



Genetic Improvement of Sorghum for Resistance to Fungal Pathogens

Progress Report

Tesfaye Mengiste

Participants & Institutions

Alemu Tirfessa, EIAR, Melkassa
Alemnesh Bekele, Haramaya University
Assefa Gidesa*, EIAR, Assosa
Chemeda Berhanu*, OARI, Bako
Frezer Girma, EIAR, Assosa
Gebisa Ejeta, Purdue
Getachew Ayana, EIAR, Melkassa
Gezahegn Girma, Purdue
Gudeta Bedhadha, OARI, Bako
Habte Nida, Purdue
Kebede Dessalegn, OARI, Bako
Moges Mekonen, EIAR, Melkassa
Nasria, EIAR, Jimma
Solomon Admasu
Tamirat Bejiga, EIAR, Melkassa



Objectives

- Development of disease resistant and improved varieties
- Genetic and genomic studies to identify resistance genes, or resistance loci
- Core collection
- Training



Presentations today

- **Tesfaye Mengiste:** Highlights
- **Chemeda Berhanu**
 - National and regional breeding activities
 - Released and candidate varieties
 - Seed increases, popularization efforts demonstrations...
 - Characterization of Ethiopia core collection
- **Gezahegn Girma:** mapping of new resistance loci, and genomics of core



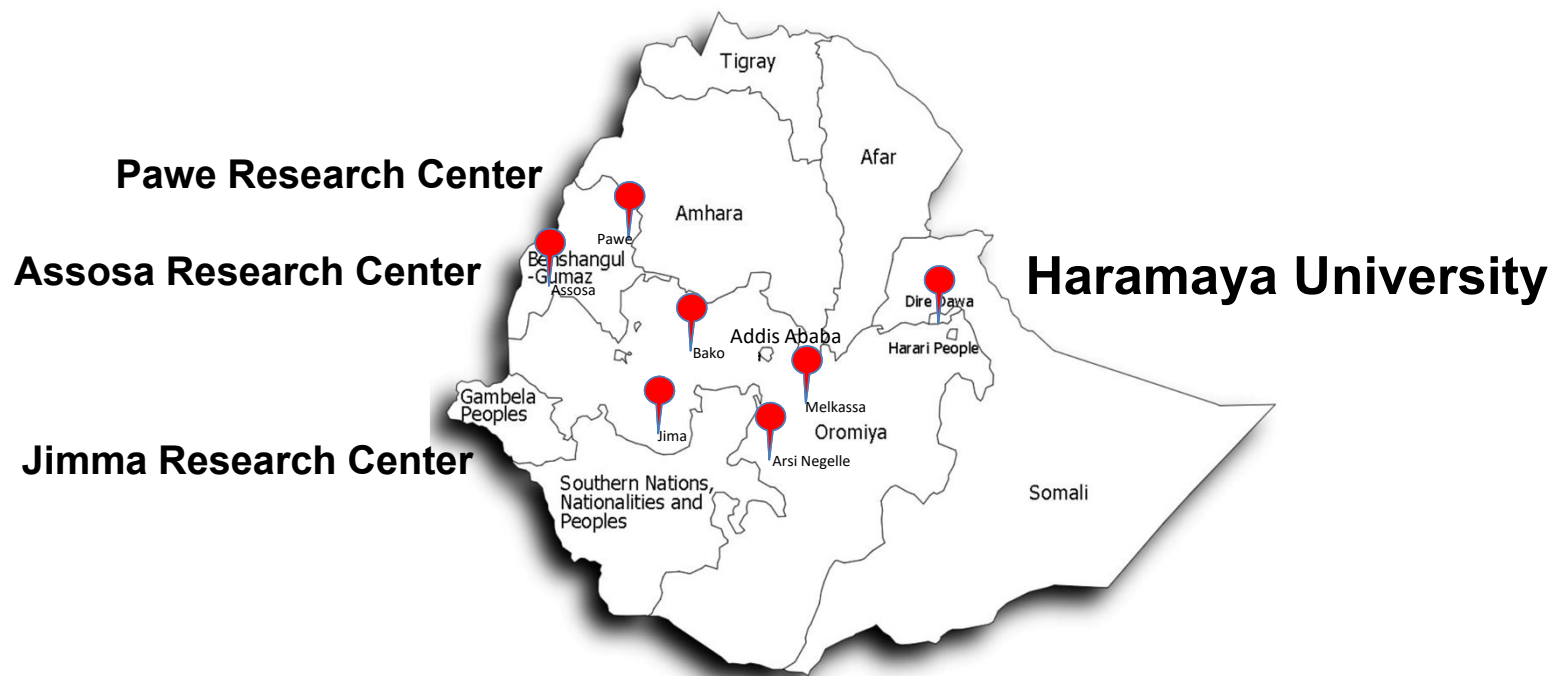
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Trial sites



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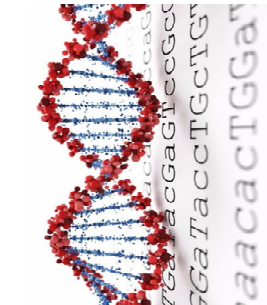
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Area of Research

- Pathology
- Molecular biology
- Resistance breeding
- Genetics and genomics



Genotypes	Fungal strains				
	Csgl_1	Csgl_2	Cs_27	Cs_29	Cs_grg
ARG1	R	R	R	R	R
ARG2	R	S	R	S	S
ARG3	S	S	S	R	R
ARG4	R	R?	?	R?	R
ARG5	R	?	S	S	R
PML981442	S	R	R	R	R
PML981475	S	R	R	R	R
PML981476	S	R	R	R	R
PML981488	S	R	R	R	R
TAM428	S	S	S	S	S
BTx623	S	S	S	S	S

Resistance genes

- ARG1, published
- ARG2, manuscript submitted
- ARG3, fine mapping complete, validation
- ARG4 and ARG5: mapping complete, *Habte? Are you listening?*
- Additional mapping for new ARGs (ARG 6-9) underway.



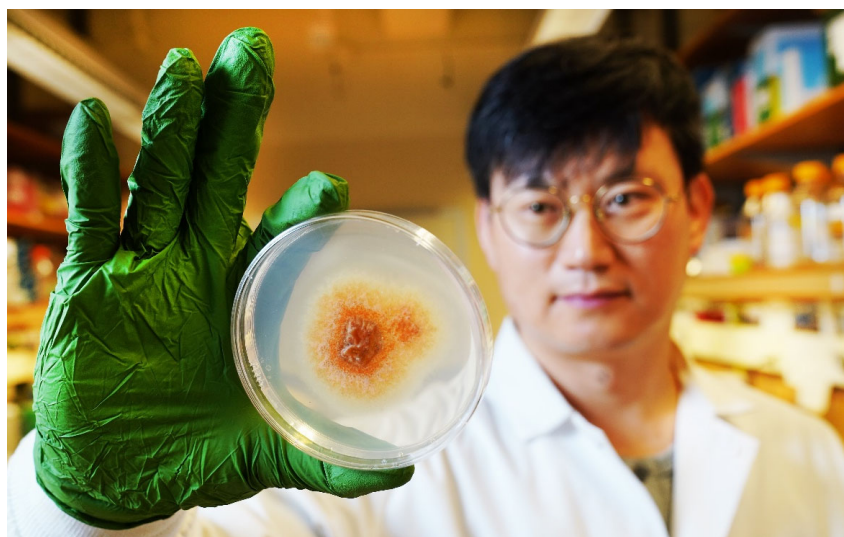
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“One gene closer to a superman sorghum”



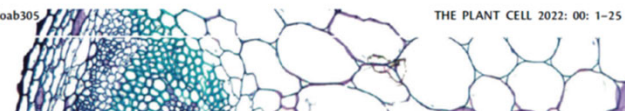
“As climate change events shift or necessitate the production of dryland crops such as sorghum into higher rainfall or irrigated regions, leaf diseases become even more significant,” “It is precisely in those situations where powerful genes become so crucially important.”

(Gebisa Ejeta)

<http://doi.org/10.1093/plcell/koab305>








THE
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CELL

THE PLANT CELL 2022; 00: 1–25



Research Article

Broad-spectrum fungal resistance in sorghum is conferred through the complex regulation of an immune receptor gene embedded in a natural antisense transcript

Sanghun Lee ¹, Fuyou Fu ¹, Chao-Jan Liao ¹, Demeke B. Mewa ¹, Adedayo Adeyanju ², Gebisa Ejeta ², Damon Lisch ¹ and Tesfaye Mengiste ^{1,*,†}

¹ Department of Botany and Plant Pathology, Purdue University, West Lafayette, Indiana 47907, USA

² Department of Agronomy, Purdue University, West Lafayette, Indiana 47907, USA

*Author for correspondence: mengiste@purdue.edu

[†]Senior author.

These authors contributed equally (S.L. and F.F.).

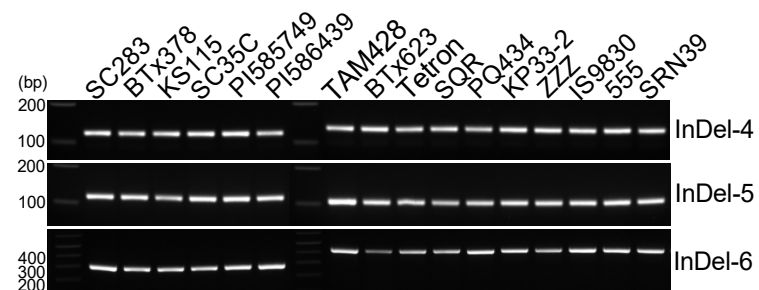
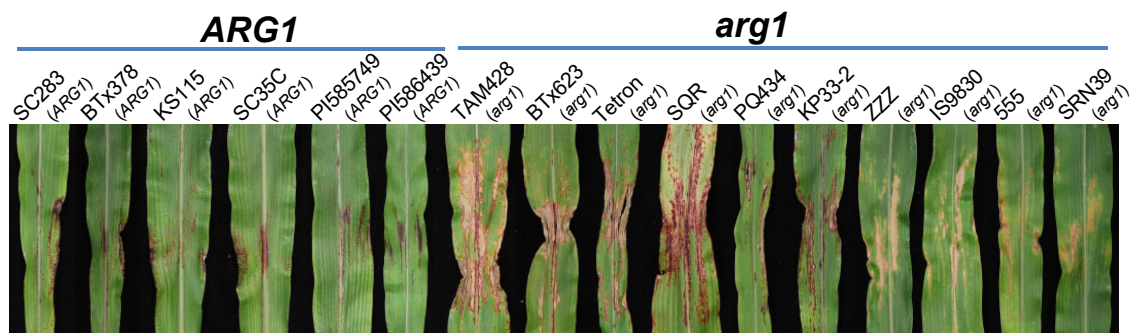
S.L. conducted marker analysis, SNP and InDel analysis, mapping and characterization of the CARG–ARG1 loci, construction of all CARG–ARG1 plasmids, generation of CARG–ARG1 Arabidopsis transgenic plants, reporter gene assays, the genetic screen and disease assays on independent sorghum lines, F2 population, and RILs, CHIP, DNA methylation, RACE, alternative splicing, and gene expression analyses, and phylogenetic analysis. F.F. conducted the genetic screen, QTL-seq, bioinformatic analysis, SNPs and InDels analysis, gene expression analyses, disease assays on the RILs, phylogenetic analysis, and small RNA identification. C.-J.L. conducted the reporter gene assay. A.A., D.B.M., conducted the additional disease assays, made the genetic crosses, and analyzed the genetic segregation data. T.M., S.L., F.F., G.E., D.L. designed the research, analyzed the data, and wrote the paper.

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (<https://academic.oup.com/plcell/advance-article/doi/10.1093/plcell/koab305/6501450>) is: Tesfaye Mengiste (mengiste@purdue.edu).

Abstract

Sorghum (*Sorghum bicolor*), the fifth most widely grown cereal crop globally, provides food security for millions of people. Anthracnose caused by the fungus *Colletotrichum sublineola* is a major disease of sorghum worldwide. We discovered a major fungal resistance locus in sorghum composed of the nucleotide-binding leucine-rich repeat receptor gene ANTHRACNOSE RESISTANCE GENE1 (ARG1) that is completely nested in an intron of a cis-natural antisense transcript (NAT) gene designated CARRIER OF ARG1 (CARG). Susceptible genotypes express CARG and two alternatively spliced ARG1 transcripts encoding truncated proteins lacking the leucine-rich repeat domains. In resistant genotypes, elevated expression of an intact allele of ARG1, attributed to the loss of CARG transcription and the presence of miniature inverted-repeat transposable element sequences, resulted in broad-spectrum resistance to fungal pathogens with distinct virulence strategies. Increased ARG1 expression in resistant genotypes is also associated with higher histone H3K4 and H3K36 methylation. In susceptible genotypes, lower ARG1 expression is associated with reduced H3K4 and H3K36 methylation and increased expression of NATs of CARG. The repressive chromatin state associated with H3K9me2 is low in CARG-expressing genotypes within the CARG exon and higher in genotypes with low CARG expression. Thus, ARG1 is regulated by multiple mechanisms and confers broad-spectrum, strong resistance to fungal pathogens.

Gene specific molecular markers

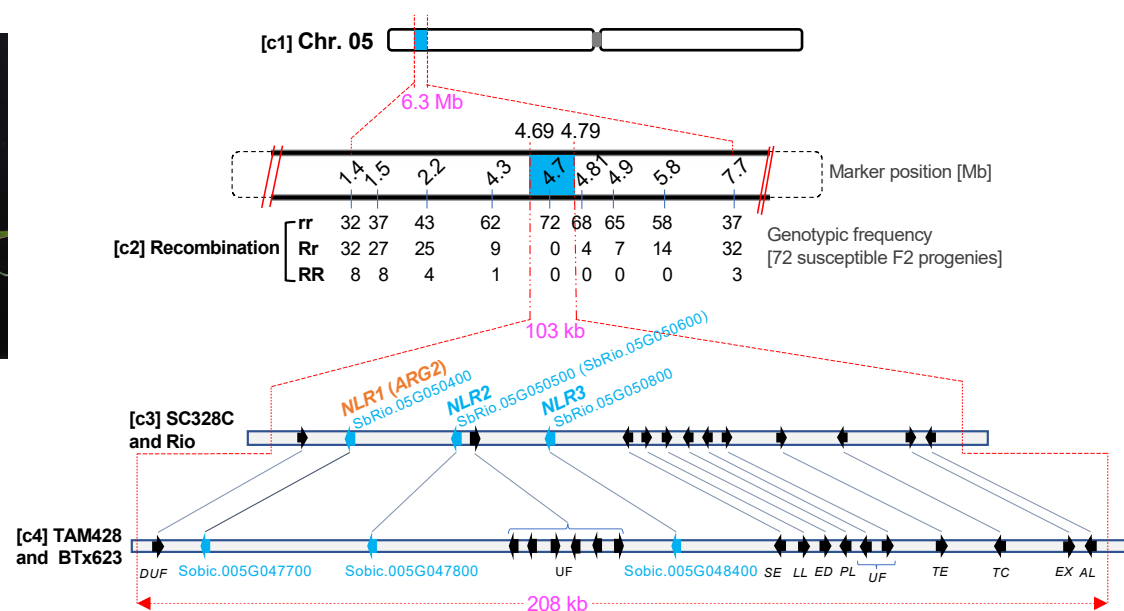
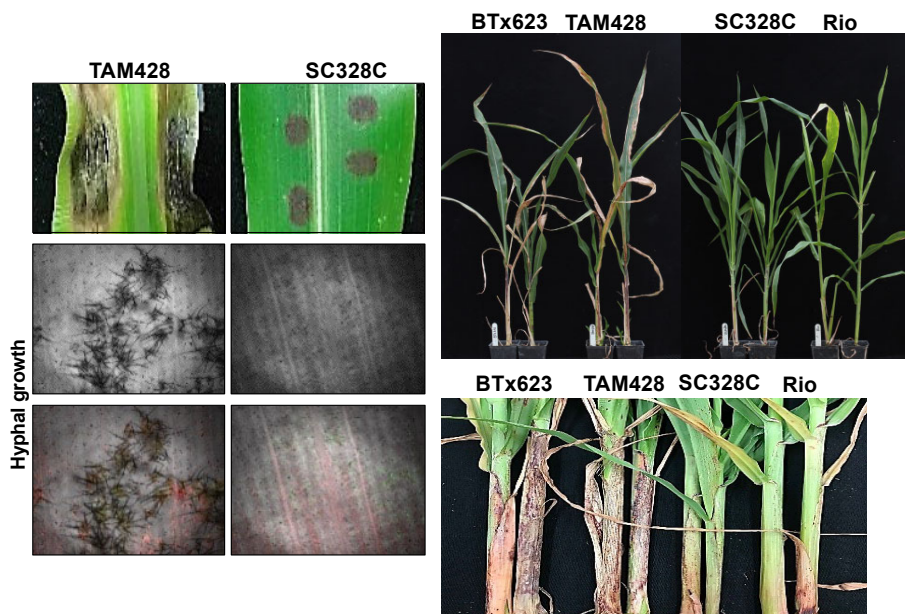


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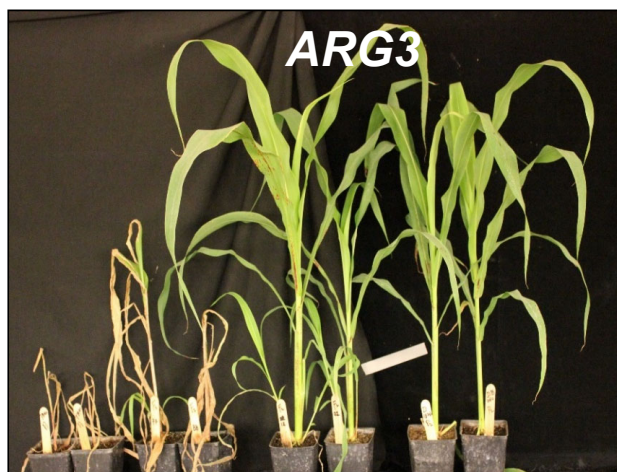
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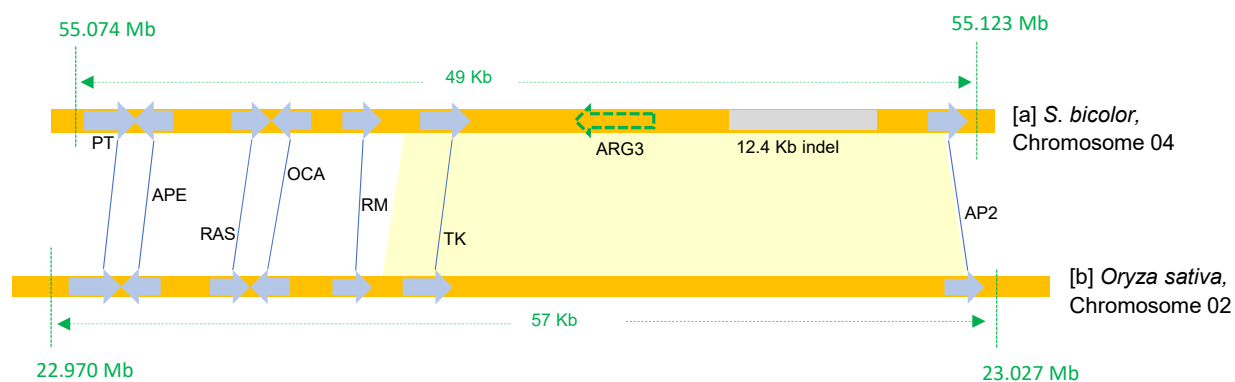
Disease with strain using Cs29



ARG3

arg3

Synteny between *S. bicolor* and *O. sativa* around ARG3 locus

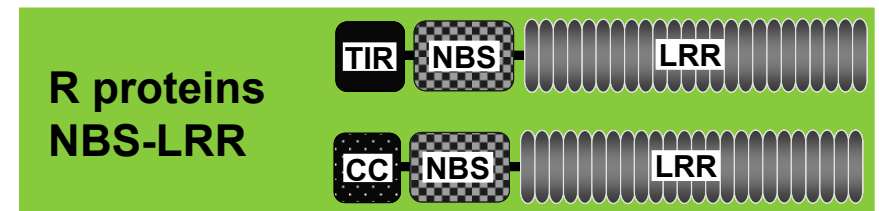


Mapping using resistance to Cs29, Csgrg

Summary

- Identified **five** major genes, closing on **one**, additional **three** loci defined
- Tightly linked or gene specific markers for **six** genes
- Four NBs-LRR proteins
- **ARG3** is protein of unknown function

ARG1, ARG2, ARG4, ARG5



Canonical R proteins have a *leucine-rich repeat*

PhD dissertation titles

Assefa Gidesa

Distribution, Pathogen Variability and Management of Sorghum Anthracnose (*Colletotrichum sublineola*) in South-Western Regions of Ethiopia

Chemed Berhanu

Genetic Diversity, Genotype by Environment Interaction and Genome Wide Association Mapping For Anthracnose (*Colletotrichum Sublineola*) Resistance in Ethiopian Sorghum Core Collection

Moges Mekonen

Genetic diversity and association mapping of virulence gene in *Colletotrichum sublineola*

Summary

- One variety released in 2020
- Multiple materials in pipeline for future release
 - Multiple lines at the variety verification stage
 - Possible release in 2022
- Introgression- materials at different levels in the national and regional programs
- Genomic and phenotypic characterization of the core

So little time so much to do

- Promote released varieties and materials in the pipeline
 - Seed production
 - Advance materials from crossing towards variety
 - Finalize trial of the core, and replace with new population
 - Open access publications for at least two ARGs, and team publication on the core
 - Training workshop in Ethiopia (Summer/Fall 2022)
 - Short term training- Chemedda at Purdue
 - Start multi-location testing of new RILs in Ethiopia
- ❖ Next phases- transfer ARGs into elite materials through a locally led effort



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The U.S. Government's Global Hunger & Food Security Initiative

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Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet

2017 Annual Review Meetings
March 6-9, 2017 - Saly, Senegal



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