

MAS, WHAT IS IT?

MAS (Marker Assisted Selection) is a technique which accelerates and simplifies the selection of the best characteristics of a plant by a series of cross-breeding.

It is based on the principle that biological diversity within the same species makes it possible to match sexually compatible varieties with those which are exploited commercially, thereby enhancing particular characteristics.

Humans have been cross breeding plants and animals for thousands of years, seeking to reproduce varieties better adapted to a particular environment and so guarantee better yields.

The practice continues today as it is an essential tool for improving animal and plant varieties. The production of new varieties, however, is often a very long process.

To be able to pinpoint the most suitable partners to reproduce, the plant must first have reached a mature state in which the desired characteristics to be selected are visible.

In the case of fruit trees, for instance, IT CAN TAKE years before the plant reaches SEXUAL maturity and it is READY to cross breed.

In addition, many characteristics are also difficult, if not impossible, to identify by observing the phenotype as the result of the interaction between the hereditary information (the genotype) with the immediate environment can inhibit or activate the expression of one or more genes present in the DNA.

Should selection concern those varieties with heightened nutritional properties or which are more drought or saline resistant, then traditional cross selection based on phenotype characteristics would call for additional effort without guaranteeing the desired results.

Marker Assisted Selection (MAS) is a way of speeding up these traditional cross selection processes by using our ADVANCED KNOWLEDGES of genetics and molecular biology.

This technique has proved particularly successful in the selection of differing plant species which are capable of producing better yields, pest resistance and greater tolerance to saline conditions or with better nutritional properties.

HOW DOES IT WORK?

All living organisms pass on specific characteristics to their progeny by way of genetic material which is made up of two DNA chains (Deoxyribonucleic acid) or RNA (Ribonucleic acid).

Each single ring of the DNA chain is made up of nucleotides which, functioning together, transmit hereditary characteristics made up of four NITROUS chemicals : adenine (A), cytosine (C), guanine (G) and tyrosine (T) (substituted by uracile in the case of RNA).

A minimum number of nucleotide particle sequences (genes) make up the basis of the hereditary character code while the majority of genetic material present in DNA still has functions yet to be discovered.

In superior organisms dual chromosomes (homologous) are the rule and, as such, single genes can codify different information, for instance, that which defines eye colour in humans.

When the same gene is able to express the same characteristic in different ways, it is described as being "allele" which can be "withdrawn", in the case that the characteristic is manifest only if same allele is present in both chromosomes (homozygous), or dominant if the characteristic of which they are carriers also manifests itself when the allele is present in a single copy (heterozygous).

MAS exploits the presence, amongst varieties of the same species, of different alleles of the same gene which are able to express the required characteristics.

With genetic mapping and the application of molecular biology techniques, it is possible to identify and, eventually, isolate those genes which codify certain characteristics and associate them with specific nucleotide sequences which are to be found at the beginning and at the end of the long DNA chain and which, during reproduction, are transferred as a whole to those genes to which they are associated.

Let's presume, for instance, that we wish to use this information to transfer a certain codified characteristic (or characteristics) from an allele which is present in a donor variety (A) and has no particular commercial value, into a receiver variety (B), which has an economic value.

Knowing the molecular marker sequence, a quick DNA test of the progeny resulting from the cross between A x B allows us to identify those individuals which make up the nucleotide sequence typical of the B variety, with the exception of the required allele spliced from the A variety which is therefore selected to be crossed again with individuals of the B variety.

This process of targeted selection is repeated until the allele becomes an integral part of the genome of the new variety (introgression).

Thanks to MAS it is possible to halve the time taken using traditional methods of hybridisation by using phenotypic selection of the adult individuals. The technique has also proved particularly suitable in the transfer of polygenic characteristics, which are regulated by the joint action of more than one gene.

► To know more

FAO, 2007. Marker-assisted selection : Current status and future perspectives in crops, livestock, forestry and fish (<http://www.fao.org/docrep/010/a1120e/a1120e00.htm>)

THE DIFFERENCES BETWEEN MAS AND GMO

Those varieties produced through MAS application do not contain DNA fragments which are alien to that species in that the introgression of the characteristics takes place through sexual reproduction by means of a simple modification of the alleles of the same gene. This means that the number and the disposition of the nucleotides in the DNA chain are identical to the individuals of the donor variety.

To create a GMO, on the other hand, the cellular cultures of the species to be modified must be bombarded with a "packet" of hereditary materials made up of the interested gene together with other genes which regulate activity (promoters).

Moreover, in some cases other genes are used which are resistant to certain antibiotics and whose only function is to aid the selection process of those cells which are to be transformed as required. After having bombarded the cell culture with the transgenic "packet", all that needs to be done is to expose it to the antibiotics to which resistance has been introduced, thereby killing all those cells which do not possess the exogenous genes in their DNA.

Even if in relative terms the genetic material added to the DNA subject to modification is in percentage terms negligible, the GMO still has more genes in its DNA than prior to the modification process and a different nucleotide sequence.

The effects of this are largely unforeseeable as the possibility of interaction between different genes, as well as the casual introduction of the transgene into another genome, could activate, suppress or modify the behaviour of other genes.

In addition, the ingestion of GMOs which are also resistant to antibiotics exposes the organism to the risk that fragments of transgenic DNA enter into the genomes of bacteria situated in the stomach and intestines of animals, humans included, thereby immunizing the bacteria to antibiotics. Should the organism find itself under attack from pathogen bacteria the hybridisation with the endogenous bacterial flora could lead to the creation of pathogen resistant strains, thus rendering ineffective therapeutic treatment with targeted antibiotics.

The combination of these risks have caused lawmakers, particularly in Europe, to enact legislation regulating such diverse factors as the release of GMO into the environment, the presence of GMO

in food and animal feed, the type of labelling and the use of markers for antibiotic resistance. The OECD has estimated that administrative costs connected to the release of a new GMO are somewhere between \$ 400,000 and \$ 13,000,000, which must be added to the research costs. Varieties which are produced by MAS are not subject to any of these uncertainties nor to these additional authorisation costs and for this reason do not meet with public opposition in the same way as GMO.