NATIONAL BIOSAFETY AUTHORITY

GUIDELINES FOR THE ENVIRONMENTAL RISK ASSESSMENT (ERA) OF GENETICALLY MODIFIED CROPS IN KENYA

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Foreword

The National Biosafety Authority (NBA) was established vide Biosafety Act of 2009 to exercise general supervision and control over the transfer, handling and use of genetically modified organisms (GMOs) in Kenya with the aim of ensuring safety of human and animal health, and provision of an adequate level of protection to the environment. The Authority regulates all activities involving GMOs in food, feed, research, industry, cultivation, trade, import, export and transboundary movements.

NBA is the National Focal Point for the Cartagena Protocol on Biosafety to the Convention on Biological Diversity (CBD) and is mandated to implement the provisions of the Cartagena Protocol on all biosafety matters pertaining to GMOs.

Since its establishment, the Authority has made great strides in establishing a strong Biosafety framework in Kenya by developing and publishing the implementing Biosafety Regulations namely; Biosafety (Contained use) Regulations, 2011, Biosafety (Environmental Release) Regulations, 2011, Biosafety (Import, Export and Transit) Regulations, 2011; and the Biosafety (Labeling Regulations), 2012. These regulations laid down clear procedures on handling GMOs whether crops, animals or microorganisms.

To support and elaborate the Regulations, the Authority has for developed a number of manuals, guidelines and standard operating procedures on various regulatory processes. These documents have been developed based on the International Organization for Standardization (ISO) standards. This guideline provides guidance for the Environmental Risk Assessment (ERA) of GM crops submitted within the framework of the Biosafety Act and Biosafety (Environmental release) Regulations, 2011. It provides a detailed stepwise process of assessing potential adverse effects of GM crops to the environment and natural ecosystems and how the identified risks shall be mitigated post release.

This guideline was prepared through a series of consultative meetings to gather experts and public views. We are grateful for the active participation and cooperation demonstrated by the Biosafety Regulatory agencies and other stakeholders during the process of developing this guideline. We sincerely thank our development partners for the support in development of these guidelines which will go a long way in improving the biosafety systems in Kenya.

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ABBREVIATIONS AND ACRONYMS

DNA	:	Deoxyribonucleic Acid
DPH	:	Department of Public Health
EMCA	:	Environmental Management and Coordination Act
ERA	:	Environmental Risk Assessment
DVS	:	Department of Veterinary Services
GM	:	Genetically Modified
GMO	:	Genetically Modified Organism
HGT	:	Horizontal gene transfer
KEBS	:	Kenya Bureau of Standards
KEPHIS	:	Kenya Plant Health Inspectorate Service
KIPI	:	Kenya Industrial Property Institute
KWS	:	Kenya Wildlife Service
NBA	:	National Biosafety Authority
NEMA	:	National Environment Management Authority
NTO	:	Non-Target Organism
OECD	:	Organization for Economic Co-operation and Development
PCPB	:	Pest Control Products Board
rDNA	:	Recombinant Deoxyribonucleic Acid
SOP	:	Standard Operating Procedure
TO	:	Target Organism
USEPA	:	United States Environmental Protection Agency

DEFINITION OF TERMS

Antagonism means the act of a gene/stack opposing the effects of another.

Applicant: means a person applying pursuant to the provisions of the Biosafety Act.

GM Breeding Stacks are gene stacks obtained via conventional crossing breeding methods.

Contained Use means any activity undertaken within a facility, installation or other physical structure, which involves genetically modified organisms that are controlled by specific measures.

Consequence: is the result of an undesired event, such as harm to health, life or the environment.

Conventional counterpart means the equivalent non-genetically modified crop variety or parental line or a near-isogenic line

Co-Transformation means techniques of modern biotechnology using two or more transformation vectors to produce a GMO. A plant is transformed with two or more independent transgenes. The transgenes of interest are in separate gene constructs and delivered to the plant simultaneously.

Donor organism means an organism from which genetic material is obtained for transfer to the recipient organism.

Enhanced fitness means characteristic of an individual or sub population of individuals that consistently produces more offspring to the subsequent generation.

Environmental release means the introduction into the environment of a genetically modified crop for which an approval has been granted in accordance with these Environmental Release Regulations and for which no specific containment measures are used to limit their contact with and to provide a high level of safety for the general population and the environment; and includes making genetically modified organisms available to the public for purposes other than sale.

Environmental risk assessment means the process of identifying significant risks to the environment, estimating the level of risk, and determining those risks that require measures to reduce the level of risk

Event means a genotype produced from the transformation of a single crop species using a specific genetic construct. For example, two lines of the same crop species transformed with the same or different constructs constitute two events.

Exposure means the contact or occurrence of a potential hazard with an environmental entity of value.

Fitness means number of seeds produced per seed sown, and includes the whole life cycle of the crop.

Harm means a negative outcome of effect of an action or event; in other words, an adverse effect.

Host organism means the crop species that was transformed to produce the genetically Modified crop.

Genetically modified organism means any organism that possesses a novel combination of genetic material obtained through the use of modern biotechnology techniques.

Hazard means a biological, chemical, or physical agent that has an inherent potential to cause an adverse effect in the environment.

Horizontal gene transfer (HGT) means any process by which an organism incorporates genetic material from another organism without being the offspring of that organism i.e. the transfer of genetic material to unrelated species such as from a crop to bacteria.

Modern biotechnology means the application of:

i. in-vitro nucleic acid techniques including the use of recombinant deoxyribonucleic acid (DNA) and direct injection of nucleic acid into cells or organelles; or

ii. fusion of cells beyond the taxonomic family, that overcome natural physiological, reproductive and recombination barriers and which are not techniques used in traditional breeding and selection:

Molecular Stacks means a plant transformed by using molecular methods, where two or more traits are simultaneously (Co-Transformation) or sequentially (Re-transformation) introduced into a host plant. This involves the introduction of gene constructs simultaneously or sequentially into the target plant by standard delivery systems such as Agrobacterium-mediated and biolistic methods.

Resistance means the occurrence of a phenotype of an individual of TO that can survive on the GM crop and produce viable offspring.

Re-transformation means transforming a transgenic organism with another/other transgene(s)

Risk, in relation to any crop, means the probability of an adverse effect on the environment and the severity of that effect, due to an environmental hazard.

Risk = *f* (Hazard x Exposure)

Risk analysis, in relation to any crop, means a process consisting of three components, i.e., risk assessment, risk management, and risk communication.
Risk assessment means the evaluation of risks to human, animals and the environment, whether direct or indirect, immediate or delayed, which the environmental release or placing on the market of genetically modified organisms may pose.

Stability means the ability of a stack to work as expected and enable transmission of genetic material from generation to generation.

Stacking means the introduction of multiple GM traits in a crop.

Synergistic effect means an interaction of elements that when combined produce a total effect that is greater than the sum of the effect of the individual elements.

Transformation means the unique DNA recombination event that took place though the integration of a transgene(s) in one crop cell for genetic modification, which was then used to generate entire transgenic crops.

Vector means an organism (e.g., virus) or a DNA molecule (e.g., plasmid, nucleic acid cassettes) used to assist in the transfer of genetic material from a donor organism to a recipient organism.

Vertical gene flow means the transfer of genetic material between sexually compatible species

CHAPTER 1

BACKGROUND INFORMATION

1.1 Background

The National Biosafety Authority (NBA) is a state corporation in Kenya mandated to ensure safety of human and animal health and provide adequate protection of the environment from harmful effects that may result from genetically modified organisms (GMOs).

The Authority was established pursuant to the provisions of the Biosafety Act, 2009 to regulate all activities involving GMOs in food, feed, research, industry, trade and environmental release and it fulfills its mandate by ensuring and assuring safe development, transfer, handling and use of GMOs in Kenya.

NBA has made great strides in establishing strong Biosafety framework in Kenya by developing and publishing the implementing Biosafety Regulations. These regulations laid down a clear procedure on handling GMOs whether crops, animals or microorganisms. NBA is the National Focal Point for the Cartagena Protocol on Biosafety to the Convention on Biological Diversity (CBD) and is mandated to implement the provisions of the Cartagena Protocol on all Biosafety matters pertaining to GMOs.

1.2 Vision Statement

A World-class Biosafety Agency

1.3 Mission Statement

To ensure and assure safe development, transfer, handling and use of genetically modified organisms (GMOs) in Kenya.

1.4 Core Values

a) Good governance and integrity

b) Professionalism

c) Customer Focus

d) Inclusiveness.

1.5 Objectives of the Biosafety Act

a) To facilitate responsible research and minimize risks that may be posed by genetically modified organisms;

b) To ensure adequate level of protection in the development, transfer, handling and use of genetically modified organisms that may have an adverse effect on the health of the people and the environment; and

c) To establish a transparent, science-based and predictable process for reviewing and making decisions on the development, transfer, handling and use of genetically modified organisms and related activities.

1.6 Core Functions

The Biosafety Act No.2 of 2009, Section 7(2) lists the functions of NBA as follows:

a) Consider and determine applications for approval for the development, transfer, handling and use of genetically modified organisms, and related activities in accordance with the provisions of the Biosafety Act;
b) Co-ordinate, monitor and assess activities relating to the safe development, transfer, handling and use of genetically modified organisms in order to ensure that such activities do not have adverse effect on human health and the environment;
c) Co-ordinate research and surveys in matters relating to the safe development, transfer, handling and use of genetically modified organisms, and to collect, collate and disseminate information about the findings of such research, investigation or survey;
d) Identify national requirements for manpower development and capacity building in biosafety;
e) Advise the Government on legislative and other measures relating to the safe development, transfer, handling and use of genetically modified organisms;
f) Promote awareness and education among the general public in matters relating to biosafety; and
g) Establish and maintain a Biosafety clearing house (BCH) to serve as a means through which information is made available to facilitate exchange of scientific, technical, environmental and legal information on, and experience with, living modified organisms;
h) To exercise and perform all other functions and powers conferred on by the Act.

CHAPTER 2

INTRODUCTION

2.1. Introduction

Modern biotechnology involving the use of recombinant DNA (rDNA) technologies, also known as genetic engineering, has emerged as a powerful tool with many potential applications in healthcare, industries and agriculture. New crop varieties developed using rDNA techniques, commonly referred to as genetically Engineered (GE), genetically modified (GM) or transgenic crop have been and are being developed with the aim of enhancing productivity, decreasing dependence on the use of agricultural chemicals, modifying the inherent properties of crops, improving the nutritional value of foods and livestock feeds, and mitigating the adverse biotic and abiotic impacts of climate variability.

The Authority has developed guidelines to provide a useful starting point for planning and conducting an environmental risk assessment in Kenya. Assessments should be conducted in compliance with pertinent national laws and regulations, as well as within international standards including but not limited to the following:

i. The Biosafety Act of 2009
ii. The Biosafety (Contained Use) Regulations, 2011
iii. The Biosafety (Environmental Release) Regulations, 2011
iv. The Biosafety (Import, Export, and Transit) Regulations, 2011
v. The Biosafety (Labeling) Regulations, 2012
vi. EMCA, 1999
vii. Consensus documents published by the Organization for Economic Cooperation and Development's (OECD) Working Group on Harmonization of Regulatory Oversight in Biotechnology.
viii. Annex III of the Cartagena Protocol on Biosafety

In enforcing the Biosafety laws, NBA collaborates with a number of regulatory agencies as specified in the First Schedule of Biosafety Act. These include:

i). Department of Public Health (DPH)
ii). Department of Veterinary Services (DVS)
iii). Kenya Bureau of Standards (KEBS)
iv). Kenya Plant Health Inspectorate Service (KEPHIS)
v). Kenya Industrial Property Institute (KIPI)
vi). Kenya Wildlife Service (KWS)
vii). Pest Control Products Board (PCPB)
viii). National Environment Management Authority (NEMA)

2.2. Objective of the Guidelines

2.2.1. Overall objective

The objective of this guideline is to provide general guidance on how environmental risk assessment of GM crops will be conducted in Kenya.

2.2.2. Specific Objectives

i. To guide applicants, expert reviewers, risk assessors and decision makers on the requirements for environmental risk assessment data required in GMO applications for environmental release.
ii. To provide a detailed stepwise process of assessing potential adverse effects of GM crops to the environment and natural ecosystems and how the identified risks shall be mitigated post release.
iii. To provide clarity on identification of potential hazards/adverse effects that are relevant for evaluation in the risk assessment of GM crops.
iv. Provide clarity on the risk assessment and regulatory approach to be taken on stacked gene events meant for commercialization in Kenya.

2.3. Scope

These guidelines shall apply to both imported and locally developed GM crops both for single and stacked gene events that are:

i. Intended for cultivation;
ii. Imported, in viable forms, for direct use in food, feed, or processing and which, if unintentionally released into the environment, could become established and persist without human intervention.

These guidelines shall not apply to the following situations:

i. The importation of non-viable products of GM crops for direct use in food, feed or processing (e.g., flour, starch, crushed meal, or oil derived from a GM crop);
ii. The environmental introduction of other types of genetically modified organisms such as recombinant microorganisms and animals;
iii. Contained and Confined field trials of experimental GM crops.

NB: These guidelines are generic and are not specific to any particular crop. Environmental risk assessment will be customized depending on the crop being evaluated.

2.4. Methodology

The underlying assumption of comparative assessment for a GM crop is that the biology of a conventional crop counterpart from which the GM version was derived is well known. This employs the concept of familiarity developed by the Organization of Economic Cooperation and Development and as guided by the Cartagena Protocol on Biosafety.

The ERA of GM crops involves generating, collecting and assessing information of a GM crop to determine its impact on human and animal health and the environment relative to its conventional counterpart, and thus assessing its relative safety. The assessment should be carried out in a scientifically sound and transparent manner based on available scientific and

technical data and on common methodology for the identification, gathering and interpretation of the relevant data.

2.5. Data Quality

The data submitted in the application should be sufficient to meet the objectives. Applicants should clearly describe the research design, data collection procedure, data analysis and data interpretation. Reference standards, quality control and quality assurance procedures, together with bibliographic references should be provided as appropriate.

CHAPTER 3

ENVIRONMETAL RISK ASSESSMENT

3.1. Principles of Environmental Risk Assessment

The Authority shall apply the listed principles in the conduct of ERA.

i) Assessment shall be carried out in a scientifically sound, transparent and a participatory manner. It shall include all relevant data (e.g. research data, scientific publications, monitoring reports) obtained prior to and/or during the risk assessment process.

ii) Lack of scientific knowledge or consensus shall not imply a particular level of risk, absence of risk or an acceptable risk

iii) Risk of a GMO shall be considered in the context of a non-GMO comparator.

iv) Risk assessment shall be carried out on a case-by-case basis.

3.2. Environmental Risk Assessment Process:

Environmental Risk Assessment shall be conducted in a six steps approach (Figure 1) as follows:

i) Problem formulation,

ii) Hazard characterization,

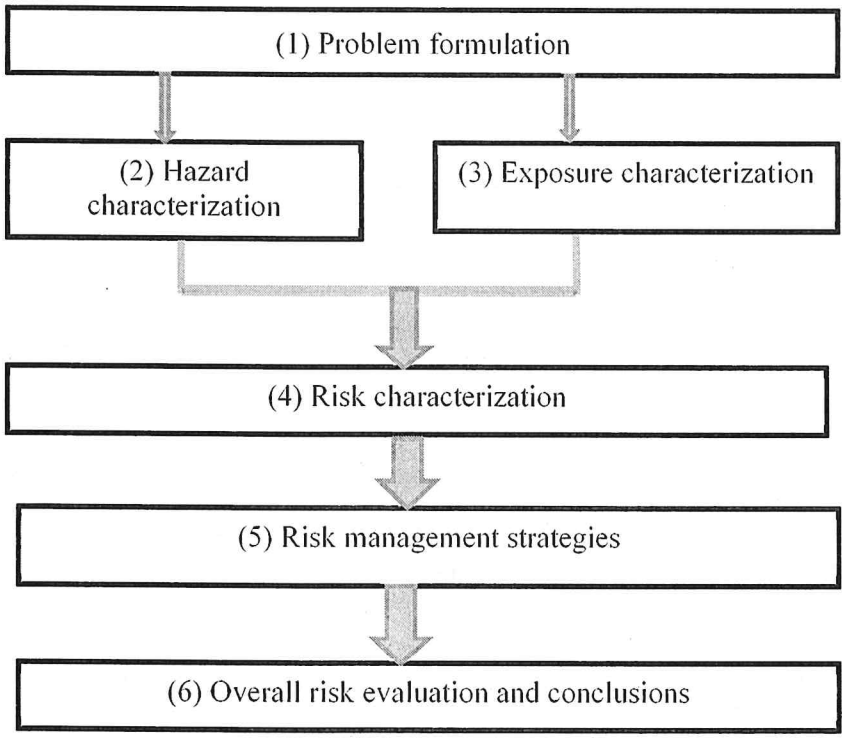
iii) Exposure characterization,

iv) Risk characterization,

v) Risk management strategies,

vi) Overall risk evaluation and conclusions.

Figure 1: **Environmental Risk Assessment Flowchart**



3.2.1 Step 1: Problem Formulation; including Hazard Identification

This is the first step in ERA. The applicant or developer shall be expected to identify any possible environmental harm that could arise from the GM crop. Problem formulation includes the identification of those characteristics of the GM crop capable of causing potential adverse effects to the environment, the nature of these effects, and the pathways of exposure through which the GM crop may adversely affect the environment. Problem formulation also defines the assessment endpoints and sets specific hypothesis to guide in the generation and evaluation of data in the next risk assessment steps.

Problem formulation starts with identification of hazards arising from the GM crop and its use. A comparison of the characteristics of the GM crop with those of its appropriate comparator enables the identification of differences in the GM crop that may in a way lead to harm. The identified potential adverse effects need to be linked to the assessment endpoints in order to derive testable hypothesis that allow for the quantitative evaluation of the harm posed to those assessment endpoints.

3.2.2. Step 2: Hazard characterization

This is the qualitative and/or quantitative evaluation of environmental harm associated with the hazard. Hazard characterization shall be categorized as having potential to cause major, intermediate, minor or marginal consequences.

(a) Major consequences: Significant changes in the numbers of one or more species of other organisms, including endangered and beneficial species in the short or long term. Such changes shall include total eradication or significant reduction of a valued species (protection goal).

(b) Intermediate consequences: Significant changes in population densities of other organisms, but not change which could result in total eradication of a valued species (protection goal). There could be long-term effects, provided there are no serious negative effects on the functioning of the ecosystem.

(c) Minor consequences: Non-significant changes in population densities of other organisms, which do not result in total eradication of any valued species, and have no negative effects on the normal functioning of an ecosystem. The only organisms that might be affected would be non- endangered, non-beneficial species either in the short or long term.

(d) Marginal consequences: No significant changes caused in any of the populations existing in the environment.

3.2.3. Step 3: Exposure characterization

This step evaluates the exposure i.e. likelihood of adverse effects occurring, and estimates the exposure quantitatively. For each hazard identified and characterized, it may not be possible to estimate the exposure (likelihood) precisely. However, applicants shall be expected to at least qualitatively give likelihood of occurrence expressed as highly likely, likely, unlikely or highly unlikely.

3.2.4. Step 4: Risk characterization

Risk is characterized by combining the magnitude of the consequences of a hazard and the likelihood that the consequences occur (Table 1)

Table 1: Risk Determination Matrix

		Severity of Harm (Consequence of hazard)			
Likelihood of hazard		**Marginal**	**Minor**	**Intermediate**	**Major**
	Highly Unlikely	Negligible	Negligible	Low	Moderate
	Unlikely	Negligible	Low	Moderate	Moderate
	Likely	Low	Low	Moderate	High
	Highly Likely	Low	Moderate	High	High
		Risk Estimate			

This model is a tool to enable identification of information and methodologies which might be useful for risk assessment. Then, in establishing that any of the steps is impossible or unlikely will lead to the conclusion of minimal risk.

3.2.5. Step 5: Risk management strategies

When risk characterization (step 4) identifies risks, then the applicant shall propose appropriate mitigation measures. These specific measures should endeavor to reduce the identified risks associated with the GM crop to a level of no concern, and should consider defined areas of uncertainties. Where the applicant has proposed mitigation measures, their adequacy shall be assessed by the NBA before final determination of the application. The applicant should also give specific post-release measures in order to monitor and verify the efficacy of the risk management measures, and to allow changes in risk management strategies in case circumstances changes or when new scientific data emerges which require changes to the risk management.

3.2.6. Step 6: Overall risk evaluation and conclusions

An evaluation of the overall risk of the GM crop shall be made taking into account the results of ERA and associated levels of uncertainty, the weight of evidence, and the risk management strategies proposed in the receiving environment. The overall risk evaluation shall be categorized as either **acceptable** or **manageable**. In instances where the overall conclusion is that the risk is manageable, appropriate post release monitoring strategies shall be put in place and assessed progressively by the NBA and any other relevant regulatory agency. High risk overall conclusion shall be considered unacceptable and the GM crop shall not be approved. On the other hand, negligible, low and moderate risks shall be mitigated by appropriate management strategies as appropriate.

Risk assessment report of a particular GM crop shall be summarized as indicated in Table 2.

Table 2: Template for the Summary Risk Assessment Report

A	B	C	D (B*C)	E	F
Potential Hazard/Adverse effect	**Likelihood of Occurrence**	**Consequences**	**Risk Estimation**	**Risk Management strategies**	**Conclusion** ***(Acceptable/ Manageable risk)***
E.g Adverse effects on Non-target organisms					
Eg Development of weediness /invasiveness characteristics					

Overall conclusion and recommendations .....

CHAPTER 4

GENERAL CONSIDERATIONS IN ENVIRONMENTAL RISK ASSESSMENT

4.1. General Considerations

Risk assessment strategy for GM crops uses appropriate methods to compare the GM crop with their conventional counterpart. The comparative safety assessment is adopted to identify similarities and differences caused by either intended or unintended effects.

Any type of genetic modification results in intended effects, but may also result in unintended effects. ERA focuses on the identification and characterization of both effects with respect to possible adverse impacts on human and animal health, and on the environment. Effects can be direct or indirect, immediate or delayed, including cumulative long-term effects. Intended effects are those that are designed to occur and which fulfill the original objectives of the genetic modification. Unintended effects of genetic modification are those which are consistent (non-transient) differences between the GM crop and its appropriate comparator, which go beyond the primary intended effect/s of introducing the transgene/s. As these unintended effects are event-specific, the applicant must supply data on the specific intended event. Data that may reveal such effects are those related to:

4.2. Description of the non-modified conventional crop

The applicant shall fulfill the information requirements under this section by referencing an appropriate biology document, where available, for the subject crop species, where this has been published by the NBA and/or by the OECD Working Group on Harmonization of Regulatory Oversight in Biotechnology and any other relevant document. In all other cases, the applicant must submit detailed information for each of the subject areas below including the sources of this information (e.g., literature citations).

1. Species or taxonomic group
    a. Classification and nomenclature
    b. Morphological characteristics
    c. Centers of origin and distribution
2. Reproductive biology
    a. Reproductive Organs i.e. flower, pollen, fruit, fruit dispersal, seed germination, and seed dormancy
    b. Sexual Reproduction i.e. Pollination type and pollinators
    c. Asexual Reproduction
3. Genetics of the species
4. Hybridization and Introgression
    a. Natural facility and success of interspecific crossing
    b. Ease of experimental crosses
    c. Information regarding gene transfer to other crops and introgression
5. Crop Production and Use
    a. Production Statistics

b. Environmental Conditions
c. Agricultural Practices
d. Management Practices

6. General Interactions with other organisms (ecology)
   a. Interactions in natural and agricultural ecosystems
   b. Potential for weediness or invasiveness
   c. Significant beneficial organisms associated with the crop species in Kenya
   d. Significant pests and pathogens of the crop species in Kenya

4.3. Description of GM Crop

The applicant should provide the following information regarding the GM crop:

a. Name of the GM event that is the subject of the application (including any commercial or trade names)
b. OECD unique identifier for the GM crop (if already allocated)
c. Scientific, common, and cultivar names of the non-modified or parental crop
d. Purpose of the genetic modification
e. Intended uses of the GM crop
f. Geographical areas within Kenya to which distribution of the product is intended.

4.4. Description of the Donor Organisms

The applicant shall provide detailed information regarding the donor organism(s) and, where appropriate, other species related to the donor. The description of the donor organism(s) should include the following:

a. Common name, scientific name, and taxonomic classification
b. Information on the history of safe use of the donor organism, or components thereof, including whether genetic elements from the donor are present in any other genetically Modified crop authorized for general release in Kenya or other countries
c. Information regarding the donor organism's ability to cause disease or injury to crops or other organisms, or if it encodes a known toxicant, allergen, pathogenicity factor, or irritant.

4.5. Description of the Genetic Modification(s)

The applicant shall provide detailed information regarding the genetic modification, identifying all genetic material potentially delivered to the host crop and providing all information necessary to characterize the DNA inserted in the crop.

The description of the genetic modification shall include the following:

a. A description of the specific method used for the modification (e.g., Agrobacterium mediated transformation or direct transformation by methods such as particle bombardment or electroporation, etc.)
   i. For Agrobacterium-mediated transformation, indicate how the Ti plasmid vector was disarmed.
   ii. A citation to a published protocol may replace a full description, as long as no significant modifications were made to the protocol.

b. Donor organism, description, and characterization of all genetic materials used to modify the crop and their intended functions in the crop
c. Details of any intentional modifications to the introduced genetic material (e.g., changes in nucleotide sequence that may affect the gene expression, amino acid sequence, or biochemical function)
d. A summary diagram (e.g., restriction map) of the introduced genetic material, including coding and non-coding sequences, and for each sequence, provide the following information:
    i. The location, order, and orientation in the vector
    ii. The name and size of the sequences inserted

4.6. Characterization of the Genetic Modification(s)

The applicant shall provide a comprehensive molecular and biochemical characterization of the inserted genetic material, including the following:

a. The number of insertion sites
b. The organization of the inserted genetic material at each insertion site including copy number and data to demonstrate if complete or partial copies were inserted
c. Sequence data of the inserted material, indicating whether the sequence of the genetic material was conserved or whether significant rearrangements have occurred upon integration
d. Sequence data of the flanking regions bordering the site of insertion
e. Identification of any open reading frames within the inserted DNA, or created by the insertions with contiguous crop genomic DNA, including those that could result in the expression of novel peptides

The applicant shall provide information[3] on any novel substances synthesized in the GM crop including the following:

i. The gene product(s) (e.g., protein, untranslated RNA, or metabolite, as appropriate)
ii. The gene product(s)' function
iii. The level and site of expression of the expressed gene product(s), and the levels of it'
iv. Metabolites if any, in the major tissues of the crop

In addition, data to demonstrate the following is also required:

v. Whether the intended effect of the modification has been achieved
vi. Whether all expected traits are expressed and inherited in a manner that is stable through several generations consistent with laws of inheritance
vii. Whether the trait(s) are function as intended.

4.6. Phenotypic and Agronomic Characteristics of the GM Crop

Information must be provided on the phenotype of the GM crop, including any observations of unintended or unanticipated characteristics, especially those that are undesirable and potentially harmful. The GM crop should be compared with a suitable conventional counterpart (e.g., near-isogenic line or parental line) and commercial cultivars to demonstrate

that, except for intentional phenotypic changes induced by the inserted genetic material, the field performance of the GM crop falls within the normal range for the crop. Data should be collected from confined field trials conducted over at least one CFT for three seasons or three CFTs for one season in a range of environmental conditions. The data from CFT will be generated locally, however, transportability of data is allowable where data is collected from equivalent or similar agro-ecologies, and with justification.

Phenotypic data may include but not limited to the following considerations:

a. Changes to the growth habit: note any changes in basic morphology of the crop including any abnormalities or changes in overall growth habit;
b. Changes to the life cycle of the crop, e.g., an annual crop becoming a perennial
c. Significant changes to crop growth and reproductive characteristics, including the following:
    i. Vegetative vigor e.g., crop height, crop biomass, etc.
    ii. Responses to biotic and/or abiotic stresses, including changes in disease susceptibility or insect predation
    iii. Ability to persist in the environment
    iv. Number of days to onset of flowering; number of days for flowering
    v. Number of days to maturity e.g., time to the production of mature fruit or seed (suitable for harvesting)
    vi. Seed production, seedling vigor, and seed dormancy
    vii. Phenotypic characteristics related to reproductive biology that could alter out crossing frequency
    viii. Phenotypic characteristics that could change impacts on beneficial species
    ix. Pollen produced, proportion of viable pollen, longevity of pollen under varying environmental conditions, physical characteristics of pollen such as stickiness, shape, and weight.
    x. Fertility and fecundity
    xi. Seed dispersal factors
    xii. Asexual reproduction

4.7. Cultivation Practices

The applicant shall provide information regarding any predictable impacts on existing agronomic practice that could arise as a consequence of cultivation of the GM crop. The following considerations shall be considered:

a. Whether the genetic modification is anticipated to change the area of current cultivation for the crop species. Describe any new ecosystems where the genetically Modified crop may be cultivated (e.g., salt tolerance that allows cultivation in degraded soils).
b. Discuss any anticipated changes to cultivation practices traditionally used for the crop, particularly how they could affect crop rotations, pesticide use, frequency of tillage, soil erosion, the management of volunteers for succeeding crops, or agro-ecosystem sustainability.

c. Describe any specific deployment strategies recommended for the genetically Modified crop (e.g., insect resistance management in the case of insect-resistant GM crops).
d. Discuss the environmental impact of any potential gene flow if the genetically Modified crop will be cultivated in areas where other sexually compatible crops exist (e.g., unmodified varieties of the same crop species, other sexually compatible species or wild relatives). The following questions should be addressed:

    i. Does the introduced trait have the potential to increase the reproductive fitness or confer a selective advantage on the wild relative? Would any increase in fitness be expected to significantly affect the establishment and spread of populations of the wild relative (consider both the absence and presence of selection pressures)?
    ii. Is the introduced trait similar to a naturally occurring trait present in populations of a compatible wild species? If so, is it known to increase the reproductive fitness or confer a selective advantage to the wild species?

CHAPTER 5

SPECIFIC RISK AREAS TO BE CONSIDERED IN ERA

5.1. Persistence and invasiveness, including crop-to-crop (vertical) gene transfer

Some environmental concerns about GM crops relate to the potential persistence or invasiveness of the crop itself, or its sexually compatible relatives as a result of vertical gene flow.

The potential adverse effects are of two types;

a. enhanced fitness of the transgenic crop
b. enhanced fitness of the feral crops (wild species)

ERA should focus on the potential of a GM crop to be more persistent or invasive than its conventional counterparts, and on the potential for gene flow to compatible relatives whose hybrid offspring may become more-weedy or invasive. Fitness only becomes an environmental concern only if the GM crop has potential to outcross with other sexually compatible species and forms a viable hybrid.

Data to support whether the GM crop is exhibiting weedy characteristics should include information such as;

Whether the GM Crop has altered fitness characteristics such as;

i. Seed dormancy
ii. Seed germination
iii. Rapid seedling growth (vigor)
iv. Flower biology e.g. changed flowering period, attractiveness to pollinators, changed pollen viability and compatibility
v. Increased seed production per seed sown
vi. Increased seed shattering
vii. Changes in seed dispersal mechanisms

The above parameters should be compared between the GM crop and its conventional counterpart. The data may be available in the scientific literature (for crops that have already been commercialized) or locally generated during confined field trials. For locally generated crops, at least one CFT for three seasons or three CFTs for one season data shall be provided in the application.

Where there is evidence that the GM crop is exhibiting any weedy or invasive characteristic, strategies to manage these risks shall be proposed by the applicant for consideration by the Authority before authorization can be granted.

5.2. Impacts of Horizontal Gene Transfer to Microorganisms

In the context of environmental release, recombinant DNA will be released from GM crops into the environment e.g. into soil, or inside the gut of animals feeding on GM crop material. Therefore, it is critical to consider the likelihood of gene transfer into microorganisms and its effects.

Horizontal gene transfer (HGT) is any process by which an organism incorporates genetic material from another organism without being the offspring of that organism. Although HGT from crop to microorganism is a rare phenomenon under natural conditions, there may be consequences for human and animal health and the environment, and therefore shall be considered in ERA.

The following shall be considered in the evaluation of HGT in the ERA and the applicant shall be required to provide adequate data on;

i. Detailed molecular characterization of the inserted genetic elements, including coding sequences, promoters and terminators
ii. Presence of antibiotic resistance selectable marker genes
iii. Presence of recipient microorganisms in the receiving environment
iv. Presence of inserted coding sequences showing similarities with DNA sequences from relevant microbial recipients enhancing the probability of recombination and subsequent stabilization.
v. Routes of exposure of the DNA of the GM crop to the recipient microorganism
vi. Persistence of the GM crop material after harvesting e.g. potential of volunteer crops thriving without human intervention.
vii. Ecological consequences if HGT were to occur.

5.3. Development of Resistance by target organisms

Target organisms (TO) are organisms on which the inserted trait is expected to act on, and are generally pests or pathogens of the crop. All other organisms are considered as non-target organisms (NTO). The primary focus when dealing with TO is whether they are likely to develop resistance, in the case of pests, or become more virulent in the case of pathogens. Therefore, this hazard will only be considered if the inserted traits are intended for pest or disease resistance.

Development of resistance is considered an environmental concern since it may compromise other pest control products, can destabilize pest control strategies and may lead to increased pesticide use. Development of resistance is not a new phenomenon in crop protection strategies using chemicals and it is likely that resistance to GM crops expressing certain Pesticidal toxins can also occur. Therefore, applicants shall be required to consider development of resistance and design strategies of mitigation.

The potential of these TO to develop resistance to GM shall be evaluated based on their history of developing resistance to conventional pesticides and resistant host crops. Applicants shall be required to provide information on;

i. Nomenclature, biology, life cycle, ecology or behavior of the TO
ii. Distribution of the TO in Kenya
iii. Host range of the TO
iv. Epidemiology of susceptible and resistant TO
v. Mode of action of active GM crop product towards TO
vi. Existing and baseline data on susceptibility of TO to the inserted genes

The above data may be obtained from literature sources.

5.4. Impact on Non-Target Organisms

One major concern is that GM crops may have an adverse effect on biodiversity and its functioning at several levels, through interactions with non-target organisms (NTO). Non target organisms are organisms not targeted by the genetic modification. They may be directly feeding on the GM crop (herbivores) or indirectly through feeding on herbivores hosts e.g. predators such as ladybird beetle feeding on aphids, for GM crops with an intentional adverse impact on specific target organisms, (e.g., insect or nematode resistant crops), the applicant should provide data that can be used to evaluate the potential for adverse environmental impacts on NTO. The ERA should address the potential environmental impact on population levels of organisms with an important ecological function e.g. pollinators, predators, decomposers etc. When considering NTO, both terrestrial and aquatic ecosystems should be considered.

Table 3 below illustrates the NTOs to be studied. The applicant should therefore undertake studies in the most relevant NTO for each ecological function and provide justification of why that species was selected.

Table 3: Surrogates/test species that are commonly used in regulatory risk assessment studies of NTOs (USEPA 2001, OECD 2007)

Ecological function/ NTO Group	Representative surrogate species and (Order)
Pollination	Honey bee *(Apis mellifera)* (Hymenoptera)
Parasitoid/Parasite	Parasite Wasp *(Ichneumon promissorius)* (Hymenoptera) Jewel wasp *(Nasonia vitripennis)* (Hymenoptera) Parasitic Wasp *Pediobius foveolatus* (Hymenoptera) Nees *(Brachymeria intermedia)* (Hymenoptera)
Predator	Spotted ladybird beetle *(Coleomegilla maculate)* (Coleoptera) Seven-spot ladybird (*Coccinella septempunctata)* (Coleoptera) Convergent lady beetle *(Hippodamia convergens)* (Coleoptera) Ground beetle *(Poecilus cupreus)* (Coleoptera) Rove beetles *Aleochara bilineata* (Coleoptera) Green Lacewing *(Chrysoperla carnea)* (Neuroptera) Insidious flower bug *(Orius insidiosus)* (Hemiptera)
Decomposer	The Springtail *(Folsomia candida)* (Collembola) Springtail sp (*Xenylla grisea)* (Collembola) Earthworm (*Lumburicus terrestris*) (Lumbricidae)
Aquatic organisms	Freshwater water flea (*Daphnia magna)* (Crustacea: Diplostraca) Bay fly (*Chironomus dilutes)* (Diptera)
Mammalian	Mice (*Mus musculus*) (Muridae)

Tiered approach to NTO testing

Typically, NTO testing shall follow a tiered approach whereby hazards are evaluated within different tiers that progress from worst-case scenario conditions framed in highly controlled laboratory environments to more realistic conditions in the field. Three main tiers can be used, which comprise experimental tests under controlled conditions (e.g. laboratory tests under tier 1 and semi-field tests (tier 2), and field tests (tier 3).

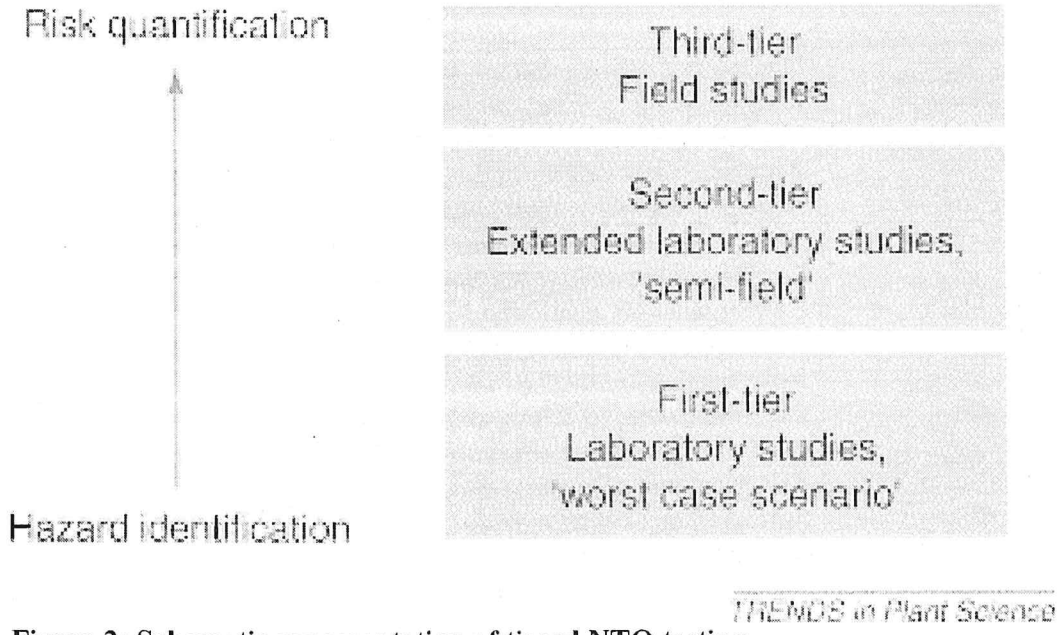


Figure 2: Schematic representation of tiered NTO testing

Within a tier, relevant data shall be gathered to assess whether there is sufficient information to conclude on the level of risk at that tier. In case no reliable risk conclusions can be drawn, further data might be needed in subsequent higher tiers. Decision of moving between tiers needs to be driven by determined trigger values. The NTO testing phase can be terminated at any of the 3 tiers when sufficient information is compiled to reject the set hypotheses. Applicants, who conclude that further tests in higher tiers are not required, based on available information, are required to explain the rationale for this conclusion.

Typically, all applications targeting pests and diseases shall be required as a minimum to conduct tier 1 tests. Tier I tests are conducted under highly conservative exposure conditions but at concentration doses far much higher than the real field situation.

All laboratory tier 1 tests shall satisfy the following requirements:

a. The endpoint (e.g. mortality rate, fecundity, reproductivity etc.) and species are identified;
b. The rationale for the selection of the species and endpoint is given. Test species selected to represent potentially impacted NTOs should provide adequate taxonomic coverage to enable a confident prediction that the GM crop will not adversely affect NTOs.
c. Variability is sufficiently low for precise effect level estimation;
d. Exposure to known quantities of testing material is maintained throughout the study;
e. The experiment is conducted for a time span adequate to reliably estimate measurement endpoints.

When reproduction is an assessment endpoint, the following requirements shall also be fulfilled:

f. The processes of the reproductive biology must be included in the testing phase;
g. The life-history must be known: age at maturation, duration of egg development, and instars subjected to exposure;
h. Optimization of conditions for growth and reproduction must be provided by the test substrate and food supply.

Applicants shall use standard protocols for particular NTO species that are considered in the ERA. In this case, it is requested that, among others, the following aspects of the experimental protocols are correctly addressed:

i. Organisms used during tests shall be healthy and of similar age;
ii. The biological performance of organisms used as controls shall be within acceptable limits (control mortality less than e.g. 20% depending on the testing system and organism);
iii. Environmental conditions in growth chambers and greenhouses shall be described explicitly and justified;
iv. Crop material shall be checked for transgene expression;
v. Direct and indirect exposure pathways shall be clearly identified in the experimental setup.
vi. The protocols selected must be validated for all test species selected, to ensure the test results are consistent and reproducible.

When designing experiments with natural enemies/predators, the following additional requirements shall be considered:

i. The suitability of artificial diet or surrogate host/prey species vs. natural food (e.g. some species do not grow well or do not reproduce when reared on artificial diet);
ii. Host/prey herbivores have to be properly exposed (possibly from hatching) to the right treatments;
iii. A uniform supply of prey/host quality, age, etc.;
iv. The availability of additional food sources for species with mixed feeding habits (e.g. availability of pollen, honey or sugar solution, possibility for sucking from crops, etc.);
v. The availability of an appropriate oviposition surface for predators;
vi. The provision of particular microhabitats (e.g. providing additional sources of water-saturated surfaces).

Semi-field tests (Tier 2) shall be conducted if data in tier 1 is not conclusive. This shall entail outdoors tests carried out with some containment that controls for variability, with manipulation treatments on relatively small experimental units (e.g. caged crops, greenhouses). Field trials (Tier 3) shall be conducted if there is no conclusive data from tier 1 and 2 or if the results from these tiers indicate that NTOs may experience significant harm under

environmentally relevant conditions. Experimental complexity and variability increase from tier 1 (e.g. toxicological studies), to semi field studies to field assemblage studies. Laboratory testing provides the best way to control and manipulate experimental conditions (environmental factors, set-up) and to limit complexity and variability. In contrast, field tests allow the evaluation of trait x environment interactions, but they exhibit the highest experimental complexity and provide the lowest ability to control experimental conditions due to large natural variability.

The objectives of field trials are:

i. To identify and study exposure routes (including trophic relationships) and confirm observed effects in lower tier experiments;
ii. To discover potential unintended effects not anticipated in lower tier tests;
iii. To provide feedback for further testing hypotheses;
iv. To study NTO food chain and indirect effects;
v. To determine effects of scale on NTO populations, including effects on generations and other spatial/temporal interactions;
vi. To study effects of interactions between several NTOs species in the field trials

Design and analysis of field trials for NTOs should be performed according to documented and validated protocols.

CHAPTER 6

EVALUATION OF GM STACKED EVENTS

6.1. Introduction

Stacking of traits is accomplished through two methods: 1) by conventional plant breeding, where parents with one or more GM events of interest are crossed to produce progeny that contain two or more GM events, commonly referred to as stacked trait products (also known as "breeding stacks"), or 2) by using molecular methods, where two or more traits are simultaneously or sequentially introduced into a host plant. In contrast to Molecular Stacks which will always result in new events, GM stacked trait products produced via conventional breeding do not result in a new event(s) even though the variety is new. In other words, events that are stacked through conventional or traditional breeding may have undergone regulatory assessments by regulators either locally or globally. Most of the commercially available stacks, like triple stack, and quadruple stack, are products of serial hybrid stacking.

Different approaches have been adopted for the regulation of stacked trait products among various countries. Approval of GM breeding stacks may not be subjected to the same regulatory scrutiny as new GM events. A simplified approval process based on the regulatory status of the singles may be adopted to avoid duplication in the regulatory process.

6.2. Approval Process for GM Stacked Events

6.2.1 Molecular Stacking techniques

New stacks events produced through molecular stacking techniques will be subject to existing process for new event approval.

6.2.2 GM Breeding Stacks

The Kenyan regulatory framework identifies the following as possible GM Breeding Stacked events which are subject to regulation as outlined in Table 4.

i. Stacking of GM Events through conventional/traditional breeding where the single events have already undergone regulatory approvals in Kenya.

ii. Stacking of GM Events through conventional/traditional breeding where one or more of the single events have **not** already undergone regulatory approvals in Kenya.

iii. Stacking of GM Events through conventional/traditional breeding where **none** of the single events have already undergone regulatory approvals in Kenya.

Table 4: Categories for Regulation of GM Stacks

Category	Considerations
1. Stacking of GM Events through conventional/traditional breeding where the single events have already undergone regulatory approvals in Kenya.	Applicant to submit a Notification to NBA (**Annex II**) accompanied with applicable fees as prescribed. In the notification request, Applicant to detail; i). A confirmation of gene expression levels of each of the single events; i). An assessment for all potential interactions - synergistic or antagonistic; ii). Confirmation of event stability. NBA will review the notification request and communicate its decision within 60 days. **NB:** Once the single events and highest order stacks are approved by NBA, any other sub-combinations of those events will require a notification to the Authority for approval for use as a parental line or for commercialization. Natural segregation leading to possible stacking of genes in cultivated fields will not lead to a notification unless where the developer/applicant uses any of the approved event as a parent or for commercialization.
2. Stacking of GM Events through conventional/traditional breeding where one or more of the single events have not undergone regulatory approvals in Kenya	a. Applicant to submit separate applications for the new or unapproved single events and the highest order stack in the prescribed format to the NBA for full safety assessment; b. A simultaneous review process to be adopted for unapproved single event(s) and the highest order stack (single events and the stack to be reviewed concurrently but as separate applications) to ensure seamless decision-making. c. Biosafety data generated locally or in equivalent environments in other countries will only be required for the combination product(s) that the applicant intends to make commercially available to end users. For the highest order stack, the applicant will be required to provide;

	i). A confirmation of gene expression levels of each of the single events; ii). An assessment for possible interactions - synergistic or antagonistic; iii). A confirmation of event stability. A full Risk Assessment will be conducted on all of the unapproved single events and the highest order stack. The NBA will review the application request(s) and communicate its decision on all products for which an application was submitted within 90-150 days. **NB:** Once the single events and highest order stacks are approved by NBA, any other sub-combinations of those events will require a notification to the Authority for approval for use as a parental line or for commercialization. Natural segregation leading to possible stacking of genes in cultivated fields will not lead to a notification unless where the developer/applicant uses any of the approved event as a parent or for commercialization.
3. Stacking of GM Events through conventional/traditional breeding where **none** of the single events have already undergone regulatory approvals in Kenya.	a. Applicant to submit separate applications for all single events and the highest order stack. b. A simultaneous review process to be adopted for all single event(s) and the highest order stack (single events and the stack to be reviewed concurrently but as separate applications) to ensure seamless decision making. c. Biosafety data generated locally or in equivalent environments in other countries will only be required for the combination product(s) that the applicant intends to make commercially available to end users. For the highest order stack, the applicant will be required to provide; i. A confirmation of gene expression levels of each of the single events; ii. An assessment for possible interactions - synergistic or antagonistic; iii. A confirmation of event stability.

	A full Risk Assessment will be conducted on all of the unapproved single events and the highest order stack. The NBA will review the application request(s) and communicate its decision on all products for which an application was submitted within 90-150 days. **NB:** Once the single events and highest order stacks are approved by NBA, any other sub-combinations of those events will require a notification to the Authority for approval for use as a parental line or for commercialization. Natural segregation leading to possible stacking of genes in cultivated fields will not lead to a notification unless where the developer/applicant uses any of the approved event as a parent or for commercialization.

6.2.3 Decision making

For GM Stacks where all the single events have previously been approved by the Authority, the applicant will be required to submit a notification to NBA in the prescribed format outlined in Annex 2 for Stack events to assess the adequacy of the Risk Assessment report of the single events as well as any other assessments or analyses submitted for any possible gene interactions prior to a decision that will be communicated by the Authority within 60 days to inform the approval or a further request for additional information to conduct full risk assessment.

For GM Stacks where at least one of the single events have not been approved by the Authority, the applicant will be required to submit full GMO application(s) on all unapproved events which shall be processed using the normal approach employed for new GM events. Additionally, the same approval process shall be adopted for GM Stacks where none of the parent single events have been given prior approval by the Authority. In this case, applicants will be required to submit data on all the un-approved singles as part of the breeding stacks application and these singles data shall be reviewed simultaneously (concurrently but as separate applications) with the breeding stack product.

CHAPTER 7

REFERENCES

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3. OECD Environment, Health and Safety Publications Series on Harmonization of Regulatory Oversight in Biotechnology No. 53.

4. The Biosafety (Contained Use) Regulations, 2011: http://www.biosafetykenya.go.ke/index.php?option=com_content&view=article&id=164:biosafety-contained-use-regulations-2011&catid=84&Itemid=498

5. The Biosafety (Environmental Release) Regulations, 2011: http://www.biosafetykenya.go.ke/index.php?option=com_content&view=article&id=166:biosafety-environmental-release-regulations-2011&catid=84&Itemid=498.

6. The Biosafety (Import, Export, and Transit) Regulations, 2011: http://www.biosafetykenya.go.ke/index.php?option=com_content&view=article&id=165:biosafety-import-export-and-transit-regulations-2011&catid=84&Itemid=498.

7. The Biosafety (Labeling) Regulations, 2012: http://www.biosafetykenya.go.ke/index.php?option=com_content&view=article&id=163:biosafety-labeling-regulations-2012&catid=84&Itemid=498

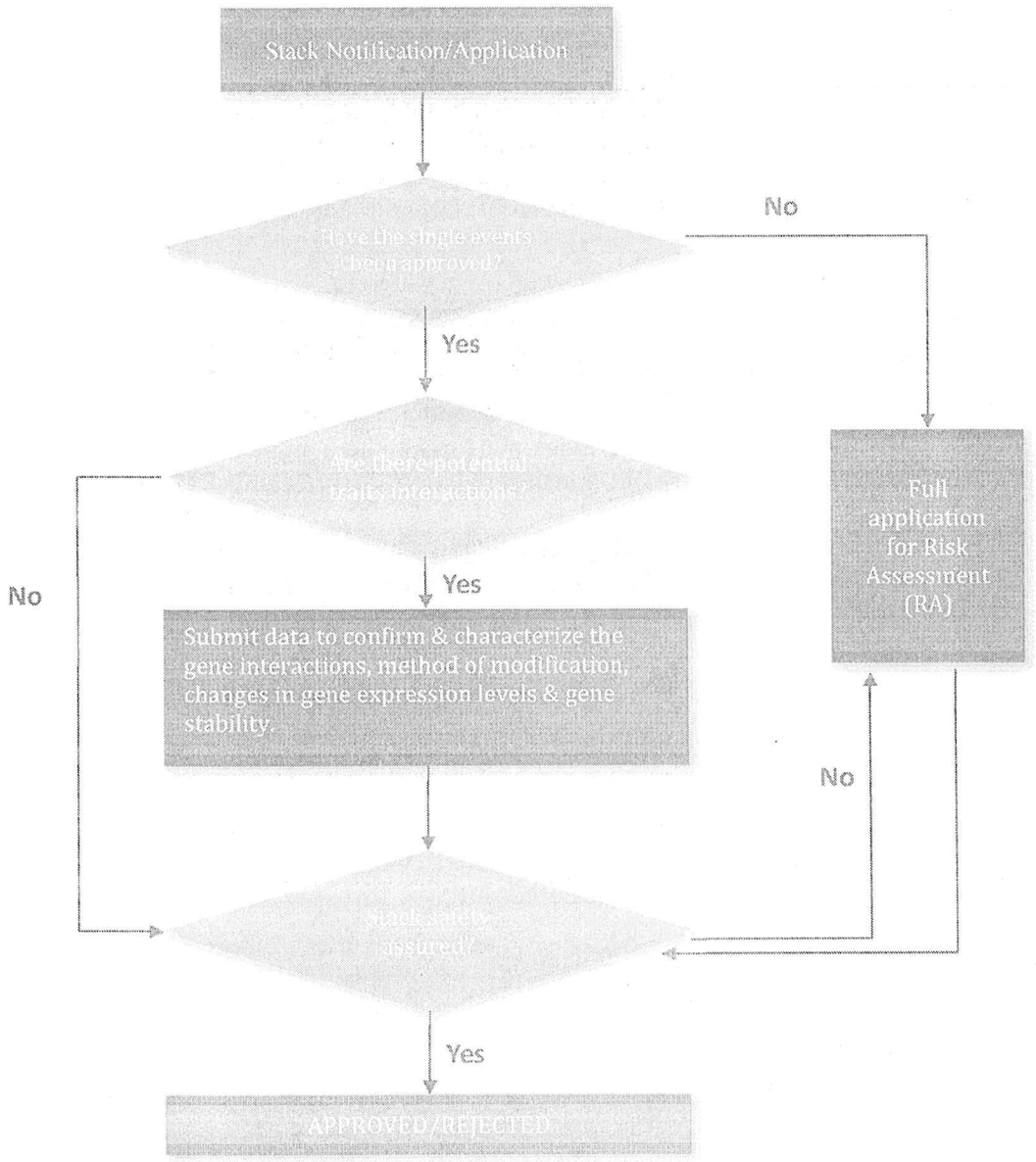
8. Consensus Documents for the Work on Harmonization of Regulatory Oversight in Biotechnology: Biology of plants(Consensus documents): http://www.oecd.org/env/ehs/biotrack/consensusdocumentsfortheworkonharmonisationofregulatoryoversightinbiotechnologybiologyofcrops.htm

9. BioTrack Product Database (identifier): http://www2.oecd.org/biotech/byIdentifier.aspx

10. Vision 2030: http://www.vision2030.go.ke/

ANNEXES

ANNEX I: FLOW CHART FOR THE REGULATORY OPTIONS OF STACKED GENE EVENTS



ANNEX II: STACK EVENT NOTIFICATION FORM IN KENYA

This form will guide in the determination of how stack events are regulated under the Biosafety Act.

SECTION I: APPLICANT INFORMATION	
Name of Applicant: Address: Email: Telephone:	
1.2. Affiliated Institution: Address: Email: Telephone: Website:	
SECTION II: SINGLE EVENTS (List all events/ traits in the Stack)	
2.1. Trait/ Event Name	Approval Status in Kenya (Approved/ Not Approved)
2.2. Intended use (Research, Import, Environmental release, Placing in the market, etc.)	
SECTION III: ORGANISM DESCRIPTION	
3.1. Description of the host organism (or parent organisms) before and after stacking: 3.2. Description of the gene products, their functions and the affected pathways before and after stacking (where applicable): 3.3 Description of the GM trait combination	
SECTION IV: METHODOLOGY	

4.1. Give a summary of the techniques used to make events in the stack:

4.2. Indicate the method of stacking used (multigene cassette transformation, co-transformation, retransformation, conventional crossing):

4.3. Provide the names of vectors used and their genetic map (where applicable)

4.3.1 Is the vector naturally pathogenic?	4.3.2 Is the vector disarmed?	4.3.3 If yes, how was the vector disarmed?
☐ Yes ☐ No	☐ Yes ☐ No	

4.4. Describe delivery methods used for transformation, retransformation or co-transformation (where applicable)

SECTION V: GENE AND/ OR GENE PRODUCTS

5.1. Are there any interactions and/ or epistatic effects between the introduced genes or/ and their expression products?

☐ Yes ☐ No

If Yes;
Describe the possible interactions (synergistic, additive, antagonistic or silencing effects) taking into account their modes of action, metabolic pathways involved, etc.

5.2. Has the stack event been approved anywhere in the World? If YES, where and for what purpose?

SECTION VI: DETECTION METHODS

6.1. Outline the detection methods applicable

SECTION VII: REFERENCES

Section VIII: Declaration of Correctness of Information
I certify that the above information is true to the best of my knowledge.

Principal Investigator/Applicant

Name _____

Name of Institution_____

Signature _____ Date _____

Affix institution stamp

Collaborator(s) (if applicable)

Name(s) _____

Signature _____ Date _____