BETTER MICROBES
BETTER CROPS
BETTER WORLD

USCCN Workshop, 20 August 2023

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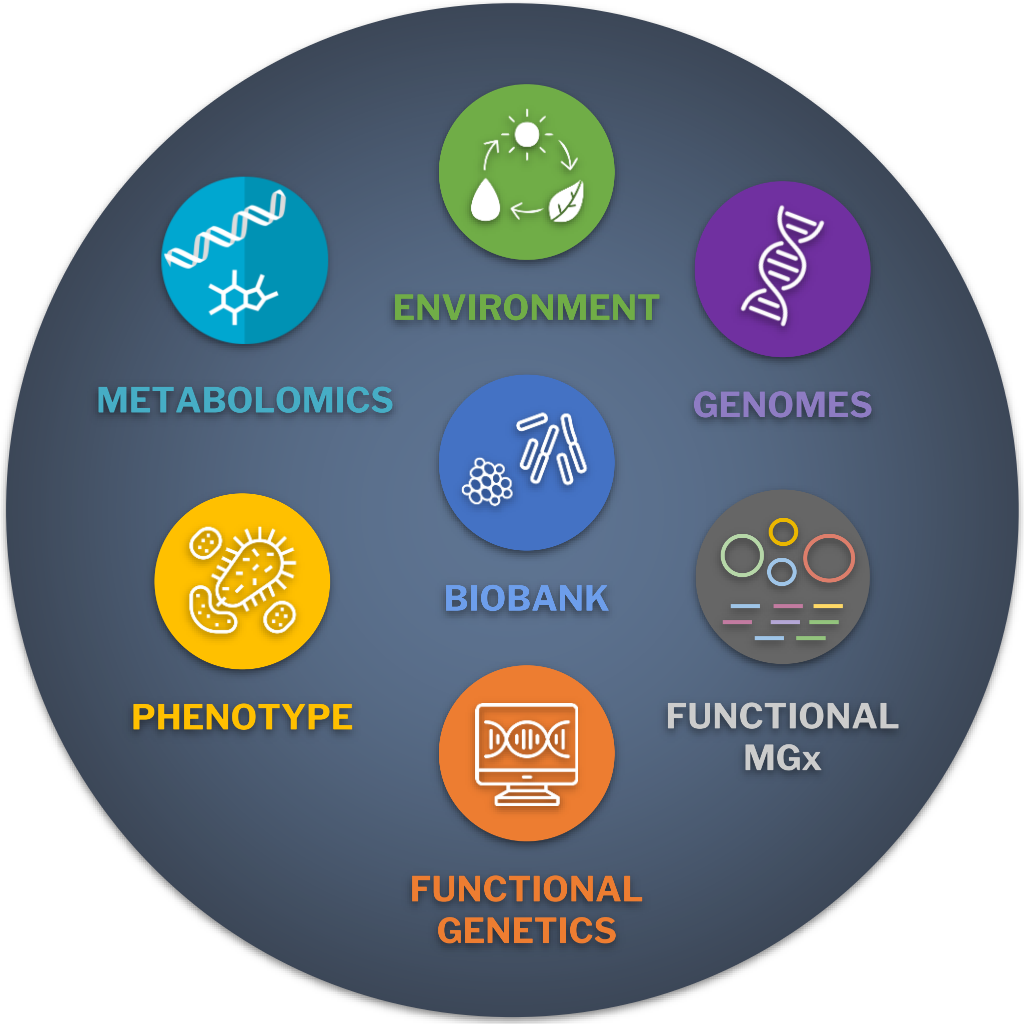
AGBIOME®

- Introduction to the **AgBiome Culture Collection**
- What we find **Valuable** about the collection
- A few **Examples** of discoveries from our collection
- Public/Private **Collaboration** opportunities and challenges

AgBiome GENESIS™ Platform



- ➢ Focused on **Broad Environmental Samples**
- ➢ Biobank of **100,000+ Individual Isolates**
- ➢ **Fully Sequenced Genomes** for each isolate
- ➢ Archived **Environmental Samples**
- ➢ **Metagenomics** for unculturable microbes
- ➢ **Functional Genomics** on half a billion genes
- ➢ **Phenotypic Screens** with real-world translation
- ➢ Diverse Chemistry via **Biosynthetic Gene Clusters**
- ➢ Complete **Meta-Data** for every isolate

The AgBiome Culture Collection

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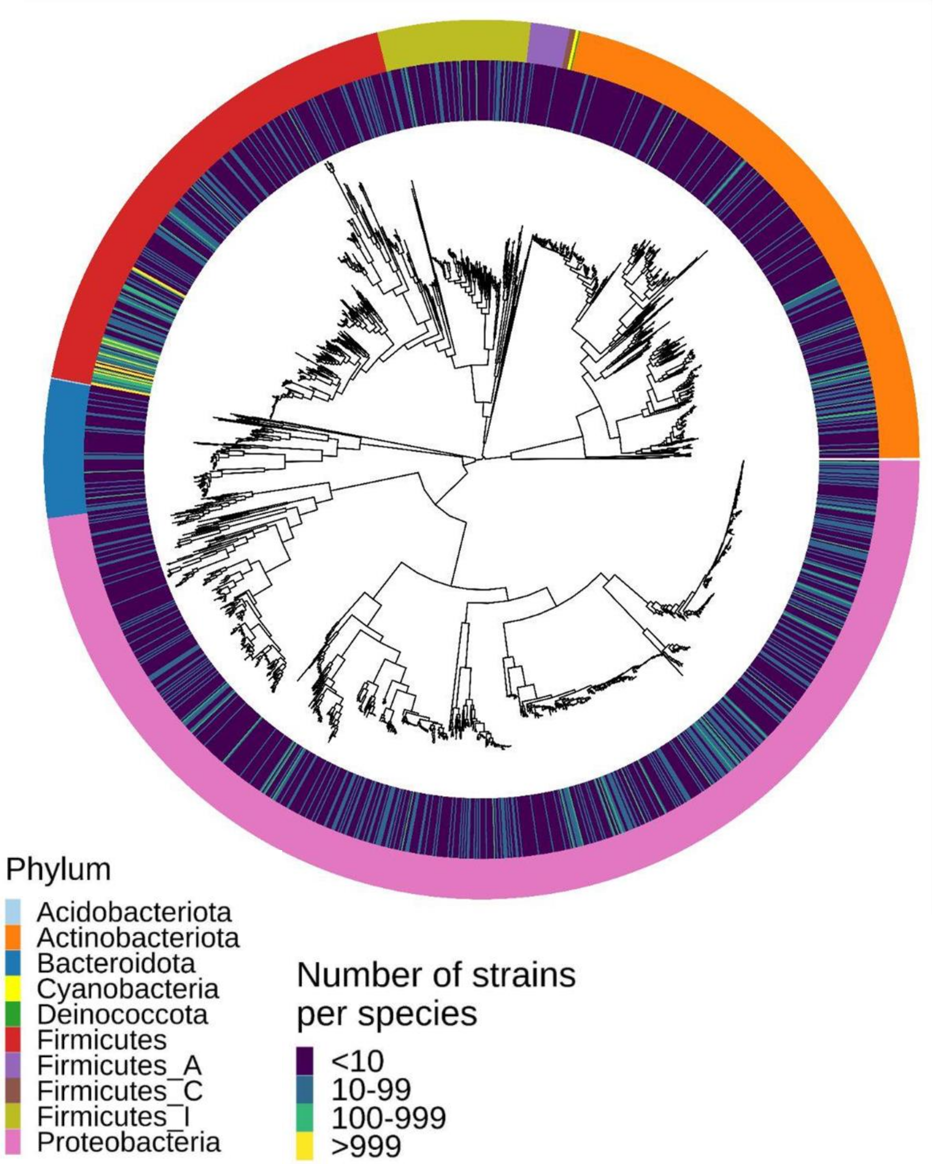
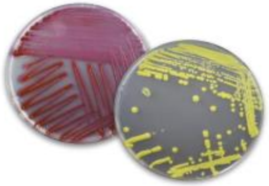
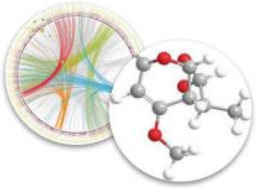


8,000+ unique environmental samples from North America and Africa



Highly diverse collection of **100,000+** fully sequenced microbes comprising **1,460** species and **431** genera



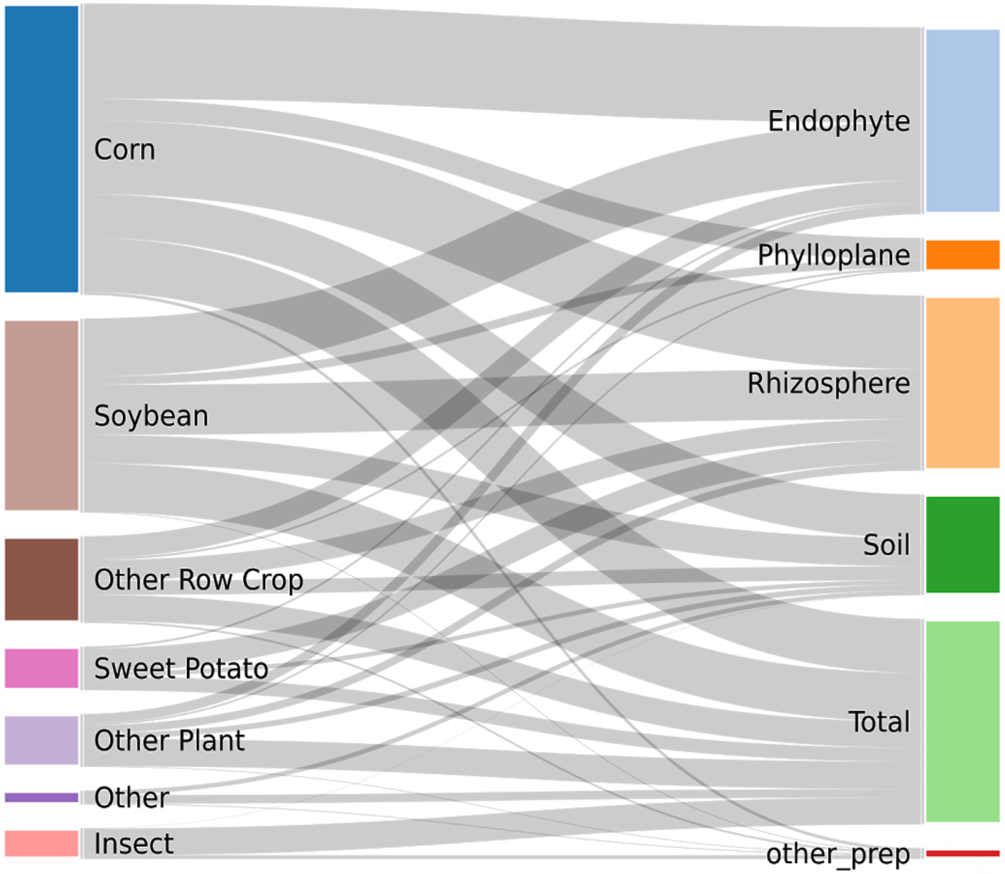
High quality genomic sequence of each microbe representing **500,000,000+** genes and **1,000,000+** BGCs

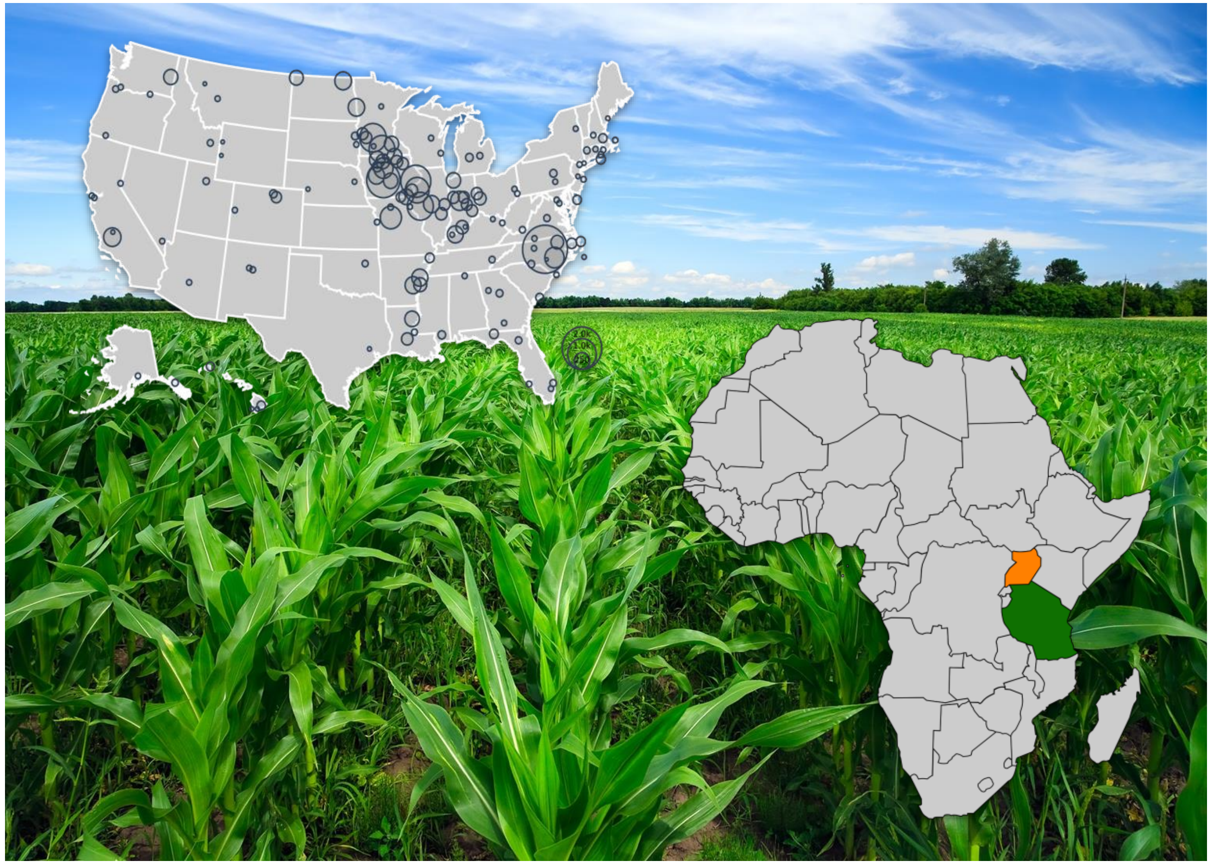
Broad access to Functional Diversity

Specific Functions per Taxa

Ability to find the Best of the Best

To build our collection, we emphasize **Broad Environmental Sampling**

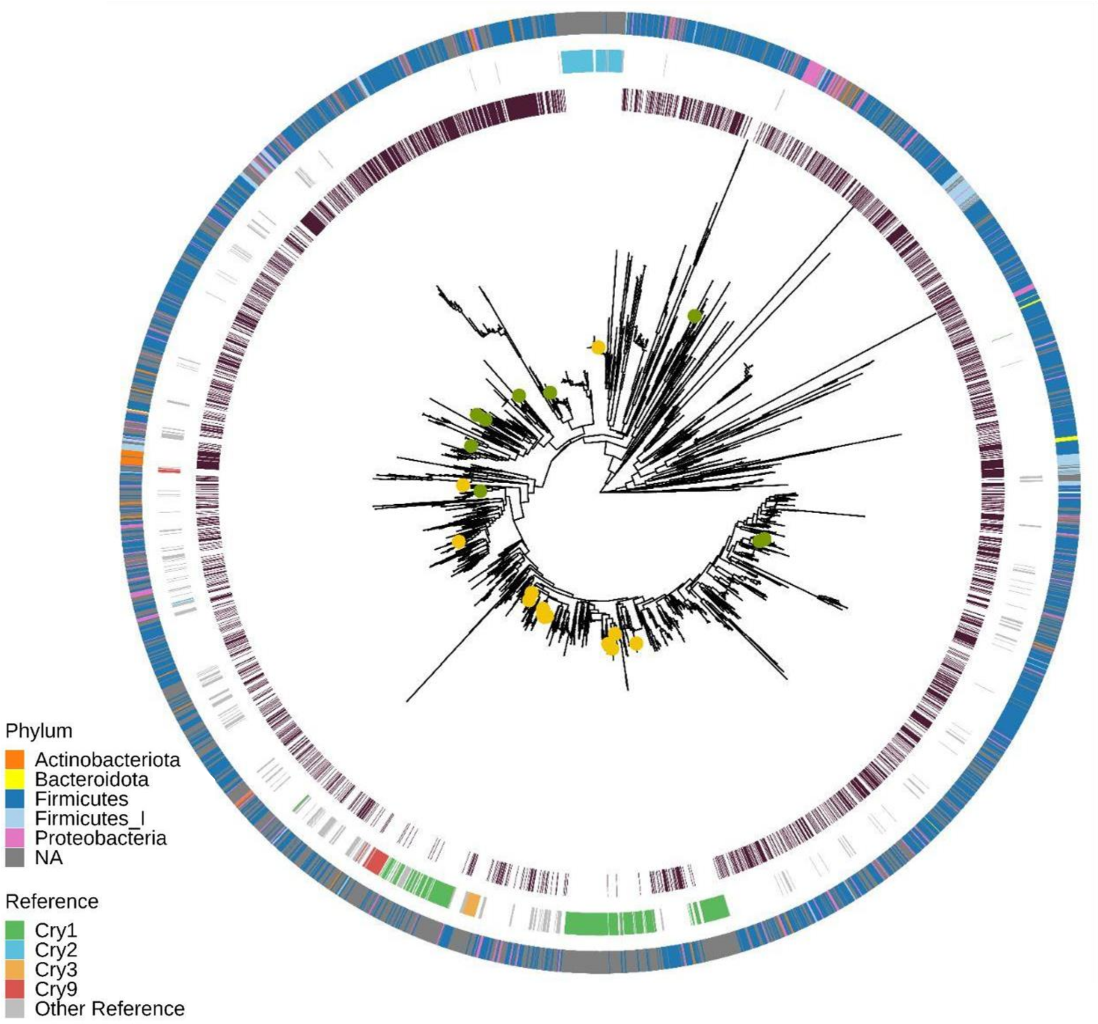


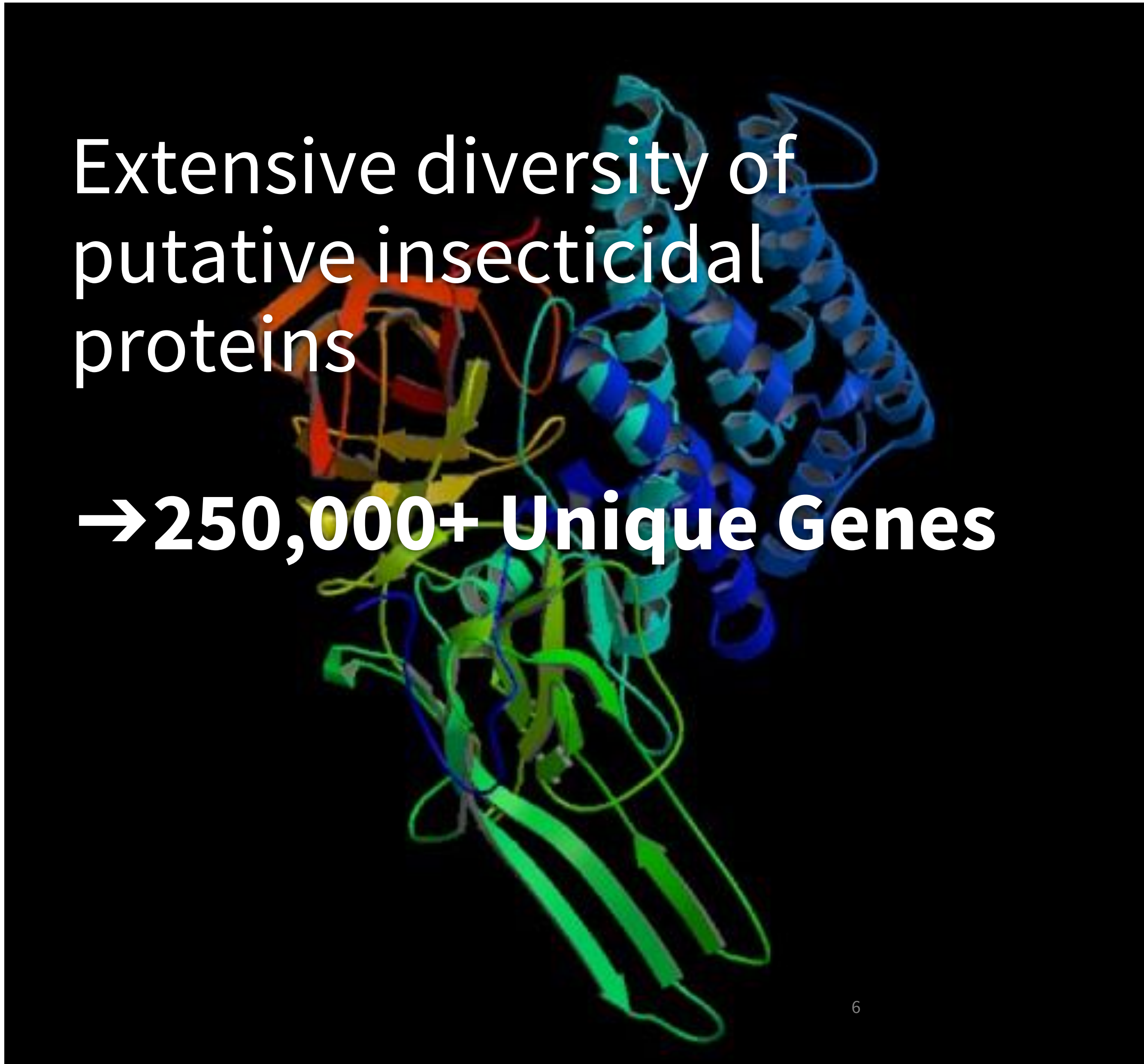


Primarily from Agricultural Fields and High-Diversity Environments

Over 8,000 Unique Environmental Samples Archived

Complete Genomes deliver **Gene Diversity**

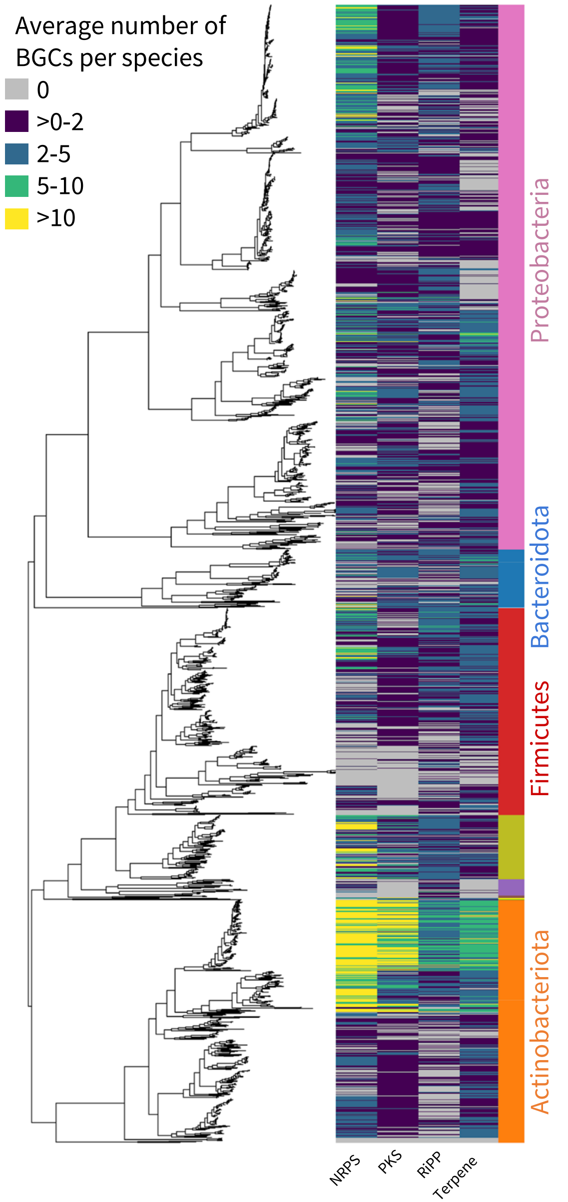




Extensive diversity of putative insecticidal proteins

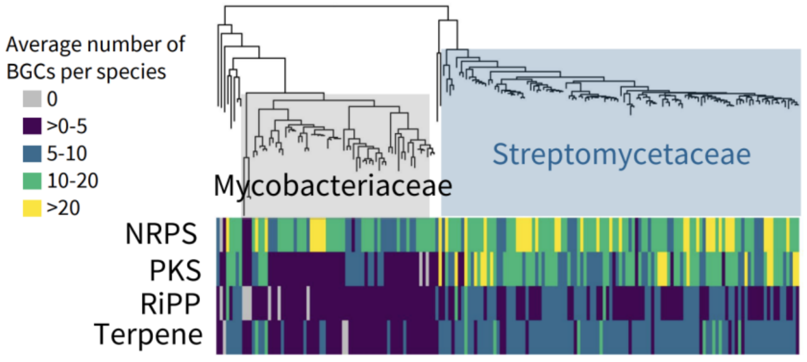
➔250,000+ Unique Genes

Microbial Universe delivers **Diverse Chemistry**

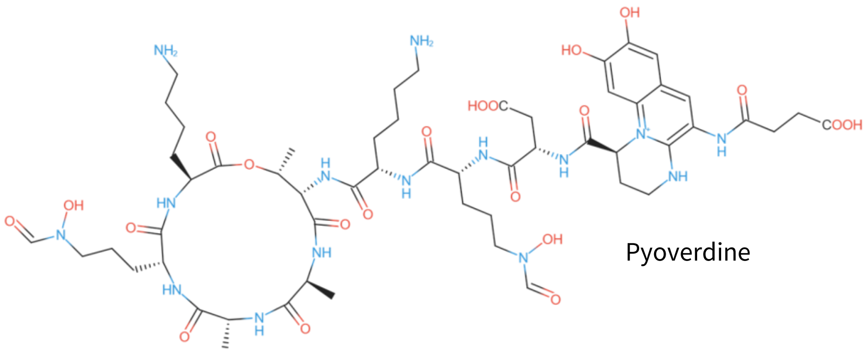


Over 1 million Biosynthetic Gene Clusters

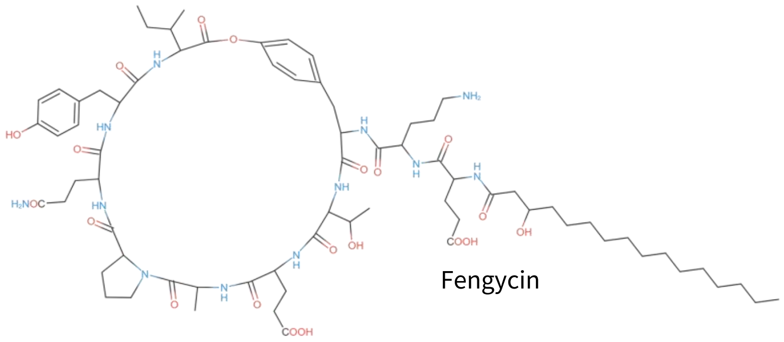
- Extensive Potential for Chemical Diversity
- Novel Natural Product Discovery



Partial representation of Actinobacteriota with two subclades. Streptomycetaceae is gifted with all BGC classes, especially PKS. Mycobacteriaceae are similarly gifted with NRPS, PKS, and Terpenes, but have fewer RiPPs.



Pyoverdine



Fengycin

Realizing Value from our Collection

Discovery for Broad Spectrum Disease Control

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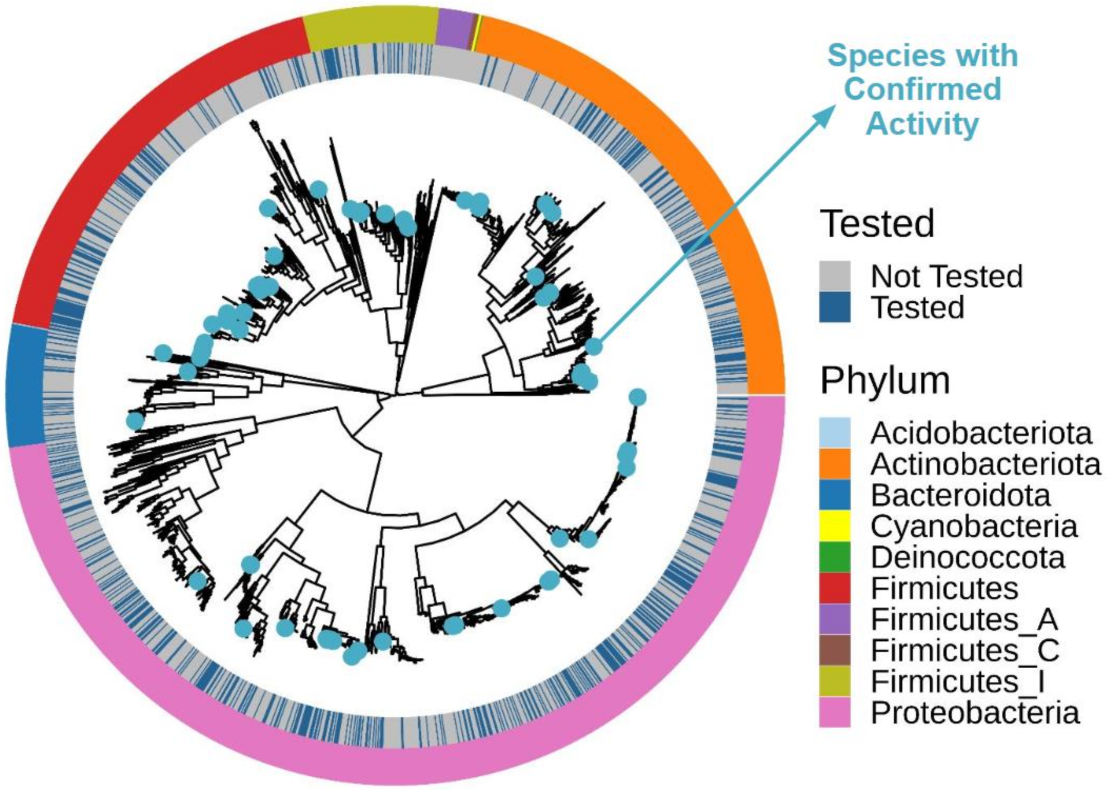
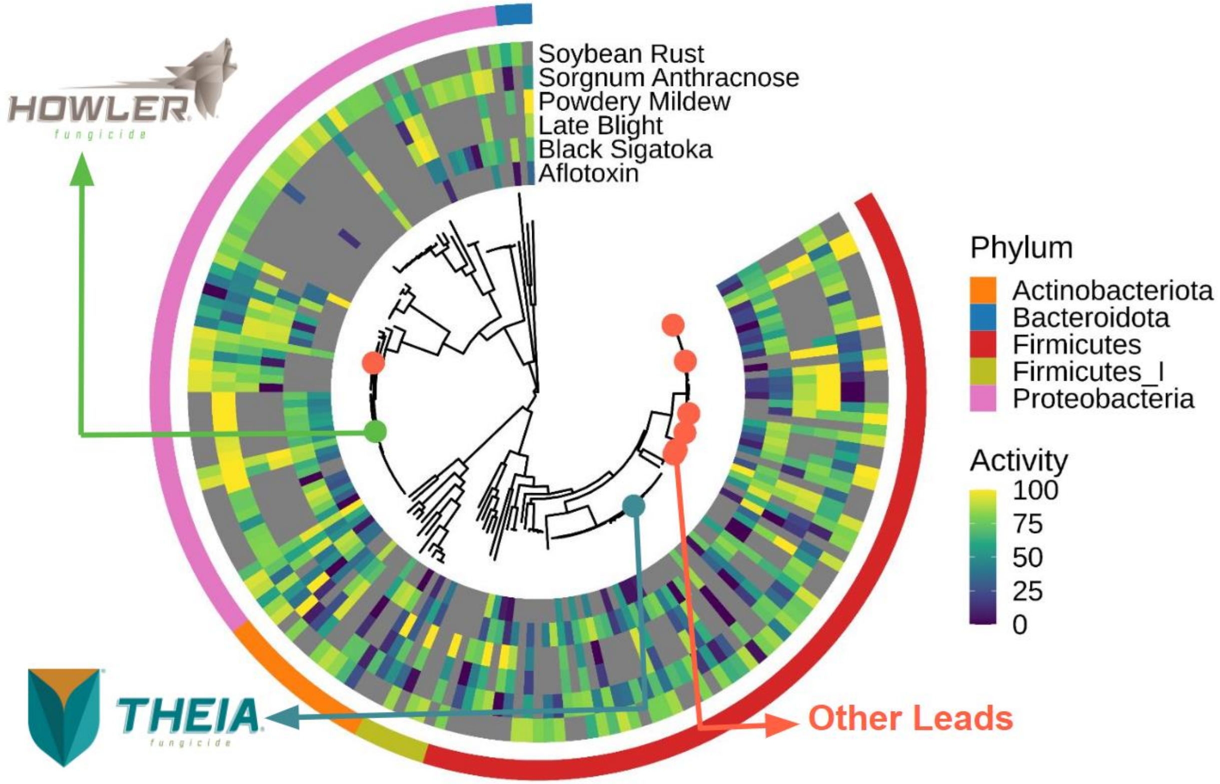
Diverse Isolates screened across 10 different phyla



Confirmed Activity across 5 Phyla



Diversity of Actives = Diversity of Modes of Action

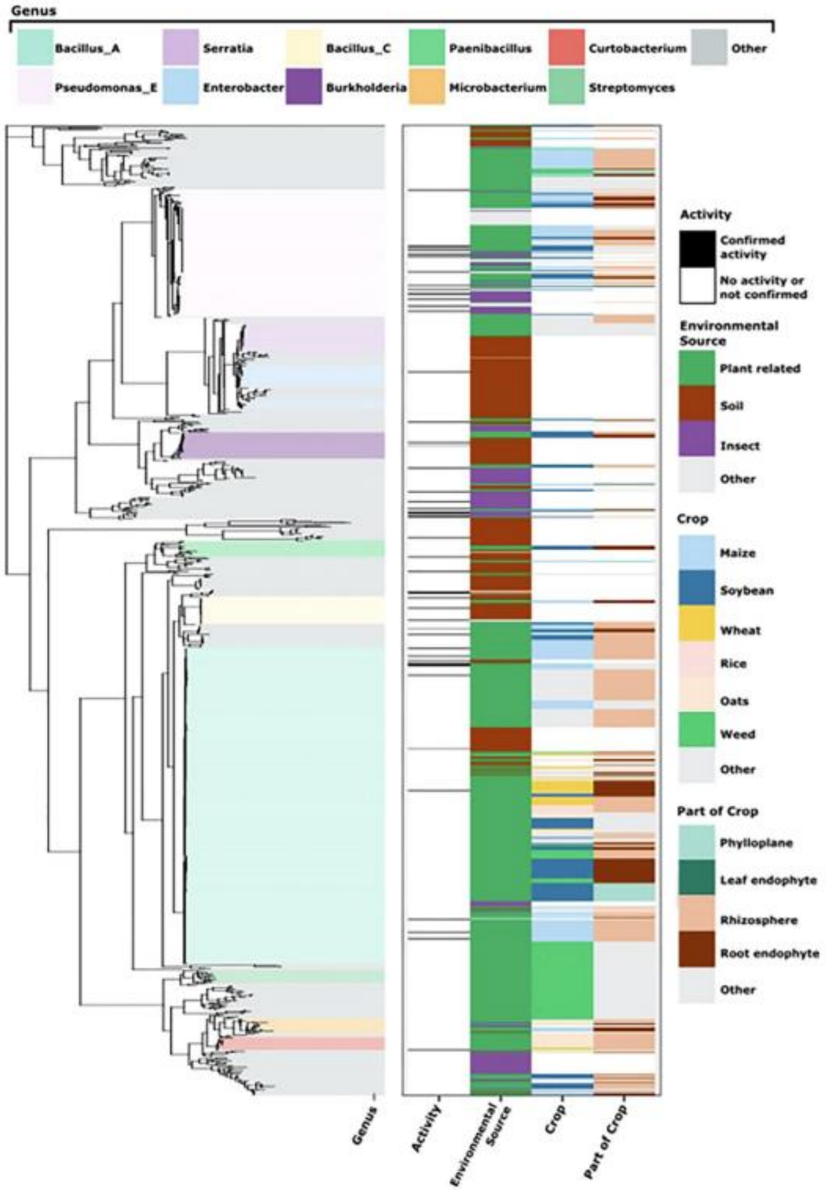


FIGURE 2
Metadata associated with bacterial isolates evaluated in the initial screen. On the left is the SSU phylogenetic tree with the most abundant genera highlighted as classified by the Genome Taxonomy Database (GTDB) (see key at the top). On the right we indicate activity against soybean rust (at least 75% reproducible rust reduction), environmental source of the isolate, and for plant-associated isolates, the crop, and the part of the crop/plant from which bacteria were isolated (see key to the right).

Diverse environmental bacteria displaying activity against *Phakopsora pachyrhizi*, the cause of soybean rust

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Antifungal activity can be found in any environment and across a broad diversity of taxa

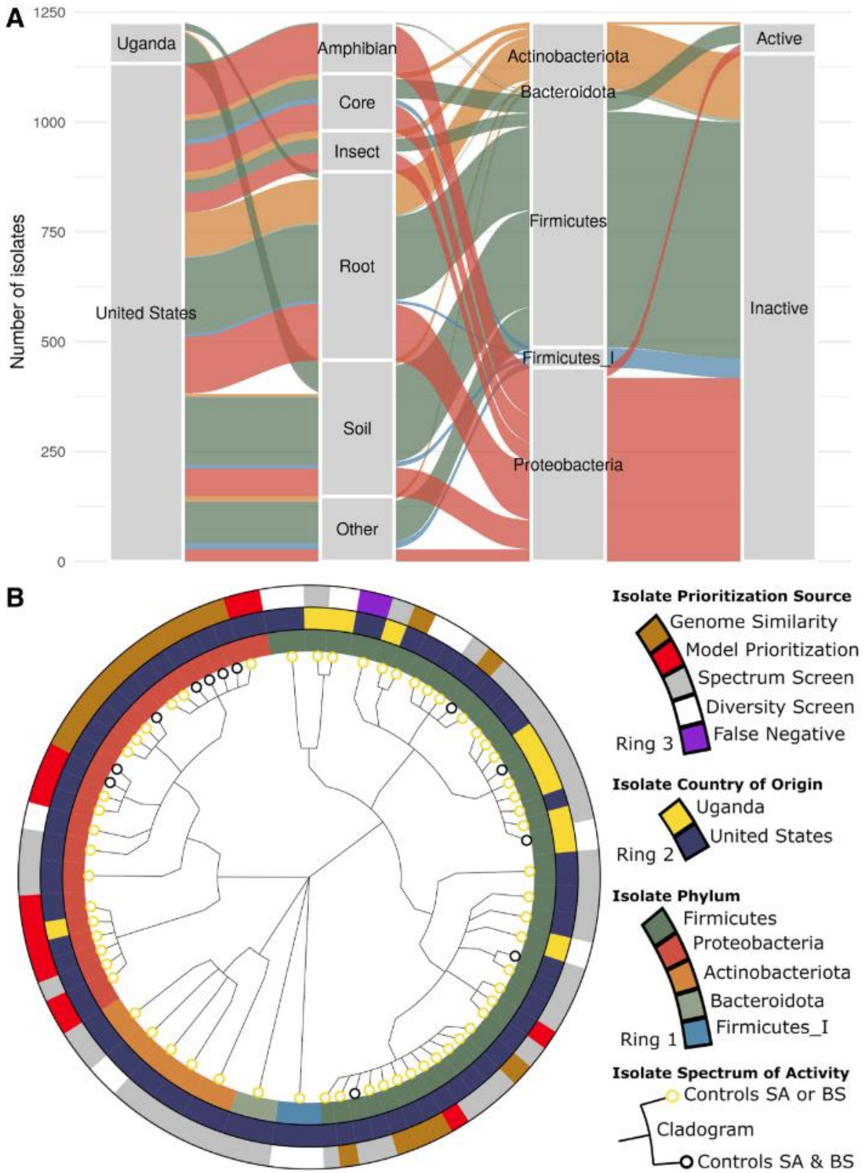

Fig. 2. Scope of screening effort, and diverse isolates with confirmed fungicidal activity. **A,** Alluvial diagram illustrates the source country, sample type (the less abundant types were combined into "Other"), phylum membership, and fungicidal activity of the 1,227 isolates screened in this work. Band colors indicate phylum membership (see legend in panel B). **B,** Cladogram in the center highlights the diversity of the biocontrol isolates discovered in this work (five phyla represented by the center branches, 14 genera, and 22 species). SA = sorghum anthracnose and BS = black sigatoka. The cladogram was constructed using whole-genome-based taxonomic IDs (see Materials and Methods). Multiple isolates displayed activity against both diseases (black leaf nodes). The outer ring shows the isolate prioritization strategies that led to each discovery, including predictive models. The "false-negative" isolate in purple was predicted to be inactive by all modeling approaches and yet was found to be reproducibly active against sorghum anthracnose.

Genomics- and Machine Learning-Accelerated Discovery of Biocontrol Bacteria

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Machine Learning Algorithms developed to accelerate our Discovery:

- ➢ Identify additional **more effective** isolates
- ➢ Counter-select to enrich for additional **modes of action**

Summary of AgBiome Collection

Breadth and Depth across collection

- 100,000+ **Fully Sequenced** Isolates
- **Complete Metadata** for each Isolate
- Archived **Environmental Samples**
- Documented **Ownership**
- **Potential value** for many industries

Public/Private Opportunities and Challenges

Maintain Intellectual Property rights

Metagenomics “collections” to expand into unculturable space

Systematic and consistent connection of all metadata for isolates

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