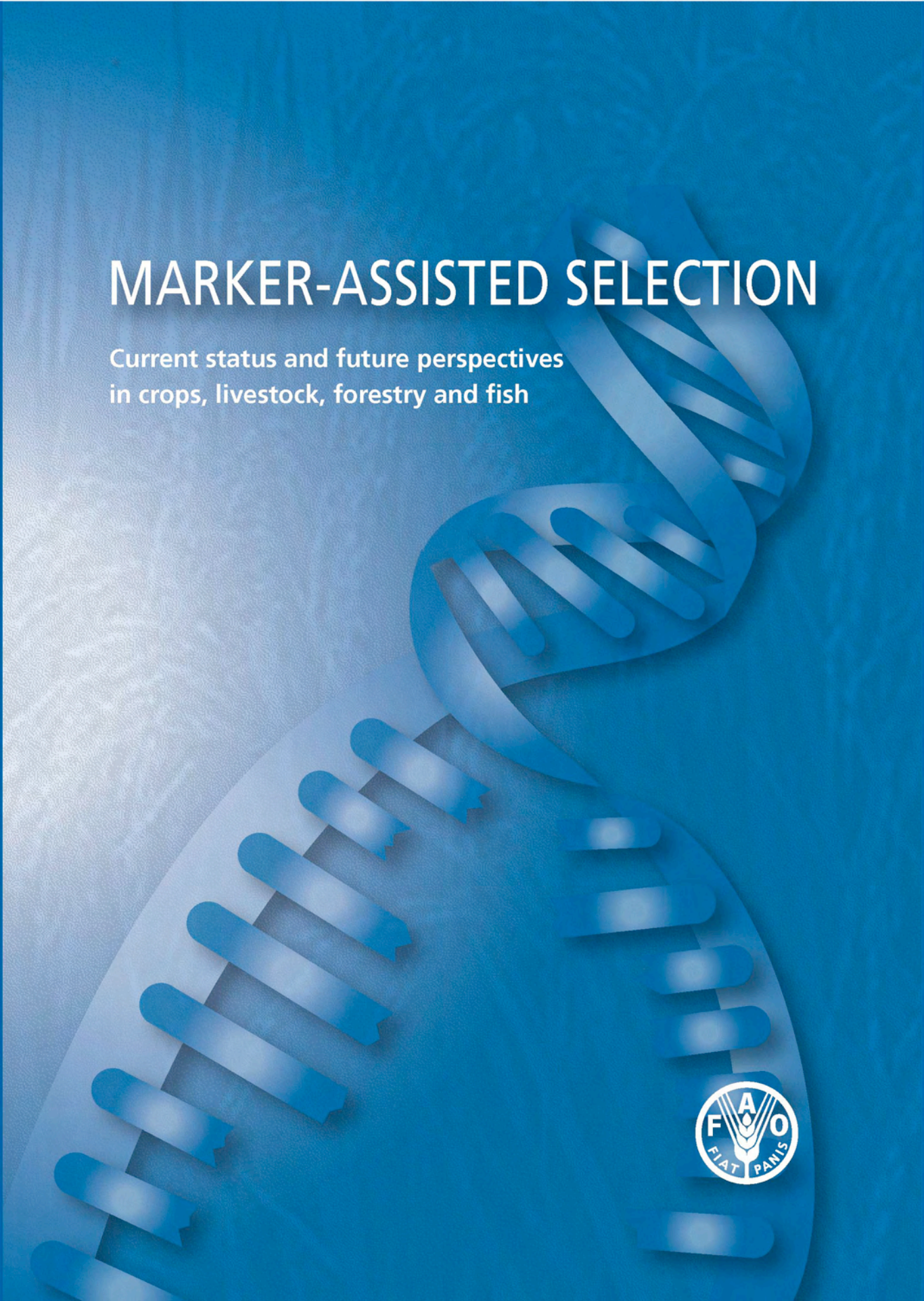
MARKER-ASSISTED SELECTION

Current status and future perspectives in crops, livestock, forestry and fish



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Current status and future perspectives in crops, livestock, forestry and fish

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Foreword

Since almost the beginning of human civilization, exploiting variation in the characteristics of the plant and animal genetic resources that are used for producing food and other agricultural products through breeding has been at the heart of efforts to increase and diversify agricultural production and productivity, enhance food security and incomes, and adapt farming to changing environmental conditions and social needs. Initially, this was achieved simply by selecting and reproducing preferred individuals or spontaneous variants, and indeed this practice remains important today as the basis for producing new generations of cultivated landraces and indigenous breeds. However, the crops, trees, livestock and fish that are farmed today have arisen largely from the introduction of scientific breeding at the beginning of the twentieth century, with the inclusion of crosses into breeding schemes prior to artificial selection and application of Mendel's laws of inheritance to improve both simple and quantitative traits providing the foundations for modern genetics.

Today, thanks to continuing investments made in research and technology development, the process of producing improved varieties, clones, breeds and strains of agriculturally important species has become progressively more accurate, reliable and efficient. Nevertheless, one of the continuing technical constraints to more effective breeding is that selecting material with one or a combination of the characteristics required by farmers, foresters, industry and consumers still relies mainly on physical and agronomic attributes (phenotype). Some of these characteristics are influenced by the environment and are therefore not necessarily a good guide to the actual heritable genetic composition (genotype) of the material in question. Others may not be visible or may only be detected in mature plants and animals. Others again may be difficult or very costly to screen, and many characters such as drought tolerance and milk composition are controlled by a large number of genes whose mode of action as well as their interaction with each other and with various environmental triggers is mainly unknown. Improving the identification, selection and monitoring of specific characters in plants and animals through breeding schemes is therefore a critical need to secure future improvements in genetic resources for food and agriculture.

Since the first description of DNA structure over 50 years ago, scientists have made tremendous strides in identifying genes and gene functions, making it increasingly possible to detect genetic differences (DNA polymorphisms) for traits among individual plants and animals in a much more direct way, thereby assisting in the selection of desired traits. The central technology involved is molecular marker-assisted selection (MAS), using sequences and/or banding patterns of DNA that have been shown through linkage mapping to be located in or near genes that affect the phenotype. These molecular markers can then be used to assist breeders track whether

the specific gene or chromosome segment(s) known to affect the phenotype of interest is present in the individuals or populations of interest.

Although the ultimate goal of identifying the location, function and most favourable alleles of each gene through genome sequence and post-genomics research, and then using markers to select for economically important genes in breeding programmes, is still decades away, in recent years the use of MAS in agriculture has moved progressively from theory to practical application. In the process, it has generated both high expectations for increasing genetic progress through breeding, and raised a number of unresolved challenges. These include: selection of the most appropriate methods and tools for MAS among the many now available for the task at hand, analysing and managing the data produced given the increasing trend towards high-throughput techniques and the constraints imposed by suboptimal levels of resources currently attached to breeding and science and technology including biotechnology, and dealing with intellectual property rights, especially in developing countries.

Since its foundation, FAO has recognized that the biological basis for sustainable agricultural production, fighting hunger and world food security lies in the genetic resources used for food and agriculture. It has also recognized the enormous contributions that have been made to the improvement of these resources through both traditional and more advanced breeding, as well as the ever-increasing role played by biotechnology in improving breeding processes and products. As a knowledge organization, one of FAO's major roles is to provide its Members and their institutions with factual, comprehensive and current information relevant to sound stewardship of crops, livestock, forestry and fisheries, thereby ensuring its availability as a global public good. This book, by providing a comprehensive description and assessment of the use of MAS for increasing the rate of genetic gain in crops, livestock, forestry and farmed fish, including the related policy, organizational and resource considerations, continues the Organization's tradition of dealing with issues of importance to agricultural and economic development in a multidisciplinary and cross-sectoral manner. As such it is hoped that the information and options presented and the suggestions made will provide valuable guidance to scientists and breeders in both the public and private sectors, as well as to government and institutional policy- and decision-makers.

Shivaji Pandey
Chairperson
FAO Working Group on Biotechnology

Abbreviations and acronyms

AATF	African Agricultural Technology Foundation
AB-QTL	Advanced backcross QTL
ACMV	African cassava mosaic virus
AFLP	Amplified fragment length polymorphism
AI	Artificial insemination
AMBIONET	Asian Maize Biotechnology Network
AMMANET	African Molecular Marker Applications Network
AnGR	Animal genetic resources
ASARECA	Association for Strengthening Agricultural Research in Eastern and Central Africa
BAC	Bacterial artificial chromosome
BCMNV	Bean common mosaic necrotic virus
BCMV	Bean common mosaic virus
BecA	Biosciences eastern and central Africa
BGYMV	Bean golden yellow mosaic virus
BIO-EARN	East African Regional Programme and Research Network for Biotechnology, Biosafety and Biotechnology Policy Development
BLUP	Best linear unbiased prediction
bp	Base pairs
BSAPs	Biodiversity Strategies and Action Plans
Bt	*Bacillus thuriengensis*
BTA	*Bos taurus* chromosome
BYDV	Barley yellow dwarf virus
CAADP	Comprehensive Africa Agriculture Development Programme
CAPS	Cleaved amplified polymorphic sequences
CBB	Cassava bacterial blight
CBS	Cassava brown streak
CBSD	Cassava brown streak disease
CCN	Cereal cyst nematode
cDNA	Complementary DNA
CGIAR	Consultative Group on International Agricultural Research
CGM	Cassava green mite
CI	Confidence interval

CIAT	International Center for Tropical Agriculture (Centro Internacional de Agricultura Tropical)
CIMMYT	International Maize and Wheat Improvement Center (Centro Internacional de Mejoramiento de Maíz y Trigo)
CIP	International Potato Center Centro (Internacional de la Papa)
CIRAD	French Agricultural Research Centre for International Development (Centre de coopération internationale en recherche agronomique pour le développement)
cM	Centi-Morgan
CMD	Cassava mosaic disease
CMV	Cassava mosaic virus
CORPOICA	Colombian Agricultural Research Corporation (Corporación Colombiana de Investigación Agropecuaria)
CR	Country report
CT	Computer tomography
DArT	Diversity array technology
DFID	United Kingdom's Department for International Development
DH	Double-haploid
DHPLC	Denaturing high pressure liquid chromatography
DMC	Dry matter content
DNA	Deoxyribonucleic acid
DYD	Daughter yield deviation
EACMV	East Africa cassava mosaic virus
EBV	Estimated breeding value
EC	European Commission
ECOSOC	Economic and Social Council of the United Nations
eQTL	Expressed gene QTL
EST	Expressed sequence tag
ESTP	Expressed sequence tagged polymorphism
EU	European Union
EUCAGEN	*Eucalyptus* Genome Network
F_1	First filial generation
F_2	Second filial generation
FAO	Food and Agriculture Organization of the United Nations
FAO-BioDeC	FAO Biotechnology in Developing Countries
FHB	*Fusarium* head blight

FIVIMS	Food Insecurity and Vulnerability Information and Mapping Systems
FNP	Functional nucleotide polymorphism
FSC	Forest Stewardship Council
FSIL	Full-sib intercross line
GABI	Genome analysis of the plant biological system
GAS	Gene-assisted selection
GCA	General combining ability
GCP	Generation Challenge Programme
GDP	Gross domestic product
GE	Genetic engineering
GH	Growth hormone
GIS	Geographical information systems
GMOs	Genetically modified organisms
GRDC	Grains Research and Development Corporation
GRFA	Genetic resources for food and agriculture
GRM	Gametic relationship matrix
h^2	Heritability
HIPC	Heavily indebted poor countries
HWE	Hardy-Weinberg equilibrium
IAC	InterAcademy Council
IAP	InterAcademy Panel
IARCs	International agricultural research centres
IBD	Identity by descent
ICAR	Indian Council for Agricultural Research
ICMV	Indian cassava mosaic virus
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICSU	International Council for Science
IFPRI	International Food Policy Research Institute
IHN	Infectious haematopoietic necrosis
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
INIFAP	National Institute for Forestry, Agriculture and Livestock Research (Instituto Nacional de Investigaciones Forestales y Agropecuarias)
IP	Intellectual property
IPGRI	International Plant Genetic Resource Institute
IPR	Intellectual property right
IRR	Internal rate of return
IRRI	International Rice Research Institute
ISAG	International Society for Animal Genetics

ISNAR	International Service for National Agricultural Research
ISSR	Inter-simple sequence repeats
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
JGI	Joint Genome Institute
KARI	Kenya Agricultural Research Institute
LD	Linkage disequilibrium
LDL	Linkage disequilibrium and linkage
LD-MAS	Linkage disequilibrium MAS
LE	Linkage equilibrium
LE-MAS	Linkage equilibrium MAS
LIMS	Laboratory information management system
LOD	Logarithm of the odds ratio
MABC	Marker-assisted back-crossing
MA-BLUP	Marker-assisted best linear unbiased prediction
MAI	Marker-assisted introgression
MALDI-TOF	Matrix-assisted laser desorption/ionization-time of flight
MARS	Marker-assisted recurrent selection
MAS	Marker-assisted selection
MBL	Medical biotechnology laboratories
MC	Molecular characterization
MD	Marek's disease
MDG	Millennium Development Goals
MFA	Microfibril angle
MHC	Major histocompatibility complex
miRNA	MicroRNA
ML	Maximum likelihood
MoDAD	Measurement of domestic animal diversity
mRNA	Messenger RNA
MSV	Maize streak virus
MTA	Material Transfer Agreement
NARES	National agricultural research and extension systems
NARS	National agricultural research systems
NDA	Non-disclosure agreement
NEPAD	New Partnership for Africa's Development
NGO	Non-governmental organization
NIRS	Near infrared reflectance spectroscopy
NPV	Net present value
NUE	Nitrogen use efficiency

OBM	Orange blossom midge
OECD	Organisation for Economic Co-operation and Development
OIE	World Organisation for Animal Health
OPV	Open-pollinated variety
PAGE	Polyacrylamide gel electrophoresis
PBRs	Plant breeders' rights
PCR	Polymerase chain reaction
PGRFA	Plant genetic resources for food and agriculture
PIC	Polymorphic information content
PPB	Participatory plant breeding
PPD	Post-harvest physiological deterioration
PRSPs	Poverty reduction strategy papers
PT	Progeny test
PVP	Plant variety protection
QPM	Quality protein maize
QTL	Quantitative trait loci (or locus)
QTL-NILs	Near isogenic lines for QTL
QTN	Quantitative trait nucleotide
R&D	Research and development
RAPD	Random amplified polymorphic DNA
rDNA	Ribosomal DNA
RFLP	Restriction fragment length polymorphism
RGA	Resistance gene analogues
RNA	Ribonucleic acid
RRA	Rapid rural appraisal
S&T	Science and technology
SACMV	South African cassava mosaic virus
SAGE	Serial analysis of gene expression
SBMV	Soil-borne mosaic virus
SCA	Specific combining ability
SCAR	Sequence characterized amplified region
SCN	Soybean cyst nematode
SCS	Somatic cell score
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
siRNA	Short interfering RNA
SLS-MAS	Single large-scale MAS
SLU	Swedish University of Agricultural Sciences
SMA	Simple marker analysis
SNP	Single nucleotide polymorphism

SoW-AnGR	State of the World's Animal Genetic Resources
SPS Agreement	WTO Agreement on the Application of Sanitary and Phytosanitary Measures
SSCP	Single strand conformation polymorphism
SSLP	Simple sequence length polymorphism
SSR	Simple sequence repeat (syn. microsatelllite)
STB	*Septoria tritici* blotch
STS	Sequence-tagged sites
SW	Seed weight
SWaps	Sector-wide approaches
TBT Agreement	WTO Agreement on Technical Barriers to Trade
TC	Tissue culture
TEs	Transposable elements
TMV	Tobacco mosaic virus
ToMV	Tomato mottle virus
TRIPS Agreement	WTO Agreement on Trade-Related Aspects of Intellectual Property Rights
TSWV	Tomato spotted wilt virus
TUA	Technology Use Agreement
TYLCV	Tomato yellow leaf curl virus
UN	United Nations
UPOV	International Union for the Protection of New Varieties of Plants
USAID	United States Agency for International Development
USDA	United States Department of Agriculture
WEC	Worm egg count
WFS	World Food Summit
WIPO	World Intellectual Property Organization
WRI	World Resources Institute
WSC	Wood specific consumption
WTO	World Trade Organization
YMV	Yellow mosaic virus

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