

## **Project Goal**

The goal of this research project is **to identify and document genomic resources for drought, aluminium and salt tolerance in diverse Ethiopian finger millet germplasm** by using whole-genome sequencing (WGS)-based genome-wide association studies (GWAS) and RNA sequencing (RNA-Seq)-based differential gene expression analysis. A genome-wide association study is an approach that involves rapidly scanning markers across the complete sets of DNA, or genomes, of many individuals to find genetic variations associated with a particular phenotype. Drought decreases crop yields due to the associated moisture stress and high temperatures. Acid soils reduce crop productivity because of the detrimental effects of the toxic aluminium forms they contain, while saline soils hamper productivity due to the harmful effects of sodium and chloride ions. The negative impacts of these abiotic stresses are further aggravated by climate change, which is expressed as variations in precipitation and temperature. There are various abiotic stress management strategies, but the development of tolerant varieties is the most sustainable approach since it is both economically and technically feasible and ecologically sound.

## **Description of Research**

In this project, we will first **evaluate up to 500 diverse finger millet accessions** that originated in Ethiopia for their tolerance to drought, aluminium and salt stresses at an early seedling stage under hydroponic conditions. Hydroponics is a method of growing seedlings in a nutrient solution that is supplied with air. The seeds of each finger millet accession will be surface disinfected and germinated for three days. The seedlings will then be grown under "control" and "stress" conditions for seven days for each type of stress. A "control" condition is a hydroponic or plant nutrient solution devoid of a stress-inducing compound, while a "stress" condition is a nutrient solution containing the stress-inducing compound. The root length of each accession grown in "control" and "stress" conditions will be measured and analyzed to determine their tolerance level. Accessions representing all tolerance classes for each abiotic stress will be selected for WGS-based GWAS. Likewise, accessions representing tolerant and sensitive classes will be selected for gene expression analysis based on RNA-Seq approaches. Leaf and root samples will be collected from the selected accessions for DNA and RNA isolation, which will be used for library preparation. The libraries will then be sequenced using the WGS and RNA-Seq methods. The sequence data and phenotype data will be collected following standard procedures.

## **Reasons for Attempting the Topic**

The **global population, projected to surpass 9 billion by 2050, is increasing**, particularly in sub-Saharan Africa, and Central and Southern Asia. Agricultural production has to increase by 60%–70% to meet the **food demand, which is predicted to increase** by 59%–102%. However, an **increase in crop production is hindered by abiotic stresses such as drought, soil acidity, and salinity**, among others. The negative impacts of these stresses are further aggravated by climate change. Therefore, it is **necessary to select and/or design proper crop ideotypes** to increase global agricultural production and avoid food and nutrition insecurity.

**For several reasons, finger millet can be considered one of the ideal candidate crops in which a significant yield increase can be gained** because of several reasons. Finger millet is adaptable to adverse environmental conditions since it is tolerant to moisture stress, acidic and saline soils; requires minimum inputs; and generally thrives on marginal land where other crops fail. Finger millet grain is gluten-free, rich in calcium, fiber and iron, has excellent malting qualities, with a low glycemic index, and because of these properties, finger millet is a choice food for diabetics. **Regardless of its importance, little effort has been made to improve its productivity, particularly in terms of drought, acidity, and salinity tolerance.** Because Ethiopia is the center of origin and diversity for finger millet and possesses extensive areas of drylands (75%), acid soils (34%), and saline soils (43%), valuable levels of drought, soil acidity, and salinity tolerance genes might have evolved through strong selection pressure imposed by the abiotic stresses.

## **Substantial Results Expected**

We expect that the project will unravel the molecular mechanisms of drought, soil acidity, and salinity tolerance in finger millet germplasm. Specifically, the project will identify abiotic stress tolerance genes, construct a detailed genetic map for the identified stress tolerance genes, and characterize differential gene expression profiles in finger millet germplasm in response to the abiotic stresses. Additional benefits of the project will be the development of molecular markers that would enable rapid screening of finger millet germplasm for tolerance to drought, soil acidity, and salinity so that the negative effects of abiotic stresses and the worsening impact of climate change on finger millet production will be alleviated. A gene is a DNA sequence that specifies one or more sequence-related RNAs or proteins, while a genetic map is a graphic representation of the order of genes within chromosomes by means of detailed analysis of the DNA. The genomic resources that will be generated by this project will be used by plant breeders to develop improved finger millet cultivars that can survive and provide high yields in areas affected by drought, soil acidity, and salinity.