GENOME EDITING IN AFRICA'S AGRICULTURE 2021

AN EARLY TAKE-OFF

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ABBREVIATIONS AND ACRONYMS

CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
DNA	Deoxyribonucleic acid
GM	Genetically Modified
GMO	Genetically Modified Organism
HDR	Homology Directed Repair
ISAAA	International Service for the Acquisition of Agri-biotech Applications
NHEJ	Non Homologous End Joining
PCR	Polymerase Chain Reaction
RNA	Ribonucleic Acid
LGS1	Low germination stimulant 1

1.0 INTRODUCTION

Genome editing (also referred to as gene editing) comprises a group of technologies that give scientists the ability to change an organism's DNA. These technologies allow addition, removal or alteration of genetic material at particular locations in the genome. The technologies make use of site-directed nucleases that create breaks in the DNA strands and thereafter use the cell DNA repair mechanisms to introduce desired changes.

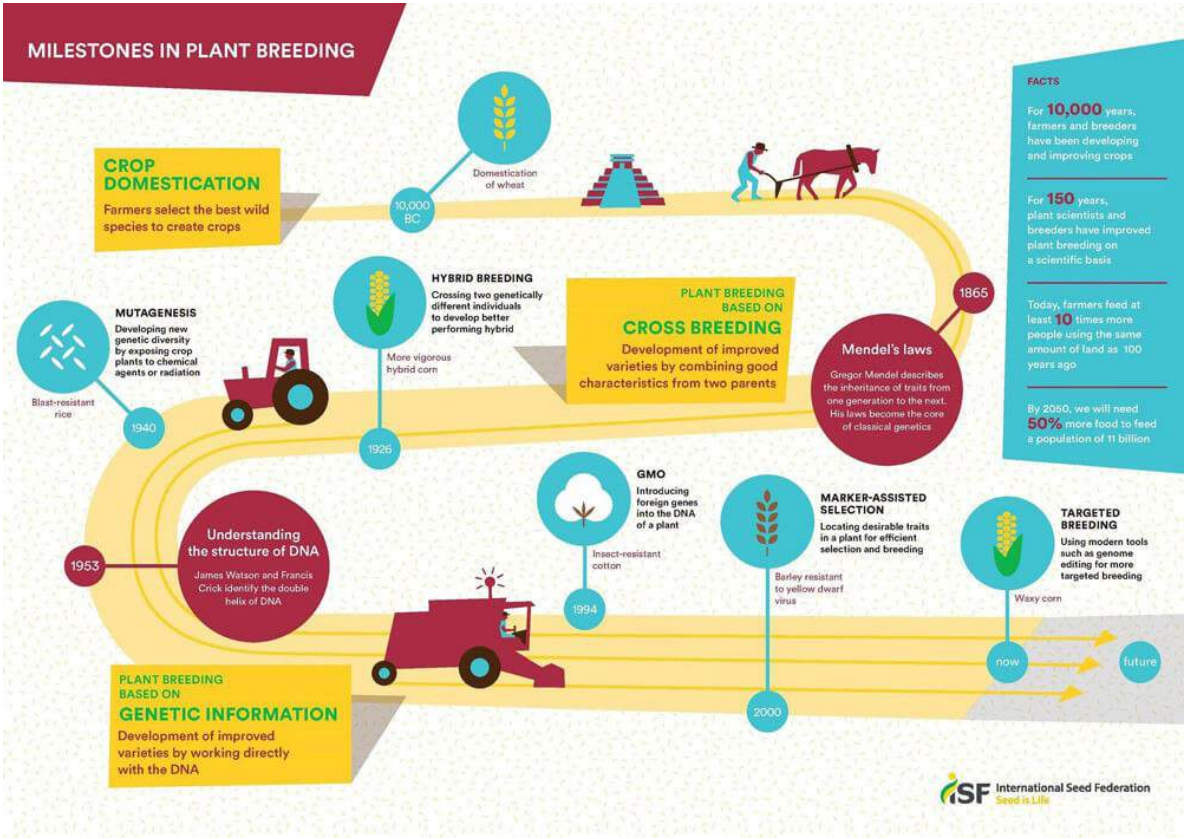
In 2012, Jennifer Doudna, Emmanuelle Charpentier, and their teams elucidated the biochemical mechanism of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) technology. By making precise targeted cuts in DNA, CRISPR ushered in endless potential in areas of medicine, agriculture, biomaterials and so on. In nature, CRISPR-Cas9 is a bacterial adaptive immune system, whereby pieces of DNA from invading viruses are cut by a bacterial nucleases, CRISPR associated proteins. The DNA fragment that is cut off is saved as memory for fighting future infections. The CRISPR-Cas9 system can be engineered to edit eukaryotic DNA by designing guide RNA complementary to the target sequence.

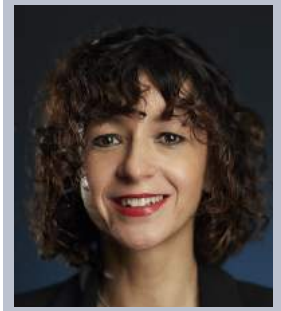
The guide RNA has a 20 base pair protospacer motif with flanking homology to the cut site of interest. Cas9 binds to this protospacer motif in the guide RNA, which in turn binds to the site of interest. Cas9 then binds to a protospacer adjacent motif (PAM) in the genomic DNA, and catalyzes a double strand break (DSB) in the DNA at a position three base pairs upstream of the PAM. If a homology arm is provided with the CRISPR-Cas9 cassette, homology-directed repair (HDR) will occur, otherwise the cell will employ non-homologous end joining (NHEJ) to create small indels at the cut site of interest.

To date, CRISPR genome editing technology has been applied in studying gene function, human disease research including pathogenesis of hereditary diseases, gene therapy, livestock and crop genetic improvement. Genome editing differs from genetic modification in that the latter generates modifications in the genome via stable integration of DNA elements which do not occur naturally. The resulting organisms and (most) products thereof can be identified with event-specific polymerase chain reaction (PCR)-based methods targeting the insertion site. New breeding techniques such as genome editing have diversified the breeder's toolbox for generating useful genetic variability in both plants and animals. Several of these techniques can introduce single nucleotide changes without integrating foreign DNA while generating organisms with the intended phenotypes.

Since the discovery of CRISPR technology, scientists in many parts of the world have sought to use it to achieve different objectives in their research involving plants or animals. The purpose of this booklet is to highlight genome editing projects and experts in Africa making use of this technology in their respective fields.

1.1 MILESTONES IN PLANT BREEDING





Emmanuelle Charpentier

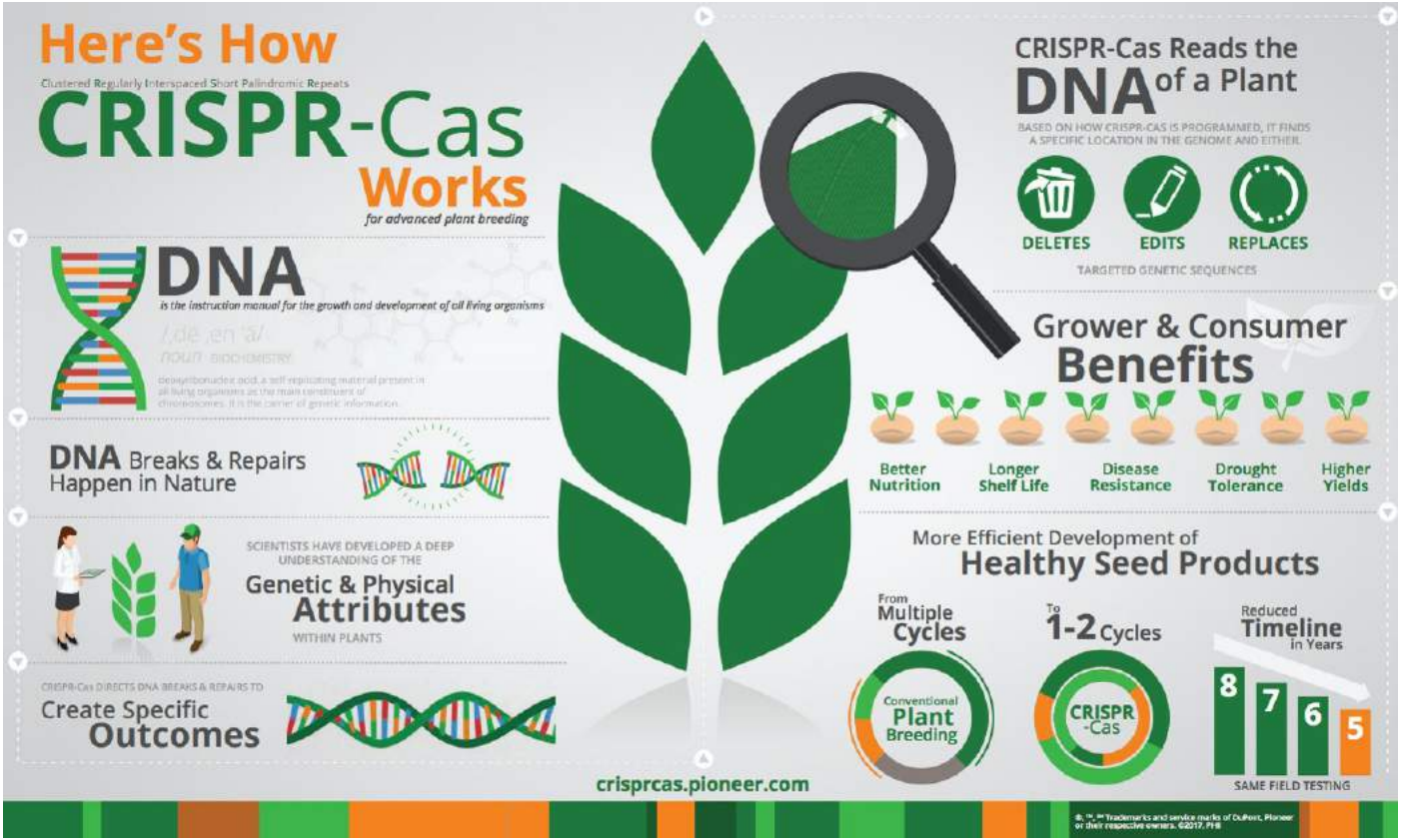
Max Planck Unit for the Science of Pathogens, Berlin, Germany

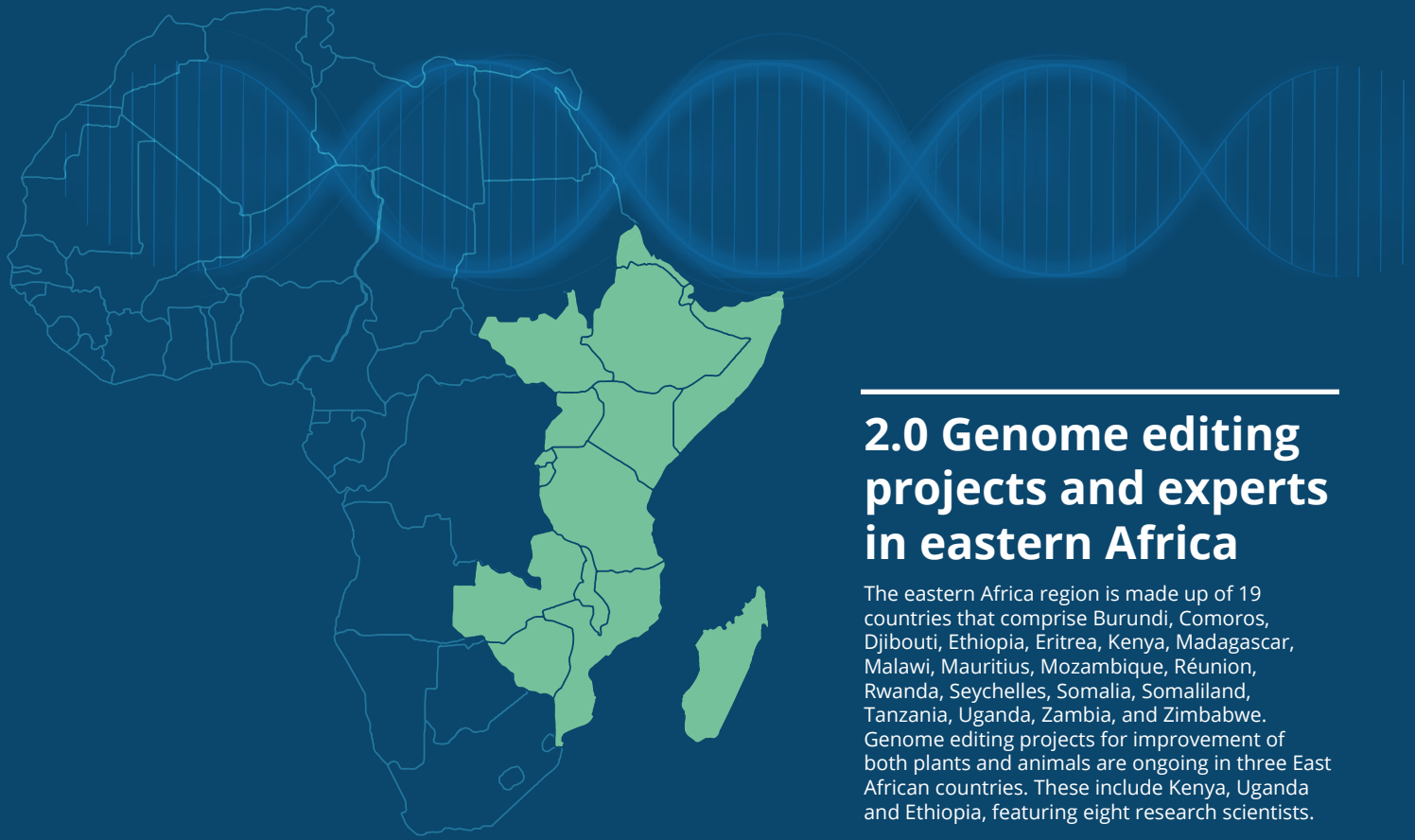
Jennifer Doudna

University of California, Berkeley, USA

The pair won the Nobel Prize in Chemistry 2020 for development of CRISPR/Cas9, a method for genome editing.

1.2 HOW CRISPR GENOME EDITING WORKS IN AGRICULTURE





2.0 Genome editing projects and experts in eastern Africa

The eastern Africa region is made up of 19 countries that comprise Burundi, Comoros, Djibouti, Ethiopia, Eritrea, Kenya, Madagascar, Malawi, Mauritius, Mozambique, Réunion, Rwanda, Seychelles, Somalia, Somaliland, Tanzania, Uganda, Zambia, and Zimbabwe. Genome editing projects for improvement of both plants and animals are ongoing in three East African countries. These include Kenya, Uganda and Ethiopia, featuring eight research scientists.

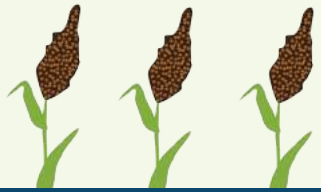
KENYA

PROJECT TITLE: Evaluation of Striga resistance in Low Germination Stimulant 1 (LGS1) mutant sorghum

Prof. Steven Runo

Professor of Molecular Biology

Affiliation: Kenyatta University



The challenge being addressed:

Parasitic weed Striga is a huge constraint to production of sorghum and other cereal crops. Most cultivated cereals, including maize, millet, sorghum, and rice, are parasitized by at least one Striga species, leading to enormous economic losses. The Striga genus has over thirty species distributed over 50 countries in sub-Saharan Africa (SSA), causing an estimated 7 billion dollars´ worth of crop losses every year.

Objectives of the project:

Evaluate LGS1 gene knock-out in conferring Striga resistance in sorghum.

Specifics of the target gene(s) and phenotype(s):

LGS1

Mutant alleles at the LGS1 locus drastically reduce Striga germination stimulant activity.

PROJECT TITLE:

Application of reproductive biotechnologies to develop a transgenic goat as a model for genetic control of animal diseases

Wilkister Nakami Nabulindo

PhD Graduate Fellow

Affiliation: International Livestock Research Institution

The challenge being addressed:

Animal trypanosomiasis is one of the diseases that cause huge losses to livestock-dependent communities in sub-Saharan Africa and efforts for its control and eradication have not been successful for decades. Scientists have in the recent past discovered a gene (Apolipoprotein L1) in primates that encodes proteins that cause lysis of trypanosomes in the body hence making the primates resistant to trypanosomiasis. A group of scientists from New York State University (Jayne Raper and co- team) have developed a synthetic version of the ApoL 1 gene that is compatible with caprine genome. This gene could be transferred to livestock to develop genetically resistant animals through transgenesis

Objectives of the project:

1. To investigate the feasibility of introducing a synthetic APOL1 gene into the genome of a group of goats and confirm its expression pattern
2. Generation of African indigenous goat carrying the APOL1 transgene that confers resistance to trypanosomiasis

Specifics of the target gene(s) and phenotype(s):

Genomic regions that have been validated in mice and encompassing the validated synthetic APOL1 sequence will be transferred into the 'protected' ROSA26 locus using a ROSA26 miniBAC. Establish cultures of donor spermatogonial stem cells from the Kenyan Galla goats' testis, after which the ApoL 1 clone will be introduced into the ROSA26 locus of the spermatogonial stem cells by homologous recombination (CRISPR- Cas9 system). Validate synthetic APOL1 in the goat ROSA26 sequence between intron 1 and exon 2, which will also carry the neor selection marker gene. Integrants will be selected with G418 and single copy integration events will be selected by quantitative PCR-based loss of allele assay. The antibiotic resistance genes that will be used to select transformed cells will be excised before creation of transgenic animals.

KENYA

KENYA

PROJECT TITLE: Gene editing to control maize lethal necrosis in Africa for improved maize productivity and grain harvests

James Kamau Karanja

Senior Research Scientist, Head of Maize Lethal Necrosis (MLN) Section

Affiliation: Kenya Agriculture and Livestock Research Organization (KALRO)
National Agricultural Research Laboratories (NARL), Kabete

Partnership with other institutions & Roles:

- CIMMYT - Initial mapping, germplasm, breeding, phenotyping
- Corteva - Genotyping, fine mapping, cloning, editing, phenotyping
- USDA-ARS - Phenotyping support (validation of edits)
- KALRO – Field support, advocacy, consulting, deployment

The challenge being addressed:

Maize lethal necrosis (MLN) disease causes severe losses to maize in Kenya and neighbouring countries. Traditional breeding approaches are time consuming and disrupt the favorable characteristics of elite varieties, whereas gene editing can achieve MLN resistance without altering desirable traits and performance of the target susceptible elite lines and varieties.

Objectives of the project:

- Introduce resistance against MLN disease directly into parent inbred lines of popular commercial maize varieties, which are currently susceptible to the disease, and reintroduce them into the farmers' fields in Kenya with possible scaling out to other countries in East Africa
- Build expertise of Kenyan scientists and stakeholders through seminars, workshops, scientific visits, support and mentor one Kenyan student to conduct PhD research within the project.

Specifics of the target gene(s) and phenotype(s):

- A strong quantitative trait locus (QTL) on maize chromosome 6 confers a high-level of resistance against MLN disease.

PROJECT TITLE: CGIAR research program on roots, tubers and banana (CRP-RTB)

Genome editing disease susceptibility loci of popular Roots, Tubers and Banana varieties and promising breeding stocks

Dr. Leena Tripathi

Principal Scientist

Affiliation: International Institute of Tropical Agriculture (IITA)

Jaindra Tripathi
Group member

Valentine Ntui
Group member

The challenge being addressed: Banana diseases

Objectives of the project: To develop disease resistant varieties of banana

Specifics of the target gene(s) and phenotype(s) - Phenotype: Disease resistance

KENYA

KENYA

PROJECT TITLE:

Modulation of energy homeostasis in maize to develop lines tolerant to drought, genotoxic and oxidative stresses

Dr. Elizabeth Njuguna

Former doctoral fellow

Affiliation:

- VIB-UGENT Center for Plant Systems Biology, Ghent University, Belgium
- Plant Transformation Laboratory, Kenyatta University, Kenya

The challenge being addressed:

Maize – drought susceptibility

Objectives of the project:

- Overall objective: Metabolic engineering of Poly(ADP-ribosyl)ation pathway (a stress response pathway) to broaden stress tolerance in plants by maintaining energy homeostasis during stress conditions.
- One approach: Knock-down of the maize PARP gene expression using CRISPR/CAS9 gene editing as a strategy for abiotic and genotoxic stress tolerance

Specifics of the target gene(s) and phenotype(s):

Genes: Poly(ADP-ribose) polymerase (PARP1 and PARP2)

Expected Phenotype: Maize tolerant to drought, DNA damage and oxidative stresses.

PROJECT TITLE:

1. Accelerating African Swine Fever Virus (ASFV) vaccine development via CRISPR-Cas9 and synthetic biology technologies
2. CRISPR/Cas9 gene editing of Theileria parva for the development of vaccine against East Coast fever (ECF)

Dr. Hussein Abkallo

Post-Doctoral Fellow

Affiliation: Vaccine Biosciences/

Animal and Human Health (AHH)/

International Livestock Research Institute (ILRI)

The challenge being addressed:	Animals: pigs (African Swine Fever Virus) and cattle (Theileria parva)
Objectives of the project:	Generation of live-attenuated vaccines
Specifics of the target gene(s) and phenotype(s):	Targets viral (ASFV) and parasite (Theileria parva) virulence genes to weaken (reduce the virulence of) the pathogen to elicit strong a strong and effective immune response when animals are vaccinated.

KENYA

ETHIOPIA

PROJECT TITLE: Improving oil qualities of Ethiopian mustard (Brassica carinata) through application of CRISPR/CAS 9-based genome editing

Prof. Teklehaimanot Haileselassie Teklu

Associate Professor

Affiliation: Institute of Biotechnology, Addis Ababa University

Misteru Tesfaye

PhD Student /Senior Oilseeds Researcher

Affiliation: Addis Ababa University, Institute of Biotechnology (IoB)

Tileye Feyissa

Associate Professor

Affiliation: Institute of Biotechnology, Addis Ababa University

The challenge being addressed:

Studies show that the level of erucic acid in Ethiopian germplasm materials as well as in Brassica carinata varieties released earlier is in the range of 31-51% of total fatty acid much beyond the nutritionally acceptable level (<5%). The emergence of novel gene editing tools like CRIPR/Cas9 has opened a good opportunity for improving the quality of B. carinata through editing targeted genes so that the crop can be applicable for both food/feed and oleochemical industries.

Objectives of the project:

i. To explore the distribution of metabolites among 144 B. carinata genotypes for its bio-industrial applications
ii. To develop B. carinata genotype with low erucic and glucosinolate for food and feed application
iii. To develop B. carinata genotypes with wax ester for industrial application
iv. To enhance the level of erucic acid for industrial applications.

Specifics of the target gene(s) and phenotype(s):

Target gene

- For food- FAE1 and FAD2 genes,
- For feed – GTR1 and GTR2 genes
- For industry- FAR and WS genes

PROJECT TITLE: Application of targeted gene editing for development of high yielding, stress resistant and nutritious crops

Dr. John Odipio

Scientist (Biotechnologist)

Affiliation: National Agricultural Research Organization (NARO)

National Crops Resources Research Institute (NaCRRI)-Namulonge Campus

The challenge being addressed:

Cassava:

1) Limited knowledge of molecular basis of flowering

2) Lack of double haploid lines and efficient methods for double haploid induction in cassava

Rice: No sources of resistance to rice yellow mottle virus

Maize: No sources of resistance to maize lethal necrosis

Objectives of the project:

Completed:

1. Efficient proof of concept developed for gene editing in cassava (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5651273/)
2. Production of fertile flowers and seeds by CRISPR/Cas9 mediated editing of endogenous anti-flowering genes in cassava (under peer publication)

On-going project:

Demonstration of proof of concept for gene editing by targeting marker gene PDS under NARs tissue culture system

Scheduled

1. Generation of knowledge and methods for haploid induction for rapid cassava breeding and faster delivery of stress resistant, high yielding and nutritious farmer preferred varieties
2. Development of novel sources of resistance to devastating rice yellow mottle virus through gene editing
3. Development of novel sources of resistance to maize lethal necrosis through gene editing

UGANDA

Specifics of the target gene(s) and phenotype(s):

Genes:

Completed

1. Phytoene desaturase
2. Terminal flower 1

Scheduled

1. Centromere localized genes
2. Host susceptibility genes

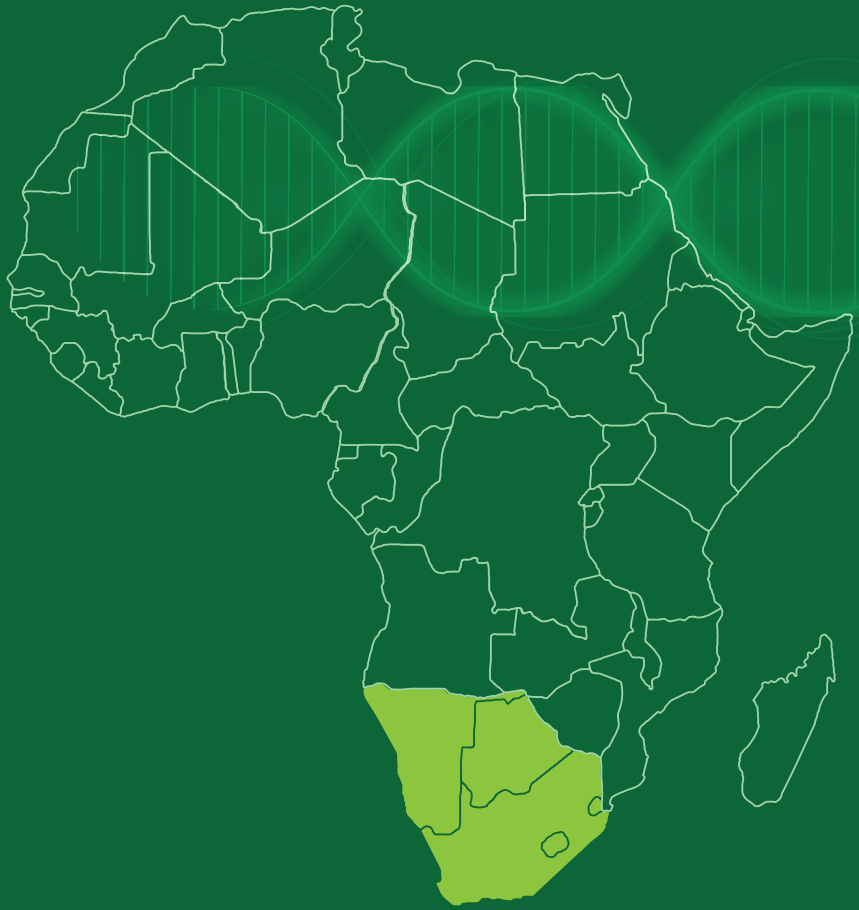
Phenotypes:

Completed

1. Photo bleaching
2. Early flowering

Scheduled

1. Short homozygous plants
2. Virus resistant edited plants



3.0 Genome editing projects and experts in southern Africa

Southern Africa is made up of 5 countries. These include Botswana, Lesotho, Namibia, South Africa, and Eswatini.

PROJECT TITLE:

High-throughput screening of genes associated with the response of cassava to geminivirus South African cassava mosaic virus (SACMV).

Chrissie Rey

Professor and Principal Investigator

Patience Chatukuta

Postdoctoral Research Fellow

Affiliation: School of Molecular and Cell Biology

University of the Witwatersrand

The challenge being addressed:

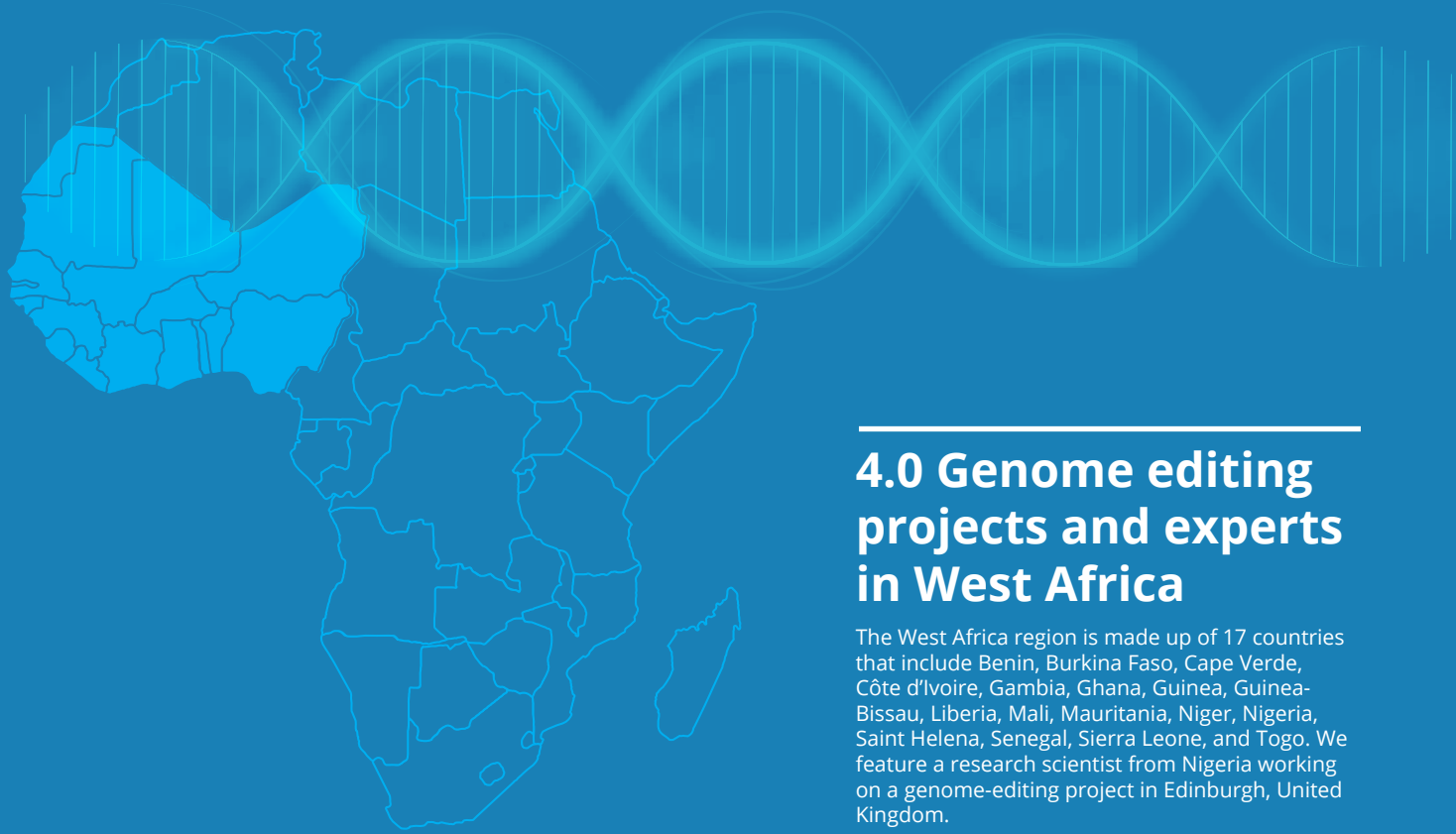
Cassava is recalcitrant to transformation, thus making reverse genetics approaches of studying the plant's response to cassava mosaic disease (CMD) time-consuming, taking at least 8 months. We exploit the use of protoplasts to study genes putatively associated with cassava's tolerance to CMD. The use of protoplasts in combination with gene editing techniques drastically reduces the time in which key genes involved with the response to CMD can be identified to 6 weeks. These key genes can then be targeted for biotechnological improvement of African cassava varieties for improved tolerance/resistance to CMD and improvement of yields thereby.

Objectives of the project:

1. To silence genes putatively associated with the response to SACMV infection in susceptible and tolerant cassava landrace protoplasts using CRISPR gene editing
2. To measure target gene expression and viral load in wild and mutant (gene-edited) SACMV-infected cassava protoplasts
3. To identify the hub or key genes associated with SACMV tolerance in cassava protoplasts

Specifics of the target gene(s) and phenotype(s):

Target host genes are those which are known to be targeted by or respond to geminiviruses, such as the ubiquitin proteasome system genes (e.g. E3 ligases), transcription factor genes (e.g. WRKYs), and resistance genes (e.g. NLRs).



4.0 Genome editing projects and experts in West Africa

The West Africa region is made up of 17 countries that include Benin, Burkina Faso, Cape Verde, Côte d'Ivoire, Gambia, Ghana, Guinea, Guinea-Bissau, Liberia, Mali, Mauritania, Niger, Nigeria, Saint Helena, Senegal, Sierra Leone, and Togo. We feature a research scientist from Nigeria working on a genome-editing project in Edinburgh, United Kingdom.

NIGERIA

PROJECT TITLE: Investigating the role of ANP32 proteins in the replication of Avian influenza Virus

Dr. Alewo Idoko-Akoh

Research Fellow

Affiliation: McGrew Group, Division of Functional Genetics & Development, The Roslin Institute & Royal (Dick) School of Veterinary Studies, The University of Edinburgh

The challenge being addressed:

Developing novel genetic anti-viral strategies to prevent avian influenza infections in poultry

Objectives of the project:

i. To identify the specific regions of ANP32 proteins needed for influenza virus protein interactions.
ii. To use genome editing tools that we have developed to modify chicken cells to identify genetic variations in ANP32 genes that will have the most significant restrictive effect on avian influenza virus replication.
iii. Assess any global changes in the transcriptome of genome-edited chicken cells containing modified ANP32 proteins
iv. Investigate in vivo replication of avian influenza virus in genome-edited chickens expressing modified ANP32 proteins

This information will inform control strategies for protection of poultry from avian influenza infection. It will also be of interest to researchers studying influenza virus in humans and livestock. See the following publication for some background information (Jason S. Long, Alewo Idoko-Akoh, Bhakti Mistry, Daniel Goldhill, Ecco Staller, Jocelyn Schreyer, Craig Ross et al. “Species specific differences in use of ANP32 proteins by influenza A virus.” eLife 8 (2019): e45066)

Specifics of the target gene(s) and phenotype(s):

ANP32 genes encode a family of nuclear proteins implicated in many molecular functions including transcriptional regulation, apoptosis, tumour suppression, protein phosphatase inhibition, messenger RNA export and regulation of intracellular transport. ANP32 genes include ANP32A, ANP32B, ANP32C, ANP32D and ANP32E. Differences between mammalian and avian ANP32A genes account for the poor replication of some avian influenza viruses in mammalian cells.

5.0 Genome editing projects and experts in Central Africa

The Central Africa region consists of seven countries that include Cameroon, Central African Republic, Chad, Congo Republic - Brazzaville, Democratic Republic of Congo, Equatorial Guinea, Gabon, São Tomé & Principe. We feature a research scientist from Cameroon working on a genome-editing project in Canada.

CAMEROON

PROJECT TITLE:

A combination of genome editing and BioID approaches to characterize a mitochondrial STAT3 function as a therapeutic strategy for multiple myeloma

Dr. Serges P. Tsofack

Scientific Research Associate

Affiliation: University Health Network (UNH) /University of Toronto

The challenge being addressed:

Genome editing in cancer cells, tissues and CRISPR/Cas9 approach to develop a new treatment regimen base on genomic instability

Objectives of the project:

CRISPR/Cas9 gene editing in genetic diseases (cancers). Understanding the mechanisms behind cancer drugs failure using different models and developing a next generation of drugs targets developing a new drug targets.

Approach:

1. Understand a genomic instability in cancer patient particularly after a drug relapse;
2. Use a genetic variation to find new treatments. We strongly believe a functional genomics approach can lead us to molecular mechanism, which can be used for genetic disease treatment in human. These approaches can be easily translated to animals and plants disease special in agriculture areas. We employ in vitro and in vivo models, patient samples and bioinformatics tools.

Specifics of the target gene(s) and phenotype(s):

Specifics of the target gene(s) and phenotype(s): STAT3

6.0 Genome editing projects and experts in North Africa

North Africa consists of six countries including Algeria, Egypt, Libya, Morocco, Sudan and Tunisia. We feature a research scientist in Egypt running a collaborative genome editing project on wheat improvement.

PROJECT TITLE: Developing sal1 mutant drought tolerant wheat using CRISPR/Cas genome editing

Joint project between Faculty of Agriculture- Cairo University and USDA-ARS WRRC, Albany, CA

Prof. Naglaa Abdallah

Professor of Genetics

Affiliation: Department of Genetics, Faculty of Agriculture, Cairo University Egypt

The challenge being addressed:

Drought is one of primary stresses that limit crop productivity and cause economic losses. Development of abiotic stress tolerant crops like wheat is an important avenue to mitigate these problems and enable good agricultural yields, despite environmental challenges.

Objectives of the project:

1. Construction of the CRISPR/Cas9 transformation vectors
2. Generation of transgenic wheat plants
3. Screening of sal1 wheat mutants
4. Screening for stress tolerance in the sal1 mutant plants

Approach:

Use of genome editing techniques to generate drought stress tolerant wheat. Employing CRISPR-Cas9 to inactivate the Sal1 genes in wheat.

Specifics of the target gene(s) and phenotype(s):

Sal1

7.0 CONCLUSION

CRISPR genome editing technology offers a precise and efficient way of changing an organism's genetic material. This has presented the scientific community with an opportunity to address a myriad of challenges in health, agriculture, industry, environmental conservation and restoration. The inexpensive, simple and flexible technology comprises of an endonuclease protein whose DNA-targeting and cutting specificity can be programmed by a short guide RNA. Today, CRISPR technology has become an indispensable tool in biological research.

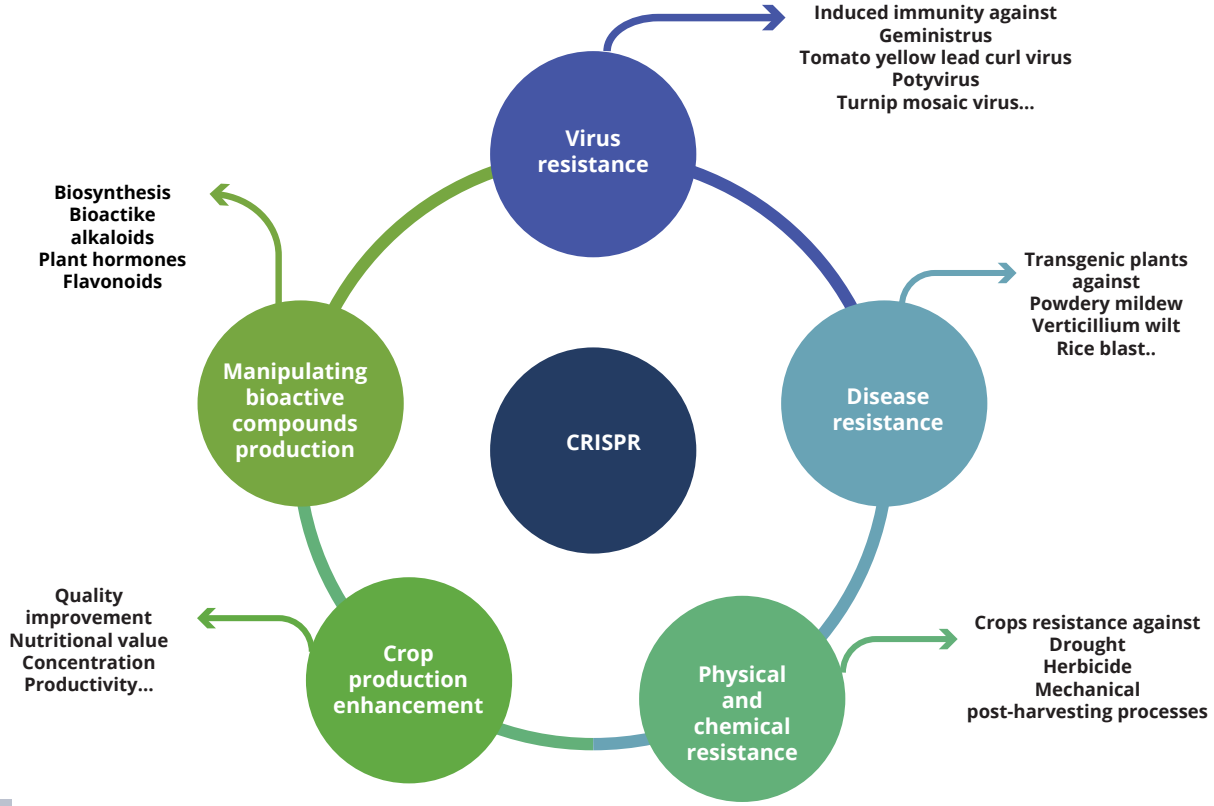
In agriculture, CRISPR genome editing is primarily being applied in improving crops with disease and pest resistance, abiotic stress tolerance and improved nutritional content. Due to its ability to generate genome-edited crops similar to those developed via conventional breeding, CRISPR technology is now regarded as one of the versatile tools for improving agricultural productivity to feed the rapidly growing population amidst climate change and dwindling arable land.

Modern biotechnologies are projected to play a critical role in building sustainable agricultural systems able to accommodate the rapidly growing demand for food. Globally, the first quarter of the 21st century has seen a major increase in undernourishment. Breeding of 'climate-change ready' and adaptable crop varieties is now more than ever critical in transforming agricultural productivity and ensuring global food and nutrition security.

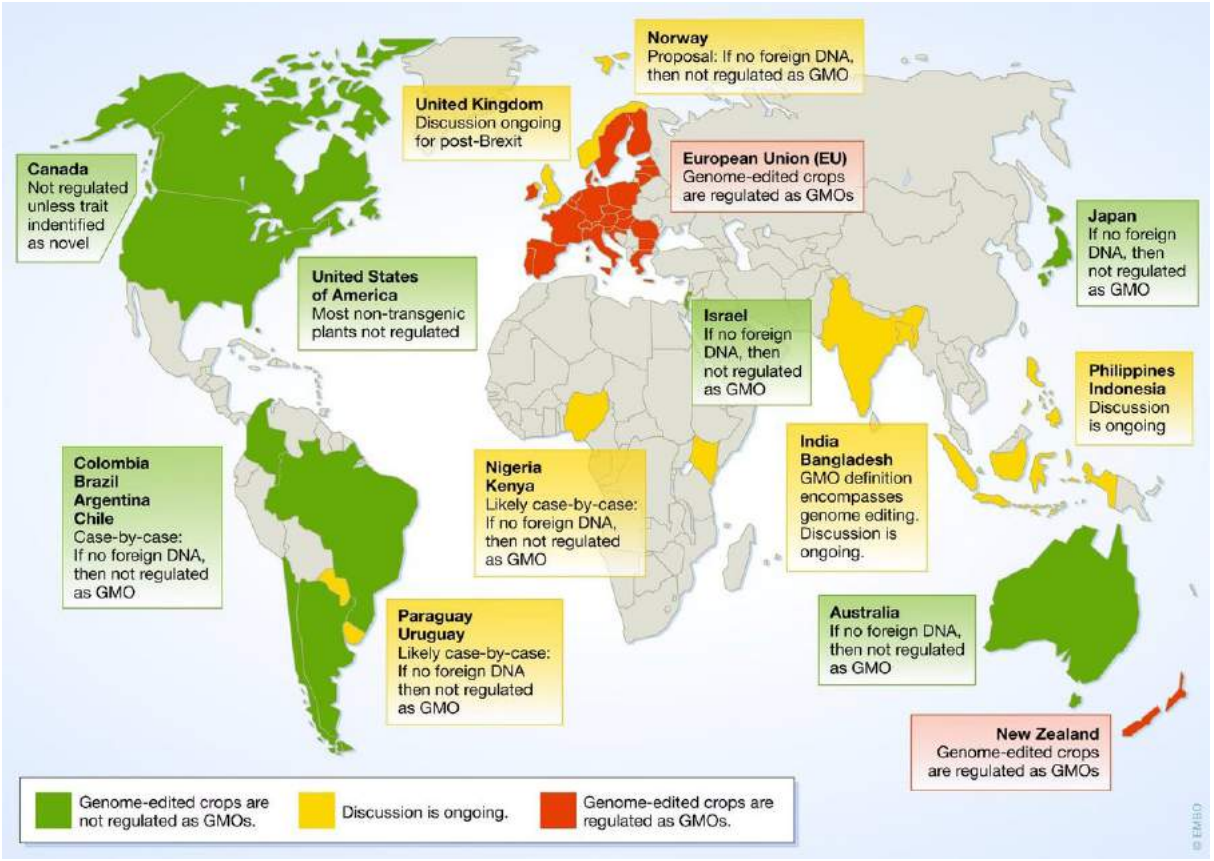
The worsening impacts of climate change on food production, coupled with the increasing demand for food due to the burgeoning population has seen an increased prevalence of undernourishment. In 2019 alone, prior to COVID-19 pandemic, almost 690 million people (8.9% of the global population) were undernourished (WFP Hunger Map 2020). Without fast and efficient interventions, the number of hungry people will reach 840 million by 2030. In Africa, over 250 million people (20 percent of the population) are undernourished. This situation has necessitated for rapid adoption of science, technology and innovations that improve the way food is produced. Genome editing is among the tools being employed in breeding crop varieties that are resilient and nutritionally superior.

As shown by the projects listed here, African scientists are moving fast to harness the potential of genome editing in developing crop varieties suited for the continent's modern agriculture. This spells a promising future where the inevitable impacts of climate change and the growing population are well mitigated through technology-supported, sustainable agricultural systems.

8.0 CRISPR GENOME EDITING: INSIDE A CROP BREEDER'S TOOLKIT



9.0 REGULATORY APPROACHES FOR GENOME EDITED PRODUCTS IN VARIOUS COUNTRIES



10 COMMUNICATING ABOUT GENOME EDITING IN AFRICA

Genome editing holds great promise and is set to transform healthcare and agriculture sectors globally. Given the precision, affordability and potential offered for quick win, Africa stands to benefit most. Although this technology poses tremendous scientific, medical, agricultural and business implications, communication approaches will either hamper or facilitate its uptake.

In 2019, ISAAA AfriCenter dedicated the 3rd Africa Biennial Biosciences Communication (ABBC) symposium held in Pretoria, South Africa, to conversations on genome editing in the region. Running under the theme "Getting it Right: Communicating about Genome Editing", the symposium provided a unique opportunity to address key components that will lay the foundation for uptake of genome editing in Africa.

The Symposium's overall objective was to interrogate best communication practices that will facilitate informed decision making on this emerging technology. It was inspired by an African proverb that says "rising early shortens the journey". We acknowledge that conversations on how to govern genome editing are gaining momentum. Consequently, public engagement needed to keep pace with these rapid advancements, to avoid inheritance of restrictive regulatory regimes. Key players in genome editing research, development, policies and regulations must embrace constructive dialogue about the technology early. We believe that starting early will enable stakeholders ample time for making informed decisions and creating an enabling environment for genome editing research and development

Recommendations from ABBC 2019;

- To work together in improving bioscience communication, including the use of new and emerging strategies to ensure effectiveness.
- To foster open and transparent dialogue with all stakeholders, including those with divergent views on genome editing, in an effort to build consensus and common understanding.
- To encourage public participation in research direction and policy formulations on genome editing.
- To create awareness among the policy and decision makers on genome editing.
- To establish an African Coalition for Communicating about Genome Editing.

To initiate the African Coalition for Communicating about Genome Editing, ISAAA AfriCenter facilitated launching of the Kenya Chapter in 2020. By developing a blueprint communication strategy for genome editing in Africa, the Kenya Chapter has set out to lay the foundation needed to ensure that Africa realizes the full potential of the technology in improving agriculture and boosting food security.

To join the coalition, contact Dr. Margaret Karembu, Director ISAAA AfriCenter at mkarembu@isaaa.org.

Citation: Karembu M. (MBS) 2021. Genome Editing in Africa's Agriculture 2021: An Early Take-off. International Service for the Acquisition of Agri-biotech Applications (ISAAA AfriCenter), Nairobi Kenya.

To be featured in the second edition of this booklet, contact Dr. Margaret Karembu at mkarembu@isaaa.org