow:

What is a marker? Is it a special gene? A part of DNA?

Teacher:

Molecular markers are like constant landmarks in the genome. They are identifiable DNA sequences, found at specific locations of the genome. They are transmitted from one generation to the next. They can be identified only by DNA tests.

Ekow:

So, how does MAS play a role in this matter?

Teacher:

The idea behind using marker-assisted selection in this process is that the genes with significant effects can be used specifically for selection of a specific trait. Some traits are controlled by single genes, but many important traits are complex and controlled by a number of genes. These complex traits are usually governed by a number of genes known as Quantitative Trait Loci (QTLs). Looking for the pattern of inheritance at such QTL assists the selection process.

Dhakiya:

Why is it called marker-assisted selection and not marker-based selection?

Teacher:

The word "assisted" implies that the selection is also influenced by other sources of information. One such source of information is the historical performance record.

Dhakiya:

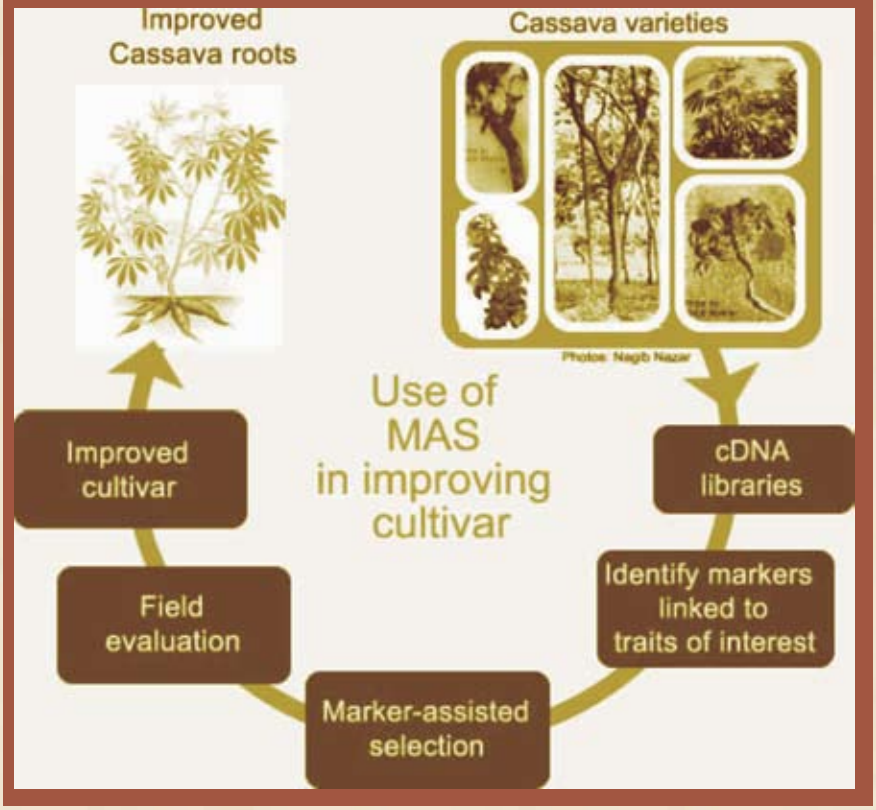
This means that in order to have a good result with MAS we must also consider the historical performance records. Tell us about historical performance records.

Teacher:

No not now, it is getting late and it is somewhat complicated. You already have a lot to remember. Soon I will explain the meaning of the historical performance records. Enjoy your evening, everyone.

Scene Thirteen

Marker-assisted selection and conservation



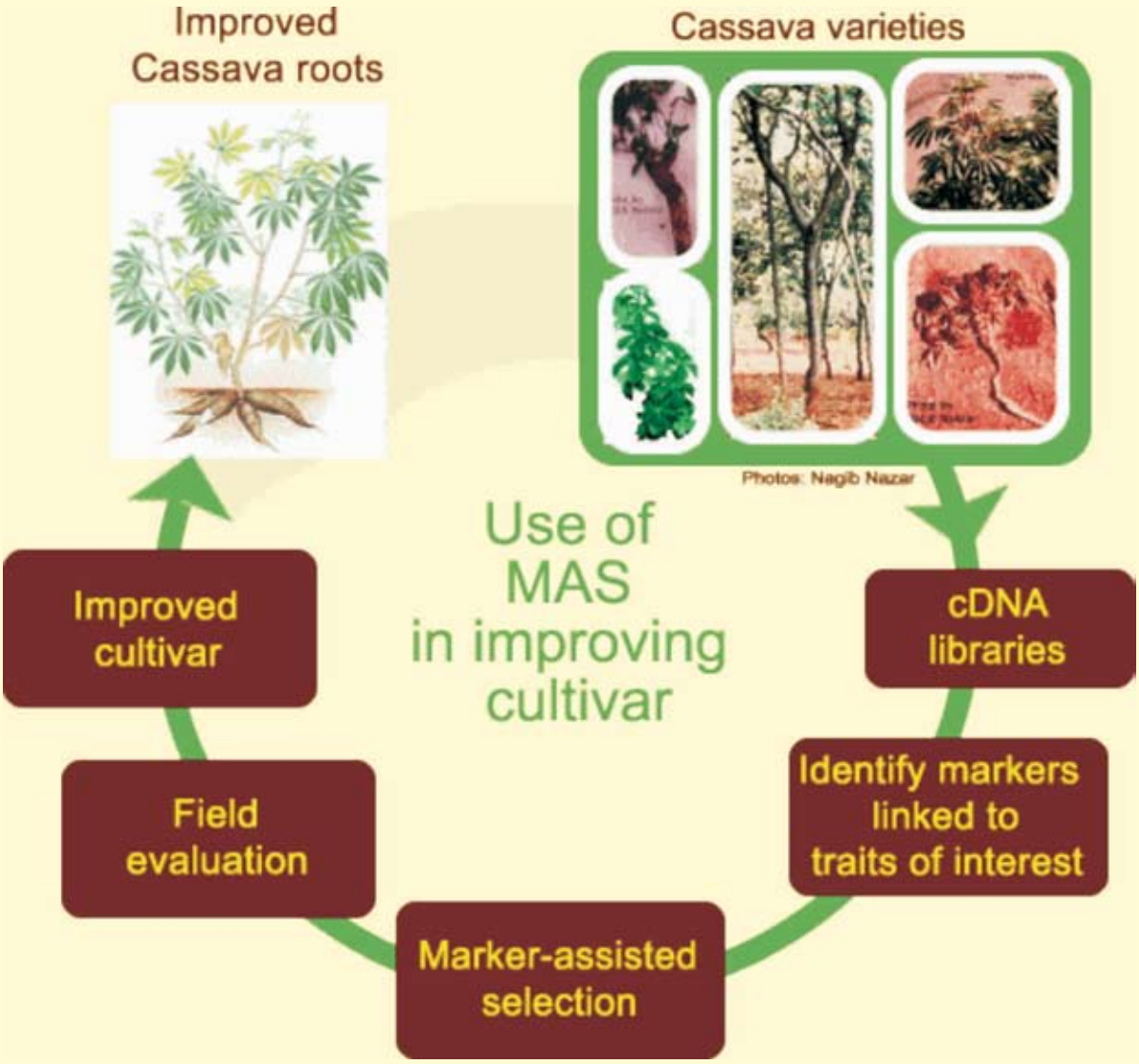
Wednesday morning

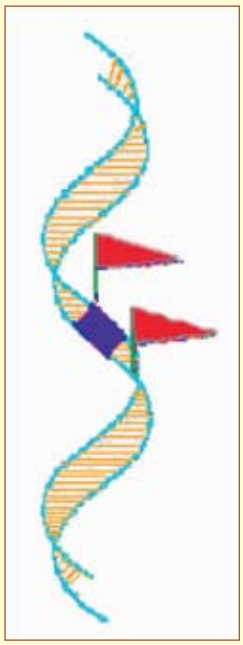
Scene Thirteen: Wednesday morning

Place: Classroom

Characters: Efia, Ekow, all other students and the biology teacher

Situation: The biology class continues with discussion on molecular markers and MAS





Genetic markers

The purple section indicates the presence of a desirable gene in an organism's genetic code. This gene is associated with a marker shown by the red flags.

Scene Thirteen: Wednesday morning

Place: Classroom

Characters: Efia, Ekow, all other students and the biology teacher

Situation: The biology class continues with discussion on molecular markers and MAS

Teacher:

Good morning, class. Today we will talk about markers. Ekow, can you tell me what MAS stands for?

Ekow:

MAS or marker-assisted selection is a biotechnology tool that uses molecular markers to select a specific trait in a plant.

Teacher:

Is MAS alone enough to choose a specific trait in a plant?

Ekow:

No. In order to make a selection decision we must consider the information from available performance records as well as the information from MAS.

Teacher:

Wonderful! So, today I will tell you about the types of markers. There are many types of markers and marker associated techniques. You will all like this because almost all of these markers and associated techniques have acronyms, like abbreviations. They are called RFLP, RAPD, AFLP, SNP and SSR.

Ekow:

Oh, my goodness! I will surely be lost now.

MAS technique can be used once traits have been mapped and a closely linked marker has been found. It is then possible to screen large numbers of samples for rapid identification of progeny that carry desirable characteristics.

Restriction Fragment Length Polymorphisms (RFLPs) often pronounced "rif-lip" is used in two related contexts: firstly, as a characteristic of DNA molecules (arising from their differing nucleotide sequences) by which they may be distinguished, secondly, as the laboratory technique which uses this characteristic to compare DNA molecules. The technique is utilized in genetic fingerprinting.

Random Amplification of Polymorphic DNA (RAPD) - It is a type of PCR reaction, but the segments of DNA that are amplified are random.
Amplified fragment length polymorphism - (AFLP) is a technique that is a highly sensitive method for detecting polymorphism in DNA

"Microsatellites" are defined as loci (or regions within DNA sequences) where short sequences of DNA (nucleotides; adenine - A, thiamine - T, guanine - G, cytosine - C) are repeated in tandem arrays. This means that the sequences are repeated one right after the other. The lengths of sequences used most often are di-, tri-, or tetra-nucleotides.
Microsatellites sometimes referred to as a variable number of tandem repeats or **VNTRs** are short segments of DNA that have a repeated sequence such as **CACACACA**. They tend to occur in non-coding DNA.
Simple Sequence Repeats (SSRs) are polymorphic loci present in nuclear DNA that consist of repeating units of 1-4 base pairs in length.
A Single Nucleotide Polymorphism or **SNP** (pronounced snip) is a DNA sequence variation occurring when a single nucleotide (A, T, C, or G) in the genome differs between members of a species or between the paired chromosomes in an individual.

Teacher:

No, Ekow, there are easy ways to know what these acronyms mean. But you don't have to worry about them now. I have hung a chart on the wall explaining all these acronyms. You can start learning them slowly for the moment. What is important to know, is that there are many types of markers and these markers may differ in their technical requirements. The ones I have mentioned are just a few examples.

The number of genetic markers that can be detected throughout the genome may be different and the amount of genetic variation found at each marker in a given population may also be different.

Kunto:

There are six types of markers. The specific characteristics of a plant are identified by several different methods used for identifying the genes that are responsible for a specific trait.

Teacher:

Very good. Let us use microsatellites as an example as they are very popular for constructing genetic maps for QTL analysis and MAS. We can use this technique to understand all the steps involved.

Dhakiya:

Teacher, can you explain the genetic map and QTL again, please?

Teacher:

Yes, of course. If you remember, we talked about quantitative trait loci or QTL. The genetic map is developed by assaying a number of DNA markers in closely related individuals; each marker identifies a position on the map called a locus.

In crop species, linkage maps are most often used to identify specific chromosomal regions controlling traits of economic importance, such as disease resistance, density or growth. These traits vary quantitatively in crop species, and the identified regions are called QTL.

Equipment used in DNA analysis

Plant tissue can be ground using a mortar and pestle.

Plant tissue can also be macerated in a genogrinder, which processes two plates at one time.

After extraction, DNA is transferred onto plates for the PCR process. Plates are sorted and organized into groups , based on the marker loci of interest. The last plate contains checks and controls.

Extracted DNA is transferred from sample plates to storage plates using robotics.

Extracted DNA is transferred from storage plates to PCR plates using robotics.

PCR is performed to amplify the regions of the genome that are to be detected. The post-PCR product is then transferred to a nitrocellulose membrane.

Robotics are used to transfer the PCR product from the PCR plate wells to the nitrocellulose membrane.

Membranes are hybridized with the appropriately labeled allele specific oligonucleotide probes. See page 106.

Ekow:

Teacher, I have a question; is MAS a biotechnology tool?

Teacher:

Ekow, don't you remember? We talked about this before. MAS is the biotechnology tool used to construct the genetic map for QTL analysis.

Efia:

Besides generating genetic maps for QTL analysis, does MAS have any other uses?

Teacher:

The practical application of MAS is well known in plant breeding, especially in crossbreeding. However, you must remember that knowledge of MAS is very important for collecting, conserving and using PGR.

Ekow:

Teacher, can you tell us more about how scientists use the MAS technique to conserve cassava PGR?

Teacher:

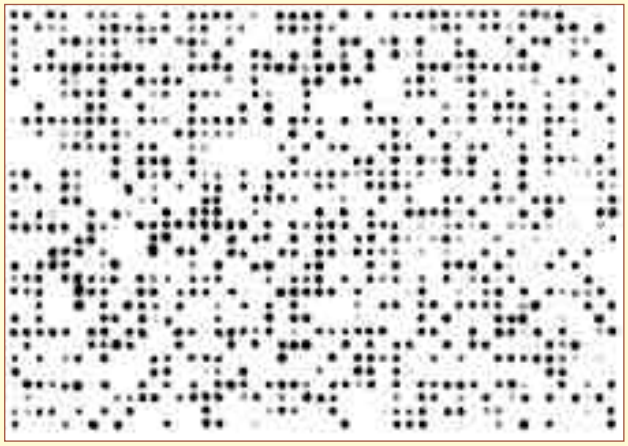
Once again let me give you some basic information before we talk about cassava. In a crop species, some traits are controlled by one or a few genes, whereas other traits may be controlled by many genes. The expression of any particular gene can be modified by the presence of other genes or by the environment in which the organism grows. The content of cassava roots may be determined by the environment where the cassava is grown.

Efia:

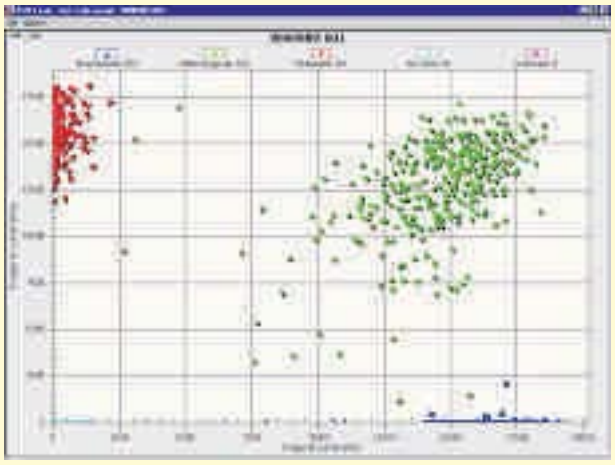
Cassava! Ekow, we can tell our grandmother about this. Teacher, could you please give us an example using MAS and QTL in cassava?

Equipment used in DNA analysis (continued)

Images are developed on X-ray film and scanned into a computer for scoring. A solid black dot on a single image would indicate that the plant sampled is homozygous for that particular marker allele; a gray to dark dot on both images would indicate that the plant sampled is heterozygous for the marker allele; no dot (no hybridization) would indicate that the plant sampled does not carry the marker allele.



16X (16 96-well plates) autorad images of complimentary alleles at one locus The images are analyzed and the results are converted into a tabular form for upload into a database. Sample results are electronically communicated to the breeders and are used to select individual plants for advancement to the next level of testing.



This is a graphical representation of sample analysis. The red data points represent samples homozygous for marker allele 1, green data points are heterozygous samples, and blue represents homozygous samples for marker allele.

Bar code readers are used to identify plants for advancement, which are then directly threshed into planting trays (in the background).

Source:
http://www.cropscience.org.au/icsc2004/symposia/3/4/133_schmidtdh.htm

Teacher:

Before I tell you about them, you must understand some fundamental facts related to MAS and QTL.
First, MAS is a fast and efficient method to analyze QTL.
Second, MAS can be a successful tool to analyze QTL without performance records.

But it is always better to have both historical performance records and MAS data, to come to a successful conclusion.

Ekow:

I also believe that besides QTL, MAS is useful for other analyses such as genotyping, right?

Teacher:

Very good, Ekow! You see, the traits that breeders observe in the field are a result of gene combinations in the plant and the influence of the environment on the expression of those genes. Thus, breeders evaluate genetic lines at different locations and in different years to make sure that they consistently out-perform commercial plants across a diversity of environments and growing conditions. The trait is usually not evaluated until after several generations of self-pollination in the breeding process when excess seed is available. This takes a long time.

Dhakiya:

However, MAS takes a much shorter time than obtaining an historical performance record.

Teacher:

Yes. Having a genetic marker associated with a gene allows one to identify the desired form of the gene or the allele from the onset of the selection process using DNA from almost any tissue of the plant. This technology allows us to rapidly identify genetic lines that have the desired allele and discard those without it. The outcome will be the development of new cultivars that have a unique processing quality. Whereas it generally takes 7-10 years to develop a cultivar, under normal practice, MAS has decreased the development time of these cultivars by several years.

Kunto:

Wow! In that case MAS is a very important biotechnology tool.

Biotechnology tools!!!!

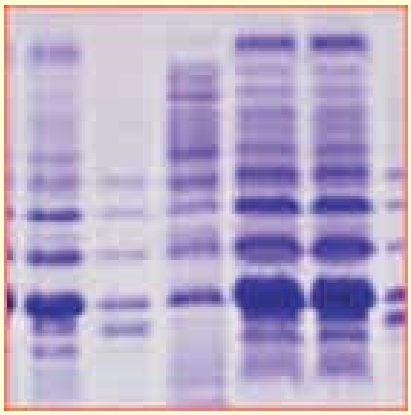
DNA extracted from a large sample (50 ml)

Top layer with DNA

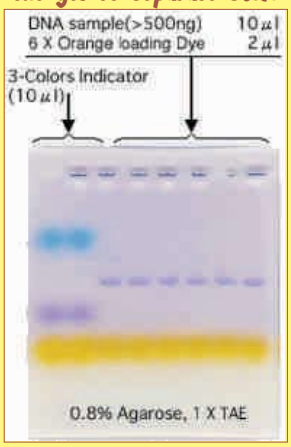
Layer with ground up sample

Steps involved in DNA extraction

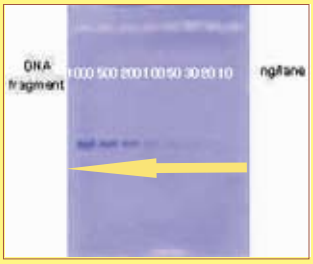
DNA separated in a gel according to their size



Standard way of setting up the gel to separate DNA



Different concentrations of same DNA samples (in ng/ml) are run in an increasing concentration showing that while the DNA fragment size remains the same, the band becomes thicker with increased concentration



The DNA band can be cut off the gel and purified for further use

The separated DNA can be visualised using ethedium bromide under ultraviolet rays

Ekow:

What do we need to know to perform MAS for plant breeding?

Teacher:

The essential requirements for MAS in a plant-breeding programme are:
one - the marker should be closely linked with the trait
two - an efficient screening mechanism for the molecular marker or markers, such as PCR, should be available
three - the screening technique should be successfully replicated in any laboratory and finally, it must be economical to use and also user-friendly.

Efia:

So, are there any problems associated with this biotechnology tool?

Teacher:

Efia, you are always cautious about everything. It is a good question. There are no problems associated with this biotechnology tool itself. But, there can be problems associated with how we use biotechnology tools. It is important to know that any tool we use could result in something that is beneficial to all human kind.

Very well, we will continue with the discussion in our next biology class. We will see how MAS has been applied in real life experience with cassava.

***A cultivar** is a cultivated plant that has received a name under the International Code of Nomenclature for Cultivated Plants (the ICNCP, commonly known as the "Cultivated Plant Code"). For this, it must be distinct from other cultivars and it must be possible to propagate it reliably, in the manner prescribed for that particular cultivar.*

Advantages of molecular markers in plant breeding:
Decreased number of breeding generations
Uniform method for scoring
No need to use phenotypic scoring until the end
Tells % of genome from each parent
Tells WHICH PARTS OF EACH CHROMOSOME come from each parent