Marker Assisted Selection (MAS)

Key issues for Africa

William Stafford



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Acronyms

AATF	African Agricultural Technology Foundation
AFLP	Amplified fragment length polymorphisms
AGRA	Alliance for a Green Revolution in Africa
CGIAR	Consultative Group on International Agricultural Research
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo
	(International Maize and Wheat Improvement Center)
DNA	Deoxyribonucleic acid
FAO	Food and Agricultural Organisation
GEF	Global Environmental Facility
GMO	Genetically Modified Organism
IAASTD	International Assessment of Agricultural Science and
	Technology for Development
ILRI	International Livestock Research Institute
IPR	Intellectual Property Rights
KARI	Kenya Agricultural Research Institute
MAS	Marker Assisted Selection
NERICA	New Rice for Africa
QPM	Quality Protein Maize
QTL	Quantitative Trait Loci
PCR	Polymerase Chain Reaction
SSR	Simple Sequence Repeats
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SNP	Single Nucleotide Polymorphism
UNDP	United Nations Development Programme
UNEP	United Nations Environment Programme
UNESCO	United Nations Educational, Scientific and Cultural Organisation
WARDA	West Africa Rice Development Association
WEMA	Water Efficient Maize for Africa
WHO	World Health Organisation

"history has many records of crimes against humanity, which were also justified by dominant commercial interests and governments of the day. today, patenting of life forms and the genetic engineering which it stimulates, is being justified on the grounds that it will benefit society... but, in fact, by monopolising the 'raw' biological materials, the development of other options is deliberately blocked. farmers therefore, become totally dependent on the corporations for seeds." Prof. Wangari Mathai of the Green Belt Movement, Kenya http://ngin.tripod.com/feedingorfooling.htm

executive summary

Recent developments in genomics and the growing recognition that the Genetically Modified Organisms (GMOs) on the market carry unacceptable biosafety risks has prompted the use of new tools for the development of new crop, tree and livestock varieties. Marker Assisted Selection (MAS) is one such tool. MAS uses molecular markers as tools in a plant or animal breeding programme to select for agricultural traits of interest, such as nutritional quality, drought tolerance, disease and pest resistance.

It has been suggested that MAS has the potential to increase food production and help initiate a new Green Revolution in Africa. Proponents of the African Green Revolution view insufficient productivity as the cause of rural poverty and promote proprietary hybrid, MAS, and GMO seeds, and large-scale application of agrochemicals (fertilisers, herbicides and pesticides) as technological solutions to increase yields. The Green Revolution in Africa is motivated by the desire to transform agriculture into an industrial sector with an emphasis on export crops and the integration of poor, small-scale farmers into the global economy.

This New Green Revolution for Africa was given renewed impetus two and a half years ago when the Rockefeller and Bill & Melinda Gates Foundations launched the Alliance for a Green Revolution in Africa (AGRA). These Foundations have donated millions of dollars to AGRA, on the pretext of helping small-scale farmers lift themselves out of poverty and hunger by significantly boosting farm productivity with Green Revolution-type technologies, such as MAS.

Globally, most of the MAS programmes are in the research and development phase and focused on cereals; particularly maize, rice, wheat and barley. Nevertheless, several MAS programmes involve pulses (beans, chickpea and soybean), root and tuber crops (potato, sweet potato and cassava) and fruit trees (banana, cocoa, coconut and papaya, apple and pear). There are also several MAS programmes involving vegetables, industrial crops (sugar cane, cotton, rubber, jute, coffee, flax and oil palm) and industrial tree plantations (eucalypts, pines and acacia). There are a few MAS programmes focusing on crops of importance in developing countries; such as sorghum, amaranthus, teff, lentil, pigeon pea, groundnut, yam and taro.

A much celebrated MAS and Green Revolution programme is the 'New Rice for Africa', (NERICA) that was developed by the West Africa Rice Development Association (WARDA). NERICA is a hybrid rice, developed through the forced breeding of African rice (*Oryza glaberrima*) and Indian rice (*O. sativa*) – different species that do not naturally inter-breed. The NERICA breeding programme used MAS to select for a combination of traits from the African rice such as drought and disease resistance with that of traits for higher yields from the Asian rice. The NERICA breeding programme made extensive use of indigenous knowledge systems and the diversity of rice landraces in the hands of local farmers during the initial varietal selection. Nevertheless, there is no evidence for the fair and equitable sharing of benefits. An additional disconcerting issue is that WARDA has recently registered NERICA as a trademark, thereby obtaining exclusive rights to use the name.

MAS and GMOs are produced by fundamentally different techniques of modern biotechnology. Nevertheless, the distinction between the two is often deliberately blurred by Agricultural-biotechnology companies. For example, Monsanto's 'Vistive' line of soybeans is disingenuously promoted as solely "produced through conventional breeding". However, 'Vistive' soybeans contain not only the trait for reduced linolenic acid content obtained through MAS, but they also contain the transgene for resistance to the Roundup Ready herbicide. 'Vistive' has received limited biosafety assessment because the transgenic parent of 'Vistive' had acquired prior biosafety approval and 'Vistive' is not perceived as a GMO. In addition, the lack of biosafety regulations for MAS produced seeds compared to that of GMOs means that Agricultural-biotechnology companies can avoid many biosafety costs (for testing, risk assessment, field trials, monitoring, labeling, and segregation) and thereby more rapidly bring their products to the market. Monsanto who has cornered 23% of the global seed market and 9% of the global agrochemical pesticide market, is rapidly adopting and developing MAS for their breeding programmes.

When comparing MAS to conventional breeding, the economics is an important consideration that should be evaluated on a case-by-case basis.

While the genetic benefits of a MAS variety may be passed onto the commercial farmer, Agricultural-biotechnology companies stand to gain the greatest economic benefits because MAS methods and products can be protected by patents. Patenting enables companies to obtain an even greater portion of the global seed market and maintain their market dominance while forcing the farmer to be more dependent on these external inputs (yearly purchase of patented proprietary seed and the associated agrochemicals). This undermines food security and food

sovereignty.

There are other biosafety risks associated with MAS that are of concern. In contrast to conventional breeding that observes nature's limits of time and reproductive boundaries, the use of modern biotechnology can create novel organisms that are not part of our natural evolution and food chain. The products developed by MAS often lack genetic diversity and the process of selection for desirable traits in the laboratory removes the plant from the natural, evolving gene pool. The maintenance of agricultural genetic diversity and dynamic gene pools is vital to protect crops from new diseases or climatic changes. This was aptly demonstrated by the selection of horizontal resistance that saved maize production from destruction in tropical Africa after the unintentional introduction of the fungal disease, tropical rust. Agricultural genetic diversity has been developed and maintained over thousands of years by farmers and traditional breeders to produce numerous open-pollinated varieties (landraces), which are also part of their indigenous knowledge systems. The diversity of these landraces needs to be preserved by isolation and segregation practices so that the biodiversity of landraces are protected from the intellectual property rights of patented Agricultural-biotechnology products.

MAS is being used within a 'business as usual' approach to food production and will therefore contribute to undermining food sovereignty and food security, and increasing global inequalities, hunger, poverty and environmental degradation. A new approach to this industrial model of agriculture is urgently needed. The adoption of ecological models as well as certain changes in policy that address the multifunctionality of agriculture are required in order to attain sustainable agriculture. The support and research for agroecological methods, grassroots information campaigns, and policies that support the rights of pastoralists and small-scale farmers will help to achieve these aims. Similarly, changes in policy and agricultural practices are required to conserve the environment and maintain ecosystem services so that climate change can be halted and the natural resources and biodiversity preserved for future generations.

introduction and context

The field of **Biotechnology** was stimulated by the sequencing of DNA and developments in the science of **genomics**. Genetic information is now available about the **genetic loci** that control important agricultural traits such as nutritional quality, drought tolerance, disease and pest resistance. These traits are identified through the use of **molecular markers**. **Marker assisted selection (MAS)** is the use of molecular markers as tools in a plant or animal breeding programme.

"There may be some mechanisms common to all crops that contribute to major characteristics, such as yield, but genes that control yield are complex. In the past, the number of samples that could be analysed limited exploitation of DNA marker technology. Automation has greatly increased throughput, so projects that until recently seemed impossible are now feasible".¹

Dr Peter Jack, Monsanto.

The worldwide proprietary seed and agrochemicals market is dominated by a few Agricultural-biotechnology companies, based in the developed world (headquarters in the USA or Europe). The top ten Agricultural-biotechnology companies account for two-thirds (67%) of the global proprietary seed market.^{2,3} It is thus not surprising that these same companies are also dominating the application of MAS in agriculture. Monsanto, the company with the greatest market share (23% of the global seed market and 9% of the global agrochemical pesticide market), is rapidly adopting and developing MAS for their breeding programmes. Their operations in the past five years are reported to include: "...the development of thousands of new marker assays, a 17-fold increase in the acquisition rate of marker data, and a decrease in unit data point cost of 75%".⁴

Research into MAS in developing countries is fragmented and not well developed. The majority of MAS research is linked to the Consultative Group on International Agricultural Research (CGIAR). These MAS programmes typically rely on the pooling of the large capital expenditure and skilled personnel of the CGIAR centres and national public research institutions. For example, CIMMYT,

the International Livestock Research Institute (ILRI) and Kenya's Agricultural Research Institute (KARI), are providing central infrastructure, technical access and training for African breeders.⁵

In addition to capital expenditure and skilled human resources for the **genotyping** in the laboratory, the application of MAS requires effective capabilities in cultivation, phenotypic evaluation and selection. The genomics era represents the technological advances in molecular biology that are enabling Agriculturalbiotechnology companies to rapidly develop genotyping facilities that can be used for MAS, the development of transgenics, and in varietal characterisation and selection.

"These sequencing efforts will not only identify preferred genes for our research and development pipelines, but move us into a high-definition molecular breeding era that uses a combination of sequence and markers to derive future higher-yielding hybrids globally".⁶ Dr. Robert Fraley, Monsanto Chief Technology Officer

The Green Revolution and MAS

It has been suggested that MAS has the potential to increase food production and initiate a new Green Revolution in Africa.^{7,8,9} Crops developed through MAS and an increased use of chemical fertilisers are being promoted as the technological solution to achieve this new Green Revolution. The CGIAR is actively involved and the Rockefeller and Bill & Melinda Gates Foundations have formed the Alliance for a Green Revolution in Africa (AGRA) to promote this approach with the provision of millions of philanthropic dollars.¹⁰

Current MAS products developed for the Green Revolution in Africa include the New Rice for Africa (NERICA), Quality Protein Maize (QPM), and the Water Efficient Maize for Africa (WEMA). NERICA was developed by WARDA (a division of the CGIAR), using a MAS breeding programme that selected for a combination of benefits from African rice (resistant to drought and several diseases) and traits for higher yields from the Asian rice.^{11,12} The NERICA breeding programme utilised the diversity of rice landraces and involved farmer-participation and indigenous knowledge systems in the initial varietal selection, but there is no evidence of agreements for the fair and equitable sharing of benefits.¹³ The cultivation of NERICA rice requires the farmer to purchase proprietary seeds annually as well as the use of associated agrochemicals (chemical fertilisers, pesticides and herbicides)

and therefore can compromise food sovereignty and food security. NERICA also threatens the biodiversity of traditional rice landraces because segregation and co-existence of rice will be difficult to achieve. This is exacerbated by the lack of regulations for MAS products that results in no mandatory segregation practices being carried out.

Quality Protein Maize (QPM) was developed by the CIMMYT using MAS to identify maize plants rich in complete protein (enriched in the amino acids lysine and tryptophan). Quality Protein Maize is the result of more than three decades of scientific development by the CIMMYT and several QPM varieties are now grown on over three million hectares in developing countries.¹⁴ Although many of these varieties are well-adapted to local conditions, they are hybrids that require the purchase of new F1 hybrid seeds each year. Since maize is wind-pollinated, these hybrids maize plants will freely cross pollinate with neighbouring maize varieties; causing problems with segregation and co-existence. The QPM is being promoted by Sasakawa Global 2000 and has received funding from the USA and Canadian International Development agency.¹⁵

The drought tolerant maize, WEMA, is a recent initiative by the African Agricultural Technology Foundation (AATF) and involves a partnership between the CIMMYT; Monsanto and the national agriculturural agencies from Kenya, Uganda, Tanzania, and South Africa. The first hybrids developed by WEMA using MAS could be available after six to seven years and will be followed by the incorporation of transgenes so that drought-tolerant maize transgenic hybrids will be available in about ten years time (2020). CIMMYT is to provide the conventionally developed drought tolerant high-yielding maize varieties that are adapted to African conditions and expertise in conventional breeding; Monsanto will provide proprietary (trans) genes, advanced breeding tools and expertise; and the national agricultural research systems will contribute project governance, seed testing, production, and distribution.¹⁶ WEMA has received initial funding of US\$47 million from the Bill & Melinda Gates Foundation and the Howard G. Buffett Foundation.¹⁷

marker assisted selection (mas)

What is Marker Assisted Selection?

Plant breeding involves the selective mating of individuals of a population to isolate or combine desired morphological, physiological or genetic traits that characterise appearance, yield, taste and resistance to pests, diseases and adverse environmental conditions (i.e. drought or frost). Breeding has been practiced for centuries in the improvement of plant crops and domesticated animals- the breeder observes favourable traits and saves the seed or offspring from these parents to select for improved characteristics of the next generation.

Marker assisted selection (MAS), also known as Marker Assisted Breeding, (MAB), is the use of molecular markers as tools in a plant or animal breeding programme. MAS makes use of genotyping (the results of DNA testing using molecular markers) to select and breed individuals with the desired traits for the next generation. The logic is that the information from the genotyping, combined with the observed performance records for individuals, can improve the accuracy and speed of the selection process in a breeding programme.¹⁸ MAS is thus a laboratory process that uses genetic testing to dispense with testing the performance of every individual in the field.

MAS does not involve genetic engineering in the laboratory, as is the case with GMOs, but uses molecular markers as tools for selection. MAS, like several other biotechnology approaches of genetic modification, avoids the introduction of transgenes and the associated elements of the transgenic cassette (such as viral promoters and antibiotic resistance marker genes).^{19,20}

MAS uses genotyping tests that can be carried out at an early stage in the breeding programme. This enables the identification of individuals with the desired trait(s) to be identified and selected without having to wait for plants to mature for assessment in the field. For example, in an initial varietal selection (see Figure A, below) a molecular marker could be used to select for maize plants by testing seed for desired traits of pest resistance and improved nutrition/taste and therefore avoids having to grow and test the maize plants in the field. In a breeding program that uses recurrent selection and backcrossing, MAS can be used at

several stages (recurrent selection in Figure B). This application of MAS allows the accumulation of several desirable traits through repeated selection in the breeding program and enables an early detection of traits; such as identifying plants that are resistant to several known pests or whose maize cobs have improved taste/ nutrition without having to grow the plants to maturity in the field to test them.



Laboratory genotyping





pest resistance and improved nutrition/taste. This new variety is deemed ready for market and is inbred to generate seed for sale and planting by farmers.

A typical application of MAS in a breeding program.

A. In varietal selection, the laboratory genotyping enables the testing of different seeds with molecular markers for certain desired traits. Using molecular markers, seeds containing the desired traits of pest-resistance (R) and improved taste (S) can be selected and then grown and cross-pollinated to generate a new maize hybrid carrying both of these traits. Varietal selection is often used to screen many different varieties or landraces for a breeding program and also to identify and characterise seed banks.

B. In a breeding program using recurrent selection, plants are tested by genotyping in the laboratory for the desired traits such as resistance to pests (resistant to two pests, R1 and R2) and improved taste (S). These traits may be controlled by many genes or QTL and are tested using several molecular markers for these traits (R1, R2 and S). The process is carried out recurrently (with or without backcrossing) to select for offspring that contain both these traits. This enables the introgresson of the QTL into a new variety and, after seed-bulking through inbreeding, is ready for market.

The unfilled arrows show progressive stages of MAS in the breeding programme Filled arrows show the laboratory selection of individual seeds or plants with the desired traits using genotyping.

MAS requires a known association between a DNA sequence (genetic marker) and a certain characteristic (trait or phenotype). If the organisms' entire DNA sequence (genome) is known, a large number of higher quality molecular markers can be developed. However, when a genome sequence is limited in the organism of interest, related species may aid as a source for the development of molecular markers by identifying genetic marker-phenotype associations across species (so that discoveries in one species may be applied to others). Molecular markers are usually not genes whose function for a desired trait is known, but are adjacent DNA sequences that are linked to these traits. Molecular markers thereby represent constant landmarks in the genome. MAS involves the use of these molecular markers, that are transmitted by the standard laws of inheritance, as tools to select individuals with the desired trait.^{21,22}

The methods and technology of MAS

There are several molecular marker methods and these differ from each other in their technical requirements, sensitivity and reliability. Restriction fragment length polymorphisms (RFLPs) detect DNA sequence variation through restriction nuclease digestions followed by probe hybridisations. These have been used in the construction of extensive genetic maps, where there is a high level of genetic diversity, such as in maize.^{23,24,25,26} These RFLP methods are robust and reproducible, and have been the methods of choice for the development of molecular markers for many plant species through the 1980s and early 1990s. The development of the polymerase chain reaction (PCR) was a breakthrough in the development of molecular markers because little DNA is required; thereby enabling seeds or young seedlings to be tested to allow for the early detection and selection of the desired trait in a breeding programme.²⁷ There are several types of PCR-based marker systems including Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphisms (AFLP), Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP).^{28,29,30,31} Simple sequence repeats (SSR, also termed microsatellites) rapidly became the system of choice since they are both sensitive and reproducible.^{32,33} Single nucleotide polymorphisms (SNPs) are the most modern method of genotyping with a greater sensitivity and ease of automation.³⁴ The table below illustrates the degree of development of molecular markers (SSR) (top ten crops are shown).35

Common name	Species	Number of SSR molecular markers
Rice	Oryza sativa	2240
Maize	Zea mays	1669
Soybean	Glycine max	597
Cassava	Manihot esculenta	318
Thale cress	Arabidopsis thaliana	290
Cotton	Gossypium spp.	217
Sugar-cane	Saccharum spp.	200
Wheat	Triticum aestivum	193
Grape	Vitis vinifera	152
Groundnut	Arachis hypogaea	110

These various molecular marker methods allow the organism's DNA sequence to be mapped onto regions of their genome. Using this map, putative DNA sequences affecting traits of interest can then be detected by testing for statistical associations between DNA sequence variants (of a particular marker) and any trait of interest. Though not necessarily genes themselves, these Quantitative Trait Loci (QTL) are stretches of DNA that are closely linked to the genes that underlie the trait. When QTLs have successfully been identified and validated, they can be applied to a breeding programme to select for the traits of interest.^{36,37,38}

What is involved in MAS?

The use of molecular markers should allow breeders to choose parents that, when mated, provide populations or gene pools enriched for combinations of desirable traits.

- The basic steps in a MAS breeding programme are:
- Screen the population for the traits of interest
- Construct genetic linkage maps
- · Identify the molecular markers that are linked to the traits of interest
- Test the applicability and reliability of the markers in predicting the traits (marker validation)
- Develop a high throughput and reproducible genotyping facilities for screening large number of samples in a time and cost effective manner
- Implement MAS into the breeding programs (monitor the introgression of desirable traits in the programme)

The molecular marker technology has been a dynamic and often expensive component in the development of MAS. Our understanding of genomics is still in its infancy since a very low percentage of the genes in crop plants have a function assigned to them on the basis of direct experimentation. The application of MAS is greatly influenced by the relationship between the markers and the genes of interest. Of greatest importance is the linkage or linkage disequilibrium between the molecular marker and trait of interest. When the combinations of genetic markers occur more or less frequently in a population than would be expected on the basis of chance (random mixing), the linkage disequilibrium can be used

to identify the QTLs. Statistical analysis is required to demonstrate that different loci interact with one another and to determine whether they produce a significant effect on the trait.³⁹ Since QTLs identify a particular region of the genome that contains a gene associated with the trait of interest, the presence of DNA sequence information greatly accelerates the development of molecular markers. This is evident in the rapid development of MAS in rice subsequent to the completion of the rice genome sequencing project.⁴⁰ However, the full genome sequence is not a requirement for MAS, and there are a number of molecular markers that have been developed without the benefit of full genome sequence. This situation is changing rapidly with developments in whole genome sequencing and functional genomics.⁴¹ To develop a MAS programme, the information resources dealing with the overwhelming amount of natural genetic diversity and the traits linked to them must be developed into a useful tool for breeding applications. Given the complexity of quantitative traits, many different lines or crosses must be carefully analysed over different years and environments to unravel important components of gene interactions. Such tool sets are beginning to emerge such as the Gramene database,⁴² the International Rice Information System (IRIS) database^{43,44} the GeneFlow database,⁴⁵ MAS wheat database⁴⁶ and software such as Real Time QTL.⁴⁷ However, relatively little has been published on the identification and mapping of DNA sequences to traits. This paucity of public information on QTLs and MAS tools most likely reflects the proprietary nature of developments of MAS in the private sector, which has resulted in poor knowledge dissemination, and has hindered research and development.

There has been considerable debate about the exact potential of MAS.^{48,49,50} Recently, several studies reported on the success rate of MAS compared to conventional breeding that relies on phenotypic selection alone.^{51,52,53,54} The rates of genetic gain or improvements attained using MAS were typically twice as high as that achieved through conventional breeding.^{54,55,56}

The economics of MAS depends on four factors: the relative cost of phenotypic versus genotypic screening, the time saved by MAS, operating capital for the breeding programme, and the benefits associated with accelerated release of the improved variety. In addition, the initial MAS development costs for QTL detection can be substantial^{57,58} and developing countries need to take this into careful consideration. Studies at the CIMMYT on the relative cost-effectiveness of conventional selection and MAS for different maize breeding applications in Mexico and elsewhere indicate that conventional breeding is less expensive, but that MAS is quicker and this factor can make MAS more cost-effective.⁵⁹ In general, MAS is more than twice as expensive as conventional breeding and

can take a similar amount of time. However, this is only true when the trait can be clearly identified visually so that the selection in the conventional breeding program can be effective. If the trait cannot be clearly identified visually in the field, then MAS may have advantages in reducing both the cost and time involved in the breeding programme. Therefore, the cost of conventional breeding methods compared to MAS must be evaluated on a case-by-case basis.⁵⁹ The benefits of MAS may accrue to the commercial farmer as a result of the genetic improvement of the crop plant. However, Agricultural-biotechnology companies stand to gain the greatest economic benefits because MAS methods and products can be protected by patents, thereby enabling companies to obtain an even greater portion of the global seed market (plant crops, trees, and livestock) and maintain market dominance.

There are several successes in identifying QTL in a number of genetic backgrounds that are associated with tolerance to drought, salt and mineral deficiencies, as well as resistance pests and diseases.^{60,61,62,63,64,65,66,67,68,69} The accumulation of several traits with resistance to diseases and/or pests involves pyramiding of resistance QTL into a single variety is being used to attain more durable forms of disease and insect resistance.⁷⁰ MAS has also been used to select for favourable traits from the diversity of landraces or wild-relatives. For example, RFLP and SSR markers have been used to monitor introgression of brown planthopper resistance from *Oryza officinalis*, bacterial blight resistance from *O. longistaminata*, aluminum tolerance or yield and quality-related traits from *O. sativa*).^{71,72,73,74,75,75,77}

As more detailed genetic maps become available, genomics methods such as comparative linkage disequilibrium will become a more important component of MAS.^{78,79,80} The comparison of genetic maps can be used to make predictions about the phenotypic consequences of a genetic locus in related species. This potentially avoids the lengthy process of practically developing molecular markers in another species. These methods have stimulated rapid advancements in the search for QTL associated with abiotic stress tolerance in cereals and a global effort is underway to identify loci associated with drought tolerance.⁸¹ Comparative genomics can also provide information on how combinations of genes of a given variety interact in a particular environment.⁸²

An entirely different application of MAS is when genotyping is used as a tool to monitor QTL or gene introgression in the development of GMOs and F1 hybrids, and in the characterisation of proprietary seeds. Although these methods are prevalent, relatively little of this knowledge is published since it is part of proprietary

methods and intellectual property (plant breeder's rights) of corporations. In many cases MAS has been used in the development of GMOs to identify the individuals with the least amount of donor DNA flanking the transgenic cassette and also in variety improvement that involves the identification and characterisation of seeds through the genotyping of seed-banks.^{83,84,85,86}

Targeted applications of MAS will also become more prevalent as our knowledge about genomics and the genetics of genotype-phenotype becomes more fully understood. For example, analysis of many QTL and the application of MAS has enabled the identification of rice candidate genes responsible for resistance to the diseases blight and blast.^{87,88,89,90,91} The knowledge of these resistance genes could inform breeding programs for varietal improvement using MAS and recurrent selection. It can also be used for the insertion of the resistant gene into another crop by engineering in the laboratory to create transgenic GMOs.

MAS can also be used as part of a monitoring programme to detect transgene contamination or adventitious presence in the field or in food products. Once introduced into the gene pool, a transgene can be tracked with the aid of molecular markers (designed to tag the transgenic cassette) in the same way that is done in a breeding programme. The detection of many GM food crops on the market use molecular markers targeting flanking regions of the transgenic cassette to detect and quantify the presence of the transgene.⁹²

biosafety of mas

The introduction of the products of modern biotechnology such as GMOs into the environment and human food chain raises new risks to the environment and to human health. Countries that are signatories to the Cartagena Protocol on Biosafety93 are required to assess and monitor these risks through appropriate methods such as long-term feeding trials, environmental and socio-economic impact assessments, and monitoring programmes. The Cartagena Protocol on Biosafety defines modern biotechnology as "the application of: in vitro nucleic acid techniques, including recombinant deoxyribonucleic acid (DNA) and direct injection of nucleic acid into cells or organelles, or fusion of cells beyond the taxonomic family, that overcome natural physiological reproductive or recombination barriers". "Natural barriers include geographical separation, separation in the time of reproductive periods of individuals, or separation in the ecology of the individuals concerned".94,95 MAS is a modern biotechnology method that overcomes the natural barriers of geographical separation (MAS often uses varieties of landraces from different geographical regions) and time (MAS typically uses laboratory genotyping for early trait detection which avoids growing plants to maturity in the field).

The biosafety assessment of MAS needs to determine the risks of this new technology using a comparative approach so that the risks of MAS are compared to both traditional breeding and to GMOs and the relative risks can be weighed against the benefits.

MAS compared to traditional breeding

MAS can be used to develop any agriculturally important species and be applied to breeding programmes in a whole range of crop, livestock, forest, tree and fish species.^{53,96} The initial focus of any MAS programme is devoted to building DNA marker maps and detecting and validating QTLs with the use of molecular markers. The identification of DNA sequences that are linked to a certain trait could then be simple in the sense that a single gene controls a single trait, or they could be complex quantitative traits involving many genes. Evidence suggests

that most traits involve many genes and are described as **polygenic**, with many Quantitative Trait Loci (QTL). For example, 47 QTL for drought tolerant traits of rice were identified using 280 molecular markers (comprising 134 RFLPs, 131 AFLPs and 15 microsatellites) and observing drought tolerance under irrigated and water stress conditions.^{97,98}

It is anticipated that MAS will be applied in different ways: to refine existing breeding programs that utilise recurrent selection; develop crossbreeds or hybrids, as well as the introgression of genes of interest into a new variety.^{39,53,99,100} An example of the use of MAS in a recurrent selection breeding programme is the Quality Protein Maize (QPM) by CIMMYT. SSR molecular markers were used to test DNA extracted from leaf tissue of very young plants for QTL, thereby allowing QPM plants to be identified early in the breeding cycle. SSR markers were used to distinguish between homozygous recessive and heterozygous plants.¹⁴

Early studies indicate that MAS is generally superior to phenotypic selection in developing a variety with the desired trait.^{49,50,51,52} Simulations have shown that MAS is between 3-20% more efficient than phenotypic selection used in traditional breeding.⁵⁴ Although research shows that MAS may be more affordable than traditional breeding methods with the reduced expenditure largely accounted for by a reduction in time. Information from molecular markers can often be obtained from any plant tissue (even from seeds or young seedlings) whereas morphological markers frequently require the observation of whole, mature plants (e.g. grain or fruit quality). Molecular markers are neutral markers and thus appear not to be affected by environmental or growing conditions, so that traits which are difficult, expensive or time consuming to isolate phenotypically (e.g. resistance to pests or diseases, tolerance to abiotic stresses such as drought and salinity, nutritional profile and taste) are amenable to MAS.

MAS compared to transgenic GMOs

GM crop plants have been developed by the insertion of genes from another organism through engineering in the laboratory. These methods cross natural reproductive barriers and are therefore unnatural. The transgenic methods also rely on the premise that one gene controls one trait which can be engineered into the host species. However, it is now widely accepted that this premise is largely unfounded; most genes control more than one trait and several genes typically act in concert to determine a particular trait.^{97,99,100} The main agricultural traits governing yield, stress resistance or long-term disease protection are quantitative

trait loci (QTL) that can be used in a MAS breeding programme. Since traits are often controlled by many genes, MAS can accomplish what would be very difficult to achieve using a transgenic approach.

"It's a numbers game and ultimately [non-transgenic] biotech offers the greatest potential. Aligning 20 segments of desired genetic material using conventional breeding would take a one-in-a-trillion chance. Using molecular markers we can achieve it in three cycles".¹⁰² Tom Crosbie, Monsanto's head of plant breeding.

The process of MAS where molecular markers are used to speed up the selection time of the traditional breeding process differs from transgenics that have been genetically engineered in the laboratory and carry intrinsic biosafety risks. The transgenic cassette is the set of sequences introduced into the host genome during the engineering of a transgenic and includes not only the transgenes for the trait of interest, but also other DNA sequences such as viral promoters and antibiotic resistance genes. These DNA sequences raise certain risks to human health such as increasing antibiotic resistance and enabling the creation of new disease-causing viruses. Furthermore, transgenic food crops developed to date are mainly for resistance to proprietary herbicides or to produce insecticidal toxins (93% of transgenic crops on the market are for herbicide resistance or produce insecticidal toxins).¹⁰³ In contrast, MAS is typically applied as a tool to develop crops that have improved resistance to biotic and abiotic stresses such as drought tolerance and resistance to diseases.

"The public is lukewarm on [transgenic] GMO products. Now we have a technology that doesn't have an image problem".¹⁰⁴ George Kotch, research director of Syngenta, on MAS.

The distinctions between MAS and GMOs are deliberately being blurred by Agricultural-biotechnology companies. For example, Monsanto's 'Vistive' line of soybeans is disingenuously promoted as solely being "produced through conventional breeding" However, these 'Vistive' soybeans contain not only the trait of reduced linolenic acid content obtained by MAS, but also contain the transgene for resistance to the Roundup Ready herbicide (the transgenic parent of 'Vistive' soybean is the soybean line GTS40-3-2 from event MON-04032-6 which is tolerant to glyphosate).^{105,106} The biosafety assessments of 'Vistive' have

therefore largely been overlooked since GTS40-3-2 had received prior biosafety approval and 'Vistive' is not perceived as a GMO.

Biosafety concerns with MAS

When assessing whether to introduce a new agricultural variety that has been developed through the use of modern biotechnology, an environmental, health, and socio-economic risk assessment should be carried out. Decisions should be made within the framework of a **precautionary approach** and with the **sustainability** of the agricultural ecosystem in mind. Forestalling disasters usually requires acting before there is strong proof of harm, and requires a precautionary approach to decision-making. The European Environment Agency published a report on developing emerging technologies responsibly – "Late lessons from early warnings: the precautionary principle 1896-2000" – where case studies spanning the past century are used to illustrate that late lessons were learnt despite the early warnings of harm being present. In many cases, heeding the early warnings and applying a precautionary approach can prevent harm to the environment or human health and be more economical in the long term.¹⁰⁶

Additionally, a post release monitoring system must be put in place to observe unpredictable effects that may occur once MAS produced seeds are released into the environment for agricultural planting (trial or general release) or imported into a country for food and feed (bulk shipments). The monitoring programme should observe changes in human health, biodiversity and the ecosystem as a function of time, scale and agricultural practice. It is also important to establish aspects of identity preservation, tracking and traceability so that observed changes can be linked to a particular causative agent.^{107,108}

It is recognised that the diversity of the crops that we grow and consume are rapidly diminishing. Approximately 10 000 different plant species have been used by humans for food and fodder production since the dawn of agriculture thousands of years ago. Today, only 150 crops feed most human beings on the planet, and just 12 crops provide 80% of human's food energy.¹⁰⁹ The erosion of this genetic diversity means that the reservoir for future varietal improvement is diminishing so that there are fewer options for ensuring more diverse nutrition, enhancing food production, and coping with environmental constraints like new disease or climatic changes. Agricultural-biotechnology exacerbates this problem since it typically relies on breeding isogenic lines with little genetic diversity and relies

on the cultivation of monocultures. This contrasts sharply with that of traditional breeders who have maintained genetically diverse open-pollinated varieties (landraces), often as part of polycultures. The genetic diversity of landraces and the saving of seed for the selection of horizontal resistance was largely responsible for saving maize production from destruction in tropical Africa after the unintentional introduction of the fungal disease, *Puccinia polysora*, or tropical rust.¹¹⁰ Therefore, the diversity of these landraces needs to be preserved by identifying isolation distances and segregation practices so that the biodiversity of local varieties and landraces can be maintained and that the food security, food sovereignty and indigenous knowledge systems of farmers are protected from the intellectual property rights of patented Agricultural-biotechnology products.¹¹¹

Furthermore, monocultures and fields planted to the same crop year after year are more susceptible to devastation by disease and pests. In many cases, changing cultivation practices (e.g. intercropping or crop rotation) is often simpler, cheaper and offers more benefits compared to changing the plant's genetic makeup, whether by GMOs, MAS or traditional breeding. For example, detailed farm studies over six years have clearly demonstrated that methods of integrated pest management including inter-cropping and rotation were effective at reducing infection of Striga and increasing the yields of open-pollinated maize in western and central Africa.^{112,113,114,115}

How traditional breeding and seed-saving rescued maize production from the fungal disease, tropical rust.

There is a disease of maize called 'tropical rust' caused by a microscopic fungus, *Puccinia polysora*. It is thought that the rust was accidentally introduced in the 1940s by shipments from tropical America to West Africa. The disease in tropical Africa caused widespread damage and devastated maize production in a similar way to the potato blight that occurred during the nineteenth century in Europe. Several breeding programmes were initiated in an attempt to use modern biotechnology to breed resistant lines. Varieties from Central America were used as a source of single resistance genes (Rpp1 and Rpp1) in breeding programs in an attempt to introduce resistance. This approach continually failed.

Surprisingly, the severity of the disease appeared to slowly decline, until (about six or seven years after its first appearance), it ceased to have any importance. The problem seemed to have solved itself and only recently has therefore become clearly understood. The maize landraces planted in

tropical Africa were diverse and this diversity meant that polygenic resistance in maize could accumulate when sufficient selective pressure was applied (tropical rust fungus was introduced and began to spread). Several years of repeated seed-saving of the few maize plants that survived the damaging rust enabled the breeding of rare individuals who had accumulated quantitative trait loci (QTL) for resistance to tropical rust.

The traditional breeding succeeded where biotechnology methods failed simply because the Agricultural-biotechnology varieties are genetically homogenous and static. Many of the Agricultural-biotechnology crops are covered by intellectual property rights and patents that prevent farmers from saving seed so that the seeds are static because they do not evolve dynamically on the farm through yearly selection, seed-saving and planting. Since these seeds lack genetic diversity they are unable to adapt to future challenges such as changes in climate, new pests and diseases.¹¹⁰

application of mas in agriculture



Advances in the field of genomics have resulted in the rapid identification of DNA sequences and QTLs for many important agronomic traits. The majority of QTL identified are those for important agricultural staple crops such as for maize, rice and wheat.

"These sequencing efforts will not only identify preferred genes for our research and development pipelines, but move us into a high-definition molecular breeding era that uses a combination of sequence and markers to derive future higher-yielding hybrids globally".¹¹⁶ Dr. Robert Fraley, Monsanto Chief Technology Officer.

Different crops have received variable attention with regard to the application of MAS:- there has been considerable use of MAS in maize compared to rice, wheat and barley. In contrast to maize that offers opportunities to generate F1 hybrids which offer intellectual property protection from successful seed-saving (because F1 hybrids do not produce offspring true to type which effectively discourages saving of seed); wheat, rice and barley are naturally inbreeding species which do not easily generate F1 hybrids. Most wheat varieties are therefore bred and cultivated as inbred isogenic lines and the breeder is afforded only a limited amount of intellectual property protection. Consequently, although the volume of wheat seed sales may be comparable with that of maize, the value of the wheat seed market is much smaller, and thus the economic incentives are less.¹¹⁷ This illustrates the economic drivers of MAS deployment in different crops.

The important scientific driver of MAS is the identification of QTL and availability of molecular markers for the various agronomically important species. Currently, only some plant genomes have been extensively sequenced,¹¹⁸ but developments in high-throughput DNA sequencing and the increased understanding of the relationships among genes, genomes, phenotypes and the environment will increase the potential for the application of MAS in breeding programmes.

To date, the most pervasive use of MAS in maize by the private sector has been for the backcrossing of transgenics into inbred lines, and for the selection

of parents for commercial F1 hybrids and transgenics.^{119,120} In this manner, MAS has expedited the development of maize commercial hybrids and transgenics. MAS has also been successfully applied in breeding programmes that use recurrent selection of QTL for complex traits such as disease resistance, abiotic stress tolerance and grain yield.^{121,122,123} For example, studies on sweet-corn demonstrated the advantage of MAS over phenotypic selection for the selection of sweet phenotypes.^{124,125}

There has also been some research on MAS for the development of virus resistance in beans and improved nutritional qualities in sorghum, but these less globally important crops have only received limited regional attention. The progress of MAS in arable crops is nevertheless quite advanced compared with horticultural crops such as apples and pears, where development of molecular marker maps has been slower.¹²⁶

The table below summarises the use of molecular markers in crop and forestry breeding programs.¹²⁷

Plant group	Number of MAS projects
Cereals and pseudo-cereals	134
Pulses	54
Root and tubers	51
Fruit trees	53
Vegetables	29
Industrial crops ^a	74
Fodder crops ^b	16
Forestry °	188
Aromatics ^d	5
Other ^e	73
Total	677

a Crops processed for cotton, rubber, sugar-cane, jute, flax and palm oil

b Alfalfa, sorghum and other cereals for fodder

c Trees such as pines, Acacia, Eucalyptus, poplar, willow

d Herbs and spices

e Crops not listed, unspecified

FAO data (2007)

This data shows that most MAS programmes are focused on cereals, and pseudo-cereals; particularly wheat, barley, maize and rice. There are also numerous MAS programmes on the pulses (beans, chickpea and soybean), root and tuber crops (potato, sweet potato and cassava) and fruit trees (banana, cocoa, coconut and papaya, apple and pear). There are also many MAS programmes for vegetables, industrial crops (sugar cane, cotton, rubber, jute, coffee, flax and palm oil) and forestry crops (eucalyptus, pines and acacia).^{128,129} However, crops important in developing countries such as sorghum, amaranth, teff, lentil, pigeon-pea, groundnut, yam and taro have received less attention.

The table below¹²⁷ highlights the fact that most breeding programmes using MAS are in the experimental and field trial stage for the crop and forestry sectors. Therefore, it will be several years before the products of MAS are brought to market.

Phase	Crop ^a	Forestry ^b	Total
Experimental phase	344	179	523
Field tests	107	8	115
Commercial phase	4	1	5
Unspecified	34	0	34
Total	489	188	677

^a Crops are all agricultural products (listed in the plant groups of the previous table) except for Forestry (^b trees for timber).

FAO data (2007)

There has also been some development of MAS in livestock with molecular maps for chicken, cattle, pigs and sheep, goat, horse, rabbit and turkey.¹²⁸ SSR molecular markers have been of major importance and there are several marker tests available on a commercial basis for pedigree breeding.¹²⁹ Molecular marker maps have also been constructed for a number of aquaculture species such as tilapia, catfish, prawns, Japanese flounder, Atlantic salmon, rainbow trout. Many of the molecular maps rely on AFLPs and microsatellites with relatively few molecular markers;¹³⁰ although molecular markers for several traits such as cold and salinity tolerance have been detected. It is predicted when the molecular maps become sufficiently detailed, the application of MAS in fish aquaculture and animal husbandry will increase.¹³¹

ipr issues

Agricultural-biotechnology and intellectual property rights (IPRs) are playing an increasingly greater role in food and agriculture. Not only can genes be patented, but the methods used to develop them can also be covered by intellectual property rights and patents. For example, the AFLP molecular marker technique is patented to Keygene and several molecular markers are patented since they contain innovations of the method (e.g. the microsatellite-AFLP method is patented.¹³²

The patenting of Agricultural-biotechnology products can attract investment in agricultural research, but it enhances monopolies by concentrating the ownership of resources. The patenting and monopoly over the food and feed chain undermines the conservation and use of biological diversity. The farmer cannot save these patented seeds and is forced to rely on the purchase of seed and associated herbicides and payment of licensing fees every year. These proprietary seeds are usually isogenic lines that have little genetic variability and rely on a model of planting monocultures that result in an ever-increasing decline in the variety of food crops grown today. There are also concerns that patented genetically modified seeds will displace existing varieties that are landraces and form part of a country's agricultural biodiversity and indigenous knowledge systems. The enforcement of these patents can also mean new liabilities. For farmers for example, the discovery of contamination (or adventitious presence) of propriety seeds in an Organic farmer's crop may result in liability for patent infringement and the farmer would be required to pay compensation to the Agricultural-biotechnology company. Even if the contamination was unintentional and occurred through wind-pollination and the farmer lost their Organic certification and livelihood, they would need to resort to litigation for redress. Patenting therefore typically escalates costs and threatens the conservation of agricultural diversity (landraces). It also undermines local farming practices and indigenous knowledge systems, and reduces food security and food sovereignty by preventing the practice of seed-saving.¹³³

The Agricultural-biotechnology industry is aggressively patenting their products in order to protect their property rights and there has been rapid growth, convergence and consolidation in this sector. For example, from thousands of

seed companies and public breeding institutions in the market three decades ago, only ten companies now control more than two-thirds of global proprietary seed sales with the top three Agricultural-biotechnology companies (Monsanto, Pioneer-DuPont, and Syngenta) together accounting for 47% of the worldwide proprietary seed market and 75% percent of the global agrochemicals market.^{2,134} In South Africa, Monsanto's purchase of local seed companies Sensako and Carnia in the late 1990s gave it an estimated 40% share of the grain seed market.

The overall patenting activity related to MAS using a cursory search of 'markerassisted selection' revealed 860 patents for "Pioneer", 396 for "Monsanto", and 44 for "Syngenta".¹³⁵ These numbers do not include many patents covering DNA sequences from genome sequencing projects and innovations of the molecular marker methods. A company could potentially file a patent application for each marker that it identifies, but a more general strategy appears to be the patenting of DNA sequences even without direct evidence of their application. For example, the completion of the rice genome sequencing project resulted in both Monsanto and Syngenta having patented huge portions of the rice genome without referring to novel use in patent applications. Furthermore, a single patent can cover many crops since DNA sequences can be responsible for the same traits in different crops. For example, Syngenta's patent claim (WO03000904A2/3) for DNA that regulates flowering development, flower formation and whole plant architecture in rice extends to 23 major food crops which effectively allows them to claim ownership and monopoly over the flowering process of many crop species.^{136,137}

The enforcement of patents and intellectual property rights is recognised as an expensive option and Agricultural-biotechnology companies have been developing technology to make plant seeds sterile so that seed-saving is not possible and the farmer is reliant on purchasing seed every year. The terminator technology is a patented technology that was developed so that seeds are sterile, but it has not been released onto the market because of huge concerns about gene escape resulting in widespread plant sterility. However, it is receiving recurrent interest and support from the United States Department of Agriculture (USDA) and the Canadian government.¹³⁸ There are also other patents filed for plants developed using MAS that produce sterile seeds, such as the Syngenta patent for sterile inbred maize line PH185 and the Pioneer-DuPont patent for controlling female fertility.¹³⁹

It is also clear that there is frequently a lack of full disclosure of the MAS process in the patent. Alternatively, the product may not be patented, but considered a trade-secret of Agricultural-biotechnology company and can be protected by other intellectual property rights such as plant breeder's rights and trademarks.

Similarly, the infringement (non-authorised disclosure or misappropriation) of a trade-secret can also result in liability. In general, the continual assertion and protection of intellectual property has often inhibited knowledge dissemination, research and development.

agroecology and sustainable agriculture



The earth's natural resources, especially those of soil, water, plant and animal diversity, climate and ecosystem services are fundamental for the structure and function of agricultural systems and in support of life on earth. Historically, the developments in agriculture have concentrated on increasing productivity and effectively exploiting natural resources, but have ignored complex interactions between agricultural activities, local ecosystems, and society. There is overwhelming evidence of the negative impacts of modern agriculture on the environment and the subsequent cost in the provisioning of ecosystem services, that many scientists consider modern agriculture to be an ecological crisis.¹⁴⁰ The global United Nation's Millennium Ecosystem services (such as air and water purification, pollination of crops, natural pest control, food, fibre, fish and wood, and the ability of the ecosystem to mitigate the effects of natural disasters) have been degraded.¹⁴¹

The concept of sustainable agriculture is touted in response to the decline in the quality of the natural resource base associated with modern agriculture.^{142,143} Sustainable agriculture considers the ecology of agriculture and its multifunctionality to help ensure the fair, equitable and sustainable use of resources such as biodiversity, water, soil, and fossil fuels.^{144,145} Agroecology is such an approach that promotes the health and productivity of farms through building healthy soils, intercropping with beneficial companion plants, conserving soil moisture, attracting predators of insect pests, recycling animal waste for use as fertiliser, and using biodiversity to improve resilience and productivity.¹⁴⁶

There are several benefits of diversified cropping systems.¹⁴⁷ As the biodiversity increases, the number of interactions increases and there is complementarity in crop species needs, diversification of niches and partitioning of resources. There is also an increase in coexistence and beneficial interactions that enhance agricultural production and sustainability. The attributes of an ecological approach are already being successfully applied to agricultural systems, including:- Organic agriculture, integrated pest management, maintaining natural buffers and refugia, inter-cropping, companion planting and planting in succession, saving-seed

selected for local conditions, and the use of polycultures to diversify agricultural outputs. An agroecological approach also utilises indigenous knowledge systems and works with farmers in the context of their conditions and culture to enhance food security and food sovereignty by diminishing the external inputs required while making food production more resilient and sustainable.¹⁴⁸



The inescapable interconnectedness of agriculture's different roles and functions. IAASTD/Ketill Berger, UNEP/GRID-Arendal.¹⁴⁹

Evidence from hundreds of grassroots development projects shows that increasing agricultural productivity with agroecological practices not only increase food supplies, but also increase incomes; thereby reducing poverty, increasing food access, reducing malnutrition, and improving the livelihoods of the poor.¹⁵⁰ Agroecological approaches can increase the stability and productivity of agriculture, while also ensuring soil fertility and enhancing biodiversity.^{148,151}

Agroecology: Integrated pest management with the Push-pull approach.

Push-pull is a approach in integrated pest management. It uses intercropping that consists of a repellent intercrop ('push') and an attractive trap plant ('pull'). Pests are repelled from the food crop and simultaneously attracted to the trap crop.¹⁵² This push-pull strategy has been shown to effectively control maize stemborers and the Striga weed (Striga hermonthica) in resource-poor farming systems.¹¹³ Maize is inter-cropped with desmodium (Desmodium uncinatum) and Napier grass (Pennisetum purpureum) is planted around the crop border. The desmodium produces volatile chemicals (e.g. ß-ocimene) that repel the stemborer moths from the maize ('push') while chemicals released by Napier grass (e.g.octanal) attract female moths ('pull'). The Desmodium roots produce chemical exudates (isoflavones) that stimulate Striga seed germination and inhibit their attachment to maize roots; thereby reducing Striga seed banks in the soil and the subsequent emergence of the Striga weeds in the field. There is therefore no need to rely on the proprietary seeds and associated agrochemicals from Agricultural-biotechnology companies such as "Strigaway" (BASF) - a maize variety tolerant to Imazapyr herbicide. The push-pull strategy not only helps to effectively combat the Striga weed and stemborer pests, but it also improves soil fertility through nitrogen fixation by Desmodium while both the Desmodium and Napier grass provide additional fodder for livestock.153,154

The Tigray experience: A success story in sustainable agriculture.

The results of a 10-year experiment in sustainable development and ecological land management in the Tigray region of Ethiopia has provided scientific evidence that organic and sustainable agricultural practices have brought significant benefits to poor farmers and communities, particularly to women-headed families. Among the benefits demonstrated are increased yields and productivity of crops, improved hydrology with raised water tables and permanent springs, improved soil fertility, less weeds, pests and diseases, rehabilitation of degraded lands, and increased incomes.

In particular, the impacts of compost on crop yields were clearly evident. From 2001 through 2005, data for 14 crops were collected each year from a total of 779 fields and the fields that used compost compared to fields that used chemical fertilisers and fields that had no inputs. Although the addition of both compost and fertiliser drastically improved crop yields,

the composting was shown to be more effective. The yields were 30% or more for the composted fields compared to those treated with synthetic fertiliser; and for some grains (barley, wheat millet) the yields for composted fields were nearly 100% more than using chemical fertiliser. This evidence highlights the fact that increased productivity and improved livelihood of the environment and community can be achieved through adding compost and using locally adapted crop varieties. There is no need for proprietary seed from Agricultural-biotechnology companies and the associated chemical inputs that make the farmer dependent on external inputs such as fertilisers, herbicides and patented genetically modified seeds. By using locally adapted crop varieties and organic farming methods the food security and food sovereignty is maintained, thereby enabling sustainable agriculture that ensures food supply for many generations to come.^{155,156}

A recent three-year study by the International Assessment of Agricultural Science and Technology for Development (IAASTD) focused on how to make better use of agricultural science, knowledge and technology to reduce hunger and poverty, improve rural livelihoods, and foster equitable and sustainable development.¹⁵⁷ The project developed out of a consultative process involving 900 participants and 110 countries and was launched as an intergovernmental process under the co-sponsorship of the FAO, GEF, UNDP, UNEP, UNESCO, the World Bank and WHO.¹ The study noted that agricultural development has been geared towards increasing productivity and exploiting natural resources, but has ignored the complex interactions between agricultural activities, local ecosystems, and society. These interactions must be considered to enable sustainable use of resources like water, soil, biodiversity and fossil fuels. Furthermore, although existing agricultural science and technology can tackle some of the underlying causes of declining productivity, further developments based on a multidisciplinary approach are needed; starting with the monitoring of how natural resources are used.¹⁵⁸ The essential flaw of the current agricultural development approach is that it is capital-centered and profit-driven. This has meant that farmers are delinked or isolated from their livelihood and culture so that "Agri-culture" becomes "Agri-business."

i The findings of the IAASTD study were reviewed and ratified by governments during the Intergovernmental Plenary Meeting (7-12 April, 2008, in Johannesburg, South Africa). Of the 61 countries attending, 58 have signed and endorsed the report. Curiously, South Africa was not present and has not signed this important document.

"We need to consider the environmental issues of biodiversity and water; the economic issues of marketing and trade, and the social concerns of gender and culture". Agriculture is far more than just production of food, and that is what we have to recognise".¹⁵⁷ Prof. Robert Watson, IAASTD

There are several possibilities for agriculture, knowledge, science and technology to combine efforts to help fulfill the aims of sustainable agriculture. These include using local knowledge and skills to develop and deploy suitable varieties adapted to site-specific conditions; improving soil, water and nutrient management and conservation; integrated pest management; and increasing small-scale farm diversification. In addition, there are several policy options that can address food security, including: developing market access for organic and fair trade products, strengthening local markets, ensuring fair and equitable trade regimes, and enabling participation, transparency and democracy.

conclusions

There are rapid advancements in the use of marker assisted selection (MAS) to develop new plant and animal varieties and many Agricultural-biotechnology companies are actively pursuing MAS programmes. This is a response to the rapid developments in DNA sequencing and genomics, the realisation that many important agronomic traits are governed by many genes or quantitative trait loci, and that the current transgenic genetically modified organisms (GMOs) carry unacceptable biosafety risks. It has been suggested that MAS has the potential to increase food production and initiate a new Green Revolution in Africa.

The products of modern biotechnology are broadly termed genetically modified organisms and are produced using a range of molecular biology techniques from marker assisted selection, mutagenesis and transgenics to cloning and human gene therapy. These products of modern biotechnology carry new biosafety risks when these organisms are released into the environment. The Cartagena Protocol on Biosafety is an international agreement that aims to protect biological diversity from the potential risks posed by the products of modern biotechnology. It requires a precautionary approach to balance the risks and benefits with regards to the environment, society, and the economy.

The traditional and conventional methods of breeding and seed-saving use open-pollinated seeds that are dynamic because they continually adapt to the local ecosystem and have a wide genetic diversity. In contrast, the Agriculturalbiotechnology seeds (HYVs, hybrids, MAS, and transgenics) are usually planted and grown as inbred monocultures and they require the early purchase of proprietary seed so that genetic diversity is limited and static. The importance of agricultural genetic diversity and the maintenance of dynamic gene pools in protecting against new diseases or climatic changes was observed when maize production in Africa was rescued from destruction after the introduction of tropical rust in the 1950s. The generation and maintenance of the world's agricultural genetic diversity has been carried out over thousands of years by farmers and traditional breeders to produce numerous open-pollinated varieties. It is vital to maintain and preserve this diversity through isolation and segregation practices so that the agricultural genetic diversity and indigenous knowledge systems of

farmers are protected from the intellectual property rights of patented Agriculturalbiotechnology products. Additionally, since the farmer is dependent on the yearly purchase of proprietary seed and the associated agrochemicals (fertilisers, herbicides, pesticides) the power has shifted from the hands of the farmer to that of the Agricultural-biotechnology company. This makes the country's food supply increasingly dependent on the external inputs from a small number of Agriculturalbiotechnology companies that now control the world's food supply.

The application of MAS in agriculture will most likely be on the basis of economics alone, with the multifunctionality of agricultural systems being given little consideration. MAS will therefore be part of the 'business as usual' approach to agricultural food production that will decrease a country's food security and food sovereignty, result in greater global inequalities with increased hunger and poverty, and cause the continued degradation of the environment.

There is such overwhelming evidence of the negative impacts of modern agriculture on the environment, and the subsequent cost in the provisioning of ecosystem services, that many scientists consider modern agriculture to be an ecological crisis. The approaches of Agroecology will help to address the sustainability of agricultural systems, but changes in policy and trade will also be needed to address inequalities in food supply, distribution and market access. A participatory approach amongst various stakeholders across multiple scales is required to ensure that the resources of biodiversity and the ecosystems services (quality of air, soil, and water) are available for future generations. It is vital to work with farmers in the development of sustainable agriculture by using indigenous knowledge systems and local open-pollinated varieties to maintain biodiversity and tackle important agricultural problems. In essence, a shift in the paradigm from "Agri-business" to one of "Agri-culture" is required.

"If we do persist with business as usual, the world's people cannot be fed over the next half-century. It will mean more environmental degradation, and the gap between the haves and have-nots will further widen. We have an opportunity now to marshal our intellectual resources to avoid that sort of future. Otherwise we face a world no one would want to inhabit".¹⁵⁷

Prof. Robert Watson, IAASTD

glossary of terms

Biodiversity is the variation of life at all levels of biological organization or the totality of genes, species, and ecosystems of a region.

Biotechnology is a broad term embracing the manipulation of living organisms and spans the large range of activities from conventional techniques of fermentation and plant and animal breeding to recent innovations in tissue culture, irradiation, genomics and marker assisted selection (MAS) to augment natural breeding. Some of the latest biotechnologies ('modern biotechnology') include the use of *in vitro* modified DNA or RNA and the fusion of cells from different taxonomic families, techniques that overcome natural physiological reproductive or recombination barriers. **Agricultural-biotechnology** refers to the use of biotechnology to develop agricultural products.

Cartagena Protocol on Biosafety (CPB, January 2002) is the first international legal agreement signed by more than 60 countries (including South Africa). It defines modern biotechnology as "the application of: *in vitro* nucleic acid techniques, including recombinant deoxyribonucleic acid (DNA) and direct injection of nucleic acid into cells or organelles, or fusion of cells beyond the taxonomic family, that overcome natural physiological reproductive or recombination barriers". "Natural barriers include geographical separation, separation in the time of reproductive periods of individuals, or separation in the ecology of the individuals concerned" (pg 50 An Explanatory Guide to the Cartagena Protocol on Biosafety, 2006, IUCN).

Food security is a situation that exists when all people, at all times, have physical, social and economic access to sufficient, safe and nutritious food that meets their dietary needs and food preferences for and active and healthy life.

Food sovereignty is defined as the right of peoples and sovereign states to democratically determine their own agricultural and food policies.

F1 hybrid. F1 stands for Filial 1, the first generation seeds/plants or animal offspring resulting from cross mating of distinctly different parental types. If these F1 hybrids are mated to produce seeds (F2), these offspring will not be true to type (they will not have the characteristics of the F1 seeds).

Genetic loci. A locus (*pl*. loci) is a fixed position on the genome and a variant of the DNA sequence at a given locus is called an allele. The ordered list of loci known for a particular genome is called the genetic map.

Genome. The genome of an organism is its whole hereditary information and is encoded by nucleic acid sequence, (generally DNA, but for some viruses, RNA). The genome includes both the genes and the regulatory or non-coding nucleic acid sequences.

Genomics is the study of an organism's entire genome. The field includes intensive efforts to determine the entire DNA sequence of organisms and fine-scale genetic mapping efforts. The field also includes phenomena such as heterosis, epistasis, pleiotrophy and other interactions between loci and within the genome

Genetically modified organism (GMO). An organism is genetically modified, if its genetic material has been changed in a way that does not occur under natural conditions through cross-breeding or natural recombination (Article 2 of the EU Directive on the Deliberate Release into the Environment of Genetically Modified Organisms, 2001/18/EG).

Genotyping refers to the process of determining the genotype of an individual by the use of biological assays. The **genotype** is the genetic constitution of a cell, an organism, or an individual (i.e. the specific allele makeup of the individual) usually with reference to a specific characteristic or trait under consideration. The inherited genotype, together with epigenetic factors, and environmental conditions contribute to the phenotype of an individual. The **phenotype** is any observable characteristic or trait of an organism: such as morphology, development, biochemical or physiological properties.

Germplasm is the collection of genetic resources for an organism. For plants, the germplasm may be stored as a seed-banks.

Inbreeding is the breeding between close relatives, whether plant or animal to produce an inbred line. If practiced repeatedly, this leads to an decrease the genetic diversity of a population and can result in inbreeding depression (reduced health and fitness and lower levels of fertility).

Indigenous knowledge systems refers to the matured long-standing traditions and practices of certain regional, indigenous, or local communities.

Introgression is the movement of a gene (gene flow) from one species into the gene pool of another by backcrossing an interspecific hybrid with one of its parents. An example of introgression is the gene flow between a transgenic plant to a wild relative as the result of a successful hybridisation.

Isogenic individuals are genetically identical (except for sex). Having originated from the same individual or from the same inbred line.

Landraces are the domesticated animals or plants adapted to the natural and cultural environment in which they live. They have been developed naturally using traditional breeding methods.

Molecular marker (genetic marker) is a fragment of DNA sequence associated with part of the genome.

Monoculture is the agricultural practice of producing or growing one single crop over a wide area.

Multifunctionality refers to the inescapable interconnectedness of agriculture's different roles and functions. The concept of multifunctionality recognises agriculture as a multi-output activity producing not only commodities (food, fodder, fibers and biofuels), but also non-commodity outputs such as ecosystem services, landscape amenities and cultural heritages. It also refers to the current patterns of agricultural subsidies, international trade and related policy frameworks that do not stimulate transitions toward equitable agricultural and food distribution or to sustainable food and farming systems and have negative impacts on natural resources and agroecologies as well as on human health and nutrition.

Open-pollinated. Open-pollination is carried out naturally in the environment by insects, birds, wind, or other natural mechanisms. Since open-pollination occurs under natural, uncontrolled conditions (and the pollen source is unknown) the breeding may result in plants that vary widely in genetic traits with increased biodiversity. Furthermore, open-pollinated seeds are dynamic because they mutate and, through seed-saving, continually adapt to the local ecosystem. In contrast, hybrids and transgenic GMOs are usually grown as inbred monocultures and require the yearly purchase of proprietary seed so that they are static with a limited biodiversity.

Polyculture is agriculture that uses multiple crops in the same field or area to create biodiversity in time (mixed-cropping) and space (succession).

Polygenic refers to the inheritance of a characteristic that varies in degree and can be attributed to the interactions between two or more genes and the environment.

Quantitative Trait Loci (QTL) are stretches of DNA (not necessarily genes themselves) that are closely linked to the genes that underlie a certain trait.

Sustainable refers to meeting the needs of the present without compromising the ability of future generations to meet their own needs. Sustainable agriculture refers to the ability of a farm to produce food indefinitely, without causing severe or irreversible damage to ecosystem health. Two key elements are the bio-physical (the long-term effects of various practices on crop productivity, which includes a range of functions and ecosystem services such as soil properties and function, water and air purification, and the maintenance of biodiversity) and socio-economic (the long-term ability of farmers to obtain inputs and manage resources).

Transgenics are genetically modified organisms (GMOs) that have had their genetic material altered using genetic engineering techniques. DNA molecules from different sources are combined into one molecule to create a new set of genes (transgenic cassette) and this DNA is engineered into the genome of an organism to create a life-form with a novel genetic makeup.

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