



Horizon 2020
Programme

FOCUS-Africa

Research and Innovation Action (RIA)

This project has received funding from the European
Union's Horizon 2020 research and innovation programme
under grant agreement No 869575

Start date : 2020-09-01 Duration : 48 Months



Report on the characterization of climate-ready rice and cowpea varieties

Authors : Dr. Shingirai NANGOMBE (CSIR), Macharia, Mercy (SSSA); Solemanegy, Marta (SSSA, INAM); Caproni, Leonardo (SSSA); Takele, Robel (SSSA); Munisse, Paulino (INAM); Amane, Manuel (INAM); Buizza, Roberto (SSSA); Dell'Amico, Valentina (SSSA); Pè, Mario Enrico (SSSA); Dell'Acqua, Matteo (SSSA))

FOCUS-Africa - Contract Number: 869575

Project officer: Javier BARRIO ALONSO

Document title	Report on the characterization of climate-ready rice and cowpea varieties
Author(s)	Dr. Shingirai NANGOMBE, Macharia, Mercy (SSSA); Solemanegy, Marta (SSSA, INAM); Caproni, Leonardo (SSSA); Takele, Robel (SSSA); Munisse, Paulino (INAM); Amane, Manuel (INAM); Buizza, Roberto (SSSA); D'Amico, Valentina (SSSA); Pè, Mario Enrico (SSSA); Dell'Acqua, Matteo (SSSA))
Number of pages	66
Document type	Deliverable
Work Package	WP2
Document number	D2.4
Issued by	CSIR
Date of completion	2023-08-26 04:47:44
Dissemination level	Public

Summary

Smallholder farmers play a crucial role in global food security yet they are amongst the most vulnerable to the impacts of the climate crisis. They typically farm in challenging production environments with limited access to inputs such as fertilizers, irrigation, and resilient seeds, thus making them particularly exposed to climate risks. Access to climate services by smallholder farmers remain challenging and quite limited throughout sub-Saharan Africa (SSA). This is due to several reasons, one of them being that existing climate services may not fully address their needs and may be ill adapted to their highly specific local contexts (Greenberg, 2016). Tailor made climate services that are co-designed with local users have the potential to support smallholder agriculture in identifying and mitigating climate risks before they manifest, however they are challenging to develop and operate (Loboguerrero et al. 2018). Case Study 3 (CS3) in the FOCUS-Africa project aims to tackle this challenge by implementing a collaborative and transdisciplinary approach combining climate science, crop genomics, and socioeconomic approaches with the final goal of contributing to food security in Mozambique. The overarching aim of CS3 is co-designing and co-developing two intertwined climate services targeted at a representative smallholder farming community in Mogovolas District, Nampula Province, Mozambique. The climate services developed by CS3 are i) a seasonal forecasting tool for the wet season calendar that local farmer communities may use to support their cropping decisions and ii) a climatic characterization of crop genetic resources, in particular cowpea and rice, to be matched with the forecasted wet season to select a short list of climate-ready varieties to enhance resilience of smallholder farmers. This report will focus on the second climate service, and in particular on the exploration of genetic resources to identify climate resilient crop varieties. This activity focuses on cowpea (*Vigna unguiculata*), and rice (*Oryza sativa*), staple crops for smallholder farmers in Mozambique and key sources for proteins and calories, respectively. Cowpea is an understudied and underutilized climate resilient crop, that is nutritionally dense and used in diverse cropping systems while rice is grown not only as a staple but also as a source of income. Below, we describe the state of the art of the characterization of cowpea and rice plant genetic resources and outline our ...

Approval

Date	By
2023-08-26 04:52:25	Dr. Shingirai NANGOMBE (CSIR)
2023-08-26 09:51:01	Mrs. Roberta BOSCOLO (WMO)



Characterization of climate-ready rice and cowpea varieties

Deliverable D2.4

Lead Beneficiary: SSSA

August 2023

¹Macharia, Mercy; ^{1, 2}Solemanegy, Marta; ¹Caproni, Leonardo; ¹Takele, Robel; ²Munisse, Paulino; ²Amane, Manuel; ¹ Buizza, Roberto; ¹D'Amico, Valentina; ¹Pè, Mario Enrico; ¹Dell'Acqua, Matteo

¹ Center of Plant Sciences, Scuola Superiore Sant'Anna Pisa, Italy

² Instituto de Investigação Agrária de Moçambique.

www.focus-africaproject.eu



This project has received funding from the European Commission's Horizon 2020 Research and Innovation Programme. The content in this presentation reflects only the author(s)'s views. The European Commission is not responsible for any use that may be made of the information it contains.

Document Information

Grant Agreement: 869575
 Project Title: Full-value chain Optimised Climate User-centric Services for Southern Africa
 Project Acronym: Focus-Africa
 Project Start Date: 1 September 2020
 Related work package: WP 2
 Related task(s): Task 2.4
 Lead Organisation: Scuola Superiore Sant'Anna, Pisa, Italy
 Submission date: 31 August 2023
 Dissemination Level: 1

History

Date	Submitted by	Reviewed by	Version (Notes)
05/08/2023	Matteo Dell'Acqua; Mercy Macharia	Shingirai Nangombe	Final draft (V.1)
13/08/2023	Matteo Dell'Acqua; Mercy Macharia; Shingirai Nangombe	Roberta Boscolo; Sebastian Grey	Final draft (V.2)

About FOCUS-Africa

FOCUS-Africa – Full-value chain Optimised Climate User-centric Services for Southern Africa – is developing sustainable tailored climate services in the Southern African Development Community (SADC) region for four sectors: agriculture and food security, water, energy and infrastructure.

It will pilot eight case studies in six countries involving a wide range of end-uses to illustrate how the application of new climate forecasts, projections, resources from Copernicus, GFCS and other relevant products can maximise socio-economic benefits in the Southern Africa region and potentially in the whole of Africa.

Led by WMO, it gathers 14 partners across Africa and Europe jointly committed to addressing the recurring sustainability and exploitation challenge of climate services in Africa over a period of 48 months.

For more information visit: www.focus-africaproject.eu

Coordinator Contact

Roberta Boscolo | Climate & Energy Scientific Officer
Applied Climate Services Division
Services Department
World Meteorological Organization (WMO)
CP 2300, 1211 Geneva SWITZERLAND
email: rboscolo@wmo.int

Table of Content

ABOUT FOCUS-AFRICA	3
TABLE OF CONTENT	4
TABLES	5
FIGURES	5
EXECUTIVE SUMMARY	6
KEYWORDS	7
1 OVERVIEW	8
1.1 AGRICULTURE IN MOZAMBIQUE	8
1.2 THE PATH TOWARDS BETTER CROPS	9
1.3 AGROBIODIVERSITY COLLECTIONS	10
1.4 GENOMIC TOOLS	11
1.5 CLIMATE AND GENOMICS	11
1.6 ASSESSING FIELD PERFORMANCE OF AGROBIODIVERSITY	12
2 CHARACTERIZING RICE AND COWPEA COLLECTIONS FROM MOZAMBIQUE	13
2.1 SOURCE OF GERMPLASM	13
2.2 PURIFICATION AND AMPLIFICATION OF SEEDS	15
3 CHARACTERIZATION OF THE COWPEA AND RICE GENOMIC DIVERSITY	16
3.1 DNA EXTRACTION FROM PLANT MATERIALS	16
3.2 DNA SEQUENCING AND GENOTYPING	17
3.3 DIVERSITY ANALYSIS	18
3.3.1. Cowpea diversity in Mozambique and southern Africa	18
3.3.2 Rice diversity in Mozambique and southern Africa	21
4 SPATIAL AND BIOCLIMATIC CHARACTERIZATION OF SOUTHERN AFRICA COWPEA LANDRACES	22
4.1 CHARACTERIZATION OF AGROECOLOGICAL DIVERSITY OF COWPEA CULTIVATION AREAS IN MOZAMBIQUE AND SOUTHERN AFRICA	24
4.2 GENOME-WIDE ASSOCIATIONS WITH BIOCLIMATIC TRAITS	26
4.3 THE POTENTIAL IMPACT OF CLIMATE CHANGE ON THE DISTRIBUTION PATTERN OF COWPEA IN SOUTHERN AFRICA	28
5 CHARACTERIZATION OF THE AGRONOMIC DIVERSITY IN THE RICE AND COWPEA CORE COLLECTIONS	29
5.1 COWPEA PHENOTYPIC EVALUATION	30
5.2 RICE PHENOTYPIC EVALUATION	30
5.3 PARTICIPATORY VARIETY EVALUATION OF COWPEA AND RICE COLLECTIONS	31
6 CONCLUSION	33
7 REFERENCES	35
8.1 COWPEA PASSPORT DATA	43
8.2 RICE PASSPORT DATA	55
8.3 DESCRIPTION OF THE SHARED SOCIOECONOMIC PATHWAY (SSP) EXPERIMENT USED	63
8.4 QTNS ASSOCIATED WITH BIOCLIMATIC VARIABLES IN THE COWPEA COLLECTION	64
8.5 PVS SCORING FORMS	66

Tables

Table 1: Pairwise Fst estimates between DAPC clusters based on cowpea SNP dataset	20
Table 2: Pairwise Fst estimates between DAPC clusters based on Rice SNP dataset.....	22
Table 3: Summary of selected CMIP6 GCMs that form the ensemble of climate projections used in this study.....	23

Figures

Figure 1: Geographic distribution of cowpea and rice accessions collection points across Southern Africa. Longitude and latitude values in WGS84 EPSG:4326 degrees are reported on the x-axis and y-axis, respectively. Each point may represent more than one accession. Samples without GPS coordinates are not shown. The sampling area is reported in shades representing altitude according to the bar on the side (meters above sea level). Colors represent cowpea and rice accessions according to legend.....	14
Figure 2: Seed purification and amplification at IIAM, Mozambique. a, b, c & d) Agronomists sorting and purifying seeds e) Preparations of fields for cowpea amplification f) Rice amplification field in Mozambique. g) Cowpea amplification field IIAM Umbeluzi station	16
Figure 3: DNA extraction. Collections of a) Rice & b), cowpea seedlings germinated for DNA extraction in c).....	18
Figure 4: Molecular diversity of cowpea landrace accessions. A. Phylogenetic tree derived from SNPs data. B. Principal component analysis derived from SNPs data. Different colors indicate region of origin as shown in the legend, with symbols indicating type of material in a) and DAPC clusters in b).	20
Figure 5: Molecular diversity of rice landrace accessions. A. Phylogenetic tree derived from SNPs data. B. Principal component analysis derived from SNPs data. Different colors indicate region of origin as shown in the legend. With symbols indicating type of material in a) and DAPC clusters in b).....	22
Figure 6: Agroecological zones of southern Africa. Each red point represents cowpea accession sampling point. Longitude and latitude values in WGS84 EPSG:4326 degrees are reported on the x-axis and y-axis, respectively. Different AEZs are represented by different colours according to legend.....	25
Figure 7: Bioclimatic variables distribution and correlation in cowpea growing areas of southern Africa. a) Histograms showing frequency of bioclimatic variables. b) Correlation between bioclimatic variables. The direction and intensity of correlations is shown by the tile color according to legend. Blank tiles mean no significant correlation.....	26
Figure 8: GWAS output for bioclimatic variable bio3 (Isothermality) and bio16 (Precipitation of Wettest Quarter). The Manhattan plots report individual SNPs across all chromosomes (x-axis) and -log10 P value of each SNP association (y-axis). The horizontal lines represent a stringent Bonferroni threshold for a nominal p-value of 0.05. points surpassing the threshold represent position on the genome in which diversity in the collection is strongly associated to climate at sampling points, suggesting the existence of adaptation mechanisms.....	27
Figure 9: Bioclimatic and spatial diversity explain genomic variation in the distribution of southern Africa cowpea landraces. a) Ranked accuracy importance of the bioclimatic and spatial variables based on Gradient Forest (GF) model. b) Biplot of the biological space, represented by Principal Components of the transformed grid with an RGB color palette relative to its first three dimensions. It displays different adaptive environments across the cropping area ("c"), where similar colors represent similar alleles at climate-responsive loci ($R^2 > 0$); in the biplot, axes report the portion of bioclimatic variance (%) explained by the PCs of the transformed grid. c) GF-	

transformed bioclimatic variables across southern Africa. Colors based on bioclimatic-genetic space in 'b'. d) Genomic offset based on SSP 585 ensemble climate projections at the horizon of 2041-2060. The color scale indicates the magnitude of the mismatch between current and projected climate-driven turnover in allele frequencies. 29

Figure 10: Participatory variety evaluation. Focus group discussions at Chokwe station as shown in a,b. Panels c, d, e, f show farmers evaluating and scoring cowpea varieties at Chokwe and Nampula stations. Panels g,h,i show rice PVS trials at Chokwe station. 32

Executive Summary

Smallholder farmers play a crucial role in global food security yet they are amongst the most vulnerable to the impacts of the climate crisis. They typically farm in challenging production environments with limited access to inputs such as fertilizers, irrigation, and resilient seeds, thus making them particularly exposed to climate risks. Access to climate services by smallholder farmers remain challenging and quite limited throughout sub-Saharan Africa (SSA). This is due to several reasons, one of them being that existing climate services may not fully address their needs and may be ill adapted to their highly specific local contexts (Greenberg, 2016). Tailor made climate services that are co-designed with local users have the potential to support smallholder agriculture in identifying and mitigating climate risks before they manifest, however they are challenging to develop and operate (Loboguerrero et al. 2018). Case Study 3 (CS3) in the FOCUS-Africa project aims to tackle this challenge by implementing a collaborative and transdisciplinary approach combining climate science, crop genomics, and socioeconomic approaches with the final goal of contributing to food security in Mozambique. The overarching aim of CS3 is co-designing and co-developing two intertwined climate services targeted at a representative smallholder farming community in Mogovolas District, Nampula Province, Mozambique. The climate services developed by CS3 are i) a seasonal forecasting tool for the wet season calendar that local farmer communities may use to support their cropping decisions and ii) a climatic characterization of crop genetic resources, in particular cowpea and rice, to be matched with the forecasted wet season to select a short list of climate-ready varieties to enhance resilience of smallholder farmers. This report will focus on the second climate service, and in particular on the exploration of genetic resources to identify climate resilient crop varieties. This activity focuses on cowpea (*Vigna unguiculata*), and rice (*Oryza sativa*), staple crops for smallholder farmers in Mozambique and key sources for proteins and calories, respectively. Cowpea is an understudied and underutilized climate resilient crop, that is nutritionally dense and used in diverse cropping systems while rice is grown not only as a staple but also as a source of income.

Below, we describe the state of the art of the characterization of cowpea and rice plant genetic resources and outline our work on the assembly of a wide portfolio of genetic resources available in local and global gene banks, their characterization for agronomic, climatic and genetic diversity, and the conduction of a participatory variety selection with local farmers to identify climate-ready varieties to support local adaptation. Our final aim is to select a small set of cowpea and rice genotypes with desirable adaptation traits to be prioritized for distribution to farmers and breeding programs. The development of the other climate service developed in CS3, *i.e.*, the forecasting tool for the wet season calendar, is narrated in detail in deliverables from WP3 (D3.2, D3.3), WP4 (D4.1, 4.2), and WP5 (D5.1, D5.2). The engagement with local stakeholders in the co-design and co-development of the services is narrated in WP2 (D2.1, D2.3), WP6 (D6.1, D6.2, D6.3), and WP7 (D7.1, D7.2).



The research tasks of CS3 under D2.4 are dynamic in nature and are adjusted as required to make the most out of the available resources and to grasp unplanned opportunities, as well as to address challenges. In this sense, this deliverable is not considered an end point regarding the characterization of crop genetic resources, but rather a description of the activities conducted, and results obtained until now. Although the current results fulfil the objectives of D2.4, we expect the activities and data analyses to continue beyond this deliverable's deadline to further refine the development of the CS3 climate services.

Keywords

food security, climatic adaptation, landscape genomics, participatory research, smallholder farming systems, rice, cowpea, Mozambique

1 Overview

1.1 Agriculture in Mozambique

Mozambique has ten Agroecological zones with two distinct climate classifications: tropical and sub-tropical in northern and central regions, and arid and semiarid in the southern regions. Most of the country receives above 400 mm of rainfall per annum, with the rainy season extending from October to April. Mozambique has not been spared from climate change in the recent years, with high rainfall variability and increased frequency of tropical cyclones (Phiri, Simwanda, and Nyirenda 2021; Arndt et al. 2011). Most of the rural farmers in Mozambique still rely on rain-fed agriculture for food production, making them poorly resilient to climate stresses. Irrigation farming is largely employed along the river valleys in the southern region (Silva and Matyas 2014), but less in the northern part of the country. The Mozambican agricultural system is characterized by millions of smallholder farmers who rely on their yearly cropping for food consumption and/or income (Ferrão et al. 2018). Smallholder farming has steadily contributed to over a quarter of the country's Gross Domestic Product (GDP) over the last decade (World bank 2020). Although crop production accounts for the largest portion of national GDP, only 7.2% of the Mozambique arable land is under cultivation (World Bank 2020). The rest of the potential agricultural land, about 47.3%, is occupied by forests.

As with most countries in SSA, agricultural production in Mozambique remains low due to several factors including low adoption of new technology, low inputs, limited extension services and climate vulnerability (Cavane, Eunice 2015). Smallholder farmers are further aggravated by the fact that most farms cover less than 2 hectares, making it difficult to close in on existing yield gaps (CGAP 2016). Further, smallholder farming is concentrated in the more densely populated North and central part of the country which has less developed transport network compared to the southern region where the capital is located, thus impacting on the effectiveness of the supply chain (CIAT; Word Bank 2017).

Mozambique is particularly vulnerable to the climate crisis because of its geographical location and its socioeconomic conditions. It has more than 2,000 kms of coastlines and major river basins both of which contribute to the diverse agroecologies in the country and support a large diversity of cultivated crops including cereals, legumes, annual and perennial horticultural products, and cash crops (Bias and Donovan 2003). Cassava, maize and rice are the most important staples followed by wheat, millet, sorghum, potatoes and cowpea (Mango et al. 2018). Despite the significant number of different crops currently under cultivation, farmers in Mozambique have reported a rapid decrease in diversity within crops (Greenberg 2016). This is partly because national policies promote technologies related to intensive agriculture, including certified seeds and synthetic fertilizers to increase productivity. Although these practices are certainly capable to support the intensification of farming and the increase in productivity, they are seldom adopted in the fields of smallholders at large due to a misalignment with local growing conditions and farmer preferences. This results in somewhat limited adoption of improved varieties, not only in Mozambique but in SSA at large (Fisher et al. 2015), and to the fact that local farmers tend to resort to local genetic materials which express traits of local adaptation. Traditional varieties otherwise known as landraces have high tolerance to biotic and abiotic stresses with intermediate yielding capacity under low input agriculture. They tend to have a higher genetic variation than in most breeding programs and are adapted to different conditions based on their origin. Local farmers maintain a wealth of this traditional agrobiodiversity that may contribute to the selection and development of new and improved varieties with the capacity to adapt to local cropping conditions, including adaptation to climate constraints. Indeed, the positive traits of landraces can be identified with the appropriate methods and incorporated into new cultivars for more sustainable agricultural production (Galuzzi et al. 2020). Here we focus on cowpea and rice landraces

from the region to explore their value for adaptation. We chose these two crops as they are particularly relevant for the farming communities in the Mogovolas region in the north of Mozambique, which are directly targeted by CS3. Indeed, rice and cowpea have been indicated as staple crops by stakeholder farmers interviewed in the initial phases of the project.

Rice is a major cereal in Mozambique with its production area covering approximately 204,000 ha and an average paddy yield of 1.27 t/ha (JICA, 2014; Ismael et al. 2021). Most rice cultivation is found in lowland rainfed ecologies, where farmers follow traditional management practices (Kajisa and Vu 2023). The major rice irrigation schemes are in Chokwe in the south and Baixo Limpopo in the center of the country. Despite the availability of lowland and wetland suitable for sustainable rice-based cropping, there is still a production deficit in Mozambique owing to challenges including the lack of high-yielding varieties that have good grain quality and resistance to biotic and abiotic stresses. Recent predictions on climate change indicate that high-temperature episodes are expected to impact rice production and productivity worldwide (Senguttuvel et al. 2021). However, climatic risk of rice cultivation is mainly related to the dependence of agriculture on rainfall. Erratic rainfall may cause droughts, and delays in the production cycle. Due to Mozambique's location, risks of droughts and floods are common all over the country. Mozambique's rice production system is heavily dependent on rainfall, with less than 3% of total rice cultivated area that is irrigated (Ismael et al. 2021). This limits the opportunity of increasing crop intensity, control weeds, and supporting higher plant growth. The problem of limited irrigated areas is aggravated by the numerous inefficiencies in water use, as reflected in largely unutilized irrigation systems already in place, lack of proper drainage resulting in soil salinity, and low capacity in managing and maintenance of existing systems. Identification of highly- yielding and wider adaptation of crop genotypes together with farmer preference would support the food security in the country and help the local farmers to fight against climate change by using their preferred varieties in a sustainable way.

In Mozambique, cowpea is one of the most important crops for food security, as leaves and grains are both used for food and to generate market income for smallholder farmers residing in rural areas. Despite its importance in the food security chain, this crop remains underutilized (Gerrano, Lubinga, and Bairu 2022). Production averages 0.27 tonnes per hectare (Boukar et al. 2019), and is vulnerable to biotic and abiotic stresses including temperature change, and extreme weather conditions such as droughts and floods, resulting in low yields (Mekonnen et al. 2022). Cowpea has immense improvement potential with regards to local adaptation, as significant differences exist among genotypes in their response to climate stresses (Gomes et al. 2020; Mwale et al. 2017). This case study focuses on fostering food security and resilience in Nampula region by characterizing cowpea diversity in relation to cultivation needs and constraints in local farming systems. Cowpea landraces may be well adapted to local conditions and might serve as a useful source of germplasm for sustainable cowpea breeding and production (Gomes et al. 2020). The development of cowpea varieties adapted to climate change would be an effective and sustainable measure for ensuring increased crop productivity, nutritional quality, and food security in Mozambique.

1.2 The path towards better crops

Conventional breeding involves crossing parent plants with desirable traits and selecting offspring with a combination of traits of interest inherited. For thousands of years, farmers have been involved in conscious or unconscious crop breeding based on selecting desirable phenotypes for key agronomic traits including yield, phenology, and adaptation to biotic and abiotic stresses, resulting in crops that are more nutritious and productive than wild ancestors and that are traditionally maintained in the form of local varieties also known as landraces. These landraces represent local agrobiodiversity, a combination of crop diversity and associated cultural and food uses, that gathers enormous potential

for resilience and adaptation thanks to unique traits that have been shaped over centuries of cultivation at the interface of human and natural selection. Prior the great acceleration of the mid-20th Century, the human population had increased to 3 billion mostly thanks to crop improvement and ability to meet the food needs (Nouman et al. 2022). Over time, the increasing population and lack of technological shift in agriculture meant the risk of famine and malnourishment particularly in developing nations. The green revolution, heralded by Norman Borlaug in the United States and Mexico, saw the rapid development and introduction of high yielding varieties in cereals such as wheat and rice, which resulted in higher food production and in an increased carrying capacity for larger populations, certainly contributing to the increase of the world population up to the current 8 billion. However, the green revolution also meant that traditional varieties under cultivation in local farming systems decreased significantly due to the focus given to the production of subsidized high-yielding hybrid crops and the emphasis of monoculture by the governments in a bid to achieve self-sufficiency (Altieri and Anderson 1986). High yielding varieties currently under cultivation have a narrow genetic variability (Govindaraj, Vetriventhan, and Srinivasan 2015). During the green revolution, productivity improved not only due to genetic improvement but also increased use of fertilizers, pesticides, and groundwater resources. Consequently, there were new environmental and social challenges impacted by this technological shift. In sub-Saharan Africa, however, the green revolution failed to take off and its practices are still particularly unsustainable to the smallholder farmers who are not able to compete with commercial farmers (Dawson, Martin, and Sikor 2016). As a result, African farmers, largely smallholders, are left out of mainstream innovation in agriculture and require tailored solutions to increase their capacity for production.

The climate crisis is now urging researchers and breeders to identify new paths towards the sustainable intensification of agriculture, moving forward and away from the resource-intensive cropping model of the green revolution (“UN Climate Experts: Green Revolution Leaves Food Systems Vulnerable to Climate Change” 2014). There are now increasing calls from the scientific and breeding community to look back into traditional varieties and landraces to harness traits of local adaptation that could be employed for accelerating the development of new, improved varieties requiring less inputs and promoting yield stability in the face of climate change (Broccanello et al. 2023). The varieties traditionally cultivated by farmers in SSA bear high potential for biotic and abiotic stress resistance; the full potential of agrobiodiversity can be disclosed by data-driven methods applied on plant genetic resources and combining genomics, climate science, and common garden experiments (Caproni et al. 2023).

1.3 Agrobiodiversity collections

The preservation of agrobiodiversity, *i.e.* the biological diversity associated with agriculture, commenced under treaties including the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) and the Convention on Biological Diversity (CBD) (Sullivan 2004). *Ex situ* seed collections, which are stored collections of plant genetic resources that aim at the preservation and conservation of plant materials outside their natural habitats, have been established in specific facilities, called gene banks, with the purpose of maintaining the genetic diversity of plants for future use in research, breeding, and agriculture. Landraces that are maintained in *ex situ* collections typically have been sampled on farmer fields via sampling campaigns and are associated with so-called passport data that includes coordinates of origin, vernacular name, and other details. These germplasm resources remain underutilized due to their high number and the heterogeneity of accessions available (McCouch et al. 2020). It is however crucial to utilize these resources in an effective way if we are to address crop improvement and global food security. There is great potential

in these reserves of agrobiodiversity, especially when it comes to the need to breed for adaptability and resilience to climate change risks. Their potential in improving agricultural productivity has been shown in breeding programs from different crops. For instance, the largest rice gene bank at the International Rice Research Institute (IRRI), has immensely contributed to variety improvement and this has increased subsequent distribution to smallholder farms in countries like Bangladesh over the years (Villanueva, Enriquez, and Capilit 2022). Traditionally, gene bank materials are characterized by passport data and provenance records in which information about highly heritable phenotypic traits are inferred as genetic after rounds of multiple seed multiplication, a labor-intensive endeavor that can focus on a small portion of the diversity available. Also because of this, gene banks and germplasm collections in SSA are largely untapped by modern research approaches and hold an enormous potential to be discovered. This is the case of the Mozambique national gene bank, which hosts hundreds of accessions carefully collected and only partially characterized, whose value CS3 has the objective to assess. To this end, it is possible to use genomics approaches coupled with available characterization data to generate information that can be implemented immediately by breeders and research programs.

1.4 Genomic tools

The Genomic revolution, that is, the capacity to sequence DNA that was realized at the turn of the 21st century, has accelerated human development in many areas including agriculture (Tian et al. 2021). The Deoxyribonucleic Acid (DNA) is the molecule that carries the genetic instructions of all biological processes. It is in the DNA that is coded the potential for expression of traits of any given organism. In crops, deciphering DNA is crucial in understanding the genetic basis of important agricultural traits that have potential for improvement, including the capacity for adaptation. The rationale of using DNA technology is that it allows to tap into the potential of agrobiodiversity and expedites breeding. Breeders can narrow down on promising lines by analyzing the DNA and accelerate the development of new and improved varieties unlike traditional methods that rely on crossing several plants over several generations to get the desired trait. Recent technological developments have made it possible to study all the genes of an organism, their interaction with each other and the environment. Advances such as high throughput DNA sequencing technologies, massive computing power for subsequent bioinformatics analysis and gene manipulation techniques have all contributed to crop breeding on an unprecedented scale (Ahmar et al. 2020; Medina-Lozano and Díaz 2022). Genomics is a powerful tool with immense potential in revolutionizing agriculture, especially when directed towards the characterization and valorization of agrobiodiversity of vast plant germplasm resources for crop improvement. Efficient, high throughput genomic tools such as single-nucleotide polymorphism (SNP) and whole-genome resequencing have been used to characterize genetic diversity and reveal relations amongst accessions. These tools have been used to describe diversity in collections and among accessions in several crops including maize (Romay et al. 2013), barley (Milner et al. 2019), and wheat (Sansaloni et al. 2020).

1.5 Climate and genomics

Ecosystems, their species distribution, and productivity are strongly associated with the climate (Leemans and Eickhout 2003). As a result, a changing climate has an impact on patterns of species

adaptation and survival. This also means that effects of climate change have different scales in different ecosystems (Malhi et al. 2020). Smallholder agricultural systems in SSA are semi-artificial ecosystems in which certain crop varieties are selected and maintained due to their productivity and adaptative capacity to local conditions. Agriculture is particularly vulnerable to climate change due to the sensitivity of the cropping cycle to abiotic and biotic stresses usually exacerbated by environmental changes. This is especially true in low-input smallholder agriculture such as that of Mozambique and SSA. The potential of adaptation of crop varieties, like their traits of agronomic interest, is written in their DNA. For this reason, transdisciplinary research encompassing different fields including climatology, ecology, genomics, and phenomics has potential to enhance agricultural adaptation to a changing climate (Palit et al. 2020). Different studies have explored the genetic basis of climate adaptation in various species (Franks and Hoffmann 2012; Wilczek et al. 2010). In plants, some traits including timing of flowering and photoperiod have a genetic basis and are related with environmental adaptation (McNamara et al. 2011).

In the advent of high throughput DNA sequencing, we can dissect molecular mechanisms underlying complex agronomic traits and effects of the environment. At the same time, we can use climate modelling to assess impacts of changing climate patterns for different future scenarios. The combination of genomics and climate science is a powerful tool that has shown potential of enhancing climate adaptation as it considers intra-species diversity under different environments (Fitzpatrick and Keller 2015). This approach has been also used to reveal a genomic vulnerability of migratory birds in a changing climate (Bay et al. 2018), further showing the need to incorporate genomics in biodiversity conservation, of which agrobiodiversity conservation is part of. Identification of potential genetic variants (*i.e.* alleles) for adaptation to a changing climate has also been shown in tree and crop species. Rhoné et al. (2020), demonstrated the need to strategize distribution of pearl millet varieties in West Africa based on their potential for future climate adaptation. A study of the ubiquitous *Quercus acutissima* tree found in East Asia identified populations in marginal areas that could be lost in future climate scenarios due to genomic maladaptation (Yuan et al. 2023). In a similar study working on *Coffea Canephora* native trees in Uganda, de Aquino et al. (2022) has shown genetic factors, existing in the accessions' genomes, having adaptative potential towards climate change. Our team has already demonstrated the value of integrating climate information data with genomics to describe potential for adaptation in future breeding programs using Ethiopian germplasm of Barley (Caproni et al. 2023) and Teff (Woldeyohannes et al. 2022). These studies show that agrobiodiversity is a reservoir of natural variation that holds potential for crop improvement and for the development of climate-ready varieties.

1.6 Assessing field performance of agrobiodiversity

To have a meaningful impact on the improvement of agriculture, agrobiodiversity must be characterized for its agronomic potential. Adaptation to climatic conditions needs to be coupled with high productivity and desirability of varieties, and this may be assessed with field experiments, in which the agrobiodiversity under study is grown in experimental field and measured for performance traits including yield, yield components, and phenology. Even this characterization, however, needs to be coupled with other sources of information to become useful, noting that farmers do not always accept innovation which, on paper, seem obvious to an external observer. Governments in developing countries have been using agricultural extension workers to support farmers in adopting technologies and products for improvement of agricultural production (Ruzzante, Labarta, and Bilton 2021), but

with mixed outcomes. Indeed, the adoption of new technologies by farmers remains a challenge since farmers' choices do not only rely on improved productivity (Yigezu et al. 2018; Nchanji et al. 2021). Smallholder farmers, particularly in SSA, have quite varied contexts in terms of environment and resource constraints that no one single technology can solve (Wainaina, Tongruksawattana, and Qaim 2016). Participatory approaches that involve farmers and other active stakeholders hold promise in overcoming these limitations (Blackstock, Kelly, and Horsey 2007). Understanding the context of farmers not only identifies the reasons for their resistance to adopting improved varieties/ technology but also identifies the incentives that would push adoption to enable farmers cope better with prevailing climate vulnerabilities (Asfaw et al. 2016). Participatory evaluation of crop varieties by farmers can contribute to solving this issue by coupling farmers' evaluations with observations of agronomic performance. Participatory Varietal Selection (PVS) usually entails evaluation of a range of varieties on garden experiments or in their own fields based on their traditional knowledge and preferences. However, the mainstream late cycle PVS involves farmers after advanced breeding efforts, close to the end of the development process of new varieties, reducing the room for discussion with farmers. A participatory evaluation study conducted in Zimbabwe revealed that farmers did not select elite high yielding and stable sorghum varieties but instead selected traditional varieties, demonstrating the need to integrate traditional knowledge with modern breeding tools to increase the chances of adoption (Magaisa et al. 2022). This is since farmers may look for traits of local adaptation that are not available in foreign materials; local adaptation that is expressed both in the agronomic potential of varieties, but also traditional and cultural uses that farmers look for in what they cultivate. Developing crop varieties takes a lot of resources and time, it is therefore crucial to take into consideration the factors that would enhance adoption by farmers prior to the intense breeding cycle. The success of PVS could further be harnessed by involving farmers for selection of pre-breeding material as well as identifying their constraints and preferences (Singh et al. 2014). Integrating social science to understand farmers' needs pre-breeding has had some success in SSA. In Tanzania, farmers were involved in development of finger millet varieties which led to significant adoption (Henry et al. 2017). In Mozambique, bean breeding varieties were developed and released having taken into consideration constraints identified by farmers through participatory processes (Burridge et al. 2019). In Ethiopia, our group has shown that PVS can be fully integrated in a genomic framework to speed up the selection of crop varieties improving local yields and farmers' satisfaction (Gesesse et al. 2023; Kidane et al. 2017; de Sousa et al. 2021).

2 Characterizing rice and cowpea collections from Mozambique

2.1 Source of germplasm

For the specific case of Mozambique, this assessment aimed at genetic, climatic, and phenotypic characterization of a large collection of cowpea and rice landraces that has never been previously explored. SSSA and partners sourced rice and cowpea landraces from *ex situ* seed collections, restricting the selection to those having a historical origin in Mozambique and neighbouring southern Africa including South Africa, Zimbabwe, Malawi, and Tanzania. Landraces are varieties of crops selected by farmers for a local agroecosystem and local practices over continued cycles of cultivation (Villa et al. 2005), and are crucial in maintaining adaptability of crop populations, including resistance to pests, diseases, and adaptation to extreme environments. In the objectives of CS3, passport data is instrumental to link landraces with specific areas of cultivation, and thus with local climatic conditions. Accessions with geographical passport are shown in Figure 1. Cowpea landraces were sourced at the national gene bank at the Agricultural Research Institute of Mozambique (IIAM), Eduardo Mondlane

University in Mozambique and from the International Institute of Tropical Agriculture (IITA) in Nigeria which holds the world's largest and most diverse collection of cowpea varieties (<https://www.iita.org/research/facilities/genetic-resources-center/>). Rice accessions were sourced from the IIAM genebank and accessions from the International Rice Research Institute (IRRI) in Philippines which has the largest collections of cultivated and wild rice varieties (<https://www.irri.org/international-rice-genebank>). Most of these plant genetic resources have never been characterized by molecular, climatic, or phenotyping means. In addition to the landrace varieties, improved varieties of cowpea and rice produced by national and international breeding programs were also included in the assessments. In total, we originally sourced 432 cowpea accessions and 650 rice accessions.

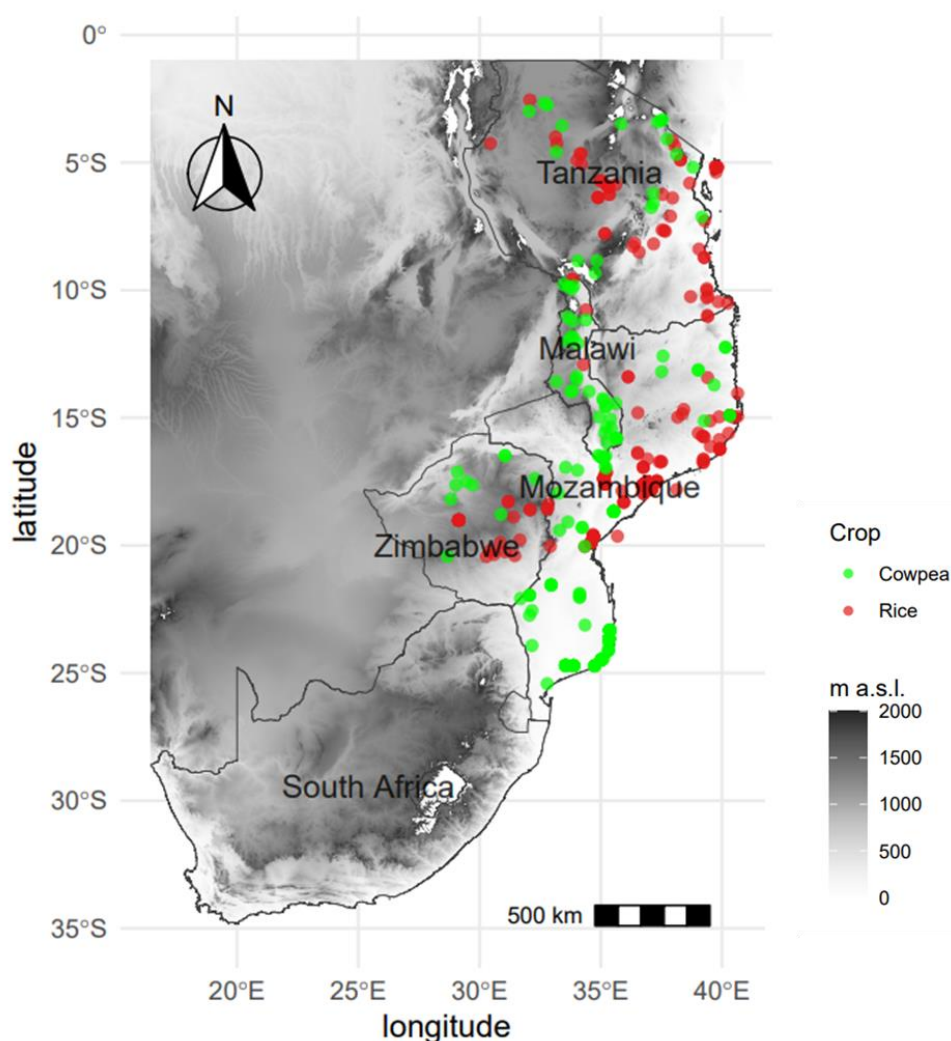


Figure 1: Geographic distribution of cowpea and rice accessions collection points across Southern Africa. Longitude and latitude values in WGS84 EPSG:4326 degrees are reported on the x-axis and y-axis, respectively. Each point may represent more than one accession. Samples without GPS coordinates are not shown. The sampling area is reported in shades representing altitude according to the bar on the side (meters above sea level). Colors represent cowpea and rice accessions according to legend.

2.2 Purification and amplification of seeds

Genebanks usually acquire material from farmers' fields, wild habitats, or markets (Hammer, Arrowsmith, and Gladis 2003). This means that most of their material may not be genetically pure. Seed purity means that a particular batch of seeds contains only the desired type of seeds and is devoid of contaminants or other types of seeds. In agriculture, gardening, and plant breeding, maintaining seed purity is crucial to ensure that the plants grown from those seeds exhibit the desired traits, characteristics, and genetic makeup. Genebanks also distribute accessions in small quantities to end users. The end user has the responsibility of ensuring germplasm purity and sufficiency of seeds for use in experiments and/or distribution. For this reason, we set up purification and seed multiplication trials for all germplasm collected in the project. In Pisa, Italy, we conducted a seed multiplication field in summer (June to August) of 2021 aimed at preliminary observation and purification of the 238 cowpea accessions obtained from IITA. In Italy, some of the accessions did not flower due to photoperiod sensitivity. Therefore, we conducted purification and multiplication of all cowpea and rice accessions in Mozambique taking into consideration the specific crop growing season of each crop. During purification and multiplication, we followed best practice for crop management and included irrigation to ensure that we harvested enough seeds for further experiments. Cowpea and rice purification trials were conducted in the growing season of 2020/2021 at Umbeluzi in Maputo province. In this cropping season, we encountered problems with the irrigation infrastructure at the experimental station and thus opted to move the experiments to other sites outside of Maputo Province. As a result only 103 rice accessions and 127 cowpea accessions were planted successfully, and 88 accessions of rice and 117 cowpea accessions were multiplied and harvested successfully. In the cropping season of 2021/ 2022, we multiplied all 432 cowpea accessions at Inhacoongo, in Inhambane province. Each cowpea accession was planted in a space of 5m by 1m plot to a total of 432 plots the space between plants was 1.6m by 1m. The crop management was done as described by IITA (1985). In the same season of 2021/2022 a total of 650 rice accessions were planted for purification and multiplication at the Chokwe station (Figure 2). Each accession occupied a 3m by 1m plot. After multiplication and purification of both cowpea and rice, we selected a core collection that was representative of the full collection based on availability of sufficient seeds to support characterization experiments. For cowpea, the core collection included accessions from Malawi (41), Mozambique (289), South Africa (34), Tanzania (19) and Zimbabwe (12). We included improved varieties, 19 of which were sourced from IITA Nigeria and three from Mozambique, totalling 417 accessions (Annex 1). The rice core collection included landraces from Mozambique (205), Tanzania (59) and Zimbabwe (29). We designated 7 accessions as of "unknown provenance" since passport data was not available. We completed the rice collection with 24 improved accessions from Mozambique to a total of 324 accessions (Annex 1). The core collections were to be used for further research activities including genetic diversity by DNA sequencing in combination with climate data and evaluation of agronomic performance by farmers and agronomists.



Figure 2: Seed purification and amplification at IIAM, Mozambique. a, b, c & d) Agronomists sorting and purifying seeds e) Preparations of fields for cowpea amplification f) Rice amplification field in Mozambique. g) Cowpea amplification field IIAM Umbeluzi station

3 Characterization of the cowpea and rice genomic diversity

3.1 DNA extraction from plant materials

All DNA extraction activities were carried out in Mozambique. We preferred this option than the simplest option of exporting seeds and conducting DNA extraction in Europe because we wanted to use this opportunity to valorize the laboratory facilities at IIAM to provide molecular biology training to IIAM staff. Rice and cowpea accessions from the core collection were germinated in pots at the greenhouse at IIAM, Maputo in Aug/Sep 2022 (Figure 3). Once the seedlings had grown to a suitable size, we proceeded with DNA extraction with a team of SSSA and IIAM researchers in the IIAM laboratories in Maputo. The extraction protocol was the same for rice and cowpea. Leaves from five seedlings per pot were sampled and pooled and total genomic DNA was isolated using the GenElute™ Plant Genomic DNA kit following the manufacturer's protocol. In a nutshell, DNA extraction works by separating the DNA from other cellular components, such as proteins and lipids, to obtain a pure and concentrated DNA sample. The process begins by breaking open the cells through mechanical or chemical means, releasing the cellular contents into a solution. Enzymes or detergents are then used to degrade proteins and disrupt cell membranes, freeing the DNA. Once the DNA is liberated, it is separated from the rest of the cellular components via binding to a matrix, and finally is purified by washing, drying, and re-suspension in a buffer suitable for storage and downstream applications. After extraction, genomic DNA quality was evaluated in 1% agarose gel and quantified using a Nanodrop spectrophotometer available at IIAM. DNA quantity and quality was deemed appropriate for all samples and was shipped to sequencing facilities for further processing: cowpea DNA was shipped to IGA Technology Services (Udine, Italy) and Rice was shipped to LGC Genomics GmbH, (Berlin Germany) for library construction and sequencing.

3.2 DNA sequencing and genotyping

For cowpea we employed a double digest restriction-site associated DNA (ddRAD) genotyping produced with a ddRAD IGATech custom protocol, with minor modifications of Peterson's double digest restriction-site associated DNA preparation (Peterson et al. 2012). The strategy is to reduce the complexity of the target genome using restriction enzymes to fragment the DNA and sequencing the resulting DNA fragments. Restriction enzymes *SphI* and *MboI* produced optimal fragment distribution and were used to digest the target DNA. For rice, restriction site-associated DNA sequencing (RAD-Seq) libraries were produced following custom protocol by LGC Genomics GmbH. In RADseq, single enzyme digestion is combined with random fragmentation and sequencing adapter to produce sequencing libraries (Baird et al. 2008). In this case, *ApeKI* produced optimal fragments. In both instances, the fragments were processed to make DNA sequencing libraries. The resulting libraries were checked for quality and quantity with both Qubit 2.0 Fluorometer (Invitrogen, Carlsbad, CA) and Bioanalyzer DNA assay (Agilent technologies, Santa Clara, CA). Libraries were sequenced with 150 cycles in paired end mode on NovaSeq 6000 instrument following the manufacturer's instructions (Illumina, San Diego, CA). This process is meant to produce the DNA sequence specific for each of the processed samples. The resulting information is a collection of bioinformatic reads, representing the DNA sequence, that were retrieved from the sequencing facility and used to derive information about the diversity existing between samples. Raw reads were de-multiplexed using the `process_radtags` utility included in Stacks v2.61 (Catchen et al. 2013). Reads from cowpea were mapped against the *Vigna unguiculata* reference genome ASM411807v2 available at (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_004118075.2/) and reads from rice were mapped against the *Oryza sativa* reference genome R498v3 available at (<https://www.mbkbase.org/R498/>) using BWA-MEM (Li and Durbin 2009) at default parameters and selection of unique reads with a mapping quality greater than 4. From the aligned reads, detection of covered loci was read using the `gstacks` program included in Stacks v2.61 (Catchen et al. 2013). Filtering of detected loci was done with option `(-R=0.75)` retaining only loci that have a 75% representation of all the samples. Heterozygosity was maintained at a maximum of 80%. HaplotypeCaller (Poplin et al. 2018) from Genome Analyzer Tool Kit package version 4.2.0.0 was used for variant calling and was run in GVCF mode (<https://github.com/broadinstitute/gatk/releases>), with suggested parameters. Only high quality (QUAL > 30.0) biallelic SNPs were retained, and further filtered for minor allele frequency above 5% and for missing calls across the collection less than 30%. SNPs, or Single Nucleotide Polymorphisms, are the most common type of genetic variation in DNA, involving a single nucleotide change in a specific position. SNPs occur throughout the genome and can influence traits and individual differences. They are valuable markers for studying genetic diversity. Minor allele frequency (MAF) refers to the frequency of the less common allele-form of a gene- in a population. Filtering SNPs based on MAF is pertinent as it removes markers that may have limited statistical power in downstream analysis or those which may not provide meaningful information. Sequencing reads produced in the project have been uploaded in an online repository and will be made available to the scientific community after publication of the results at NCBI (<https://www.ncbi.nlm.nih.gov/>) under BioProjects PRJNA951214 for *Vigna unguiculata* and PRJNA952322 for *Oryza sativa*.



Figure 3: DNA extraction. Collections of a) Rice & b), cowpea seedlings germinated for DNA extraction in c).

3.3 Diversity analysis

Genetic diversity analyses were performed on genomic data using R (“R: The R Project for Statistical Computing” 2021.) to assess different aspects of the molecular diversity in the rice and cowpea core collections and to identify subpopulations. A discriminant analysis of the principal components (DAPC) implemented in R/adegenet (Jombart, Devillard, and Balloux 2010) was used to identify the presence of genetic groups among rice and cow pea samples, separately. A neighbor-joining phylogeny was produced with R/adegenet and a PCA was performed on the SNPs dataset to survey the existence and distance of genetic clades in the collection. To assess the genetic distance existing between the genetic clusters, pairwise F_{st} values were estimated using R/hierfstat with the Weir and Cockerham estimator (Weir and Cockerham 1984). F_{st}^1 , or Fixation Index, measures genetic differences between populations. It quantifies the proportion of genetic variation due to population differences rather than individual differences within populations. High F_{st} values indicate significant genetic divergence between populations, while low values suggest greater genetic similarity within populations. Summary statistics including Expected vs Observed heterozygosity were analyzed in R/adegenet. Here below we report detailed results for cowpea and rice; in both cases, the genomic analysis revealed broad diversity and hence potential for genetic contribution to traits of interest, including adaptation. Indeed, diversity is the first prerequisite for crop improvement.

3.3.1. Cowpea diversity in Mozambique and southern Africa

The sequencing of cowpea landraces from southern Africa, including 22 improved varieties, produced more than 3,245,002,228 Illumina paired-end reads. Reads were aligned to the cowpea reference genome resulting in 202,946 high-quality SNPs markers distributed on the entire genome. We further filtered our data to gain on reliability and retained 49,727 SNP markers with higher frequency ($MAF > 0.05$).

¹ F_{st} refers to a statistical measure used in population genetics to quantify the degree of genetic differentiation between subpopulations within a larger population. It provides insight into how genetic variation is distributed among different groups of individuals.

To assess cowpea diversity, we computed a phylogenetic tree based on SNP data (Figure 4a). Overall, the accessions did not show obvious geographical structuring, however, there was a distinct clade consisting of landraces from Mozambique (Figure 4a). This means that cowpea accessions from Mozambique, which have been sourced from the IIAM genebank and originally come from Mozambique farmer fields, have unique genetic diversity. We further assessed the population structure by Discriminant Analysis of Principal Components (DAPC) clusters, a powerful statistical technique that analyzes genetic variation among individuals or populations. The DAPC unveiled three genetic clusters best describing the allelic frequencies within southern Africa cowpea landraces (Figure 4b). A PCA computed on SNP data shows these clusters with PC1 and PC2 explaining 7.79% and 21.45% of the variance, respectively. We noted that over 80% of landraces from Mozambique were placed in cluster 2 further corroborating the phylogenetic analysis. Interestingly, two improved cowpea varieties, IT98K-1263 and IT98K-166-4, were also in cluster 2. IT98K-1263 is an elite IITA variety resistant to bean common mosaic virus (BCMV), an important virus affecting cowpea in Sub-Saharan African (Boukar et al. 2019). IT98K-166-4 is a grain producing variety previously used in breeding programs targeting development of dual-purpose cowpea varieties (Moalafi, Asiwe, and Funnah, 2010). The genetic similarity of these IITA varieties with the Mozambique samples suggest that they may share a common origin. The majority of the other improved varieties from IITA were placed in cluster 1. Regardless, we found that there were samples from Mozambique in all the three clusters suggesting that other factors besides geographical origin account for genetic diversity in these cowpea genotypes.

We then sought to assess genetic distance amongst these genetic clusters by pairwise F_{st} analysis. The F_{st} is a value between 0 and 1, which quantifies the proportion of genetic variation due to differences between populations relative to the total genetic variation. Generally, we observed low genetic variation between the clusters ranging from 0.009549 to 0.045462 (Table 1), suggesting that there is extant exchange of genetic diversity between all clusters, possibly because of crossing, mixing, or seed circulation. The clusters account for a slight proportion of the total variance displayed by the whole population and thus suggests that selection would be more efficient between genotypes rather than between clusters. We also assessed heterozygosity as a measure of genetic variability within the population. Heterozygosity is a measure of genetic diversity and is usually assigned a value between 0 and 1 with higher heterozygosity generally indicating a greater degree of genetic variation within a population. Genetic diversity is important for the adaptation and survival of populations in changing environments as it can potentially be harnessed for breeding towards disease resistance, resilience to environmental stress, and productivity. We observed that heterozygosity varied among the 49,727 loci, suggesting moderate genetic diversity. However, the overall mean Observed heterozygosity (H_o) was low at 0.09 while the mean expected heterozygosity (H_e) was 0.28. The F_{is}^2 value was also high at 0.68 suggesting that most of the accessions were inbred. The F_{is} statistic also known as inbreeding coefficient, is a statistic used in population genetics to measure the level of inbreeding. This inbreeding phenomenon in our findings may be ascribed to the self-pollinating nature of cowpea and has been previously reported in other studies (Fatokun et al. 2018). However, higher heterozygosity (0.4) has also been reported in Chinese cowpea germplasm (Chen et al. 2017). This suggests that there may be some additional factors including cultural/agricultural practices associated with cowpea farming in southern Africa such as selective breeding whereby only a few plants or specific traits are selected for breeding (Smýkal et al. 2015). Cowpea landraces are traditional varieties maintained in farmer fields, they are selected for adaptation to local environments and local farmer preferences through

² F_{is} index provides insight into whether a subpopulation's observed genetic diversity matches the expected diversity based on the allele frequencies, helping researchers understand patterns of inbreeding and genetic health within populations.

continued cycles of local cultivation practices and overtime could be isolated from other populations leading to increased inbreeding (Nkhoma et al. 2020). Although we observe high inbreeding in our study population, there is still significant genetic variation within and between different landraces. In addition, this genetic data is crucial in understanding the genetic basis of important agronomic traits and bioclimatic adaptation potential as discussed in subsequent sections of this report.

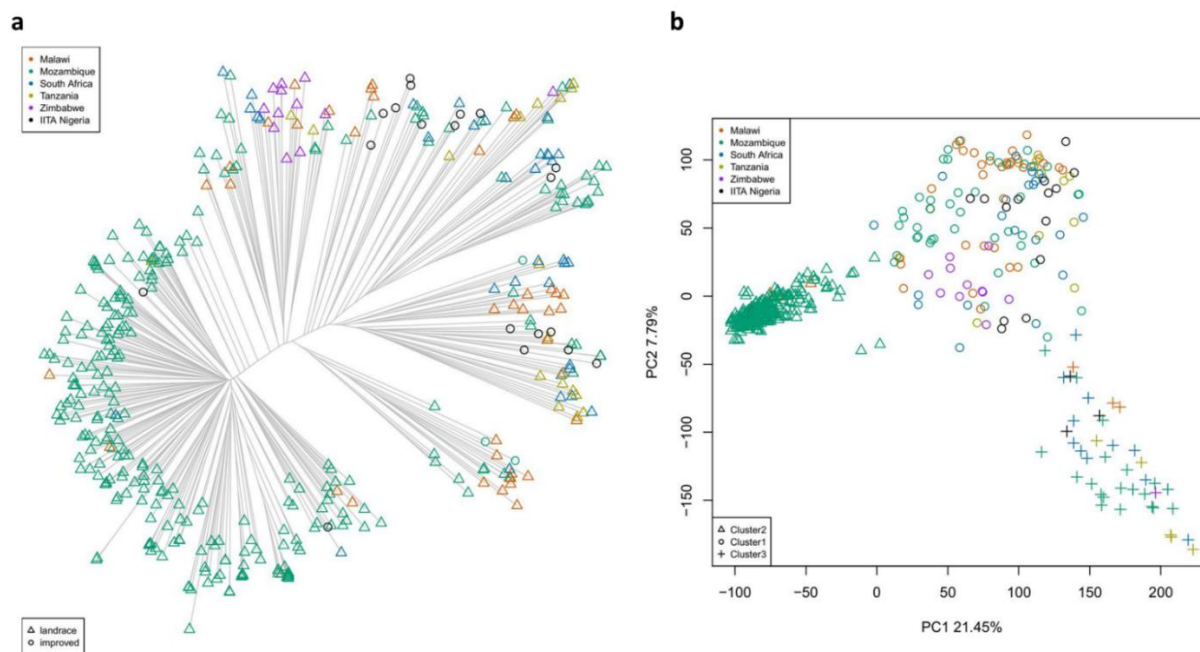


Figure 4: Molecular diversity of cowpea landrace accessions. A. Phylogenetic tree derived from SNPs data. B. Principal component analysis derived from SNPs data. Different colors indicate region of origin as shown in the legend, with symbols indicating type of material in a) and DAPC clusters in b).

Table 1: Pairwise F_{st} estimates between DAPC clusters based on cowpea SNP dataset

	Cluster1	Cluster2	Cluster3
Cluster1	0	0.009549	0.045462
Cluster2	0.009549	0	0.03013
Cluster3	0.045462	0.03013	0

3.3.2 Rice diversity in Mozambique and southern Africa

Genotyping-by-sequencing of rice accessions included 324 accessions that produced more than 331 million read pairs. Aligning the reads to the rice reference genome resulted in 100,000 high quality SNPs. These SNPs were further filtered at $MAF > 0.01$ and resulted in 22,589 high quality SNP markers to be utilized for downstream analysis. We used a different MAF threshold than that used in cowpea to account for the different diversity expressed in the rice dataset; we expected to use a uniform SNP calling pipeline in the two species in further steps of the project. A phylogenetic analysis revealed that improved varieties generally grouped into one clade. Most accessions from Zimbabwe also grouped together as was the case with Tanzanian accessions, suggesting geographical structuring to an extent. Accessions from Mozambique were distributed evenly across the clusters (Figure 5a). DAPC analysis unveiled five genetic clusters best describing the allelic frequencies across southern Africa rice accessions (Figure 5b). PC1 and PC2 explained 18.63% and 10.83% of the variance, respectively and reported some degree of geographical structure within the DAPC clusters. Cluster 1 was made up samples from Mozambique and includes both landraces and improved varieties. The majority of accessions in Cluster 2 were landraces from Tanzania. Cluster 5 was predominantly composed of accessions from Zimbabwe. Cluster 3 and 4 had an admixture of landraces with Mozambique accessions being predominant in both scenarios. Pairwise F_{st} distances were relatively high between these clusters, suggesting significant levels of genetic differentiation between them (Table 2). The highest genetic distance was observed between cluster 2 and 5 at 0.7. The lowest was between cluster 2 and 4 at 0.2. This implies that these subpopulations are highly diversified, and may have diverged due to farmer selection, environmental adaptation, or lack of seed circulation (Nhamo et al. 2014; Wang et al. 2016). Tanzania landraces have already been shown to be distinct implying their uniqueness (Suvi et al. 2020). However, we do not rule out exchange of genetic materials among the neighboring farmers and traders in the region as occasioned by some admixtures within clusters. Expected heterozygosity (H_e) across the population was 0.1 while observed heterozygosity (H_o) was lower at 0.06. Rice is self-pollinated and therefore not unexpected as most traditional rice cultivars are usually inbred lines (Huang et al. 2015). These findings, that will be further explored in combination with data analysis in WP5, already suggest the need to understand rice germplasm diversity prior to selection of suitable parents for use in local breeding programmes.

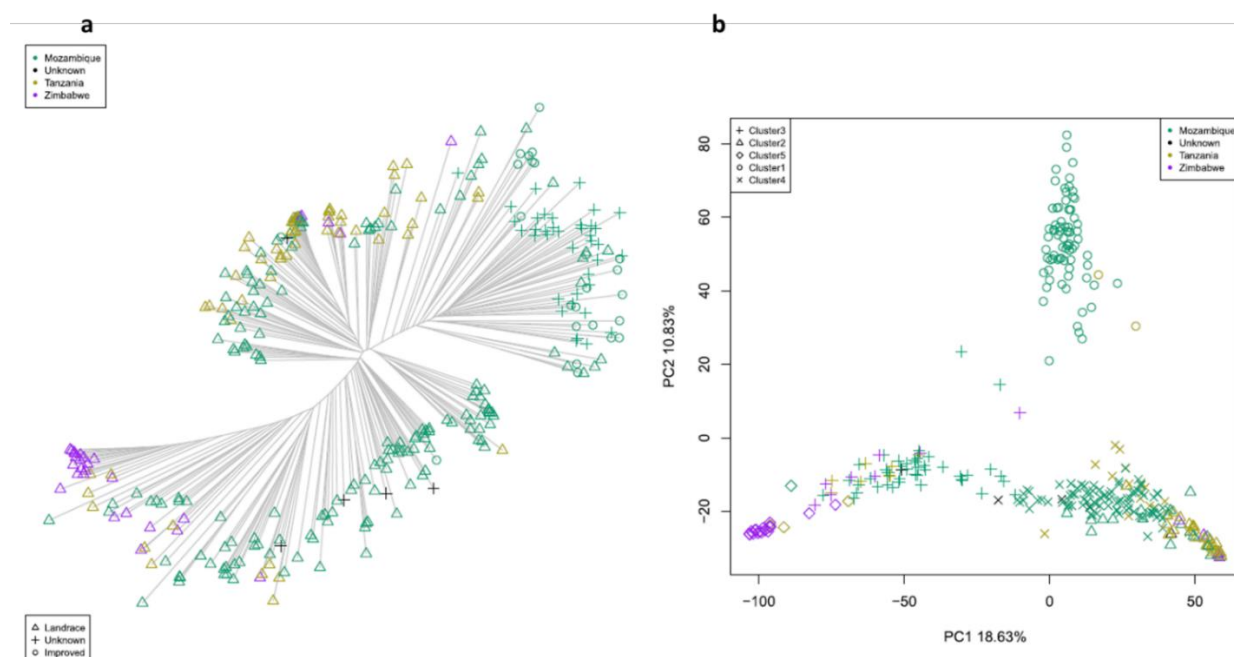


Figure 5: Molecular diversity of rice landrace accessions. A. Phylogenetic tree derived from SNPs data. B. Principal component analysis derived from SNPs data. Different colors indicate region of origin as shown in the legend. With symbols indicating type of material in a) and DAPC clusters in b)

Table 2: Pairwise Fst estimates between DAPC clusters based on Rice SNP dataset

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
Cluster1	0	0.38637	0.302914	0.270908	0.530728
Cluster2	0.38637	0	0.453469	0.225803	0.733454
Cluster3	0.302914	0.453469	0	0.287794	0.324987
Cluster4	0.270908	0.225803	0.287794	0	0.564139
Cluster5	0.530728	0.733454	0.324987	0.564139	0

4 Spatial and Bioclimatic Characterization of southern Africa cowpea landraces

Once genomic data is available, it becomes possible to link it with climatic diversity at sampling points and to look at the relationship existing between genetic diversity and historical and projected climates. For the moment, this analysis was conducted on cowpea, while rice data is still being analyzed in detail. For this reason, the next sections focus on the analysis conducted on the cowpea collection, with the assumption that similar results will be achieved on rice too. GPS sampling locations of cowpea landraces were obtained from available genebank passport data. South Africa has been left out of these analyses as passport data was unavailable. Sampling points were projected onto the southern Africa country maps (Tanzania, Mozambique, Malawi and Zimbabwe) using R/raster (Hijmans 2018) and altitudes of sampling points were derived using the CGIAR SRTM database at 90 m resolution (Reuter, Nelson, and Jarvis 2007). Agroecological Zones (AEZs) were derived from Food and Agricultural Organization (FAO) GAEZ v4 database. Historical climate data was derived from WorldClim version 2.1. The data is available at 2.5 minutes ($\sim 21 \text{ km}^2$ at the equator) horizontal resolution (Fick

and Hijmans 2017). Similarly, CMIP6 downscaled future climate projections were obtained from WorldClim. The downscaling and calibration (bias correction) was done with WorldClim v2.1 as baseline climate. We used the available 13 models (Table 3) to prepare multi-model ensembles (MME) for future projected climates with the same spatial resolution as historical data for Shared Socio-economic Pathway (described Annex 2).

Table 3: Summary of selected CMIP6 GCMs that form the ensemble of climate projections used in this study

Model Name	Modelling Centre	Released
ACCESS-CM2	CSIRO-ARCCSS (Commonwealth Scientific and Industrial Research Organisation, Australian Research Council Centre of Excellence for Climate System Science)	2019
BCC-CSM2-MR	Beijing Climate Center (BCC)	2017
CMCC-ESM2	CMCC (Centro Euro-Mediterraneo per I Cambiamenti Climatici)	2017
EC-Earth3-Veg	EC-Earth-Consortium	2019
FIO-ESM-2-0	FIO-QLNM (First Institute of Oceanography (FIO) and Qingdao National Laboratory for Marine Science and Technology (QNLN))	2018
GISS-E2-1-G	NASA-GISS (National Oceanic and Atmospheric Administration, Goddard Institute for Space Studies)	2019
HadGEM3-GC31-LL	MOHC NERC (Met Office Hadley Centre, Natural Environmental Research Council)	2016
INM-CM5-0	INM (Institute of Numerical Mathematics)	2016
IPSL-CM6A-LR	IPSL (Institut Pierre-Simon Laplace)	2017
MIROC6	MIROC (Atmosphere and Ocean Research Institute (AORI), Centre for Climate System Research - National Institute for Environmental Studies (CCSR-NIES))	2017
MPI-ESM1-2-HR	MPI-M DWD DKRZ (Max Planck Institute for Meteorology (MPI-M), German Meteorological Service (DWD), German Climate Computing Center (DKRZ))	2017
MRI-ESM2-0	MRI (Meteorological Research Institute, Japan)	2017
UKESM1-0-LL	MOHC, NERC, NIMS-KMA, NIWA (Met Office Hadley Centre, Natural Environmental Research Council, National Institute of Meteorological Science / Korean Meteorological Administration (NIMS-KMA), National Institute of Weather and Atmospheric Research (NIWA))	2018

Using historical and future climate data, 19 biologically meaningful indicators, called bioclimatic variables, were derived using R/dismo (Hijmans et al. 2017). These 19 indicators provide valuable information for assessing the suitability of specific regions for agricultural activities and crop production. Bio1-11 bioclimatic variables refer to temperature while Bio 12-19 refer to rainfall. They include:

- Bio1, Annual Mean Temperature;
- Bio2, Mean Diurnal Range (Mean of monthly (max temp - min temp));
- Bio3, Isothermality (Bio2/Bio7) (×100);
- Bio4, Temperature Seasonality (standard deviation ×100);
- Bio5, Max Temperature of Warmest Month;
- Bio6, Min Temperature of Coldest Month;
- Bio7, Temperature Annual Range (Bio5-Bio6);

- Bio8, Mean Temperature of Wettest Quarter;
- Bio9, Mean Temperature of Driest Quarter;
- Bio10, Mean Temperature of Warmest Quarter;
- Bio11, Mean Temperature of Coldest Quarter;
- Bio12, Annual Precipitation;
- Bio13, Precipitation of Wettest Month;
- Bio14, Precipitation of Driest Month;
- Bio15, Precipitation Seasonality (Coefficient of Variation);
- Bio16, Precipitation of Wettest Quarter;
- Bio17, Precipitation of Driest Quarter;
- Bio18, Precipitation of Warmest Quarter;
- Bio19, Precipitation of Coldest Quarter.

We assessed collinearity among bioclimatic variables with the `ensemble.VIF()` function in R/Biodiversity (Kindt and Coe 2005), with retention of only variables with a variance inflation factor below 10 for downstream analysis.

4.1 Characterization of agroecological diversity of cowpea cultivation areas in Mozambique and southern Africa

Agroecological zones refer to distinct geographical regions with specific climatic and ecological characteristics that influence agricultural management and crop production practices (Redclift 1990). In this study, about 95% of the cowpea landraces samples were coming from either one of two agroecologies: low land semiarid, and low land subhumid (Figure 6). Lowland semi-arid zones in southern Africa experience a semi-arid climate, characterized by limited rainfall and high evaporation rates (Murungweni et al. 2016). The region typically receives less than 600 millimeters of rainfall annually, which is insufficient to support extensive vegetation growth. Lowland semi-arid zones face several challenges, including water scarcity, soil degradation, and vulnerability to climate change. This reinforces the importance of cowpea cultivation, thanks to its resilience and capacity to tolerate harsh environmental conditions (Fussell, Bidinger, and Bieler 1991). We expect that cowpea accessions with an origin in this zone possess crucial adaptation traits such as drought and heat tolerance, shorter growth cycles and photoprotection (Kumari et al. 2021). These traits are particularly useful in plant breeding programs to enhance production especially now that global temperatures have been on the rise and anticipated to keep rising in the future and will further affect crop production (Long and Ort 2010). The lowland subhumid zone, on the other hand, experiences a moderate amount of rainfall throughout the year that ranges between 800 and 1,200 millimeters. Nevertheless, this zone is still vulnerable to periodic droughts particularly now with the changing climate (Byakatonda et al. 2021). We expect cowpea landraces originally sourced in this area to bear traits of adaptation to these specific conditions. Understanding this diversity would allow to gain insights on the potential of specific cowpea accessions to contribute to measures that may promote food security and sustainable agriculture in regions characterized by specific climatic conditions.

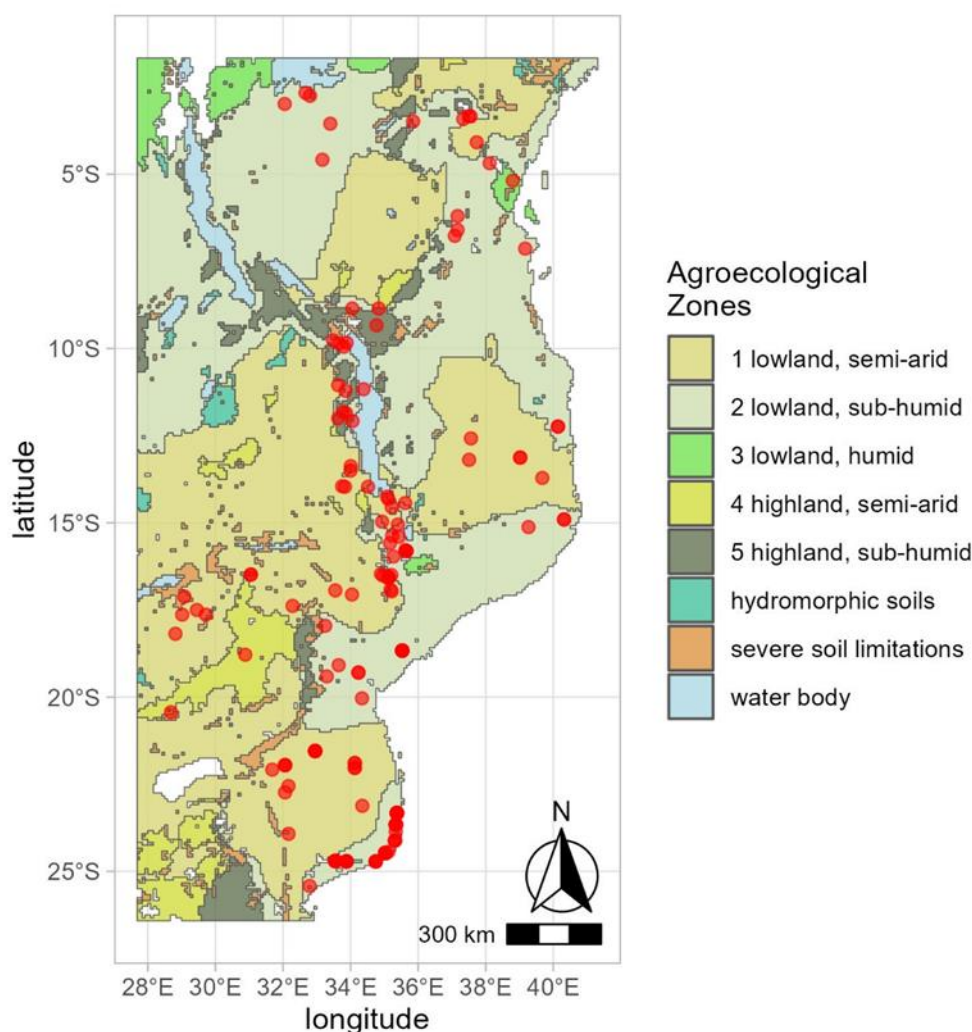


Figure 6: Agroecological zones of southern Africa. Each red point represents cowpea accession sampling point. Longitude and latitude values in WGS84 EPSG:4326 degrees are reported on the x-axis and y-axis, respectively. Different AEZs are represented by different colours according to legend.

Taking advantage of the availability of sampling points, we further studied the climatic diversity represented in the cowpea collection. Overall, we found large climatic diversity at cowpea sampling points (Figure 7a), suggesting an opportunity to harness for traits conferring climate adaptation that may have been selected for by local farmers cultivating cowpea landraces in local fields. Looking into historical bioclimatic data, we observed annual precipitation (bio12) of between 233 to 1,732 mm, typical of semi-arid and subhumid AEZs. Annual mean temperature at cowpea sampling points (bio1) ranges from 16.4°C to 26.3°C. The distribution of bioclimatic variables shows that the core collection of cowpea is representative of a large climatic diversity. This is the prerequisite of identifying climate-ready accessions, as we expect that some cowpea landraces will be adapted to specific conditions. Their adaptation traits, that eventually are encoded in their DNA, may provide a positive contribution to cowpea breeding in the long term, and to the selection of climate-ready accessions to be distributed to farmers in the short term.

R/corrplot (Taiyun 2017) was used to study the correlation among bioclimatic variables at cowpea sampling points, including altitude (Figure 7b). Altitude in cowpea sampling points showed a strong

negative correlation with temperature related variables bio1, bio8 and bio9 meaning that, expectedly, as altitude increases the average temperature tends to decrease. Annual precipitation (bio12) showed a strong positive correlation with bio13 (precipitation of wettest month) and bio16 (precipitation of wettest quarter). This is expected as they are all derivatives of precipitation data. Precipitation seasonality (bio15) and isothermality (bio3) show a negative correlation meaning that with high variation in timing and distribution of precipitation throughout the year, there is a lower degree of temperature variation throughout the year, and regions with low precipitation seasonality tend to have high isothermality. This negative correlation can be explained by the influence of atmospheric circulation patterns (Horton et al. 2015).

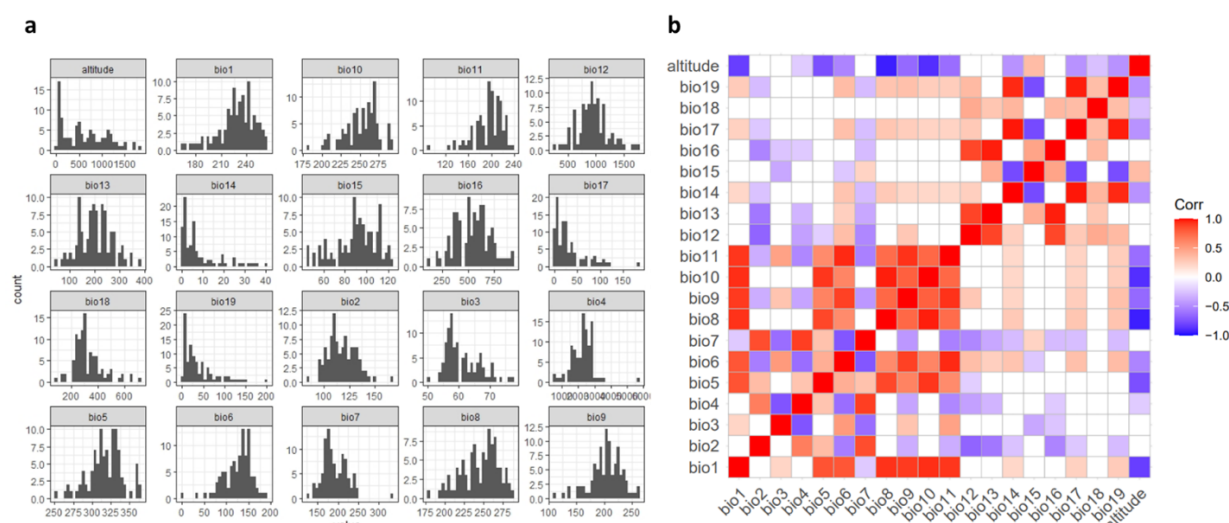


Figure 7: Bioclimatic variables distribution and correlation in cowpea growing areas of southern Africa. a) Histograms showing frequency of bioclimatic variables. b) Correlation between bioclimatic variables. The direction and intensity of correlations is shown by the tile color according to legend. Blank tiles mean no significant correlation.

4.2 Genome-wide associations with Bioclimatic traits

In crop breeding, GWAS (Genome-Wide Association Study) is a valuable tool that may be used to identify parts of the genome associated with desirable traits. By analyzing the entire genome of a diverse population, GWAS can pinpoint regions of DNA that influence specific traits like yield, disease resistance, and even adaptation to specific climatic conditions. This information helps breeders select individuals with favorable genetic variations for mating, increasing the chances of producing offspring with improved traits. Here, we conducted a so-called environmental GWAS combining genetic data and bioclimatic data at sampling locations. By this, the GWAS statistical approach was used to identify genetic variations associated with climate adaptation in the cowpea core collection. The aim was to find genetic markers, in this case SNPs, that are correlated with certain bioclimatic variables. These markers are usually found throughout the entire genome and can assist in locating genes or regions of the genome which in turn are useful to breeders for developing climate smart crop varieties. The SNPs identified are usually referred to as quantitative trait nucleotides (QTNs) as they are potential key genetic variants that may contribute to the observed differences in quantitative traits, including climate adaptation, between cowpea accessions. GWAS is not an endpoint but is a first step towards unravelling the genetic mechanism behind complex traits such as climate adaptation. GWAS was implemented using a fixed and random Circulating Probability Unification (FarmCPU) model (Liu et al. 2016) implemented in the package in R/GAPIT (Lipka et al. 2012) using the first PC calculated on

genotypic data as covariate. QTNs were defined when SNPs surpassed the significance threshold of a false discovery rate of 0.05 based on Storey's method (Storey and Tibshirani 2003). With this analysis we identified 27 unique QTNs for six bioclimatic variables namely, bio1, bio3, bio4, bio6, bio11 and bio16 (Annex 3). Four QTNs were common among some variables including QTN at 4.02Mb on chromosome 5 for bio1 and bio11 and 22.5Mb on chromosome 7 for bio6 and bio11. On chromosome 6, QTN at 19.5Mb was common for bio6 and bio11 and at 20.6Mb for bio3 and bio4. Isothermality (bio3), which was among the most important climatic drivers of the GF model was associated with 9 QTNs (Figure 8). Precipitation of Wettest Quarter (bio16) was the only precipitation variable with 4 QTNs identified on chromosomes 10 and 11 (Figure 9). These QTNs represent genomic regions that are associated to climatic diversity and may be indicative of the molecular basis of adaptation mechanisms in Mozambiquan cowpea. Further analysis will be done to investigate the climatic adaptive loci identified and if they have any role in phenology. It is the first time that adaptation QTN are described in cowpea, and the work of CS3 will be relevant not only for the content of FOCUS-Africa but aims at establishing a legacy in cowpea breeding after the project ends.

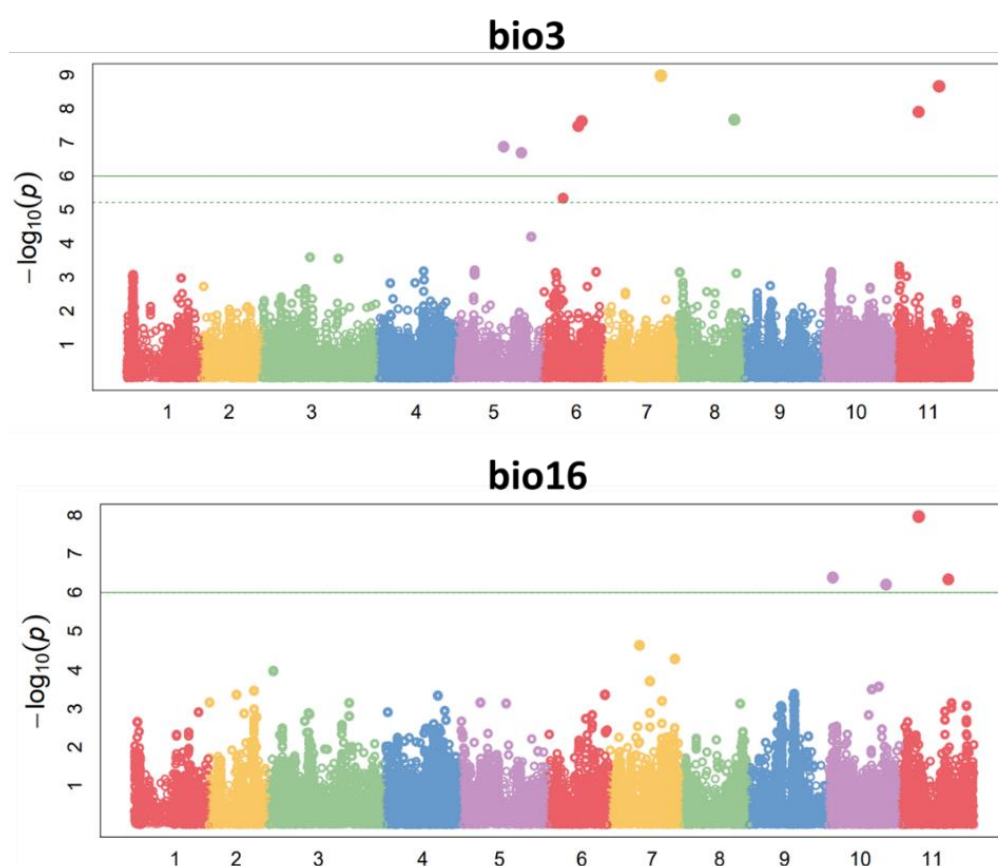


Figure 8: GWAS output for bioclimatic variable bio3 (Isothermality) and bio16 (Precipitation of Wettest Quarter). The Manhattan plots report individual SNPs across all chromosomes (x-axis) and $-\log_{10} P$ value of each SNP association (y-axis). The horizontal lines represent a stringent Bonferroni threshold for a nominal p-value of 0.05. Points surpassing the significant threshold represent positions on the genome in which diversity in the collection is strongly associated to climate at sampling points, suggesting the existence of adaptation mechanisms.

4.3 The potential impact of climate change on the distribution pattern of cowpea in southern Africa

After looking at the historical climatic diversity in cowpea sampling points, we assessed the adaptability of cowpea landraces to future climate projected scenarios in southern Africa. Assessing the vulnerability of cowpea cultivation in a future climate allows for adaptation and resilience measures that will ensure food security and sustainable agriculture. To this end, we developed a GF model using historical climate and MEMs as predictors with 4210 SNPs ($MAF > 0.05$) as response variables. The allelic turnover in the cowpea collection was best predicted by MEM5, describing spatial distribution (Figure 9a). Bioclimatic variables including precipitation seasonality, precipitation of warmest quarter, isothermality, max temperature of warmest month, annual precipitation, precipitation of driest month and mean diurnal range were among the most important variables that influence the current and future distribution of cowpea in southern Africa (Figure 9a). We then used the bioclimatic predictors to estimate climate-driven genomic variation across the landscape (Figure 9b, c). Out of all the SNPs tested as response variables, about 36.1% ($n = 1519$, $R^2 > 0$) were predicted by the model. Based on the current landscape-genome relations modelled through GF, we estimated the expected genomic composition at SSP 585 (2041-2060) scenario. We then derived the future cowpea genomic offset as the difference between the current genetic variation and the genetic variation that would be needed under a changed climate for the tested scenario. Overall, we observed moderate offset in most areas of southern Africa (Figure 9d). Zimbabwe and Tanzania had a few regions with high offset at >0.004 . We observed an average offset throughout Mozambique at <0.004 , showing moderate vulnerability of cowpea to climate change. In areas where the offset is greater, our model predicts substantial maladaptation of current cowpea genotypes to future climates, suggesting the need for complementation with other diversity either via breeding or via distribution of different landraces. Further germplasm collection efforts around southern Africa could be useful to capture more diversity that could further compensate for the offset predicted by our analyses. It is also important to note that although we observe an average offset throughout southern Africa, most farmers currently have a high incentive to abandon these landraces for high yielding varieties and thus, they may fall out of cultivation in the years to come, further contributing to genomic vulnerability of this species towards climate change. Our findings, which will undergo further scrutiny as new data will become available from field experiments, reinforce the need to harness existing plant resources to develop crop varieties adaptable to the current and future climate. Indeed, the cowpea core collection presented here could be useful for this endeavour and could support smallholder farmers against future climate eventualities.

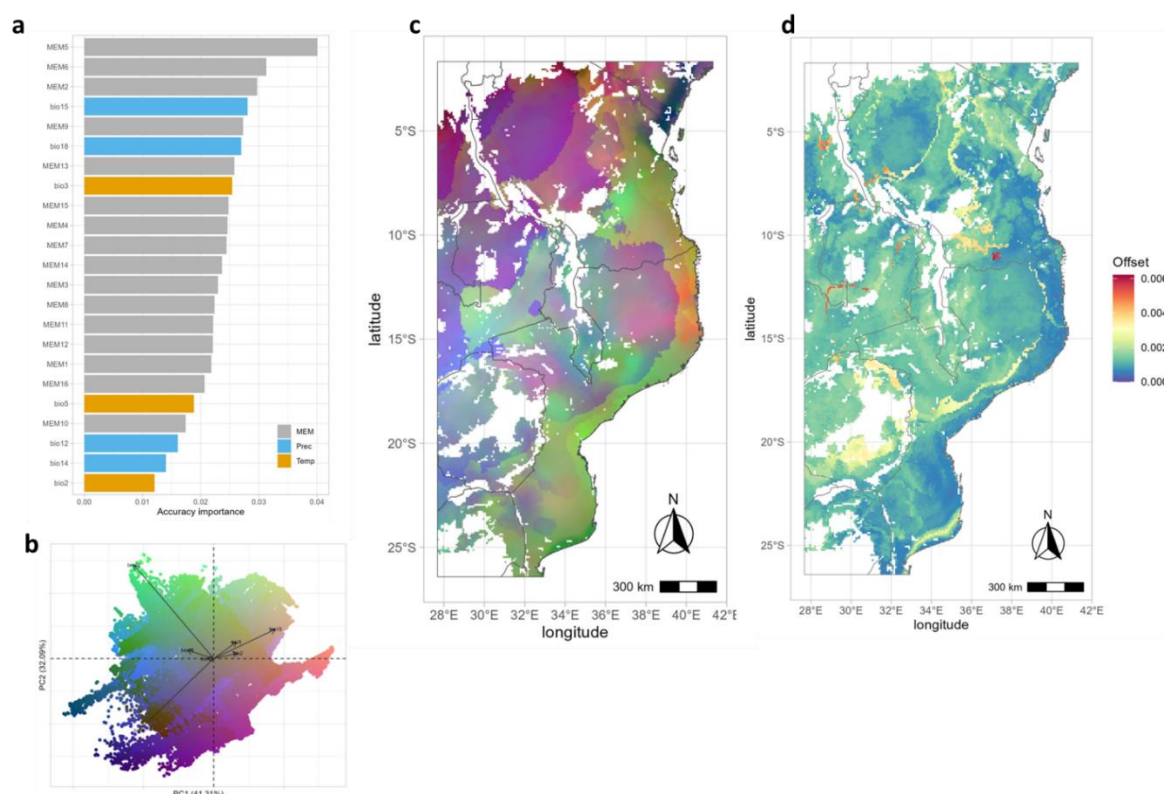


Figure 9: Bioclimatic and spatial diversity explain genomic variation in the distribution of southern Africa cowpea landraces. a) Ranked accuracy importance of the bioclimatic and spatial variables based on Gradient Forest (GF) model. b) Biplot of the biological space, represented by Principal Components of the transformed grid with an RGB color palette relative to its first three dimensions. It displays different adaptive environments across the cropping area ("c"), where similar colors represent similar alleles at climate-responsive loci ($R^2 > 0$); in the biplot, axes report the portion of bioclimatic variance (%) explained by the PCs of the transformed grid. c) GF-transformed bioclimatic variables across southern Africa. Colors based on bioclimatic-genetic space in 'b'. d) Genomic offset based on SSP 585 ensemble climate projections at the horizon of 2041-2060. The color scale indicates the magnitude of the mismatch between current and projected climate-driven turnover in allele frequencies.

5 Characterization of the agronomic diversity in the rice and cowpea core collections

The phenotyping characterization of cowpea and rice accession follows the genomic characterization and the climatic characterization described in the sections above. This activity has been conducted during the main cropping season of 2022-2023, and the results reported below are part of an ongoing workflow that requires to organize the field observations and conduct appropriate data analysis. However, the data collected is fully integral to the achievement of the objectives of CS3 and as such is described below.

A subset of cowpea and rice collections were grown in common garden experiments to evaluate phenotypic performance in a participatory research framework. The subset was selected based on the following criteria: availability of sufficient seeds, representativity of the collection, passport data information availability, and budget resources available for labour management during the field trials. The field experiments were conducted in two locations in the provinces of Nampula and Gaza. The field experiment in Gaza was conducted at the IIAM Chokwe station and involved both rice and

cowpea. Chokwe is located at (S 24° 31' 42.0"; E 033° 00' 40.7"; Altitude.: 32 m). The climate is semi-arid, the average temperature is about 24.5°C, with the highest and lowest of 33°C and 17°C respectively. During the day, the average annual temperature reaches 27.7°C, while at night the annual average is 21.8°C. Cowpea accessions were also characterized near the city of Nampula, capital of the Nampula province and in proximity with the smallholder farmer villages that have been engaged in the co-design and co-development of the climate services. The Nampula field station is located at (S 15°09' 10" E 39 18'21"; Altitude: 364m). The area has an average daily maximum temperature of 31°C. The climate is classified as tropical humid and is one of the warmest regions in the country. In each station, the crop collection(s) were grown and characterized for their agronomic potential and for farmers' appreciation following a participatory variety selection (PVS) approach. Cowpea at Chokwe was planted in February 2023 and PVS conducted in May 2023. Rice genotypes at Chokwe were planted in December 2022 and PVS conducted in May 2023. At Nampula cowpea was planted in January 2023 and PVS followed in mid-April 2023. The information derived from the characterization is key to be integrated with the genomic and climatic characterization of the core collections to prioritize genetic materials that not only have the potential for genomic adaptation to climate constraints but also that are carrying desirable agronomic traits that are approved and desired by farmers. It is by combining all the characterization data that CS3 will pick the most promising lines and couple them with the seasonal forecasting information developed in parallel to the crop characterization. A more detailed description of the field activities is given below.

5.1 Cowpea phenotypic evaluation

Cowpea field experiments were conducted in two locations: Nampula and Chokwe. 351 genotypes were selected based on criteria listed above. At Chokwe, the 351 cowpea genotypes were evaluated in a randomized incomplete block design (Latinized Alpha lattice design) with two replications under irrigated conditions. The plot size for each genotype was 3m², and the planting geometry was 75 cm × 100cm. Improved cowpea varieties were used as checks and received the same management as landraces. The same protocol was duplicated in Nampula, following the same field design, however in Nampula the field trial was conducted under rain fed conditions. Selected phenotypic traits were collected for cowpea genotypes following the standard guidelines and descriptors developed by IITA (1985). Phenotypic traits were recorded on five randomly selected plants per plot. Border plants were excluded to avoid border effects. The following traits were collected before harvesting, at the stage when 50% of plants have begun to flower: shape of leaf, growth habit, days to flowering time, days to maturity and pods per plant per plant. We also collected the following traits after harvesting: yield per plot, pod length, number of seeds per pod and 100-seed weight.

5.2 Rice phenotypic evaluation

The rice field experiment was conducted only at Chokwe station. A total of 220 rice genotypes were selected for the field experiment. The accessions were evaluated in a Randomized incomplete block design (Latinized Alpha lattice design) with two replications in lowland irrigated conditions, the rice was transplanted in December 2022. Each accession was planted in a 5m² plot with a planting geometry of 25 cm × 30 cm. Each replication contained 10 Blocks, in each block 22 plots were used to minimize the variation and reduce the experimental area in the field. All improved rice varieties were used as control or checks, and all received the same conditions as local varieties. Phenotypic traits were recorded on five randomly selected plants per plot. Border plants were excluded to avoid border effects. The following traits were collected: grain yield, plant height (cm), days to 50% flowering, days to maturity, tillers per meter of row crop, panicles per meter of row crop, panicle length(cm), seed humidity and 100-grain seed weight.

5.3 Participatory Variety Evaluation of cowpea and rice collections

Participatory variety selection was conducted on 351 cowpea lines in May of 2023 at Chokwe and Nampula field stations. PVS on rice was conducted on 220 genotypes at Chokwe in May 2023. Due to differences in maturity amongst the tested varieties, some varieties were at the pod-filling stage whereas others were approaching physiological maturity at the time of PVS. At Nampula field station 10 farmers from the Nampula district (5 men, 5 women) participated in the activity while at Gaza, 20 farmers (10 male and 10 female) from Guija and Chokwe districts participated in the activity. The selection of farmers was based on their willingness to participate as well as their experience in cowpea and rice production. We included people of different ages and an equal number of men and women to ensure gender balance and representation. Five Staff members from the agricultural extension services, who have experience in guiding previous participatory research, guided the farmers in the activities. Participating farmers were informed about their roles as well as the objectives and expectations of PVS activities. Evaluations were conducted following a guide developed by the CS3 team. In each case, farmers were divided into groups of 5, separating men and women. Each group of farmers was guided by an extension officer. The groups moved into the field from random entry points and asked to evaluate each accession for their overall appreciation (OA) based on a Lickert scale from 1 (very low) to 5 (very high) (Annex 4). The farmers would bear small stones equivalent to the score to be given, and were asked to pick a score and then show it at once in an effort to reduce bias from leadership dynamics within farmer groups (Figure 10e). The scoring of each farmer for each of the accessions was independently recorded.



Figure 10: Participatory variety evaluation. Focus group discussions at Chokwe station as shown in a,b. Panels c, d, e, f show farmers evaluating and scoring cowpea varieties at Chokwe and Nampula stations. Panels g,h,i show rice PVS trials at Chokwe station.

As of July 2023, the post-harvest data collection was ongoing. Some genotypes were lost in the field during the trials therefore the phenotypic data and PVS data were collected on 349 genotypes for cowpea and 218 genotypes for rice. Once data analysis is complete, promising genotypes will be selected based on farmers preference, climatic and phenotypic trait data. PVS and phenotypic data will also be combined with genotypic data to conduct a GWAS and bioclimatic evaluation that will inform on the genetic basis of preferences and traits observed.

The farmers' overall appreciation is usually guided by traditional knowledge and thus it is important to include them in pre-breeding trials to enhance adoption of varieties developed by breeders. It is worth reporting that focus group discussions were conducted after PVS trials to assess farmers' perceptions and rationale behind their preferences in cowpea varieties. Data collected in WP6 established that cowpea is almost exclusively grown by women in the southern and Northern regions of Mozambique region. Farmers used various criteria to select cowpea varieties such as high grain and leaf yield, large seed size, earliness, smoothness of the taste, and potential marketability of the variety. The PVS trials were conducted in different regions with different climatic conditions and thus the stresses affecting crops are different. The implication of this for breeders is that different types of varieties need to be bred for different districts focusing on agroecological zones to meet the challenge faced by climate change. During the breeding process, an integrated selection index needs to be

adopted whereby phenological, climate adaptation traits and farmer preferred varieties are incorporated. Integrated methods of variety selection involving farmers are crucial. Ideally, the genotypes prioritized under these field activities will undergo further intensive evaluations in the pipeline of developing breeding materials to meet farmers' needs.

6 Conclusion

Climate change and its impacts are prominent in Mozambique, and local small-scale farmers are affected disproportionately by its adverse effects. CS3 operated an innovative transdisciplinary strategy that utilizes existing wealth of plant genetic resources to fuel research aimed at mitigating food insecurity amidst the climate crisis to increase resilience to farmers in Nampula region. We may summarize our key findings as follows:

- Cowpea and rice landraces traditionally cultivated by smallholder farmers in Mozambique and in the SADC region hold enormous untapped genetic diversity;
- The geographic distribution of cultivation of these varieties is suggestive of the presence of adaptation potential towards current and projected climate stress, including heat and drought;
- The local agrobiodiversity of cowpea and, expectedly, of rice contains genetic factors associated with climatic diversity, and that can be harnessed by pre-breeding and breeding programs to speed up the development of new, climate-ready varieties;
- Future climate scenarios show areas of vulnerability for cowpea cultivation in Mozambique that call for tailored breeding efforts, possibly leveraging landrace diversity.

With FOCUS-Africa, we created a vast catalogue of genetic, climatic, and phenotypic diversity of cowpea and rice landraces in Mozambique, including participatory evaluation of varieties. We hope by this to provide a lasting contribution to the breeding community in the region. Our initiative is aimed at characterizing existing plant genetic resources to support development and distribution of climate-resilient varieties to rural farmers in Mozambique. Although this case study is based in Mozambique, we sourced additional germplasm from neighbouring southern African countries as these countries share similar climatic and environmental conditions and may therefore provide genetic materials with adaptation traits of relevance and, could also in turn, benefit from FOCUS-Africa results in CS3. PVS and agronomic data analysis, combined with climate and genomic data, will inform further about the potential contribution of genotypes sourced from the southern African region to address the needs of farmers from Mozambique and beyond. The findings of this report highlight the importance of combining genetic, climatic, farmer participatory approaches and agronomy. We have identified genomic loci with potential for local adaptation and also shown the adaptation of existing germplasm in a projected climate scenario. Our data shows that the cowpea (and potentially rice) core collections characterised in this study have potential to contribute to the enhanced resilience and adaptation in light of current variability and future climate change and should be explored further. All rice and cowpea crop varieties used in this study are now available at the IIAM genebank in Maputo, Mozambique. Once the data is fully analyzed, the data will be made publicly available through additional peer reviewed publications.

As the project comes to its final year, further work involves prioritizing germplasm to be distributed to farmers and for advancement into breeding programs. At the time of writing, we aimed to select the top 10-20 promising accessions for each crop. Our criteria for selection criteria will be based on an index that incorporates genetic, climatic, phenotypic diversity and overall appreciation by the farmer. The selected lines will then be distributed to farmers in Nampula to further validate them for



climate adaptability and preference within the region. A full description of the transdisciplinary results achieved by the Case Study 3 approaches, including the further work under WP2, will be included in D5.5 ("A data catalogue providing the complete genotypic, climatic, and phenotypic characterization of the rice and cowpea accessions used in CS3").

REFERENCES

- Ahmar, Sunny, Sumbul Saeed, Muhammad Hafeez Ullah Khan, Shahid Ullah Khan, Freddy Mora-Poblete, Muhammad Kamran, Aroosha Faheem, et al. 2020. "A Revolution toward Gene-Editing Technology and Its Application to Crop Improvement." *International Journal of Molecular Sciences* 21 (16): 5665. <https://doi.org/10.3390/ijms21165665>.
- Altieri, Miguel A., and M. Kat Anderson. 1986. "An Ecological Basis for the Development of Alternative Agricultural Systems for Small Farmers in the Third World." *American Journal of Alternative Agriculture* 1 (1): 30–38. <https://doi.org/10.1017/S0889189300000771>.
- Aquino, Sinara Oliveira de, Catherine Kiwuka, Rémi Tournebize, Clément Gain, Pierre Marraccini, Cédric Mariac, Kévin Bethune, et al. 2022. "Adaptive Potential of *Coffea Canephora* from Uganda in Response to Climate Change." *Molecular Ecology* 31 (6): 1800–1819. <https://doi.org/10.1111/mec.16360>.
- Arndt, Channing, Kenneth Strzepeck, Finn Tarp, James Thurlow, Charles Fant, and Len Wright. 2011. "Adapting to Climate Change: An Integrated Biophysical and Economic Assessment for Mozambique." *Sustainability Science* 6 (1): 7–20. <https://doi.org/10.1007/s11625-010-0118-9>.
- Asfaw, Solomon, Nancy McCarthy, Leslie Lipper, Aslihan Arslan, and Andrea Cattaneo. 2016. "What Determines Farmers' Adaptive Capacity? Empirical Evidence from Malawi." *Food Security: The Science, Sociology and Economics of Food Production and Access to Food* 8 (3): 643–64.
- Baird, Nathan A., Paul D. Etter, Tressa S. Atwood, Mark C. Currey, Anthony L. Shiver, Zachary A. Lewis, Eric U. Selker, William A. Cresko, and Eric A. Johnson. 2008. "Rapid SNP Discovery and Genetic Mapping Using Sequenced RAD Markers." *PLOS ONE* 3 (10): e3376. <https://doi.org/10.1371/journal.pone.0003376>.
- Bay, Rachael A., Ryan J. Harrigan, Vinh Le Underwood, H. Lisle Gibbs, Thomas B. Smith, and Kristen Ruegg. 2018. "Genomic Signals of Selection Predict Climate-Driven Population Declines in a Migratory Bird." *Science (New York, N.Y.)* 359 (6371): 83–86. <https://doi.org/10.1126/science.aan4380>.
- Blackstock, K. L., G. J. Kelly, and B. L. Horsey. 2007. "Developing and Applying a Framework to Evaluate Participatory Research for Sustainability." *Ecological Economics* 60 (4): 726–42. <https://doi.org/10.1016/j.ecolecon.2006.05.014>.
- Boukar, Ousmane, Nouhoun Belko, Siva Chamarthi, Abou Togola, Joseph Batieno, Emmanuel Owusu, Mohammed Haruna, et al. 2019. "Cowpea (*Vigna Unguiculata*): Genetics, Genomics and Breeding." *Plant Breeding* 138 (4): 415–24. <https://doi.org/10.1111/pbr.12589>.
- Broccanello, Chiara, Diana Bellin, Giovanni DalCorso, Antonella Furini, and Francesca Taranto. 2023. "Genetic Approaches to Exploit Landraces for Improvement of *Triticum Turgidum* Ssp. *Durum* in the Age of Climate Change." *Frontiers in Plant Science* 14. <https://www.frontiersin.org/articles/10.3389/fpls.2023.1101271>.
- Burridge, James D., Jill L. Findeis, Celestina N. Jochua, Magalhaes A. Miguel, Fridah M. Mubichi-Kut, Maria L. Quinhentos, Soares A. Xerinda, and Jonathan P. Lynch. 2019. "A Case Study on the Efficacy of Root Phenotypic Selection for Edaphic Stress Tolerance in Low-Input Agriculture: Common Bean Breeding in Mozambique." *Field Crops Research* 244 (December): 107612. <https://doi.org/10.1016/j.fcr.2019.107612>.
- Byakatonda, Jimmy, Geoffrey Openy, Jotham Ivan Sempewo, and Dominic Banaga Mucunguzi. 2021. "Over a Century Evidence of Historical and Recent Dryness/Wetness in Sub-Humid Areas: A Uganda, East African Case." *Meteorological Applications* 28 (5): e2028. <https://doi.org/10.1002/met.2028>.
- Caproni, Leonardo, Basazen Fantahun Lakew, Seyoum Asefie Kassaw, Mara Miculan, Jemal Seid Ahmed, Simona Grazioli, Yosef Gebrehawaryat Kidane, Carlo Fadda, Mario Enrico Pè, and Matteo Dell'Acqua. 2023. "The Genomic and Bioclimatic Characterization of Ethiopian Barley

- (*Hordeum Vulgare* L.) Unveils Challenges and Opportunities to Adapt to a Changing Climate.” *Global Change Biology* 29 (8): 2335–50. <https://doi.org/10.1111/gcb.16560>.
- Catchen, Julian, Paul A. Hohenlohe, Susan Bassham, Angel Amores, and William A. Cresko. 2013. “Stacks: An Analysis Tool Set for Population Genomics.” *Molecular Ecology* 22 (11): 3124–40. <https://doi.org/10.1111/mec.12354>.
- CIAT; World Bank. 2017. Climate-Smart Agriculture in Mozambique. CSA Country Profiles for Africa Series. International Center for Tropical Agriculture (CIAT); World Bank. Washington, D.C. 25 p.
- CGAP. 2016. National Survey and Segmentation of Smallholder Households in Mozambique. The Consultative Group to Assist the Poor.
- Chang, Christopher C., Carson C. Chow, Laurent Cam Tellier, Shashaank Vattikuti, Shaun M. Purcell, and James J. Lee. 2015. “Second-Generation PLINK: Rising to the Challenge of Larger and Richer Datasets.” *GigaScience* 1 (4): 1–16. <https://doi.org/10.1186/s13742-015-0047-8>.
- Chen, Honglin, Hong Chen, Liangliang Hu, Lixia Wang, Suhua Wang, Ming Li Wang, and Xuzhen Cheng. 2017. “Genetic Diversity and a Population Structure Analysis of Accessions in the Chinese Cowpea [*Vigna Unguiculata* (L.) Walp.] Germplasm Collection.” *The Crop Journal* 5 (5): 363–72. <https://doi.org/10.1016/j.cj.2017.04.002>.
- Dawson, Neil, Adrian Martin, and Thomas Sikor. 2016. “Green Revolution in Sub-Saharan Africa: Implications of Imposed Innovation for the Wellbeing of Rural Smallholders.” *World Development* 78 (February): 204–18. <https://doi.org/10.1016/j.worlddev.2015.10.008>.
- Dray, S., R. Péliissier, P. Couteron, M.-J. Fortin, P. Legendre, P. R. Peres-Neto, E. Bellier, et al. 2012. “Community Ecology in the Age of Multivariate Multiscale Spatial Analysis.” *Ecological Monographs* 82 (3): 257–75. <https://doi.org/10.1890/11-1183.1>.
- Ellis, Nick, Stephen J. Smith, and C. Roland Pitcher. 2012. “Gradient Forests: Calculating Importance Gradients on Physical Predictors.” *Ecology* 93 (1): 156–68. <https://doi.org/10.1890/11-0252.1>.
- Fatokun, Christian, Gezahegn Girma, Michael Abberton, Melaku Gedil, Nnanna Unachukwu, Olaniyi Oyatomi, Muyideen Yusuf, Ismail Rabbi, and Ousmane Boukar. 2018. “Genetic Diversity and Population Structure of a Mini-Core Subset from the World Cowpea (*Vigna Unguiculata* (L.) Walp.) Germplasm Collection.” *Scientific Reports* 8 (1): 16035. <https://doi.org/10.1038/s41598-018-34555-9>.
- FAOSTAT. 2016. Food and Agriculture Organization of the United Nations Statistics Division.
- Ferrão, Jorge, Victoria Bell, Luis Alfaro Cardoso, and Tito Fernandes. 2018. “Agriculture and Food Security in Mozambique.” *Journal of Food, Nutrition and Agriculture*, March, 7–11. <https://doi.org/10.21839/jfna.v1i1.121>.
- Fick, Stephen E., and Robert J. Hijmans. 2017. “WorldClim 2: New 1-Km Spatial Resolution Climate Surfaces for Global Land Areas.” *International Journal of Climatology* 37 (12): 4302–15. <https://doi.org/10.1002/joc.5086>.
- Fisher, Monica, Tsedeke Abate, Rodney W. Lunduka, Woinishet Asnake, Yoseph Alemayehu, and Ruth B. Madulu. 2015. “Drought Tolerant Maize for Farmer Adaptation to Drought in Sub-Saharan Africa: Determinants of Adoption in Eastern and Southern Africa.” *Climatic Change* 133 (2): 283–99. <https://doi.org/10.1007/s10584-015-1459-2>.
- Fitzpatrick, Matthew C., and Stephen R. Keller. 2015. “Ecological Genomics Meets Community-Level Modelling of Biodiversity: Mapping the Genomic Landscape of Current and Future Environmental Adaptation.” *Ecology Letters* 18 (1): 1–16. <https://doi.org/10.1111/ele.12376>.
- Franks, Steven J., and Ary A. Hoffmann. 2012. “Genetics of Climate Change Adaptation.” *Annual Review of Genetics* 46 (1): 185–208. <https://doi.org/10.1146/annurev-genet-110711-155511>.
- Fussell, L. K., F. R. Bidinger, and P. Bieler. 1991. “Crop Physiology and Breeding for Drought Tolerance: Research and Development.” *Field Crops Research* 27 (3): 183–99. [https://doi.org/10.1016/0378-4290\(91\)90061-Y](https://doi.org/10.1016/0378-4290(91)90061-Y).

- Galluzzi, Gea, Aseffa Seyoum, Michael Halewood, Isabel López Noriega, and Eric W. Welch. 2020. "The Role of Genetic Resources in Breeding for Climate Change: The Case of Public Breeding Programmes in Eighteen Developing Countries." *Plants* 9 (9): 1129. <https://doi.org/10.3390/plants9091129>.
- Gerrano, Abe Shegro, Moses H. Lubinga, and Michael Wolday Bairu. 2022. "Genetic Resources Management, Seed Production Constraints and Trade Performance of Orphan Crops in Southern Africa: A Case of Cowpea." *South African Journal of Botany* 146 (May): 340–47. <https://doi.org/10.1016/j.sajb.2021.11.007>.
- Gesesse, Cherinet Alem, Bogale Nigir, Kauê de Sousa, Luca Gianfranceschi, Guido Roberto Gallo, Jesse Poland, Yosef Gebrehawaryat Kidane, et al. 2023. "Genomics-Driven Breeding for Local Adaptation of Durum Wheat Is Enhanced by Farmers' Traditional Knowledge." *Proceedings of the National Academy of Sciences* 120 (14): e2205774119. <https://doi.org/10.1073/pnas.2205774119>.
- Gomes, Ana Maria Figueira, David Draper, Pedro Talhinhos, Paula Batista Santos, Fernanda Simões, Nascimento Nhandumbo, Rafael Massinga, José C. Ramalho, Isabel Marques, and Ana I. Ribeiro-Barros. 2020. "Genetic Diversity among Cowpea (*Vigna unguiculata* (L.) Walp.) Landraces Suggests Central Mozambique as an Important Hotspot of Variation." *Agronomy* 10 (12): 1893. <https://doi.org/10.3390/agronomy10121893>.
- Govindaraj, M., M. Vetriventhan, and M. Srinivasan. 2015. "Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives." *Genetics Research International* 2015: 431487. <https://doi.org/10.1155/2015/431487>.
- Greenberg, Stephen. 2016. *Mapping Farmer Seed Varieties in Manica, Mozambique: Initial Investigations into Agricultural Biodiversity (ACB Report)*.
- Hammer, Karl, Nancy Arrowsmith, and Thomas Gladis. 2003. "Agrobiodiversity with Emphasis on Plant Genetic Resources." *Naturwissenschaften* 90 (6): 241–50. <https://doi.org/10.1007/s00114-003-0433-4>.
- Henry, Fred Ojulong, Letayo Elias, Sakwera Loveness, Ziwa Rukwa, Mgonja Frida, Sheunda Patrick, Kibuka Joseph, et al., eds. 2017. "Participatory Variety Selection for Enhanced Promotion and Adoption of Improved Finger Millet Varieties: A Case for Singida and Iramba Districts in Central Tanzania." *African Journal of Rural Development (AFJRD)*. <https://doi.org/10.22004/ag.econ.263302>.
- Hahsler, M., & Piekenbrock, M. 2022. Density-based spatial clustering of applications with noise (DBSCAN) and related algorithms (R package version 1.1-10). <https://cran.r-project.org/package=dbscan>
- Hijmans, Robert J. 2018. "Raster: Geographic Data Analysis and Modeling." *R Package Version 2: 8*.
- Hijmans, Robert J., Steven Phillips, John Leathwick, Jane Elith, and Maintainer Robert J. Hijmans. 2017. "Package 'Dismo.'" *Circles* 9 (1): 1–68.
- Horton, Daniel E., Nathaniel C. Johnson, Deepti Singh, Daniel L. Swain, Bala Rajaratnam, and Noah S. Diffenbaugh. 2015. "Contribution of Changes in Atmospheric Circulation Patterns to Extreme Temperature Trends." *Nature* 522 (7557): 465–69. <https://doi.org/10.1038/nature14550>.
- Huang, Xuehui, Shihua Yang, Junyi Gong, Yan Zhao, Qi Feng, Hao Gong, Wenjun Li, et al. 2015. "Genomic Analysis of Hybrid Rice Varieties Reveals Numerous Superior Alleles That Contribute to Heterosis." *Nature Communications* 6 (1): 6258. <https://doi.org/10.1038/ncomms7258>.
- Ismael, Fátima, Aires A. Mbanze, Alexis Ndayiragije, and David Fanguero. 2021. "Understanding the Dynamic of Rice Farming Systems in Southern Mozambique to Improve Production and Benefits to Smallholders." *Agronomy* 11 (5): 1018. <https://doi.org/10.3390/agronomy11051018>.
- JICA. 2014. *The Project for Rice Productivity Improvement in Chokwe Irrigation Scheme*; JICA: Maputo, Mozambique, 2014.

- Jombart, Thibaut, Sébastien Devillard, and François Balloux. 2010. "Discriminant Analysis of Principal Components: A New Method for the Analysis of Genetically Structured Populations." *BMC Genetics* 11 (1): 94. <https://doi.org/10.1186/1471-2156-11-94>.
- Kajisa, Kei, and Trang Thu Vu. 2023. "The Importance of Farm Management Training for the African Rice Green Revolution: Experimental Evidence from Rainfed Lowland Areas in Mozambique." *Food Policy* 114 (January): 102401. <https://doi.org/10.1016/j.foodpol.2022.102401>.
- Kidane, Yosef G., Chiara Mancini, Dejene K. Mengistu, Elisabetta Frascaroli, Carlo Fadda, Mario Enrico Pè, and Matteo Dell'Acqua. 2017. "Genome Wide Association Study to Identify the Genetic Base of Smallholder Farmer Preferences of Durum Wheat Traits." *Frontiers in Plant Science* 8. <https://www.frontiersin.org/articles/10.3389/fpls.2017.01230>.
- Kindt, Roeland, and Richard Coe. 2005. *Tree Diversity Analysis: A Manual and Software for Common Statistical Methods for Ecological and Biodiversity Studies*. World Agroforestry Centre.
- Kumari, Venugopalan Visha, Anirban Roy, Roshni Vijayan, Purabi Banerjee, Vivek Chandra Verma, Arpita Nalia, Madhusri Pramanik, et al. 2021. "Drought and Heat Stress in Cool-Season Food Legumes in Sub-Tropical Regions: Consequences, Adaptation, and Mitigation Strategies." *Plants* 10 (6): 1038. <https://doi.org/10.3390/plants10061038>.
- Leemans, H. B. J., and B. Eickhout. 2003. "Analysing Changes in Ecosystems for Different Levels of Climate Change." https://scholar.google.com/scholar_lookup?title=Analysing+changes+in+ecosystems+for+different+levels+of+climate+change&author=Leemans%2C+H.B.J.&publication_year=2003.
- Li, Heng, and Richard Durbin. 2009. "Fast and Accurate Short Read Alignment with Burrows–Wheeler Transform." *Bioinformatics* 25 (14): 1754–60. <https://doi.org/10.1093/bioinformatics/btp324>.
- Lipka, Alexander E., Feng Tian, Qishan Wang, Jason Peiffer, Meng Li, Peter J. Bradbury, Michael A. Gore, Edward S. Buckler, and Zhiwu Zhang. 2012. "GAPIT: Genome Association and Prediction Integrated Tool." *Bioinformatics (Oxford, England)* 28 (18): 2397–99. <https://doi.org/10.1093/bioinformatics/bts444>.
- Liu, Xiaolei, Meng Huang, Bin Fan, Edward S. Buckler, and Zhiwu Zhang. 2016. "Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies." *PLOS Genetics* 12 (2): e1005767. <https://doi.org/10.1371/journal.pgen.1005767>.
- Loboguerrero, Ana Maria, Francisco Boshell, Gloria León, Deissy Martinez-Baron, Diana Giraldo, Liliana Recaman Mejía, Eliecer Díaz, and James Cock. 2018. "Bridging the Gap between Climate Science and Farmers in Colombia." *Climate Risk Management, Scaling Up Climate Services for Smallholder Farmers: Learning from Practice*, 22 (January): 67–81. <https://doi.org/10.1016/j.crm.2018.08.001>.
- Long, Stephen P, and Donald R Ort. 2010. "More than Taking the Heat: Crops and Global Change." *Current Opinion in Plant Biology* 13 (3): 240–47. <https://doi.org/10.1016/j.pbi.2010.04.008>.
- Magaisa, Alec, Pepukai Manjeru, Casper Nyaradzai Kamutando, and Martin Philani Moyo. 2022. "Participatory Variety Selection and Stability of Agronomic Performance of Advanced Sorghum Lines in Zimbabwe." *Journal of Crop Improvement* 36 (3): 440–60. <https://doi.org/10.1080/15427528.2021.1974635>.
- Malhi, Yadvinder, Janet Franklin, Nathalie Seddon, Martin Solan, Monica G. Turner, Christopher B. Field, and Nancy Knowlton. 2020. "Climate Change and Ecosystems: Threats, Opportunities and Solutions." *Philosophical Transactions of the Royal Society B: Biological Sciences* 375 (1794): 20190104. <https://doi.org/10.1098/rstb.2019.0104>.
- Mango, Nelson, Lawrence Mapemba, Hardwick Tchale, Clifton Makate, Nothando Dunjana, and Mark Lundy. 2018. "Maize Value Chain Analysis: A Case of Smallholder Maize Production and Marketing in Selected Areas of Malawi and Mozambique." Edited by Len Tiu Wright. *Cogent Business & Management* 5 (1): 1503220. <https://doi.org/10.1080/23311975.2018.1503220>.

- McCouch, Susan, Zahra Katy Navabi, Michael Abberton, Noelle L. Anglin, Rosa Lia Barbieri, Michael Baum, Kirstin Bett, et al. 2020. "Mobilizing Crop Biodiversity." *Molecular Plant* 13 (10): 1341–44. <https://doi.org/10.1016/j.molp.2020.08.011>.
- McNamara, John M, Zoltan Barta, Marcel Klaassen, and Silke Bauer. 2011. "Cues and the Optimal Timing of Activities under Environmental Changes." *Ecology Letters* 14 (12): 1183–90. <https://doi.org/10.1111/j.1461-0248.2011.01686.x>.
- Medina-Lozano, Inés, and Aurora Díaz. 2022. "Applications of Genomic Tools in Plant Breeding: Crop Biofortification." *International Journal of Molecular Sciences* 23 (6): 3086. <https://doi.org/10.3390/ijms23063086>.
- Mekonnen, Tesfaye Walle, Abe Shegro Gerrano, Ntombokulunga Wedy Mbuma, and Maryke Tine Labuschagne. 2022. "Breeding of Vegetable Cowpea for Nutrition and Climate Resilience in Sub-Saharan Africa: Progress, Opportunities, and Challenges." *Plants* 11 (12): 1583. <https://doi.org/10.3390/plants11121583>.
- Milner, Sara G., Matthias Jost, Shin Taketa, Elena Rey Mazón, Axel Himmelbach, Markus Oppermann, Stephan Weise, et al. 2019. "Genebank Genomics Highlights the Diversity of a Global Barley Collection." *Nature Genetics* 51 (2): 319–26. <https://doi.org/10.1038/s41588-018-0266-x>.
- Ministry of Agriculture (2009) National Rice Development Strategy Mozambique; Ministry of Agriculture: Maputo, Mozambique, 2009.
- Moalafi, A I, J A N Asiwe, and S M Funnah. n.d. "Germplasm Evaluation and Enhancement for the Development of Cowpea (*Vigna Unguiculata* (L.) Walp Dual-Purpose F2 Genotypes."
- Murungweni, C., M. T. Van Wijk, E. M. A. Smaling, and K. E. Giller. 2016. "Climate-Smart Crop Production in Semi-Arid Areas through Increased Knowledge of Varieties, Environment and Management Factors." *Nutrient Cycling in Agroecosystems* 105 (3): 183–97. <https://doi.org/10.1007/s10705-015-9695-4>.
- Mwale, Saul Eric, Mildred Ochwo-Ssemakula, Kassim Sadik, Esther Achola, Valentor Okul, Paul Gibson, Richard Edema, Wales Singini, and Patrick Rubaihayo. 2017. "Response of Cowpea Genotypes to Drought Stress in Uganda." <https://doi.org/10.4236/ajps.2017.84050>.
- Nchanji, Eileen Bogweh, Cosmas Kweyu Lutomia, Odhiambo Collins Ageyo, David Karanja, and Eliezah Kamau. 2021. "Gender-Responsive Participatory Variety Selection in Kenya: Implications for Common Bean (*Phaseolus Vulgaris* L.) Breeding in Kenya." *Sustainability* 13 (23): 13164. <https://doi.org/10.3390/su132313164>.
- Nhamo, Nhamo, Jonne Rodenburg, Negussie Zenna, Godswill Makombe, and Ashura Luzi-Kihupi. 2014. "Narrowing the Rice Yield Gap in East and Southern Africa: Using and Adapting Existing Technologies." *Agricultural Systems* 131 (November): 45–55. <https://doi.org/10.1016/j.agsy.2014.08.003>.
- Nkhoma, Nelia, Hussein Shimelis, Mark D. Laing, Admire Shayanowako, and Isack Mathew. 2020. "Assessing the Genetic Diversity of Cowpea [*Vigna Unguiculata* (L.) Walp.] Germplasm Collections Using Phenotypic Traits and SNP Markers." *BMC Genetics* 21 (1): 110. <https://doi.org/10.1186/s12863-020-00914-7>.
- Nouman, Muhammad, Dilawar Khan, Ihtisham Ul Haq, Nabeela Naz, Bibi Taharat E. Zahra, and Arif Ullah. 2022. "Assessing the Implication of Green Revolution for Food Security in Pakistan: A Multivariate Cointegration Decomposition Analysis." *Journal of Public Affairs* 22 (S1): e2758. <https://doi.org/10.1002/pa.2758>.
- Palit, Paramita, Himabindu Kudapa, Robert Zougmore, Jana Kholova, Anthony Whitbread, Mamta Sharma, and Rajeev K Varshney. 2020. "An Integrated Research Framework Combining Genomics, Systems Biology, Physiology, Modelling and Breeding for Legume Improvement in Response to Elevated CO₂ under Climate Change Scenario." *Current Plant Biology* 22 (June): 100149. <https://doi.org/10.1016/j.cpb.2020.100149>.
- Peterson, Brant K., Jesse N. Weber, Emily H. Kay, Heidi S. Fisher, and Hopi E. Hoekstra. 2012. "Double Digest RADseq: An Inexpensive Method for de Novo SNP Discovery and Genotyping in Model

- and Non-Model Species.” *PloS One* 7 (5): e37135. <https://doi.org/10.1371/journal.pone.0037135>.
- Phiri, Darius, Matamyo Simwanda, and Vincent Nyirenda. 2021. “Mapping the Impacts of Cyclone Idai in Mozambique Using Sentinel-2 and OBIA Approach.” *South African Geographical Journal* 103 (2): 237–58. <https://doi.org/10.1080/03736245.2020.1740104>.
- Poplin, Ryan, Valentin Ruano-Rubio, Mark A. DePristo, Tim J. Fennell, Mauricio O. Carneiro, Geraldine A. Van der Auwera, David E. Kling, et al. 2018. “Scaling Accurate Genetic Variant Discovery to Tens of Thousands of Samples.” *bioRxiv*. <https://doi.org/10.1101/201178>.
- “R: The R Project for Statistical Computing.” n.d. Accessed July 10, 2023. <https://www.r-project.org/>.
- Ray, Deepak K., James S. Gerber, Graham K. MacDonald, and Paul C. West. 2015. “Climate Variation Explains a Third of Global Crop Yield Variability.” *Nature Communications* 6 (1): 5989. <https://doi.org/10.1038/ncomms6989>.
- Redclift, Michael. 1990. “Developing Sustainably: Designating Agroecological Zones.” *Land Use Policy* 7 (3): 202–16. [https://doi.org/10.1016/0264-8377\(90\)90035-W](https://doi.org/10.1016/0264-8377(90)90035-W).
- Reuter, H. I., A. Nelson, and A. Jarvis. 2007. “An Evaluation of Void-filling Interpolation Methods for SRTM Data.” *International Journal of Geographical Information Science* 21 (9): 983–1008. <https://doi.org/10.1080/13658810601169899>.
- Rhoné, Bénédicte, Dimitri Defrance, Cécile Berthouly-Salazar, Cédric Mariac, Philippe Cubry, Marie Couderc, Anaïs Dequincey, et al. 2020. “Pearl Millet Genomic Vulnerability to Climate Change in West Africa Highlights the Need for Regional Collaboration.” *Nature Communications* 11 (1): 5274. <https://doi.org/10.1038/s41467-020-19066-4>.
- Romay, Maria C., Mark J. Millard, Jeffrey C. Glaubitz, Jason A. Peiffer, Kelly L. Swarts, Terry M. Casstevens, Robert J. Elshire, et al. 2013. “Comprehensive Genotyping of the USA National Maize Inbred Seed Bank.” *Genome Biology* 14 (6): R55. <https://doi.org/10.1186/gb-2013-14-6-r55>.
- Ruzzante, Sacha, Ricardo Labarta, and Amy Bilton. 2021. “Adoption of Agricultural Technology in the Developing World: A Meta-Analysis of the Empirical Literature.” *World Development* 146 (October): 105599. <https://doi.org/10.1016/j.worlddev.2021.105599>.
- Sansaloni, Carolina, Jorge Franco, Bruno Santos, Lawrence Percival-Alwyn, Sukhwinder Singh, Cesar Petrolí, Jaime Campos, et al. 2020. “Diversity Analysis of 80,000 Wheat Accessions Reveals Consequences and Opportunities of Selection Footprints.” *Nature Communications* 11 (1): 4572. <https://doi.org/10.1038/s41467-020-18404-w>.
- Senguttuvel, P., N. Sravanraju, V. Jaldhani, B. Divya, P. Beulah, P. Nagaraju, Y. Manasa, et al. 2021. “Evaluation of Genotype by Environment Interaction and Adaptability in Lowland Irrigated Rice Hybrids for Grain Yield under High Temperature.” *Scientific Reports* 11 (1): 15825. <https://doi.org/10.1038/s41598-021-95264-4>.
- Shilomboleni, Helena. 2017. “The African Green Revolution and the Food Sovereignty Movement: Contributions to Food Security and Sustainability A Case-Study of Mozambique.” Doctoral Thesis, University of Waterloo. <https://uwspace.uwaterloo.ca/handle/10012/11323>.
- Silici, Laura, Bias Calisto, and Cavane, Eunice. 2015. “Sustainable Agriculture for Small-Scale Farmers in Mozambique - A Scoping Report.” *International Institute for Environment and Development: London, UK, 2015*.
- Silva, Julie A., and Corene J. Matyas. 2014. “Relating Rainfall Patterns to Agricultural Income: Implications for Rural Development in Mozambique.” *Weather, Climate, and Society* 6 (2): 218–37. <https://doi.org/10.1175/WCAS-D-13-00012.1>.
- Singh, Y. P., A. K. Nayak, D. K. Sharma, R. K. Gautam, R. K. Singh, Ranbir Singh, V. K. Mishra, T. Paris, and A. M. Ismail. 2014. “Farmers’ Participatory Varietal Selection: A Sustainable Crop Improvement Approach for the 21st Century.” *Agroecology and Sustainable Food Systems* 38 (4): 427–44. <https://doi.org/10.1080/21683565.2013.870101>.
- Smýkal, Petr, Clarice J. Coyne, Mike J. Ambrose, Nigel Maxted, Hanno Schaefer, Matthew W. Blair, Jens Berger, et al. 2015. “Legume Crops Phylogeny and Genetic Diversity for Science and Breeding.”

- Critical Reviews in Plant Sciences* 34 (1–3): 43–104. <https://doi.org/10.1080/07352689.2014.897904>.
- Sousa, Kauê de, Jacob van Etten, Jesse Poland, Carlo Fadda, Jean-Luc Jannink, Yosef Gebrehawaryat Kidane, Basazen Fantahun Lakew, et al. 2021. “Data-Driven Decentralized Breeding Increases Prediction Accuracy in a Challenging Crop Production Environment.” *Communications Biology* 4 (1): 1–9. <https://doi.org/10.1038/s42003-021-02463-w>.
- Storey, John, and Robert Tibshirani. 2003. “Storey JD, Tibshirani R Statistical Significance for Genomewide Studies. *Proc Nat Acad Sci USA* 100:9440–9445.” *Proceedings of the National Academy of Sciences of the United States of America* 100 (September): 9440–45. <https://doi.org/10.1073/pnas.1530509100>.
- Sullivan, Shawn N. 2004. “Plant Genetic Resources and the Law.” *Plant Physiology* 135 (1): 10–15. <https://doi.org/10.1104/pp.104.042572>.
- Suvi, William Titus, Hussein Shimelis, Mark Laing, Isack Mathew, and Admire Isaac Tichafa Shayanowako. 2020. “Assessment of the Genetic Diversity and Population Structure of Rice Genotypes Using SSR Markers.” *Acta Agriculturae Scandinavica, Section B — Soil & Plant Science* 70 (1): 76–86. <https://doi.org/10.1080/09064710.2019.1670859>.
- Taiyun W, Simko V. 2017. R package “corrplot”: visualization of a correlationmatrix (version 0.84). 2017. Available from <https://github.com/taiyun/corrplot>
- Tian, Zhixi, Jia-Wei Wang, Jiayang Li, and Bin Han. 2021. “Designing Future Crops: Challenges and Strategies for Sustainable Agriculture.” *The Plant Journal* 105 (5): 1165–78. <https://doi.org/10.1111/tpj.15107>.
- “UN Climate Experts: Green Revolution Leaves Food Systems Vulnerable to Climate Change.” 2014. Gaia Foundation. March 31, 2014. <https://gaiafoundation.org/un-climate-experts-green-revolution-leaves-food-systems-vulnerable-to-climate-change/>.
- Villa, Tania Carolina Camacho, Nigel Maxted, Maria Scholten, and Brian Ford-Lloyd. 2005. “Defining and Identifying Crop Landraces.” *Plant Genetic Resources* 3 (3): 373–84. <https://doi.org/10.1079/PGR200591>.
- Villanueva, Donald, Yuji Enriquez, and Grace Lee Capilit. 2022. “The Impact of the International Rice Genebank (IRG) on Rice Farming in Bangladesh.” *CABI Agriculture and Bioscience* 3 (1): 45. <https://doi.org/10.1186/s43170-022-00113-7>.
- Wainaina, Priscilla, Songporne Tongruksawattana, and Matin Qaim. 2016. “Tradeoffs and Complementarities in the Adoption of Improved Seeds, Fertilizer, and Natural Resource Management Technologies in Kenya: P. Wainaina et Al.” *Agricultural Economics* 47 (3): 351–62. <https://doi.org/10.1111/agec.12235>.
- Wang, Yanjie, Yanli Wang, Xiaodong Sun, Zhuoma Caiji, Jingbiao Yang, Di Cui, Guilan Cao, et al. 2016. “Influence of Ethnic Traditional Cultures on Genetic Diversity of Rice Landraces under On-Farm Conservation in Southwest China.” *Journal of Ethnobiology and Ethnomedicine* 12 (1): 51. <https://doi.org/10.1186/s13002-016-0120-0>.
- Weir, B. S., and C. Clark Cockerham. 1984. “ESTIMATING F-STATISTICS FOR THE ANALYSIS OF POPULATION STRUCTURE.” *Evolution; International Journal of Organic Evolution* 38 (6): 1358–70. <https://doi.org/10.1111/j.1558-5646.1984.tb05657.x>.
- Wilczek, A. M., L. T. Burghardt, A. R. Cobb, M. D. Cooper, S. M. Welch, and J. Schmitt. 2010. “Genetic and Physiological Bases for Phenological Responses to Current and Predicted Climates.” *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* 365 (1555): 3129–47. <https://doi.org/10.1098/rstb.2010.0128>.
- Woldeyohannes, Aemiro Bezabih, Sessen Daniel Iohannes, Mara Miculan, Leonardo Caproni, Jemal Seid Ahmed, Kauê de Sousa, Ermias Abate Desta, Carlo Fadda, Mario Enrico Pè, and Matteo Dell’Acqua. 2022. “Data-Driven, Participatory Characterization of Farmer Varieties Discloses Teff Breeding Potential under Current and Future Climates.” Edited by Kelly Swarts, Detlef Weigel, and Bela Teeken. *ELife* 11 (September): e80009. <https://doi.org/10.7554/eLife.80009>.

- World Bank .2020. Cultivating Opportunities for Faster Rural Income Growth and Poverty Reduction (Rural Income Diagnostic). Overview Policy Report. Washington DC: The World Bank.
- Yigezu, Yigezu Atnafe, Amin Mugera, Tamer El-Shater, Aden Aw-Hassan, Colin Piggin, Atef Haddad, Yaseen Khalil, and Stephen Loss. 2018. “Enhancing Adoption of Agricultural Technologies Requiring High Initial Investment among Smallholders.” *Technological Forecasting and Social Change* 134 (September): 199–206. <https://doi.org/10.1016/j.techfore.2018.06.006>.
- Yuan, Shuai, Yong Shi, Biao-Feng Zhou, Yi-Ye Liang, Xue-Yan Chen, Qing-Qing An, Yan-Ru Fan, Zhao Shen, Pär K. Ingvarsson, and Baosheng Wang. n.d. “Genomic Vulnerability to Climate Change in *Quercus Acutissima*, a Dominant Tree Species in East Asian Deciduous Forests.” *Molecular Ecology* n/a (n/a). Accessed January 25, 2023. <https://doi.org/10.1111/mec.16843>.

8. ANNEX

8.1 Cowpea passport data

ID	Accession	Variety	country	material	Province	District	Village	Lat	Long
Vu001	1254	Timbawene Mo	Mozambique	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu002	1255	Massava-II	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu003	1288	Muikuha	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu004	1350	Ecúte	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu005	2094	Timbawene	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu006	2106	Xidjaiandlala	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu007	2109	Timbawene (va	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu008	2110	Timbawene	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze	-24.7132	33.87833
Vu009	2117	Thoane	Mozambique	Landrace	Inhamban	Massinga	P.Ad Sede	-23.3252	35.37005
Vu010	2131		Mozambique	Landrace	Inhamban	Massinga	P.Ad Sede	-23.3252	35.37005
Vu011	2143	Ecute	Mozambique	Landrace	Inhamban	Massinga	P. Ad Sede	-23.3252	35.37005
Vu012	2167	Ecute	Mozambique	Landrace	Inhamban	Massinga	P. Ad Sede	-23.3252	35.37005
Vu013	2174	Ecute - yoyevac	Mozambique	Landrace	Inhamban	Massinga	P. Ad Sede	-23.3252	35.37005
Vu014	2183	Mui nana-lawe	Mozambique	Landrace	Inhamban	Massinga	P. Ad Sede	-23.3252	35.37005
Vu015	2186	Desconhecido	Mozambique	Landrace	Inhamban	Massinga	P. Ad Chic	-23.3252	35.37005
Vu016	2222	Desconhecido	Mozambique	Landrace	Inhamban	Massinga	P. Ad Chic	-23.3252	35.37005
Vu017	2295	Congondzo (vag	Mozambique	Landrace	Inhamban	Massinga	P. Ad Chic	-23.3252	35.37005
Vu018	2300	Thonhuane	Mozambique	Landrace	Inhamban	Massinga	P. Ad Chic	-23.3252	35.37005
Vu019	2301	Tyhulo	Mozambique	Landrace	Inhamban	Massinga	P. Ad.Gum	-23.3252	35.37005
Vu020	2313	Desconhecido (Mozambique	Landrace	Inhamban	Massinga	P. Ad.Gum	-23.3252	35.37005
Vu021	2427	Desconhecido (Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Sitila	-23.659	35.33896
Vu022	2435	Desconhecido	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu023	2480	Desconhecido	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu024	2524	Namuathapuat	Mozambique	Landrace	Inhamban	Morrumbene	P. Ad.Gotit	-23.659	35.33896
Vu025	2590	Nhemba	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu026	2625	Desconhecido	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu027	2651	Desconhecido	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu028	2692	Nhabubo Norte	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu029	2764	Tatykulo	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit	-23.659	35.33896
Vu030	2801	Desconhecido	Mozambique	Landrace	Inhamban	Jagamo	P.Ad. Bam	-24.1136	35.31326
Vu031	3236	Xlinhawane cor	Mozambique	Landrace	Inhamban	Jagamo	P.Ad. Bam	-24.1136	35.31326
Vu032	3246	Tihulu	Mozambique	Landrace	Inhamban	Jagamo	P.Ad. Bam	-24.1136	35.31326
Vu033	3247	Xiinhawanehan	Mozambique	Landrace	Inhamban	Inharrime	P.Ad. Don	-24.4747	35.02641
Vu034	3252	Tinhawawanha	Mozambique	Landrace	Inhamban	Inharrime	P.Ad. Don	-24.4747	35.02641



This project has received funding from the European Commission's Horizon 2020 Research and Innovation Programme. The content in this presentation reflects only the author(s)'s views. The European Commission is not responsible for any use that may be made of the information it contains.

Vu035	3257	Tsonguane	Mozambique	Landrace	Inhamban	Inharrime	P.Ad. Don	-24.4747	35.02641
Vu036	3260	Sacana vermelh	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu037	3262	Xinhawane	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu038	3264	Desconhecido T	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu039	3269	Nantchenga	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu040	3270	Nhabubo	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu041	3271	Desconhecido	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu042	3280	Desconhecido c	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong	-24.4747	35.02641
Vu043	3282	Desconhecido	Mozambique	Landrace	Inhamban	Inharrime	Zamdamel	-24.4747	35.02641
Vu044	3283	Xingove/Banch	Mozambique	Landrace	Inhamban	Inharrime	P. Ad Mac	-24.4747	35.02641
Vu045	3285	Desconhecido c	Mozambique	Landrace	Inhamban	Inharrime	Macugela	-24.4747	35.02641
Vu046	3293	Nhantchengue	Mozambique	Landrace	Inhamban	Zavala	Chissico	-24.7156	34.74383
Vu047	3298	Timbawene Ta	Mozambique	Landrace	Inhamban	Zavala	Quissico	-24.7156	34.74383
Vu048	3301	Nhantshengue	Mozambique	Landrace	Inhamban	Zavala	Quissico	-24.7156	34.74383
Vu049	3306	Nhantshengue	Mozambique	Landrace	Inhamban	Zavala	Quissico	-24.7156	34.74383
Vu050	3355	Kubassa	Mozambique	Landrace	Inhamban	Zavala	Chissibuca	-24.7156	34.74383
Vu051	3356	Nholoyolo	Mozambique	Landrace	Manica	Borue	NA	-17.9539	33.24808
Vu052	3360	Tiyulo-Kutsuka	Mozambique	Landrace	Manica	Sussundenga	NA	-19.4054	33.29603
Vu053	3361	Tlowane	Mozambique	Landrace	Sofala	Nhamatanda	NA	-19.2958	34.23217
Vu054	3362	Chimbawane	Mozambique	Landrace	Sofala	NA	NA	-19.2958	34.23217
Vu055	3365	Nhaloyodue	Mozambique	Landrace	Sofala	Buzi	NA	-20.0345	34.33794
Vu056	3368	Desconhecida	Mozambique	Landrace				-9.8333	33.8833
Vu057	3371	Tcheneca	Mozambique	Landrace				-9.95	33.8
Vu058	3375	Moconua	Mozambique	Landrace				-9.7667	33.4833
Vu059	3376	Mussotxa- cinz	Mozambique	Landrace				-13.9667	33.8333
Vu060	3377	Chixinhauane	Mozambique	Landrace				-13.9667	34.5167
Vu061	3381	Desconhecido	Mozambique	Landrace				-14.25	35.0833
Vu062	3390	Txowane	Mozambique	Landrace				-14.5667	35.2
Vu063	3397	Tinhawa	Mozambique	Landrace				-15.3667	35.2333
Vu064	3399	Massotxa	Mozambique	Landrace				-16.5833	35.1167
Vu065	3400	Movolo	Mozambique	Landrace				-16.9167	35.1833
Vu066	3401	Tluguelo	Mozambique	Landrace				-14.9667	34.9333
Vu067	3402	Mussotxa	Mozambique	Landrace				-15.5833	35.1667
Vu068	3403	Xiquidane	Mozambique	Landrace				-16.5167	34.9667
Vu069	3404	Thowane	Mozambique	Landrace				-16.4667	34.9
Vu070	3405	Kachuane	Mozambique	Landrace				-15.7833	35.6167



Vu071	3407	Hagha	Mozambique	Landrace					-15.4	35.4333
Vu072	3408	Gufuia	Mozambique	Landrace					-15.05	35.4
Vu073	3410	Desconhecida	Mozambique	Landrace					-14.4333	35.6167
Vu074	3414	Zinhemba Zacu	Mozambique	Landrace					-14.55	35.2167
Vu075	3415	Zinhemba Zazic	Mozambique	Landrace					-14.3167	35.1167
Vu076	3417	Zinhemba- Nhe	Mozambique	Landrace					-12	33.6333
Vu077	3418	Nhassengue	Mozambique	Landrace					-11.85	33.8667
Vu078	3419	Zinhemba	Mozambique	Landrace					-11.1667	34.3833
Vu079	3420	Guicacana	Mozambique	Landrace					-11.2167	33.85
Vu080	3421	Massotxa	Mozambique	Landrace					-9.85	33.6667
Vu081	3422	Desconhecida	Mozambique	Landrace					-11.05	33.6333
Vu082	3423	Blivila	Mozambique	Landrace					-11.8167	33.7833
Vu083	3424	Nhablevele	Mozambique	Landrace					-16.5819	35.1248
Vu085	3427	Nhambasse	Mozambique	Landrace					-13.5	34
Vu086	3430	Madjedje	Mozambique	Landrace					-16.55	35.12823
Vu087	3431	Guionga	Mozambique	Landrace					-16.4982	35.2062
Vu088	3433	Tsafuvila	Mozambique	Landrace					-12.0794	34.0573
Vu089	3434	Shagohaga	Mozambique	Landrace					-15.9667	35.2667
Vu090	3435	Nassengane Br	Mozambique	Landrace					-15.8064	35.6507
Vu091	3436	Tchionga	Mozambique	Landrace					-15.8064	35.6507
Vu092	3438	Youblivila	Mozambique	Landrace					-13.3753	34.0036
Vu093	3467	Nhemba Ziculu	Mozambique	Landrace					-13.5833	33.1667
Vu094	3483	Nhemba Huro	Mozambique	Landrace					-15.8064	35.6507
Vu096	3505	Murassa	Mozambique	Landrace					-13.95	33.75
Vu097	3543	Murassa	Mozambique	Landrace					-16.9667	35.2167
Vu098	3571	Buadala	Mozambique	Landrace					-18.6657	35.52956
Vu099	4201	MW80-136	Malawi	Landrace	NA	NA	NA	NA	NA	NA
Vu100	4202	MW80-148	Malawi	Landrace	NA	NA	NA	NA	NA	NA
Vu102	4204	MW80-189	Malawi	Landrace	Nampula	Monapo	25 de Junh	-14.9029	40.31746	
Vu103	4206	EX LILONGWE	Malawi	Landrace	Nampula	Nampula	Nampula	-15.1217	39.26474	
Vu104	4210	MW80-398	Malawi	Landrace	Gaza	Massingir	Massingir	-22.5508	32.16376	
Vu105	4212	MW80-462	Malawi	Landrace	Gaza	Massingir	Massingir	-23.9213	32.16376	
Vu106	4213	MW80-485	Malawi	Landrace	Gaza	Chicualacuala	Aldeia de	-21.9509	32.06144	
Vu107	4217	EX ZOMBA	Malawi	Landrace	Gaza	Chicualacuala	Aldeia de	-21.9509	32.06144	
Vu108	4224	MW80-741	Malawi	Landrace	Gaza	Chicualacuala	Aldeia de	-21.9526	32.06144	

Vu109	4225	MW80-758	Malawi	Landrace	Gaza	Chicualacuala	Mapai	-22.7331	32.06144
Vu111	4230	EX BALAKA MA	Malawi	Landrace	Cabo Delg	Montepuez	Aldeia de	-13.1273	39.0189
Vu112	4232	AG87M-201	Malawi	Landrace	Cabo Delg	Macomia	Aldeia de	-12.2378	40.13653
Vu113	4233	AG87M-216	Malawi	Landrace	Cabo Delg	Macomia	Aldeia de	-12.2378	40.13653
Vu114	4234	NGABU TOWN	Malawi	Landrace	Nampula	Monapo	Natoa, Mo	-14.9029	40.31746
Vu116	4236	AG87M-237	Malawi	Landrace	Niassa	Mavago	Aldeia de I	-12.5778	37.56236
Vu117	4237	AG87M-244	Malawi	Landrace	Niassa	Marrupa	Aldeia de	-13.1919	37.50715
Vu118	4238	AG87M-254	Malawi	Landrace	Inhamban	Mabote	Aldeia de	-22.029	34.12559
Vu119	4239	AG87M-263	Malawi	Landrace	Inhamban	Mabote	Aldeia de	-21.8921	34.12559
Vu120	4240	AG87M-265	Malawi	Landrace	Inhamban	Mabote	Aldeia de	-21.8921	34.12559
Vu121	4241	AG87M-277	Malawi	Landrace	Inhamban	Morrumbene	Aldeia 25	-23.1188	34.3467
Vu122	4245	AG87M-339	Malawi	Landrace	Inhamban	Inharime	Aldeia Cho	-24.4368	35.1192
Vu123	4246	EX CHIKANGAW	Malawi	Landrace	Inhamban	Inharime	Aldeia Cho	-24.4747	35.02641
Vu124	4247	AG87M-353	Malawi	Landrace	Inhamban	Maxixe	Aldeia de	-23.8599	35.33904
Vu125	4249	AG87M-361	Malawi	Landrace	Cabo Delg	Chiure	Aldeia de	-13.7122	39.67351
Vu126	4250	AG87M-381	Malawi	Landrace	Manica	Guro	Aldeia de	-16.9391	33.54811
Vu127	4252	AG87M-403	Malawi	Landrace	Manica	Gondola	Aldeia de	-17.0575	34.04194
Vu128	4253	AG87M-407	Malawi	Landrace	Cabo Delg	Montepuez	P.A.Mapup	-13.1273	39.0189
Vu129	4256	BANGULA NO.1	Malawi	Landrace					
Vu130	4257	CHADZUKA NO.	Malawi	Landrace	Maputo	Manhica	Manhica	-25.4158	32.78862
Vu131	4258	EX CHIROMO	Malawi	Landrace					
Vu132	4259	MAKHANGA NO.	Malawi	Landrace	Gaza	Massangena	Massange	-21.5462	32.9516
Vu133	4260	MUONA NO.1	Malawi	Landrace	Gaza	Massangena	Massange	-21.5462	32.9516
Vu134	4261	MAKANDE NO.4	Malawi	Landrace	Gaza	Massangena	Massange	-21.5462	32.9516
Vu135	4262	PHALUMBE NO.	Malawi	Landrace	Gaza	Massangena	Massange	-21.5462	32.9516
Vu136	4263	PHALUMBE NO.	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu137	4267	NCHISA NO.5	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu138	4268	CHEWEATAN N	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu139	4269	PHUMULIA NO.	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu140	4270	CHIGONELIA NO.	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu141	4272	NGABU NO.3	Malawi	Landrace	Gaza	Chigubo	Chigubo	-24.7018	33.54607
Vu142	4275	RPM 43/2	Mozambique	Landrace				-18.6657	35.52956
Vu143	4276	RPM 46	Mozambique	Landrace				-18.6657	35.52956
Vu144	4277	RPM 73	Mozambique	Landrace				-18.6657	35.52956
Vu145	4280	RPM 105	Mozambique	Landrace				-18.6657	35.52956
Vu146	4281	RPM 115/1	Mozambique	Landrace				-18.6657	35.52956



Vu147	4283	RPM 121/2	Mozambique	Landrace	-18.6657	35.52956
Vu148	4284	RPM 136-2	Mozambique	Landrace	-18.6657	35.52956
Vu149	4285	RPM 139-1	Mozambique	Landrace	-18.6657	35.52956
Vu150	4286	RPM 147	Mozambique	Landrace	-30.5595	22.93751
Vu151	4290	34C-395	South Africa	Landrace	-30.5595	22.93751
Vu152	4291	34-C-395(-A)	South Africa	Landrace	-30.5595	22.93751
Vu153	4293	51-C-142	South Africa	Landrace	-30.5595	22.93751
Vu154	4296	51C-428	South Africa	Landrace	-30.5595	22.93751
Vu155	4297	53-C-28	South Africa	Landrace	-30.5595	22.93751
Vu156	4300	53-C-91-2	South Africa	Landrace	-30.5595	22.93751
Vu157	4301	53-C-91-2	South Africa	Landrace	-30.5595	22.93751
Vu158	4306	BECHUANA WH	South Africa	Landrace	-30.5595	22.93751
Vu159	4307	BETCHWANA W	South Africa	Landrace	-30.5595	22.93751
Vu160	4309	EARLY BROWNE	South Africa	Landrace	-30.5595	22.93751
Vu161	4311	FD 68007	South Africa	Landrace	-30.5595	22.93751
Vu163	4319	IRON	South Africa	Landrace	-30.5595	22.93751
Vu164	4322	NEW ERA A2	South Africa	Landrace	-30.5595	22.93751
Vu165	4323	NEW ERA B	South Africa	Landrace	-30.5595	22.93751
Vu166	4325	NEW ERA G9	South Africa	Landrace	-30.5595	22.93751
Vu167	4326	P 268	South Africa	Landrace	-30.5595	22.93751
Vu168	4330	PI 221732	South Africa	Landrace	-30.5595	22.93751
Vu169	4332	PI 225922	South Africa	Landrace	-30.5595	22.93751
Vu170	4333	PI 257463	South Africa	Landrace	-30.5595	22.93751
Vu171	4336	PI 292894	South Africa	Landrace	-30.5595	22.93751
Vu172	4342	PI 339592	South Africa	Landrace	-30.5595	22.93751
Vu173	4343	PI 339593	South Africa	Landrace	-30.5595	22.93751
Vu174	4344	PI 339594	South Africa	Landrace	-30.5595	22.93751
Vu175	4347	PI 339596	South Africa	Landrace	-30.5595	22.93751
Vu176	4349	PI 339597	South Africa	Landrace	-30.5595	22.93751
Vu177	4350	PI 339604	South Africa	Landrace	-30.5595	22.93751
Vu178	4351	POTCHEF	South Africa	Landrace	-30.5595	22.93751
Vu179	4353	PREVIOUS TVU	South Africa	Landrace	-30.5595	22.93751
Vu180	4354	REAUSTER	South Africa	Landrace	-30.5595	22.93751
Vu181	4357	SES NO 5	South Africa	Landrace	-30.5595	22.93751
Vu182	4359	SPECKLED TEST	South Africa	Landrace	-30.5595	22.93751
Vu183	4361	WITZEN BONG	South Africa	Landrace	-30.5595	22.93751



Vu184	4362	YANDER B	South Africa	Landrace	-30.5595	22.93751
Vu185	4363	EX KITONGA	Tanzania	Landrace		
Vu186	4364	EX PEYAPEYA	Tanzania	Landrace		
Vu187	4365	EX UCHIRA	Tanzania	Landrace		
Vu188	4366	EX KIKAVU CHINT	Tanzania	Landrace		
Vu189	4368	EX OLD SHINYA	Tanzania	Landrace		
Vu190	4371	EX NTUNDU	Tanzania	Landrace		
Vu191	4374	TAMBEZI	Tanzania	Landrace		
Vu192	4375	EX SENGEREMA	Tanzania	Landrace		
Vu193	4378	EX MUHAYA M	Tanzania	Landrace		
Vu194	4380	PS87T-39	Tanzania	Landrace		
Vu195	4381	PS87T-56	Tanzania	Landrace		
Vu196	4383	PS87T-137	Tanzania	Landrace		
Vu197	4385	PS87T-245A	Tanzania	Landrace		
Vu198	4390	PS87T-90	Tanzania	Landrace		
Vu199	4391	EX CHALINZE	Tanzania	Landrace		
Vu200	4393	EX 'SAME' MAR	Tanzania	Landrace		
Vu201	4396	EX MAKAMBAK	Tanzania	Landrace		
Vu202	4399	EX MIHAMA	Tanzania	Landrace		
Vu203	4400	NJOMBE NO.2	Tanzania	Landrace		
Vu205	4403	BANIREMBIZI VI	Zimbabwe	Landrace		
Vu206	4406	PS87Z-237	Zimbabwe	Landrace		
Vu208	4408	PS87Z-285	Zimbabwe	Landrace		
Vu209	4409	PS87Z-293	Zimbabwe	Landrace		
Vu210	4410	PS87Z-320	Zimbabwe	Landrace		
Vu211	4411	PS87Z-342	Zimbabwe	Landrace		
Vu212	4412	PS87Z-351	Zimbabwe	Landrace		
Vu213	4414	PS87Z-379	Zimbabwe	Landrace		
Vu214	4415	PS87Z-444	Zimbabwe	Landrace		
Vu216	4422	IT97K-499-35	IITA Nigeria	Improved		
Vu217	4425	IT82E-60	IITA Nigeria	Improved		
Vu218	4426	IT84S-2246-4	IITA Nigeria	Improved		
Vu219	4427	IT91K-93-10	IITA Nigeria	Improved		
Vu220	4430	IT98K-1263	IITA Nigeria	Improved		
Vu221	4431	IT98K-166-4	IITA Nigeria	Improved		



Vu222	4432	IT-97	IITA Nigeria	Improved					
Vu223	4433	IT-00K	IITA Nigeria	Improved					
Vu224	4434	IT-18	IITA Nigeria	Improved					
Vu225	4435	INIA-41	Mozambique	Improved	-30.5595				22.93751
Vu226	4436	IT-16	IITA Nigeria	Improved					
Vu227	2117A	Thoane	Mozambique	Landrace					
Vu228	2295A	Congondzo (vag	Mozambique	Landrace	-30.5595				22.93751
Vu229	3212A	Congondzo	Mozambique	Landrace	-30.5595				22.93751
Vu230	3246A	Tihulu	Mozambique	Landrace	-30.5595				22.93751
Vu231	3283B	Xingove/Banch	Mozambique	Landrace	-30.5595				22.93751
Vu232	3298A	Timbawene Ta	Mozambique	Landrace	-30.5595				22.93751
Vu233	3359B	Tiyulo-ta ku Bas	Mozambique	Landrace	-30.5595				22.93751
Vu234	3377A	Chixinhauane	Mozambique	Landrace	-30.5595				22.93751
Vu235	3381A	Desconhecido	Mozambique	Landrace	-30.5595				22.93751
Vu236	3399A	Massotxa	Mozambique	Landrace	-30.5595				22.93751
Vu237	3401A	Tluguelo	Mozambique	Landrace	-30.5595				22.93751
Vu238	3402A	Mussotxa	Mozambique	Landrace	-30.5595				22.93751
Vu239	3418A	Nhassengue	Mozambique	Landrace	-30.5595				22.93751
Vu240	3418B	Nhassengue	Mozambique	Landrace	-30.5595				22.93751
Vu241	3420A	Guicacana	Mozambique	Landrace	-30.5595				22.93751
Vu242	3421A	Massotxa	Mozambique	Landrace	-30.5595				22.93751
Vu243	3424A	Nhablevele	Mozambique	Landrace	-30.5595				22.93751
Vu244	3426B	Mucra	Mozambique	Landrace	-30.5595				22.93751
Vu245	3427A	Nhambasse	Mozambique	Landrace	-30.5595				22.93751
Vu246	3430A	Madjedje	Mozambique	Landrace	-30.5595				22.93751
Vu247	3431A	Guionga	Mozambique	Landrace	-30.5595				22.93751
Vu248	3502A	Mucumbo torg	Mozambique	Landrace				-30.5595	22.93751
Vu249	4260A	MUONA NO.1	Malawi	Landrace		Gaza	Chigubo	Chigubo	-24.7018 33.54607
Vu250	3212	Congondzo	Mozambique	Landrace					-30.5595 22.93751
Vu251	4325A	NEW ERA G9	South Africa	Landrace					-30.5595 22.93751
Vu252	4403A	BANIREMBIZI VI	Zimbabwe	Landrace					
Vu253	4411B	PS87Z-342	Zimbabwe	Landrace					
Vu254	4420A	PS87Z-393	Zimbabwe	Landrace					
Vu255	4426A	IT84S-2246-4	IITA Nigeria	Improved					
Vu256	4446	IT18	IITA Nigeria	Improved					
Vu257	4445	IT98K-530-1	IITA Nigeria	Improved					



Vu258	4447	TVX3226	IITA Nigeria	Improved		
Vu259	4451	IT97K-1089-8	IITA Nigeria	Improved		
Vu260	4450	IT16	IITA Nigeria	Improved		
Vu261	4449	IT97K-1069-8	IITA Nigeria	Improved		
Vu262	4448	IT86D-880	IITA Nigeria	Improved		
Vu263	4426	IT84S-2246-4	IITA Nigeria	Improved		
Vu264	2638	Sacana	Mozambique	Landrace	-30.5595	22.93751
Vu266	4505	Variedade 1	Mozambique	Landrace	-30.5595	22.93751
Vu267	4506	Variedade Loca	Mozambique	Landrace	-30.5595	22.93751
Vu268	4507	Variedade P124	Mozambique	Landrace	-30.5595	22.93751
Vu269	4508	Variedade 3	Mozambique	Landrace	-30.5595	22.93751
Vu274	4513	variedade local	Mozambique	Landrace	-30.5595	22.93751
Vu275	4514	Variedade Loca	Mozambique	Landrace	-30.5595	22.93751
Vu277	4516	Variedade Loca	Mozambique	Landrace	-30.5595	22.93751
Vu279	4518	Variedade P.Chi	Mozambique	Landrace	-30.5595	22.93751
Vu281	4520	Variedade local	Mozambique	Landrace	-7.1333	39.1667
Vu282	4521	Variedade local	Mozambique	Landrace	-6.7667	37.0833
Vu283	4522	Variedade local	Mozambique	Landrace	-3.3333	37.5
Vu290	4529	p1-93-1 (P1)	Mozambique	Landrace	-3.4167	37.3333
Vu291	4530	Var. 12	Mozambique	Landrace	-3.55	33.4
Vu295	4534	Var. Local (P90)	Mozambique	Landrace	-2.75	32.8
Vu296	4535	Var. Local P26	Mozambique	Landrace	-6.6	37.1667
Vu299	4538	Var. 1037-298	Mozambique	Landrace	-2.6667	32.6667
Vu300	4539	Var. Local P48	Mozambique	Landrace	-5.1833	38.8
Vu301	4540	Var. Loca P24	Mozambique	Landrace	-4.6833	38.1167
Vu302	4541	Var. 119-03	Mozambique	Landrace	-3.3333	37.55
Vu304	4543	var. P. Chiulele	Mozambique	Landrace	-2.9833	32.05
Vu307	4546	Var. Local (P46)	Mozambique	Landrace	-8.85	34.05
Vu308	4547	Var. P97	Mozambique	Landrace	-3.4833	35.85
Vu309	4548	Var. Local P116	Mozambique	Landrace	-6.2	37.1667
Vu310	4549	Var. Local P110	Mozambique	Landrace	-4.0833	37.7333
Vu311	4550	P3-202-3 (P6)	Mozambique	Landrace	-8.85	34.8333
Vu312	4551	Var. Local P35	Mozambique	Landrace	-4.5833	33.1667
Vu314	4553	Var. 9	Mozambique	Landrace	-9.3333	34.7667
Vu315	4554	Var. Local P50	Mozambique	Landrace	-16.4833	31.05
Vu317	4556	Var. Local 99	Mozambique	Landrace	-17.3833	32.2833



Vu319	4558	Var. Local P103	Mozambique	Landrace					-17.6333	29.7167
Vu321	4560	Var. Local P81	Mozambique	Landrace					-17.5	29.45
Vu323	4562	Var. Local P116	Mozambique	Landrace					-17.1167	29.0833
Vu324	4563	Var. LoCAL P12	Mozambique	Landrace					-17.6333	29.0167
Vu328	4567	Var. Local P30	Mozambique	Landrace					-18.1833	28.8167
Vu329	4568	var.P. chiulele4	Mozambique	Landrace					-18.7833	30.8833
Vu334	4573	var local p119	Mozambique	Landrace					-20.4333	28.6833
Vu337	4576	variedade local	Mozambique	Landrace					NA	NA
Vu339	4578	var.local 111	Mozambique	Landrace					NA	NA
Vu340	4579	var.local p84	Mozambique	Landrace					NA	NA
Vu342	4581	var. local p63	Mozambique	Landrace					NA	NA
Vu343	4582	var local p75	Mozambique	Landrace					NA	NA
Vu344	4583	Var. 18	Mozambique	Landrace					NA	NA
Vu345	4584	P6-27-6(P7)	Mozambique	Landrace					NA	NA
Vu346	4585	Var. local p106	Mozambique	Landrace					NA	NA
Vu347	4586	var. local P07	Mozambique	Landrace					NA	NA
Vu348	4587	var local 109	Mozambique	Landrace					NA	NA
Vu349	4588	var local p1	Mozambique	Landrace					NA	NA
Vu350	4589	499-39XIT18-3-	Mozambique	Landrace	Gaza	Chicualacuala	Aldeia de		-22.0803	31.68283
Vu351	4590	1037-298P2	Mozambique	Landrace	Inhamban	Mabote	Aldeia de		-22.029	34.12558
Vu352	4591	Var. local p92	Mozambique	Landrace					NA	NA
Vu353	4592	var. local p63	Mozambique	Landrace	Gaza	Massangena	Massange		-21.5462	32.9516
Vu354	4593	2246X503(0)	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze		-24.7132	33.87833
Vu355	4594	875-355P9	Mozambique	Landrace	Gaza	Manjacaze	Manjacaze		-24.7132	33.87833
Vu356	4595	Var. local P77	Mozambique	Landrace	Inhamban	Massinga			-23.3252	35.37005
Vu357	4596	Var. 11	Mozambique	Landrace	Inhamban	Massinga	P. Ad.Gum		-23.3252	35.37005
Vu358	4597	Var. 19	Mozambique	Landrace	Inhamban	Massinga	P. Ad.Gum		-23.3252	35.37005
Vu360	4599	Var. 9	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit		-23.659	35.33896
Vu361	4600	Var. local P77	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit		-23.659	35.33896
Vu362	4601	Var. local P(105	Mozambique	Landrace	Inhamban	Morrumbene	P.Ad. Gotit		-23.659	35.33896
Vu363	4602	var. local P65	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong		-24.4747	35.02641
Vu366	4605	Var. local P51	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong		-24.4747	35.02641
Vu370	4609	Var. local P106	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong		-24.4747	35.02641
Vu371	4610	Var.3	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong		-24.4747	35.02641
Vu372	4611	Var. local 122	Mozambique	Landrace	Inhamban	Inharrime	Inhacoong		-24.4747	35.02641



Vu373	4612	Var. Local P73	Mozambique	Landrace	Inhamban	Inharrime	Zamdamel	-24.4747	35.02641
Vu374	4613	Var. local P41	Mozambique	Landrace	Inhamban	Inharrime	Zamdamel	-24.4747	35.02641
Vu375	4614	var. local P14	Mozambique	Landrace	Inhamban	Inharrime	P. Ad Mac	-24.4747	35.02641
Vu376	4615	var. local p260	Mozambique	Landrace	Inhamban	Inharrime	Macugela	-24.4747	35.02641
Vu377	4616	var . Local Maci	Mozambique	Landrace	Manica	Gondola	-19.0828		33.64706
Vu378	4617	Var8	Mozambique	Landrace			NA		NA
Vu379	4618	grupo3 var. loca	Mozambique	Landrace			NA		NA
Vu380	4619	Grupo 11 (p3)	Mozambique	Landrace			NA		NA
Vu382	4621	var. local p51	Mozambique	Landrace			-16.4833		31.05
Vu383	4622	Var.4	Mozambique	Landrace			NA		NA
Vu384	4623	var.local P1	Mozambique	Landrace			NA		NA
Vu385	4624	var. local p08	Mozambique	Landrace			NA		NA
Vu386	4625	var. local p9(0)	Mozambique	Landrace			NA		NA
Vu388	4627	var. local P4	Mozambique	Landrace			NA		NA
Vu389	4628	var. local p134	Mozambique	Landrace			NA		NA
Vu390	4629	var. local p76	Mozambique	Landrace			NA		NA
Vu392	4631	var. local p12	Mozambique	Landrace			NA		NA
Vu393	4632	var. local p101	Mozambique	Landrace			NA		NA
Vu394	4633	var.13	Mozambique	Landrace			NA		NA
Vu395	4634	INIA 152xB21-1	Mozambique	Improved			NA		NA
Vu402	4641	var.local p39	Mozambique	Landrace			NA		NA
Vu411	4650	Var. Local P430	Mozambique	Landrace					
Vu416	4655	Var. local P128	Mozambique	Landrace					
Vu420	4659	Var. local P89	Mozambique	Landrace					
Vu423	4662	Var. local P16	Mozambique	Landrace					
Vu429	4668	Var. local P5	Mozambique	Landrace					
Vu431	4670	Var. local P47	Mozambique	Landrace					
Vu434	4673	Var. local P580	Mozambique	Landrace					
Vu437	4676	Var. local P49	Mozambique	Landrace					
Vu440	4679	Var. local P203	Mozambique	Landrace					
Vu441	4680	Var. local P86	Mozambique	Landrace					
Vu445	4684	Var. local P54	Mozambique	Landrace					
Vu448	4687	Var. local P145	Mozambique	Landrace					
Vu449	4688	Var. local P38	Mozambique	Landrace					
Vu455	4694	Var. local P94	Mozambique	Landrace					
Vu457	4696	Var. local P126	Mozambique	Landrace					

Vu458	4697	Var. local P26	Mozambique	Landrace
Vu462	4701	Var. local P118	Mozambique	Landrace
Vu466	4705	Var. local P88	Mozambique	Landrace
Vu473	4712	Var. local Macia	Mozambique	Landrace
Vu477	4716	Var. 11 D	Mozambique	Landrace
Vu482	4721	Var. local P67	Mozambique	Landrace
Vu486	4725	Var. local P44	Mozambique	Landrace
Vu487	4726	Var. local (P34)	Mozambique	Landrace
Vu490	4729	Var. local P121	Mozambique	Landrace
Vu491	4730	Var. P9-27-9-P5	Mozambique	Landrace
Vu494	4733	Var. local P90	Mozambique	Landrace
Vu495	4734	Var. local P79	Mozambique	Landrace
Vu497	4736	Var. local P16	Mozambique	Landrace
Vu499	4738	Var. P6-86-6 P1	Mozambique	Landrace
Vu502	4741	Var. local P99	Mozambique	Landrace
Vu505	4744	Var. P9-11-9 P4	Mozambique	Landrace
Vu514	4753	Var.21	Mozambique	Landrace
Vu515	4754	Var.8	Mozambique	Landrace
Vu517	4756	p5-202-5p1	Mozambique	Landrace
Vu518	4757	Var.localp105	Mozambique	Landrace
Vu520	4759	Cb46x(cb46x20	Mozambique	Landrace
Vu522	4761	Var.3	Mozambique	Landrace
Vu523	4762	524Bx\524B\xl	Mozambique	Landrace
Vu524	4763	Var.local P51	Mozambique	Landrace
Vu525	4764	Var.local P108	Mozambique	Landrace
Vu528	4767	Var. 2	Mozambique	Landrace
Vu534	4773	EUA-Gileke-loca	Mozambique	Landrace
Vu537	4776	Var. 1	Mozambique	Landrace
Vu538	4777	Var. local P124	Mozambique	Landrace
Vu540	4779	EUA-Gile K loca	Mozambique	Landrace
Vu541	4780	Var. local P109	Mozambique	Landrace
Vu542	4781	Var. local P9	Mozambique	Landrace
Vu543	4782	Var.6	Mozambique	Landrace
Vu544	4783	Var. loca Chuiel	Mozambique	Landrace
Vu545	4784	Var. 4	Mozambique	Landrace
Vu548	4787	Var. local P97	Mozambique	Landrace

Vu551	4790	Var. local P28	Mozambique	Landrace
Vu554	4793	Var. local P34	Mozambique	Landrace
Vu556	4795	Var.local P5	Mozambique	Landrace
Vu557	4796	Var. local P122	Mozambique	Landrace
Vu560	4799	Var. local P7	Mozambique	Landrace
Vu562	4801	var. local p61	Mozambique	Landrace
Vu565	4804	Var.21	Mozambique	Landrace
Vu566	4805	Var.local P4	Mozambique	Landrace
Vu570	4809	Var.22	Mozambique	Landrace
Vu571	4810	var. local p11	Mozambique	Landrace
Vu573	4812	var.localp63	Mozambique	Landrace
Vu574	4813	INIA41XIT84S-2	Mozambique	Improved
Vu575	4814	var local p255	Mozambique	Landrace
Vu581	4820	Var.local 109	Mozambique	Landrace
Vu584	4823	var. local P98	Mozambique	Landrace
Vu585	4824	var.local p60	Mozambique	Landrace
Vu587	4826	var. local p84	Mozambique	Landrace
Vu588	4827	var. local p41	Mozambique	Landrace
Vu589	4828	var local p24	Mozambique	Landrace
Vu591	4830	var.local p23	Mozambique	Landrace
Vu592	4831	var.local p111	Mozambique	Landrace
Vu594	4833	Bambey21x499	Mozambique	Landrace
Vu606	4845	Var. local P961	Mozambique	Landrace
Vu610	4849	Var. local p8	Mozambique	Landrace
Vu611	4850	Var .2	Mozambique	Landrace
Vu613	4852	2049x(CB46x20	Mozambique	Landrace

8.2 Rice passport data

ID	Accession	Material	Variety name	Country	Pronvince	District	Village	Latitude	Longitude
OS001	1159	Landrace	Mata-fome	Mozambique	Zambézia	Nicoadala	Mucelo - Cerâmica	-17.5885	36.80224
OS002	1159A	Landrace	Mata-fome	Mozambique	Zambézia	Nicoadala	Mucelo - Cerâmica	-17.5885	36.80224
OS004	1160A	Landrace	Carvalho	Mozambique	Zambézia	Nicoadala	Mucelo - Cerâmica	-17.5885	36.80224
OS005	1161	Landrace	Chibiça	Mozambique	Zambézia	Nicoadala	Mucelo - Cerâmica	-17.5885	36.80224
OS006	1164	Landrace	Cantambira	Mozambique	Zambézia	Nicoadala	Nhangoma	-17.5885	36.80224
OS007	1198A	Landrace	Manteiga	Mozambique	Sofala	Búzi	Mandire, Companhia de	-19.9083	34.575
OS008	1216	Landrace	Nhacatendewa	Mozambique	Sofala	Dondo	Vale do Mandruzi	-19.6386	34.68611
OS009	1216A	Landrace	Nhacatendewa	Mozambique	Sofala	Dondo	Vale do Mandruzi	-19.6386	34.68611
OS010	1216B	Landrace	Nhacatendewa	Mozambique	Sofala	Dondo	Vale do Mandruzi	-19.6386	34.68611
OS011	1216	Landrace	Nhacatendewa	Mozambique	Sofala	Dondo	Vale do Mandruzi	-19.6386	34.68611
OS013	1224	Landrace	Bungala	Mozambique	Sofala	Marromeu	Muene Kamba	-18.3038	35.9486
OS014	1229	Landrace	Maxima	Mozambique	Sofala	Marromeu	Muene Kamba	-18.3038	35.9486
OS015	1261B	Landrace	Mussoro wotela	Mozambique	Nampula	Monapo	Karapira-Mutarawatane	-14.9029	40.31746
OS016	1345B	Landrace	Nihaya	Mozambique	Nampula	Mogovolas	Nametil-Mutamala-Cali	-15.719	39.20076
OS017	2465	Landrace	Marocha ya kuba	Mozambique	Inhambane	Muorrumben	Aldeia de Cambine	-23.659	35.33896
OS018	2465A	Landrace	Marocha ya kuba	Mozambique	Inhambane	Muorrumben	Aldeia de Cambine	-23.659	35.33896
OS019	2556	Landrace	Manda	Mozambique	Niassa	Cuamba	Cuamba-Muchehe	-14.8037	36.52748
OS020	2577A	Landrace	Desconhecido	Mozambique	Niassa	Majune	Luambala	-13.3949	36.12668
OS021	2577B	Landrace	Desconhecido	Mozambique	Niassa	Majune	Luambala	-13.3949	36.12668
OS022	2878A	Landrace	Tsingano-2	Mozambique	Tete			-17.3792	35.12389
OS023	2556B	Landrace	Manda	Mozambique					
OS024	3561	Landrace		Mozambique					
OS025	2826	Landrace	Nene	Mozambique	Zambézia	Namacura	Mutange	-17.5018	36.92186



OS026	2828	Landrace	Essenga	Mozambique	Zambézia	Namacura	Mutange	-17.5018	36.92186
OS027	2828A	Landrace	Essenga	Mozambique	Zambézia	Namacura	Mutange	-17.5018	36.92186
OS028	2828B	Landrace	Essenga	Mozambique	Zambézia	Namacura	Mutange	-17.5018	36.92186
OS029	2828C	Landrace	Essenga	Mozambique	Zambézia	Namacura	Mutange	-17.5018	36.92186
OS030	2832	Landrace	Niwayo	Mozambique	Zambézia	Namacura	Naminane	-17.5692	36.92653
OS031	2832A	Landrace	Niwayo	Mozambique	Zambézia	Namacura	Naminane	-17.5692	36.92653
OS032	2832B	Landrace	Niwayo	Mozambique	Zambézia	Namacura	Naminane	-17.5692	36.92653
OS033	2836	Landrace	Rosa	Mozambique	Zambézia	Nicoadala	Aldeia Bate Muziva	-17.6386	36.72092
OS034	2836A	Landrace	Rosa	Mozambique	Zambézia	Nicoadala	Aldeia Bate Muziva	-17.6386	36.72092
OS036	2840	Landrace	Pirizi	Mozambique	Zambézia	Nicoadala	Aldeia Bate Muziva	-17.6423	36.72169
OS037	2840A	Landrace	Pirizi	Mozambique	Zambézia	Nicoadala	Aldeia Bate Muziva	-17.6423	36.72169
OS038	2843	Landrace	Administrador	Mozambique	Zambézia	Nicoadala	Aldeia Bate Muziva	-17.6423	36.72169
OS039	2844	Landrace	M'franca	Mozambique	Zambézia	Nicoadala	Bairro Supinho	-17.6025	36.81092
OS040	2844A	Landrace	M'franca	Mozambique	Zambézia	Nicoadala	Bairro Supinho	-17.6025	36.81092
OS041	2844B	Landrace	M'franca	Mozambique	Zambézia	Nicoadala	Bairro Supinho	-17.6025	36.81092
OS042	2856	Landrace	Mugodji	Mozambique	Zambézia	Mocuba	Aldeia Machera-Caiave	-17.9699	36.76367
OS044	4149	Landrace		Mozambique					
OS045	2856C	Landrace	Mugodji	Mozambique	Zambézia	Mocuba	Aldeia Machera-Caiave	-17.9699	36.76367
OS046	2859	Landrace	Salchicha	Mozambique	Zambézia	Mocuba	Localidade Muaquiua-Q	-16.7229	37.41225
OS047	2862	Landrace	Chuabo	Mozambique	Zambézia	Mocuba	Aldeia Serote, Nigula-M	-16.718	37.49833
OS049	2872B	Landrace	Ndeca	Mozambique	Tete	Mutarara	Ndere - Canama	-17.5911	35.17961
OS050	2874	Landrace	Faia	Mozambique	Tete	Mutarara	Aldeia de Chicote-1/No	-17.1334	35.23019
OS051	2874A	Landrace	Faia	Mozambique	Tete	Mutarara	Aldeia de Chicote-1/No	-17.1334	35.23019
OS052	2883	Landrace	Nhakasonkole	Mozambique	Tete	Mutarara	Aldeia de Miphange-Ch	-17.3792	35.12389
OS053	1476	Landrace	Petroleo	Mozambique	Sofala	Dondo	Machorroto	-19.6389	34.68611
OS055	3532	Landrace		Mozambique					
OS056	4452	Improved	IR15A3666	Mozambique	Maputo	Maputo			
OS057	4453	Improved	IR107015-37-2-2-	Mozambique	Maputo	Maputo			
OS058	4454	Improved	TCHULULA MET2	Mozambique	Maputo	Maputo			
OS059	4455	Improved	ARS	Mozambique	Maputo	Maputo			
OS060	4456	Improved	ARS181-1-2-B-B	Mozambique	Maputo	Maputo			
OS061	4457	Improved	IR94 306-25-3-1-	Mozambique	Maputo	Maputo			
OS062	4458	Improved	D26-ARS-1-3	Mozambique	Maputo	Maputo			
OS063	4459	Improved	D26-ARS-1-3	Mozambique	Maputo	Maputo			
OS064	4460	Improved	ARS 844-30-2-2-2	Mozambique	Maputo	Maputo			
OS065	4461	Improved	ARS755-3-B-B-B	Mozambique	Maputo	Maputo			
OS066	4462	Improved	IR 15A2942MET2	Mozambique	Maputo	Maputo			
OS067	4463	Improved	IR15A2930 MET2	Mozambique	Maputo	Maputo			
OS068	4464	Improved	MACASSANE	Mozambique	Maputo	Maputo			
OS070	4466	Improved	ARS 844-13-5-1-1	Mozambique	Maputo	Maputo			
OS071	4467	Improved	ARS 144-5-9-B-B	Mozambique	Maputo	Maputo			

OS073		4469 Improved	Mozambique				
OS075		4437 Improved	Mozambique				
OS076		4438 Improved	Mozambique				
OS077		4439 Improved	Mozambique				
OS078		4440 Improved	Mozambique				
OS079		4441 Improved	Mozambique				
OS080		4442 Improved	Mozambique				
OS081		4443 Improved	Mozambique				
OS082		4444 Improved	Mozambique				
OS084		3559 Landrace	Mozambique				
OS099		3066 Landrace	Namuina				
OS188		3526 Landrace	Mucabo Delgado	Mozambique	Sofala	Dondo	-19.6389 34.68611
OS189	2836C	Landrace	Rosa	Mozambique	Zambézia		
OS190		3560 Landrace	Andirembui	Mozambique	Sofala	Buzi	-20.0479 34.33982
OS191	2881A	Landrace	Luabo	Mozambique	Tete		-17.3792 35.12389
OS192	2556A	Landrace	Manda	Mozambique			
OS194		3518 Landrace	Chupa	Mozambique	Sofala	Dondo	-19.6389 34.68611
OS197		4855 Unknown	AYT12	Mozambique			
OS198		4856 Unknown	AYT13	Mozambique			
OS199		4857 Unknown	AYT14	Mozambique			
OS201		4859 Unknown	AYT16	Mozambique			
OS202		4860 Unknown	AYT17	Mozambique			
OS203		4861 Unknown	AYT18	Mozambique			
OS204		4862 Unknown	AYT19	Mozambique			
OS205		4863 Unknown	AYT20	Mozambique			
OS206		4864 Unknown	AYT21	Mozambique			
OS207		4865 Unknown	AYT22	Mozambique			
OS208		4866 Unknown	AYT23	Mozambique			
OS209		4867 Unknown	AYT24	Mozambique			
OS210		4868 Unknown	AYT25	Mozambique			
OS211		4869 Unknown	AYT26	Mozambique			
OS213		4871 Unknown	AYT28	Mozambique			
OS214		4872 Unknown	AYT29	Mozambique			
OS215		4873 Unknown	AYT30	Mozambique			
OS216		4874 Unknown	AYT31	Mozambique			
OS217		4875 Unknown	AYT32	Mozambique			
OS218		4876 Unknown	AYT33	Mozambique			
OS219		4877 Unknown	AYT34	Mozambique			
OS220		4878 Unknown	AYT35	Mozambique			
OS221		4879 Unknown	AYT36	Mozambique			
OS222		4880 Unknown	AYT37	Mozambique			



OS223	4881 Unknown	AYT38	Mozambique				
OS224	4882 Unknown	AYT39	Mozambique				
OS225	4883 Unknown	AYT40	Mozambique				
OS226	4884 Unknown	AYT1	Mozambique				
OS227	4885 Unknown	AYT2	Mozambique				
OS228	4886 Unknown	AYT3	Mozambique				
OS229	4887 Unknown	AYT4	Mozambique				
OS230	4888 Unknown	AYT5	Mozambique				
OS231	4889 Unknown	AYT6	Mozambique				
OS232	4890 Unknown	AYT7	Mozambique				
OS233	4891 Unknown	AYT8	Mozambique				
OS234	4892 Unknown	AYT9	Mozambique				
OS235	4893 Unknown	AYT10	Mozambique				
OS236	4894 Unknown	AYT11	Mozambique				
OS237	3005 Landrace	Rafique	Mozambique		-16.6247	39.22834	
OS238	3092 Landrace	Mamima com ari	Mozambique	Zambézia	-17.5783	36.86136	
OS239	3146 Landrace	M'brá	Mozambique			-16.6119	36.92159
OS240	3037 Landrace	Mussoro	Mozambique			-14.8428	38.36056
OS241	3135 Landrace	Mamima	Mozambique	Zambézia			
OS242	3124 Landrace	Popothy	Mozambique		-17.5847	37.17411	
OS244	3168 Landrace	Caga	Mozambique		-17.514	37.3053	
OS245	3003 Landrace	Wipo	Mozambique		-16.6247	39.22834	
OS246	3123 Landrace	Mukabu	Mozambique		-17.5847	37.17411	
OS247	3136 Landrace	Mussador	Mozambique		-16.4012	36.52168	
OS249	3081 Landrace	Ririo	Mozambique	Zambézia	-17.5903	36.85844	
OS250	3051 Landrace	Desconhecido co	Mozambique		-14.0419	40.64174	
OS251	3090 Landrace	Namacaba Mell	Mozambique	Zambézia	-17.5783	36.86136	
OS252	3169 Landrace	Chuapa/Chuabo	Mozambique		-17.514	37.3053	
OS253	3074 Landrace	Namapupa	Mozambique	Nampula	-14.9641	39.88034	
OS254	3026 Landrace	Namacula	Mozambique				
OS255	3138 Landrace	Namuriama	Mozambique		-16.364	36.52012	
OS256	3107 Landrace	M'pulo	Mozambique		-17.543	37.12116	
OS257	3002 Landrace	China	Mozambique		-16.7508	39.22377	
OS258	3078 Landrace	Mucabo Delgado	Mozambique	Zambézia	-17.5903	36.85844	
OS259	3145 Landrace	Namaciba	Mozambique				
OS260	3064 Landrace	Namapupa	Mozambique	Nampula	-14.9982	40.50528	
OS261	3088 Landrace	M'pulo	Mozambique	Zambézia	-17.5783	36.86136	
OS262	1336 Landrace	Nihaya	Mozambique	Nampula	Angoche	Berração (Rio Mutan'la)	-16.224 39.90582
OS263	1311 Landrace		Mozambique	Nampula			
OS264	1338 Landrace	Rafique	Mozambique				
OS265	1162 Landrace	Chigude	Mozambique	Zambézia	Nicoadala		-17.5885 36.80224



OS267	1207 Landrace	Muchevuta	Mozambique	Sofala	Buzi			-19.8758	34.60778
OS268	1221 Landrace	Media	Mozambique	Sofala	Dondo			-19.6389	34.68611
OS269	1172 Landrace	Mazubo	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS270	1171 Landrace	Câssamo	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS272	1209 Landrace	Chikerere branco	Mozambique	Sofala	Buzi			-19.8758	34.60778
OS273	1219 Landrace	Petroleo	Mozambique	Sofala	Dondo			-19.6389	34.68611
OS274	1310 Landrace		Mozambique	Nampula					
OS276	1332 Landrace	Nihaya	Mozambique	Nampula	Angoche	Berração (Rio Mutan'la)		-15.8524	39.88389
OS277	1215 Landrace	Nhamacoco Maw	Mozambique	Sofala	Dondo			-19.6386	34.68611
OS278	1315 Landrace	Naminhinga?	Mozambique	Nampula	Mangicual	Muanona, Namituco		-15.6044	40.27003
OS279	1323 Landrace	Nihaya	Mozambique	Nampula	Angoche	Mueravera (aldeia)		-16.224	39.90582
OS280	1370 Landrace	Mozambique							
OS281	1380 Landrace	Mozambique		Nampula	Ribáue	Manema (Aldeia)		-14.6723	38.41889
OS282	1201 Landrace	Chikerere	Mozambique	Sofala	Buzi			-19.8686	34.58753
OS283	1218 Landrace	Administrador	Mozambique	Sofala	Dondo			-19.6389	34.68611
OS284	1208 Landrace	M'pungura	Mozambique	Sofala	Buzi			-19.8759	34.60778
OS285	1204 Landrace	Petroleo vermelh	Mozambique	Sofala	Buzi			-19.8759	34.60778
OS286	1205 Landrace	Chikerere	Mozambique	Sofala	Buzi			-19.8759	34.60778
OS287	1213 Landrace	Petroleo	Mozambique	Sofala	Dondo			-19.6386	34.69441
OS289	1325 Landrace	M'rathi	Mozambique	Nampula	Angoche	Mueravera (aldeia)		-16.224	39.90582
OS290	2829 Landrace	Munhabera	Mozambique	Zambézia				-17.5018	36.92184
OS291	2835 Landrace	Mucabo	Mozambique	Zambézia				-17.5018	36.92184
OS292	2827 Landrace	Mimima	Mozambique	Zambézia				-17.5911	36.92031
OS293	2855 Landrace	Mpulo	Mozambique	Zambézia				-16.9469	36.75989
OS294	1223 Landrace	China	Mozambique	Sofala	Marromeu			-18.3038	35.9486
OS296	1222 Landrace	Mozambique		Sofala				-19.5653	34.66694
OS297	1214 Landrace	Manda	Mozambique	Sofala	Dondo			-19.6389	35.68611
OS299	1167 Landrace	M'pulo	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS300	1174 Landrace	Administrador	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS301	1248 Landrace	Chidader	Mozambique						
OS302	1237 Landrace	Xiputuguese	Mozambique						
OS303	1168 Landrace	Muluabu	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS306	1261 Landrace	Mussoro wotela	Mozambique	Nampula	Monapo	Caripira		-14.9029	40.31746
OS307	1181 Landrace	Ingamiot	Mozambique	Zambézia	Nicoadala			-17.5885	36.80224
OS308	1206 Landrace	Muanamima	Mozambique	Sofala	Buzi			-19.8758	34.60778
OS312	2869 Landrace	Caga	Mozambique	Zambézia				-17.4755	37.30803
OS313	3001 Landrace	Nihaya	Mozambique					-16.7508	39.22377
OS315	2870 Landrace	Tsingano	Mozambique	Tete				-17.5928	35.17897
OS316	2825 Landrace	Bebé	Mozambique	Zambézia				-17.5892	36.91881

OS318	1347	Landrace	Pimpili	Mozambique	Nampula	Mogovolas	Nametil, Namicossa	-15.5978	39.02111
OS319	2846	Landrace	Indô	Mozambique	Zambézia			-17.8092	37.10292
OS321	1331	Landrace	Namararoa/Nank	Mozambique	Nampula	Angoche	Notane (Aldeia)	-16.224	39.90582
OS323	2878	Landrace	Tsingano-2	Mozambique	Tete			-17.3795	35.12392
OS324	2863	Landrace	Nene	Mozambique	Zambézia			-16.7191	37.48902
OS327	1926	Landrace	Muhinde	Mozambique					
OS329	1484	Landrace		Mozambique	Sofala	Dondo		-19.6389	34.68778
OS330	1241	Landrace	Xisaiana	Mozambique					
OS331	2854	Landrace	Nene	Mozambique	Zambézia			-16.9167	36.7443
OS332	2847	Landrace	Kangiwa kafri	Mozambique	Zambézia			-17.8081	38.12425
OS333	2871	Landrace	Manda	Mozambique	Tete			-17.5947	35.17823
OS335	2879	Landrace	Nkunta	Mozambique	Tete			-17.3792	35.12389
OS336	2867	Landrace	M'pulo	Mozambique	Zambézia			-17.4752	37.30947
OS338	2831	Landrace	Angelo	Mozambique	Zambézia			-17.5692	36.92653
OS339	2868	Landrace	Popote/Nassoko	Mozambique	Zambézia			-17.4806	37.3155
OS340	2873	Landrace	Petroleo	Mozambique	Tete			-17.59111	35.17628
OS341	2838	Landrace	Mamima	Mozambique	Zambézia			-17.6386	36.72092
OS343	2877	Landrace	Ntchenga	Mozambique	Tete			-17.3331	35.15551
OS344	2848	Landrace	Rosa bonita	Mozambique	Zambézia			-17.8068	37.10177
OS345	2830	Landrace	M'pulo pequeno	Mozambique	Zambézia			-17.5725	36.92292
OS346	1173	Landrace	Namcaba-Mell	Mozambique	Zambézia	Nicoadala		-17.5885	36.80224
OS348	2853	Landrace	Sam' Debe	Mozambique	Zambézia			-17.8015	37.001
OS349	2843	Landrace	Administrador	Mozambique	Zambézia			-17.6423	36.7217
OS350	2882	Landrace	Mangoche	Mozambique	Tete			-17.3792	35.12389
OS351	3128	Landrace	Nhaluabo	Mozambique				-17.8636	35.86956
OS352	2999	Landrace	Wipo	Mozambique				-16.1189	39.51619
OS353	2851	Landrace	Mukiri	Mozambique	Zambézia			-17.8066	37.10231
OS354	2520	Landrace	Chupa	Mozambique				-13.4244	39.40245
OS355	2833	Landrace	Nhacatendewa	Mozambique	Zambézia			-17.5698	36.97703
OS356	2842	Landrace	India pequeno	Mozambique	Zambézia			-17.6423	36.7217
OS357	2857	Landrace	Pirizi	Mozambique	Zambézia			-16.9407	36.74571
OS358	3078	Landrace	Mucabo Delgado	Mozambique	Zambézia			-17.5903	36.85844
OS359	2980	Landrace	Muma	Mozambique	Nampula	Mogovolas		-15.7589	39.2758
OS360	3053	Landrace	Desconhecido co	Mozambique				-14.9419	40.64174
OS361	2998	Landrace	Xixirica	Mozambique				-15.1189	39.51619
OS362	3119	Landrace	Muchuabo	Mozambique				-17.5651	37.13842
OS363	3023	Landrace	Desconhecido	Mozambique				-14.9763	38.16818
OS364	3118	Landrace	Nene	Mozambique				-17.5651	37.13842
OS365	1240	Landrace	Guirossana	Mozambique					
OS367	1942	Landrace	Xindeque	Mozambique					
OS369	1527	Landrace	M'franca	Mozambique					



OS370	1229 Landrace	Maxima	Mozambique Sofala	Marromeu				
OS371	1345 Landrace	Nihaya	Mozambique Nampula	Mogovolas	Nametil, Mutubala calip	-15.719	39.20076	
OS372	2164 Landrace	Desconhecido	Mozambique					
OS086	3595 Landrace	2?16	Tanzania			-6.36806	34.885	
OS087	3609 Landrace	AFAA MWANZA	Tanzania			-6.36806	34.885	
OS088	3610 Landrace	AFAA KILOMBER	Tanzania			-6.36806	34.885	
OS089	3620 Landrace	ES 9	Tanzania			-7.78333	35.16667	
OS090	3621 Landrace	SUPA INDIA	Tanzania			-7.78333	35.16667	
OS093	3625 Landrace	ES 18 (GOLD)	Tanzania			-5.88333	35.23333	
OS094	3634 Landrace	ES 32	Tanzania			-4.25	30.45	
OS096	3636 Landrace	ES 37	Tanzania			-4.13333	37.95	
OS097	3637 Landrace	FAYA SUPA KIHO	Tanzania			-4.35	38.05	
OS101	3643 Landrace	WAHI	Tanzania			-4.9	38.28333	
OS103	3655A Landrace	ES 76	Tanzania			-5.16528	39.72306	
OS104	3657 Landrace	ZIRA	Tanzania			-5.16528	39.72306	
OS105	3658 Landrace	ES 79	Tanzania			-5.3825	39.74722	
OS106	3659 Landrace	SINDANO	Tanzania			-5.18306	39.80694	
OS107	3660 Landrace	ES 82	Tanzania		-5.18306		39.80694	
OS139	3720 Landrace	TGR 1160	Tanzania		-20.4333		30.28333	
OS141	3758 Landrace	EX BUGOLA MW	Tanzania		-2.55		32.06667	
OS142	3760 Landrace	EX DAHI DODOM	Tanzania		-5.96667		35.33333	
OS144	3783 Landrace	KIHOGO MWEKU	Tanzania		-9.56667		33.83333	
OS145	3788 Landrace	MOSHI	Tanzania		-4.25		33.18333	
OS146	3790 Landrace	MWASUNGU	Tanzania		-9.56667		33.83333	
OS147	3794 Landrace	RUPA	Tanzania		-4		33.13333	
OS148	3823 Landrace	Garamata	Tanzania		-4.90569		34.01575	
OS149	3831 Landrace	India Rangi	Tanzania		-5.07103		34.208	
OS150	3837 Landrace	Kalimata	Tanzania		-8.50533		36.57592	
OS151	3845 Landrace	Kaniki	Tanzania		-11.032		39.41125	
OS152	3853 Landrace	Kibakuli	Tanzania		-6.25136		37.54883	
OS153	3857 Landrace	Kihogo	Tanzania		-10.2507		39.42406	
OS154	3884 Landrace	Lichede	Tanzania		-10.7699		34.39022	
OS155	3887 Landrace	Likwati	Tanzania		-10.4533		39.84417	
OS156	3889 Landrace	Lindunda	Tanzania		-8.28922		36.33706	
OS157	3943 Landrace	Nganyalo	Tanzania		-5.88836		35.21728	
OS158	3944 Landrace	Nganyalo	Tanzania		-6.24764		35.35364	
OS159	3950 Landrace	Nganyaro	Tanzania		-5.7105		34.98067	
OS160	3951 Landrace	Nganyaro	Tanzania		-5.95133		35.31075	
OS161	3957 Landrace	Ngwindimba	Tanzania		-10.5093		40.23117	
OS162	3962 Landrace	Ntalima Wangu	Tanzania		-10.3042		39.36425	
OS164	3967 Landrace	Nusu Upawa	Tanzania		-9.94297		39.37019	



OS165	3971 Landrace	Omana	Tanzania	-4.65497	34.19872
OS166	3987 Landrace	Sindano	Tanzania	-8.71844	39.26467
OS167	3990 Landrace	Si Nzito	Tanzania	-10.9951	39.39861
OS168	4013 Landrace	Supa	Tanzania	-7.10658	37.87431
OS169	4015 Landrace	Supa	Tanzania	-10.0099	39.38011
OS170	4019 Landrace	Supa Asilia	Tanzania	-5.711	34.97614
OS171	4020 Landrace	Supa Bahi	Tanzania	-5.95231	35.31044
OS172	4023 Landrace	Supa India	Tanzania	-7.69333	37.65647
OS173	4024 Landrace	Supa India	Tanzania	-8.18675	37.17567
OS174	4028 Landrace	Supa Kikoti	Tanzania	NULL	NULL
OS175	4032 Landrace	Supa Kinyambwa	Tanzania	-6.24764	35.35364
OS176	4037 Landrace	Supa Mbeya	Tanzania	-6.38581	37.95781
OS177	4080 Landrace	Super India	Tanzania	-8.15661	36.39692
OS178	4103 Landrace	Wahi Wahi	Tanzania	-4.6475	34.13667
OS179	4114 Landrace	Kisegese	Tanzania	-7.64253	37.53128
OS180	4120 Landrace	Nchi Kavu	Tanzania	-5.86653	35.61853
OS181	4125 Landrace	Supa Nyeupe	Tanzania	-5.80783	38.66731
OS182	4127 Landrace	Afaa	Tanzania	-8.38933	39.04694
OS183	4140 Landrace	Kampe Bwana	Tanzania	-8.71844	39.26467
OS184	4142 Landrace	Kienyeji	Tanzania	-10.2508	38.70103
OS185	4146 Landrace	Kisegese	Tanzania	-7.65931	37.60975
OS043	Unknown		Unknown		
OS054	Unknown		Unknown		
OS074	Unknown		Unknown		
OS083	Unknown		Unknown		
OS085	Unknown		Unknown		
OS186	Unknown		Unknown		
OS195	4198 Unknown		unknown		
OS109	3662 Landrace	KACHI KOPE	Zimbabwe	-12.9167	34.28333
OS110	3673 Landrace	LITWANGA TONI	Zimbabwe	-19.0131	29.14639
OS111	3674 Landrace	OS 16	Zimbabwe	-19.0131	29.14639
OS112	3675 Landrace	R 46	Zimbabwe	-19.0131	29.14639
OS113	3676 Landrace	R 89	Zimbabwe	-19.0131	29.14639
OS114	3677 Landrace	R 92	Zimbabwe	-19.0131	29.14639
OS115	3678 Landrace	R 93	Zimbabwe	-19.0131	29.14639
OS117	3680 Landrace	R 96?2	Zimbabwe	-19.0131	29.14639
OS118	3681 Landrace	R 97?1	Zimbabwe	-19.0131	29.14639
OS119	3682 Landrace	R 97?5	Zimbabwe	-19.0131	29.14639
OS120	3683 Landrace	R 101	Zimbabwe	-19.0131	29.14639
OS121	3684 Landrace	R 100?1	Zimbabwe	-19.0131	29.14639
OS122	3685 Landrace	R 102	Zimbabwe	-19.0131	29.14639

OS123	3687 Landrace	SOKONI	Zimbabwe	-19.0131	29.14639
OS124	3688 Landrace	CHIPUNGARE	Zimbabwe	-18.8833	31.4
OS125	3689 Landrace	CHITIRIGU	Zimbabwe	-18.2833	31.18333
OS126	3690 Landrace	DEMBAREMBA	Zimbabwe	-18.2833	31.18333
OS127	3691 Landrace	DEMBAREMBA	Zimbabwe	-18.6	32.08333
OS128	3692 Landrace	KASAWAYA	Zimbabwe	-18.6	32.08333
OS129	3693 Landrace	MARHARORA	Zimbabwe	-20.4	31.45
OS130	3695 Landrace	MUNGORE	Zimbabwe	-19.8833	30.85
OS131	3697 Landrace	SAMANYIKA	Zimbabwe	-18.3833	32.83333
OS132	3698 Landrace	TSINGANO	Zimbabwe	-18.5667	32.8
OS133	3698A Landrace	TSINGANO	Zimbabwe	-18.5667	32.8
OS134	3699 Landrace	TGR 46	Zimbabwe	-20.35	30.6
OS135	3700 Landrace	TGR 52	Zimbabwe	-20.2	30.43333
OS136	3702 Landrace	TGR 123	Zimbabwe	-19.7833	31.66667
OS137	3703 Landrace	TGR 172	Zimbabwe	-20.25	31.05
OS138	3713 Landrace	TGR 538	Zimbabwe	-20.0333	32.91667

8.3 Description of the Shared Socioeconomic Pathway (SSP) Experiment used

Experiment name	Description
historical	The historical experiment is a simulation of the recent past from 1850 to 2014, it is performed with a coupled atmosphere-ocean general circulation model (AOGCM). In the historical simulations the model is forced with changing conditions (consistent with observations) which include atmospheric composition, land use and solar forcing. The initial conditions for the historical simulation are taken from the pre-industrial control simulation (piControl) at a point where the remaining length of the piControl is sufficient to extend beyond the period of the historical simulation to the end of any future "scenario" simulations run by the same model. The historical simulation is used to evaluate model performance against present climate and observed climate change.
SSP5-8.5	SSP5-8.5 is a scenario experiment extending into the near future from 2015 to 2100, it is performed with a coupled atmosphere-ocean general circulation model (AOGCM). The forcing for the CMIP6 SSP experiments is derived from shared socioeconomic pathways (SSPs), a set of emission scenarios driven by different socioeconomic assumptions, paired with representative concentration pathways (RCPs), global forcing pathways which lead to specific end of century radiative forcing targets. SSP5-8.5 is based on SSP5 in which climate change mitigation challenges dominate

and RCP8.5, a future pathway with a radiative forcing of 8.5 W/m² in the year 2100. The ssp585 scenario represents the high end of plausible future forcing pathways. SSP5-8.5 is comparable to the CMIP5 experiment RCP8.5.

8.4 QTNs associated with bioclimatic variables in the cowpea collection

Variable	SNP	Chromosome	Position	P.value	maf	FDR_Adjusted_P-values	effect
bio1	100656:121:-	5	4020593	5.44E-08	0.417526	0.001947119	-8.25511
bio1	140431:113:-	6	23646216	9.57E-07	0.154639	0.011899289	-10.2837
bio1	223645:416:-	10	16101001	7.83E-08	0.474227	0.001947119	-9.33806
bio1	240301:432:-	11	6599281	2.08E-07	0.149485	0.00344328	-9.63003
bio3	114016:55:+	5	27550005	1.37E-07	0.438144	0.000970261	-3.18154
bio3	120276:128:-	5	37462233	2.06E-07	0.015464	0.001282552	5.153514
bio3	134372:235:-	6	12091971	4.57E-06	0.139175	0.025255281	-1.86908
bio3	138867:450:-	6	20637141	3.33E-08	0.041237	0.000276195	3.906096
bio3	139795:242:-	6	22516315	2.39E-08	0.149485	0.000237207	2.134785
bio3	163229:186:-	7	32429843	1.07E-09	0.103093	5.33032E-05	-2.7507
bio3	186692:374:-	8	32692323	2.17E-08	0.365979	0.000237207	-1.46567
bio3	244080:56:+	11	12563387	1.27E-08	0.041237	0.000210622	3.7957
bio3	251858:95:+	11	24030984	2.21E-09	0.061856	5.49297E-05	3.520071
bio4	62141:8:-	3	34955682	3.8E-08	0.407216	0.000945793	-187.795
bio4	132448:103:-	6	8825495	1.88E-11	0.010309	9.3302E-07	1230.62
bio4	138867:450:-	6	20637141	1E-06	0.041237	0.012470358	-416.468
bio4	229490:119:-	10	25603177	2.94E-06	0.216495	0.02924338	-223.084
bio4	237517:27:+	11	1327032	2.17E-07	0.283505	0.0035973	405.0606
bio6	1585:30:+	1	3174169	3.85E-06	0.417526	0.031883139	-13.2549
bio6	60328:446:+	3	32146557	1.66E-08	0.340206	0.000411696	-9.07262



bio6	93011:93:-	4	30764541	1.05E-06	0.113402	0.013078776	-16.312
bio6	138296:303:	6	19503613	7.7E-09	0.036082	0.000383013	-31.6368
bio6	158350:13:+	7	22546213	2.43E-06	0.43299	0.024155074	-9.19748
bio6	240257:23:+	11	6527476	7.9E-07	0.134021	0.013078776	-12.4761
bio11	32495:103:-	2	15133317	1.12E-07	0.134021	0.001850221	14.4354
bio11	100656:121:-	5	4020593	3.25E-07	0.417526	0.004034545	-8.72124
bio11	138296:303:	6	19503613	2.36E-09	0.036082	0.00011715	-30.1246
bio11	158350:13:+	7	22546213	4E-08	0.43299	0.000994558	-8.84237
bio16	215844:87:-	10	3286428	4.15E-07	0.14433	0.007671444	-94.3515
bio16	232831:507:-	10	33281042	6.31E-07	0.438144	0.007844729	-60.5422
bio16	242720:22:-	11	10413385	1.11E-08	0.484536	0.000551888	65.87711
bio16	253904:42:+	11	27034241	4.63E-07	0.134021	0.007671444	-64.8757

8.5 PVS scoring forms

Projecto FOCUS-ÁFRICA						
Ficha de dados de Seleção Participativa de genótipos de feijão nhemba						
Genótipo : _____						
1	Hábito de crescimento		1	2	3	4
	Produtor (1)					
	1. Mau					
	2. Razoável					
	3. Intermédio					
	4. Bom					
	5. Muito bom					
	Produtor (4)					
	Produtor (5)					
2	Tipo de folha		1	2	3	4
	Produtor (1)					
	1. Mau					
	2. Razoável					
	3. Intermédio					
	4. Bom					
	5. Muito bom					
	Produtor (4)					
	Produtor (5)					
3	Ramificação		1	2	3	4
	Produtor (1)					
	1. Mau					
	2. Razoável					
	3. Intermédio					
	4. Bom					
	5. Muito bom					
	Produtor (4)					
	Produtor (5)					
3	Número e vagens por planta					
	Produtor (1)					
	Produtor (2)					
	1. Mau					
	2. Razoável					
	3. Intermédio					
	4. Bom					
	5. Muito bom					
	Produtor (5)					
4	Ciclo da cultura					
	Produtor (1)					
	Produtor (2)					
	1. Mau					
	2. Razoável					
	3. Intermédio					
	4. Bom					
	5. Muito bom					
	Produtor (5)					



This project has received funding from the European Commission's Horizon 2020 Research and Innovation Programme. The content in this presentation reflects only the author(s)'s views. The European Commission is not responsible for any use that may be made of the information it contains.