Genomics & Microbiome Analysis

to identify the next generation biopesticides

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CEO
BioConsortia, Inc.

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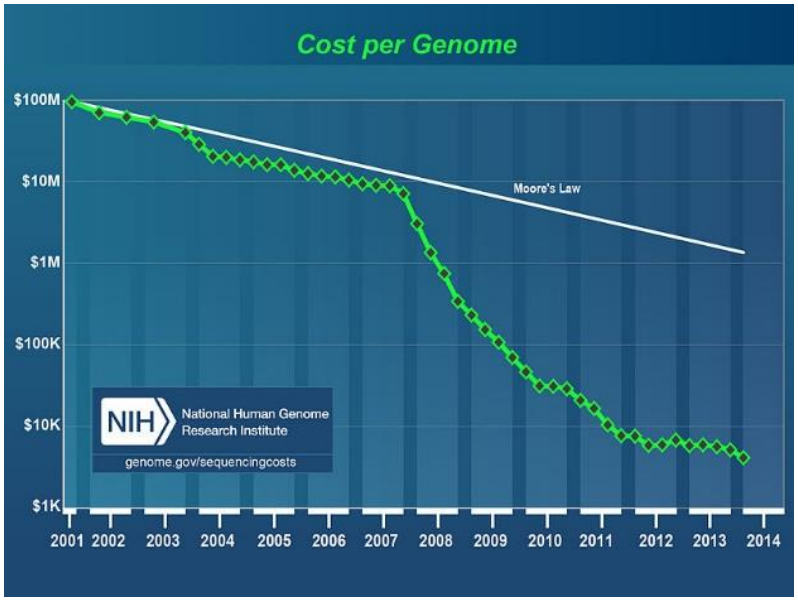
DNA Driven Discovery

Genome sequencing costs have dropped dramatically in the past decade allowing for consistent use in research programs



First human genome sequenced in 2000[1]

$100 million
9 months

Human Longevity Inc. 2016[1]

< $2,000
15 minutes

Arabidopsis genome sequenced in 2000[2]

$70 million
7 years
500 people

Arabidopsis genome sequencing in 2017[1]

$99
2 minutes

1. Technology Review: https://www.technologyreview.com/s/601842/inside-genomics-pioneer-craig-venters-latest-production/
2. Source: Jeff Ross-Ibarra from presentation by Dr. Pamela Roland at University of California Davis
   National Human Genome Research Institute

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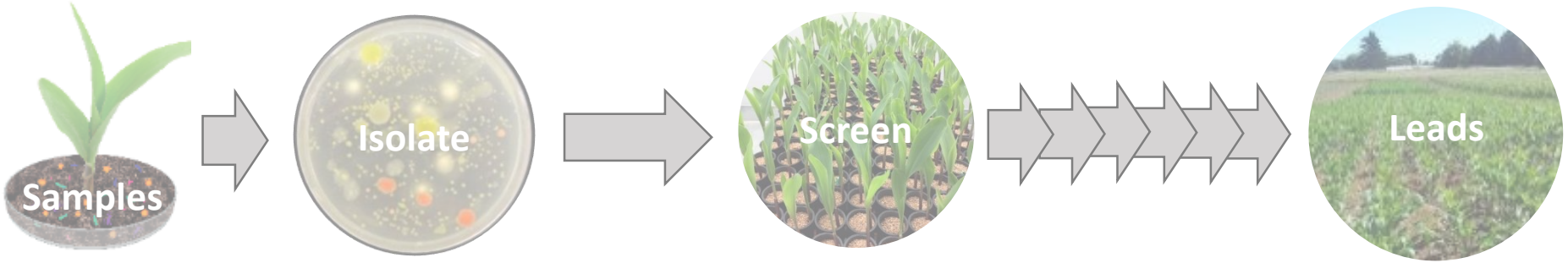
AMS - Superior Discovery Process

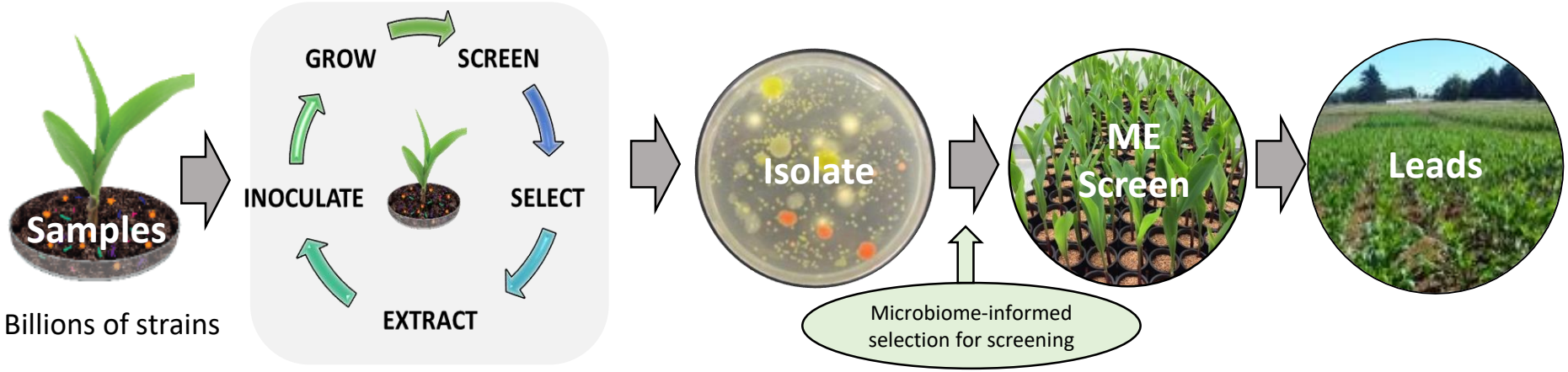
Conventional Microbial R&D Process (often years to lead discovery)



10,000s of strains | 10,000s of strains | **10,000s of strains** | **2 -3 strains**

BioConsortia's AMS process

1,000s of strains | **10s – 100s of strains** | **5 – 10 consortia**



Billions of strains

Directed selection of the microbiome, under biotic or abiotic stress, identifying teams of beneficial microbes that improve plant phenotype

Microbiome Analysis

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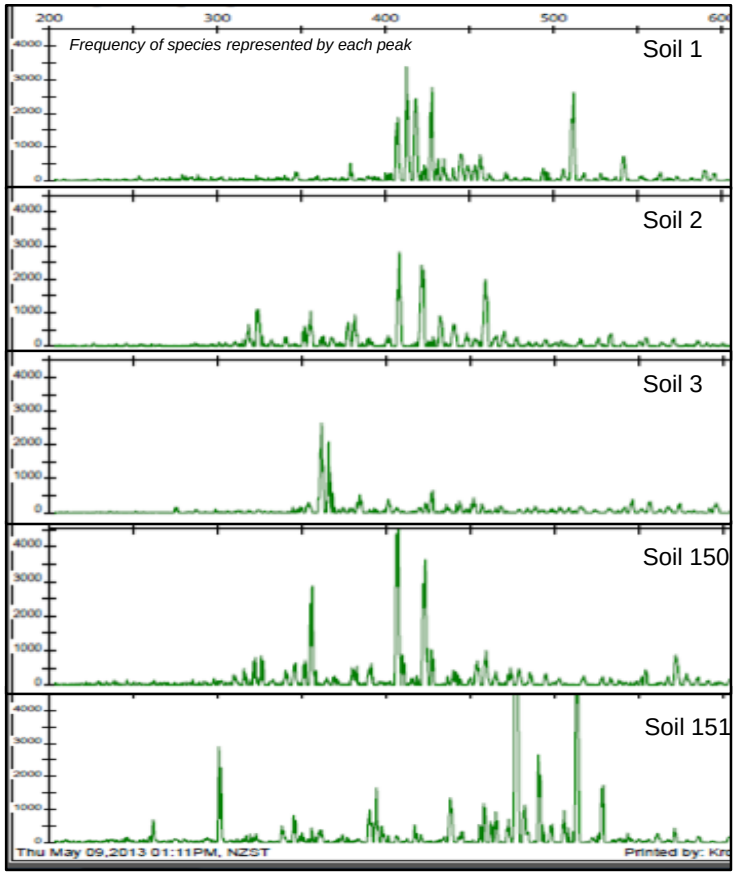
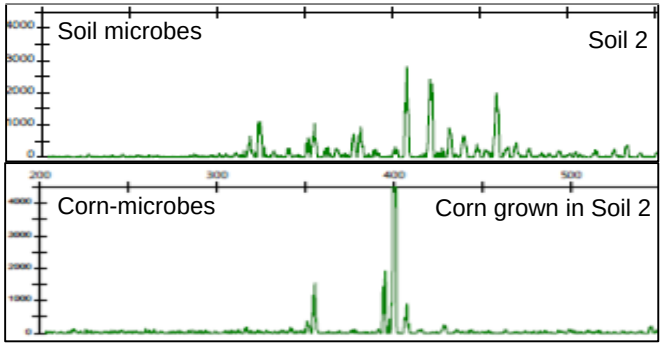
Soil Microbiome Influences Crop Yield

Each soil has a different microbial community



Community Fingerprinting: Automated Ribosomal Intergenic Spacer Analysis (ARISA)

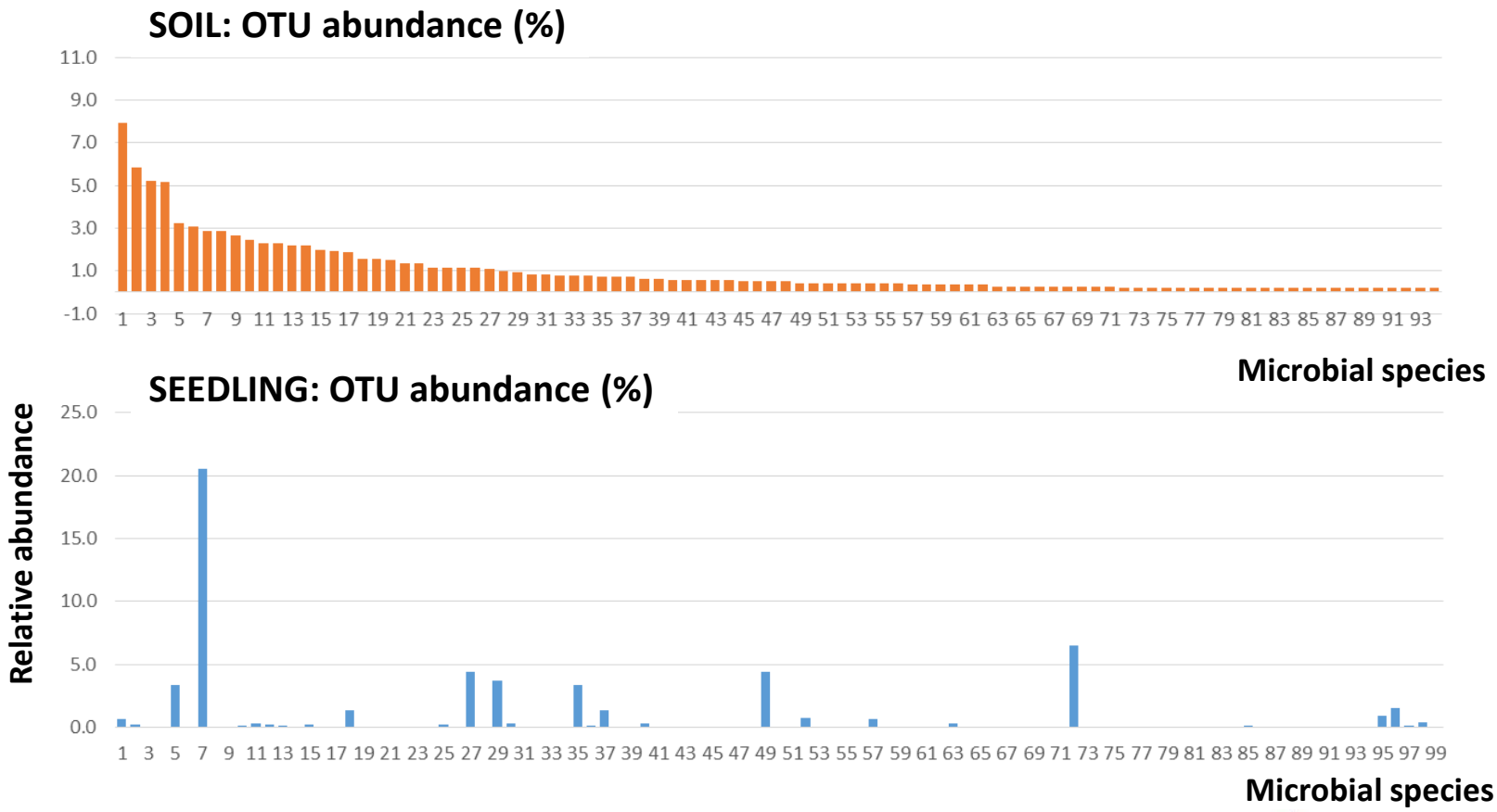
<u>Plants</u> accumulate a <u>different</u> microbial community than the <u>soil</u> in which they are grown



We exploit this natural process identifying the microbial consortia that improve plant traits

Soil and Plant Microbiomes Differ

Seedlings accumulate a different microbial community structure than that present in the soil



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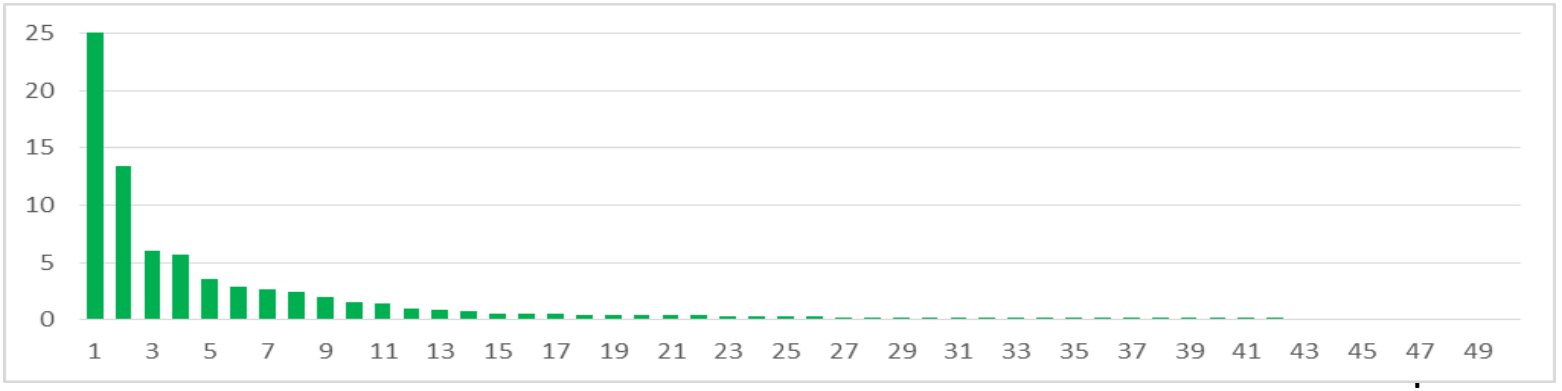
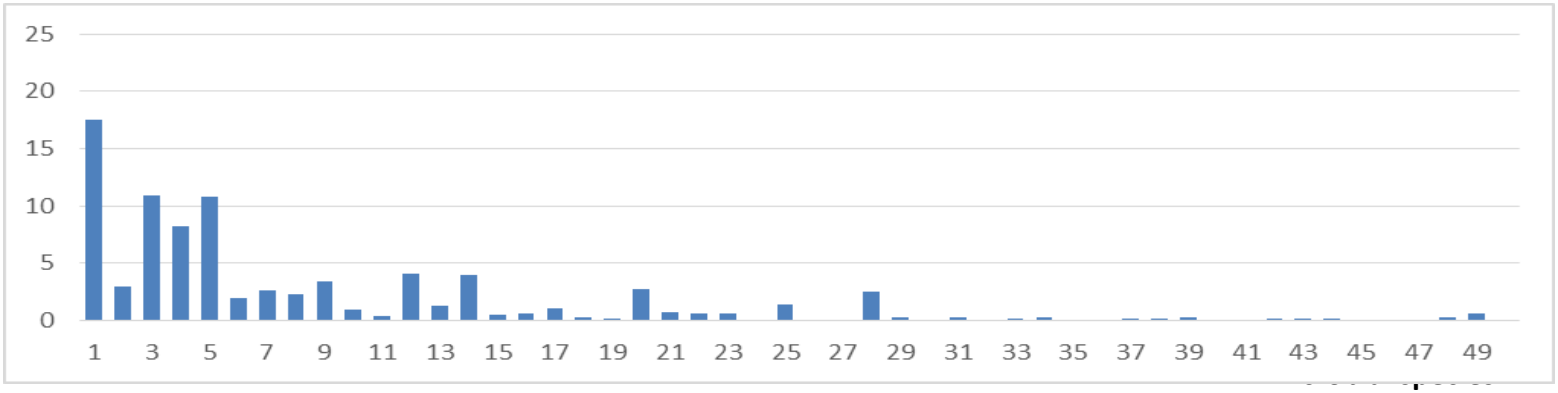
High & Low Performing Plants - Microbiomes Differ

High & low performing plants have a different microbial community
AMS - differences are tracked over successive generations

High Performing Plant: OTU abundance (%)



Low Performing Plant: OTU abundance (%)



Advanced Microbial Selection (AMS)

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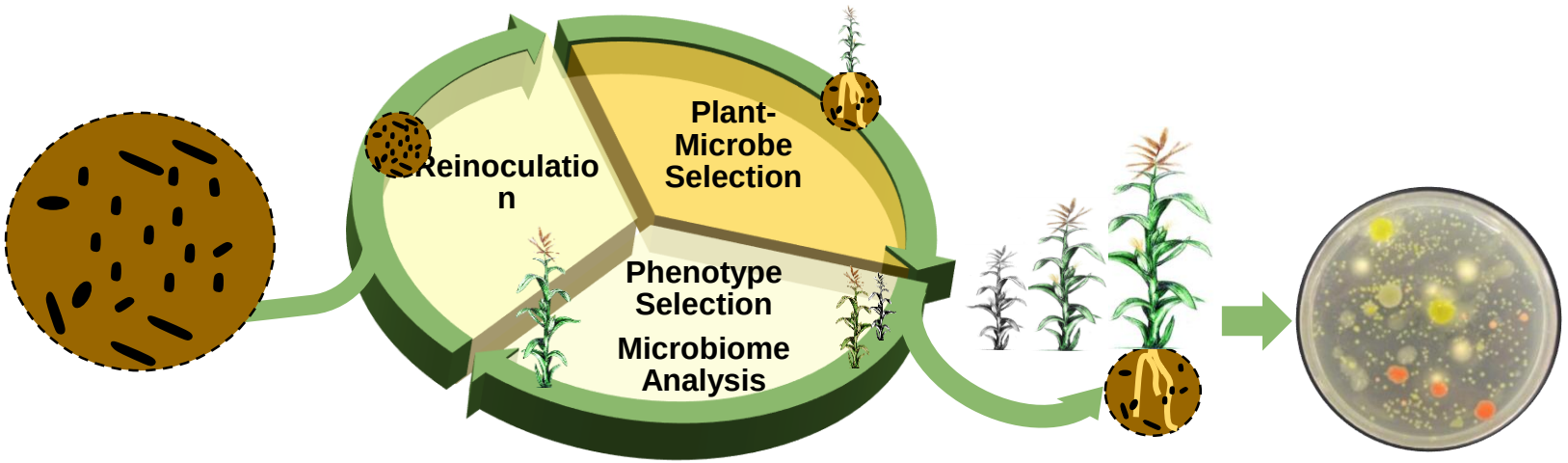
Advanced Microbial Selection (AMS)

Directed selection of the microbiome to identify teams of beneficial microbes



Diverse soil microbes → Microbe capture → Directed selection → Final selection → Microbe isolation

Conducted with or without application of stress

Process and selection informed by DNA and microbiome analysis

Proprietary, patented process

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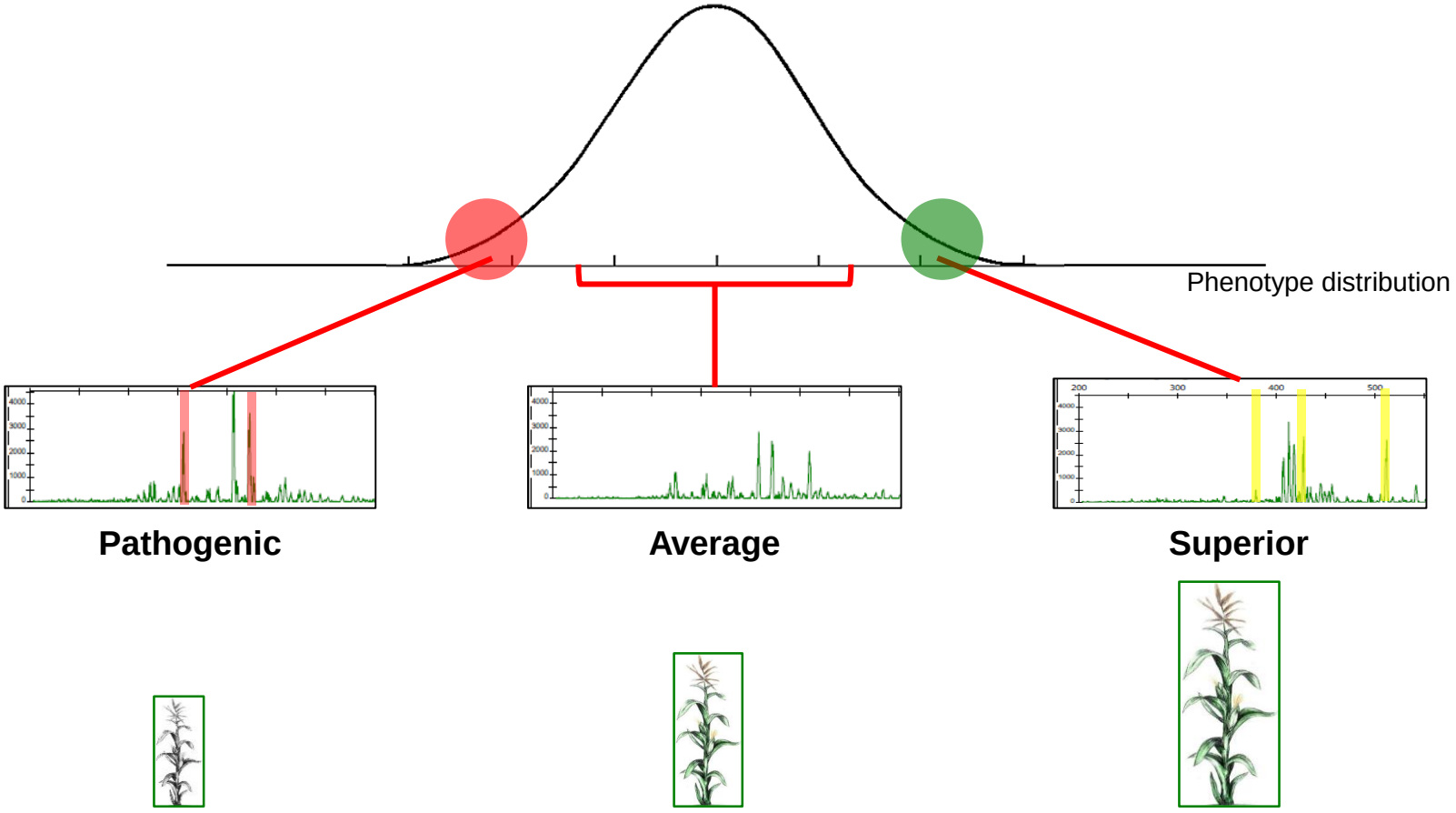
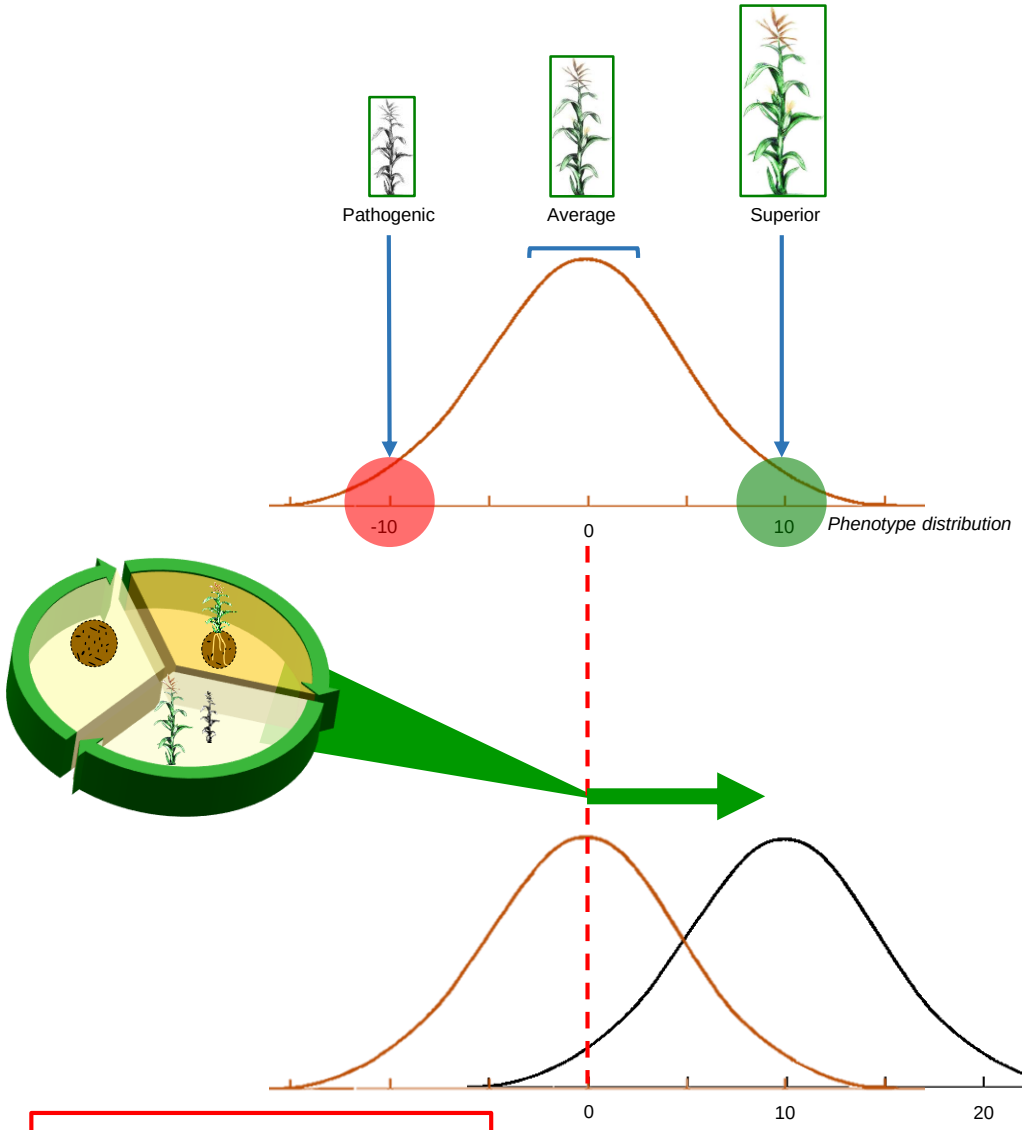
Selecting Superior Phenotypes



Selection process is completed in both ideal and stressed conditions, such as nutrient deficiency, drought, etc.

Directed Selection



The AMS Process

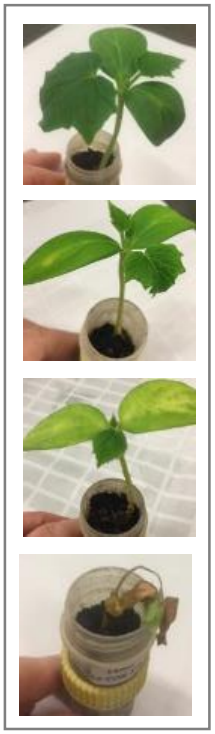
Selecting the superior phenotype

Changing the microbial community

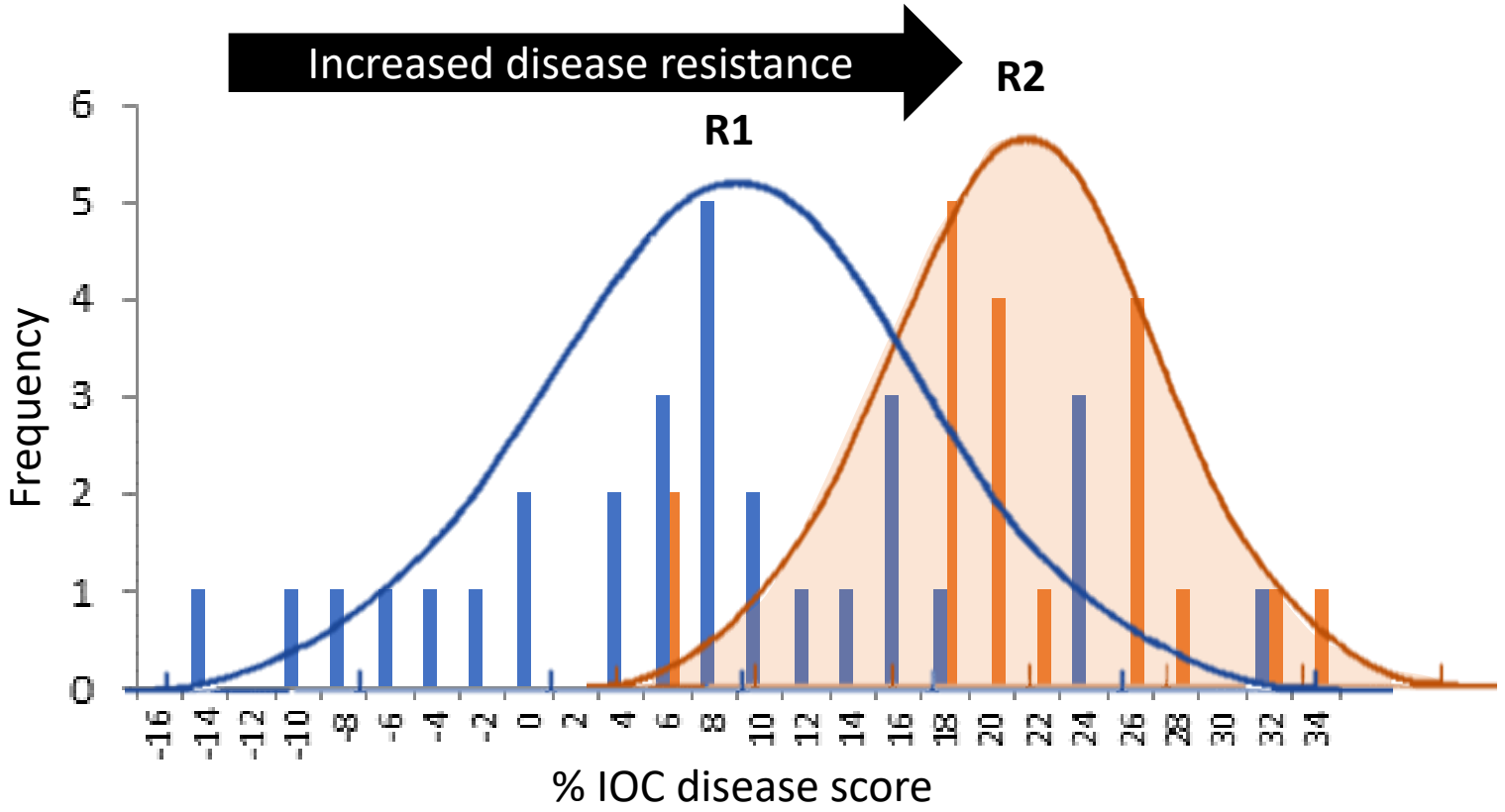
Driving an improvement in trait performance

Proprietary, patent-pending process

AMS Induces a Shift in Disease Resistance

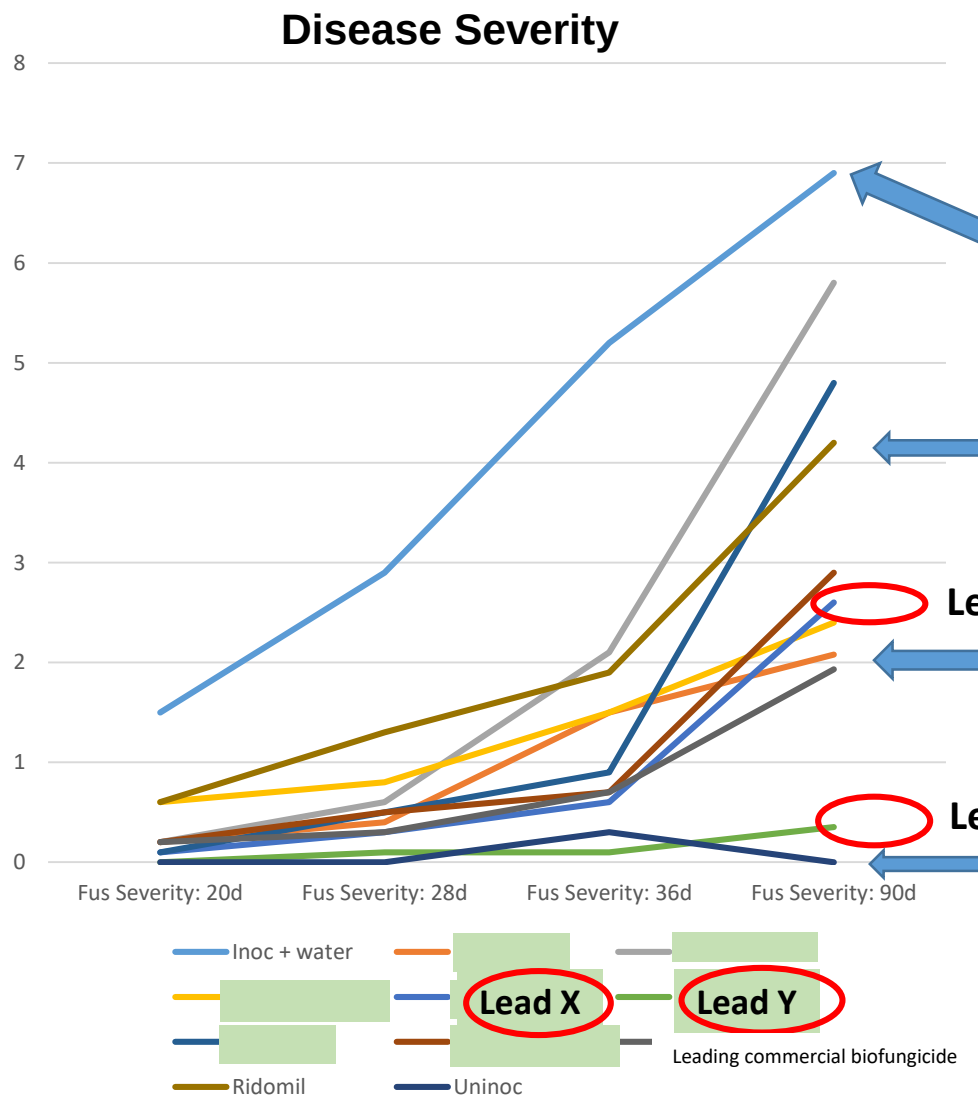


AMS for Pythium Resistance in Cucumber



Initial Biofungicide Program

Tomato - Fusarium wilt
Florida Ag



Good level of disease Challenge
Disease inoculated, UTC

Ridomil

Lead X (spore forming bacterium)

Leading commercial biofungicide

Lead Y (spore forming bacterium)

No disease inoculation UTC

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AMS + Microbiome Analysis

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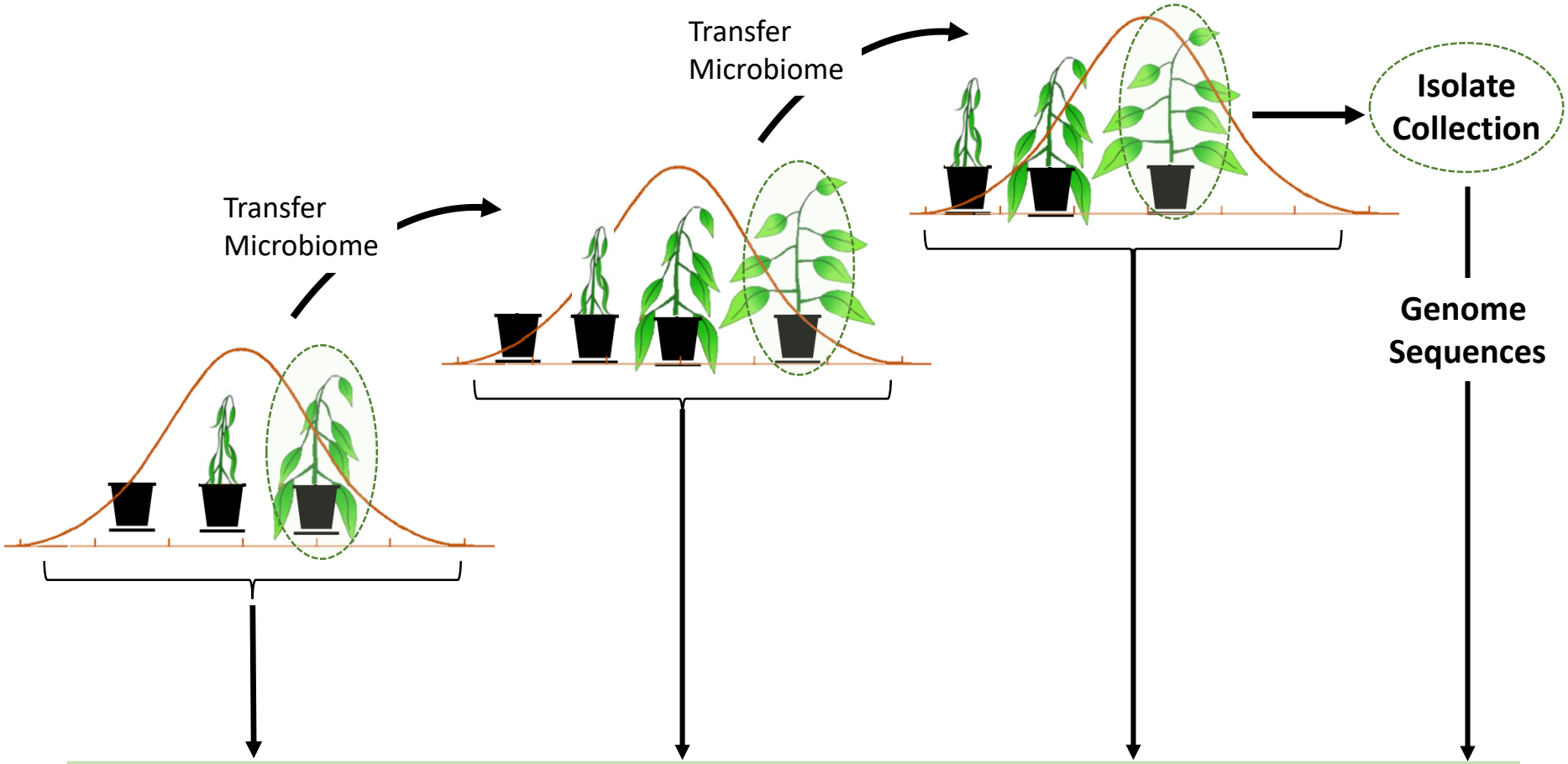
Microbiome analysis makes AMS more powerful



Microbiome Analysis - Machine Learning Identifies Key Microbes

- Comparative analysis of high and low performing plants across each AMS round
- Key species, strains and consortia (co-occurring) identified

AMS and Microbiome Analysis

AMS helps us narrow in on the members of the microbiome that matter

Filter 1

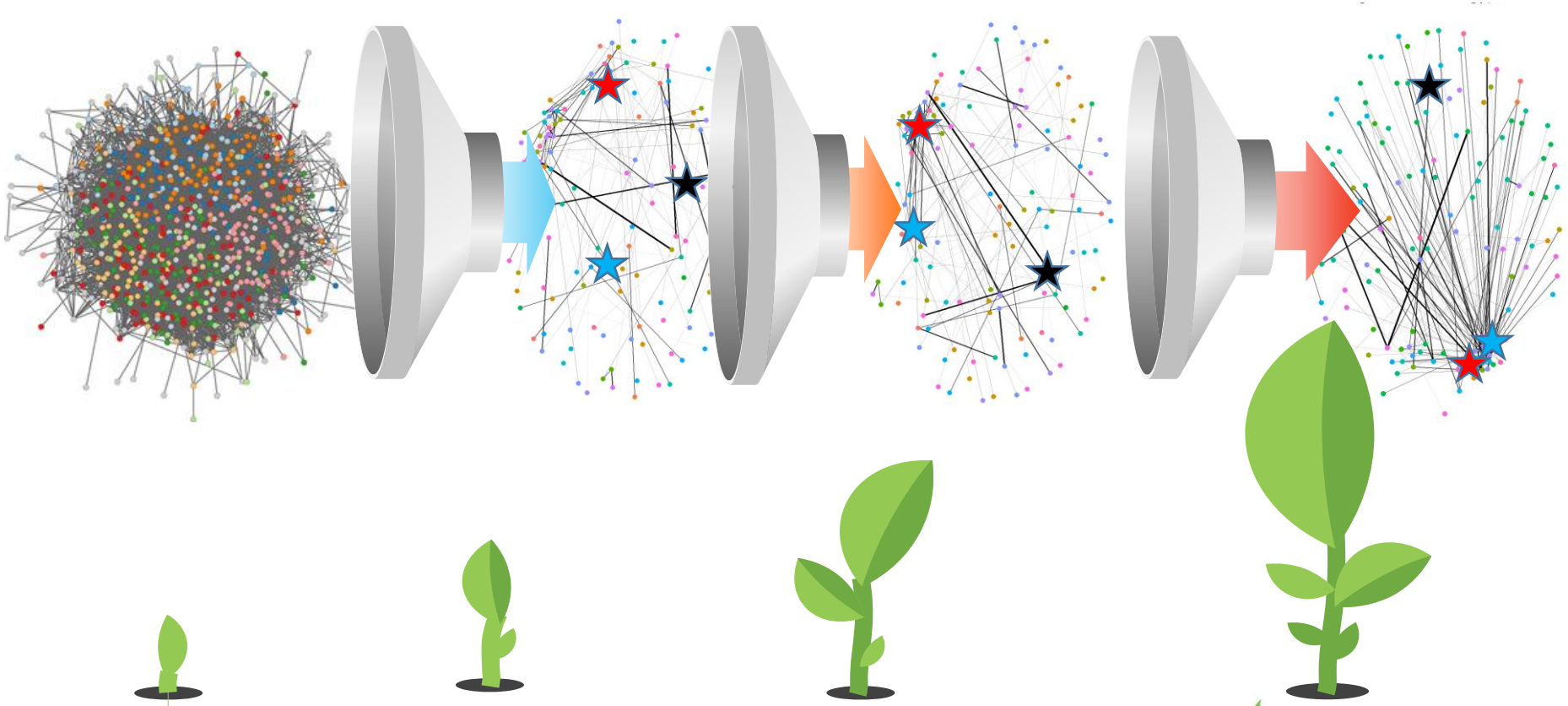
Plant-associated microbes are selected during microbe capture

Filter 2

Microbes that are retained under selective pressure are transferred

Filter 3

Microbes that consistently confer a positive effect through selection rounds are targeted for isolation



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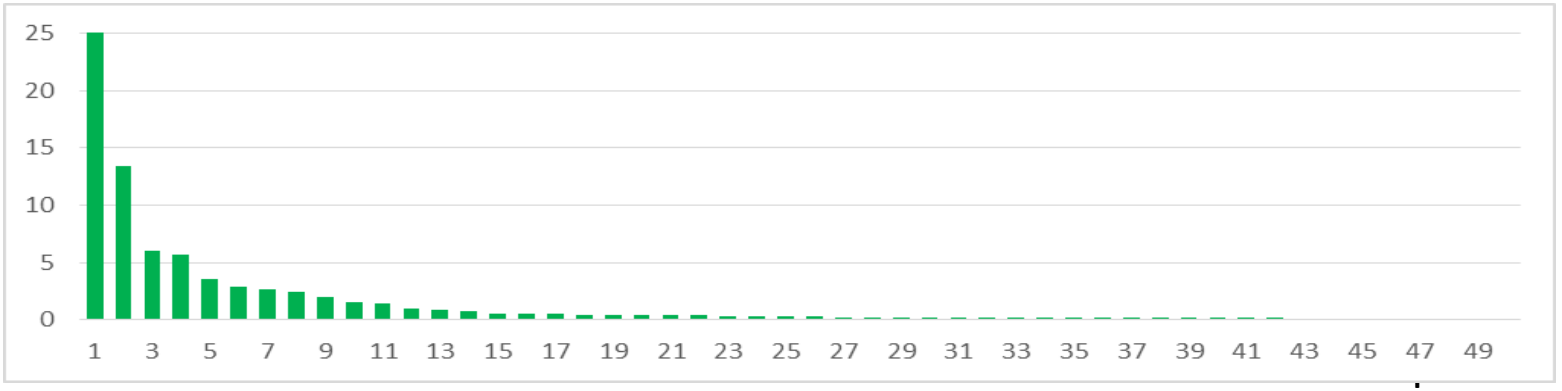
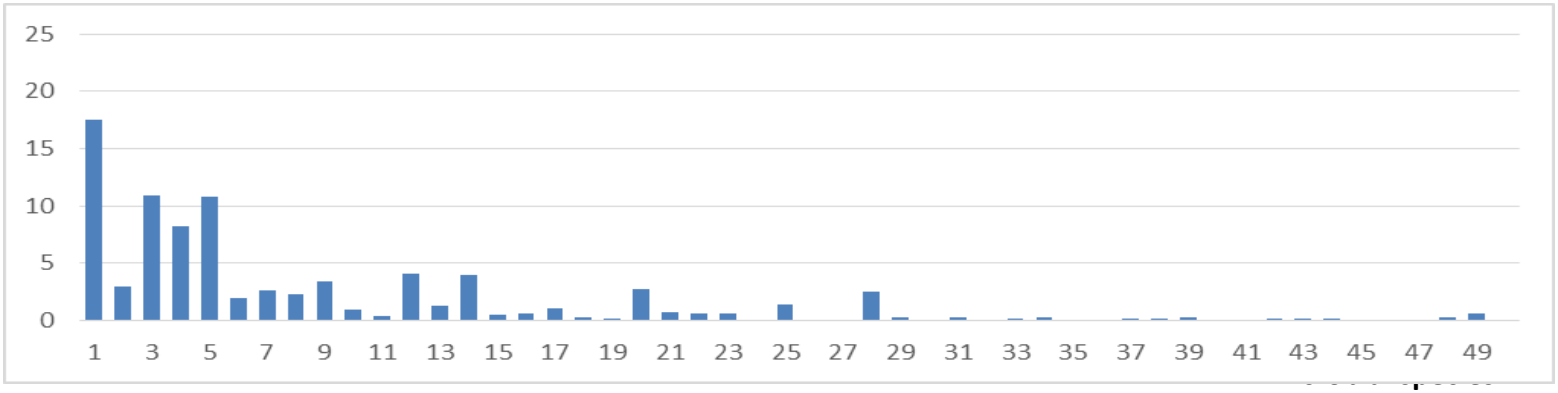
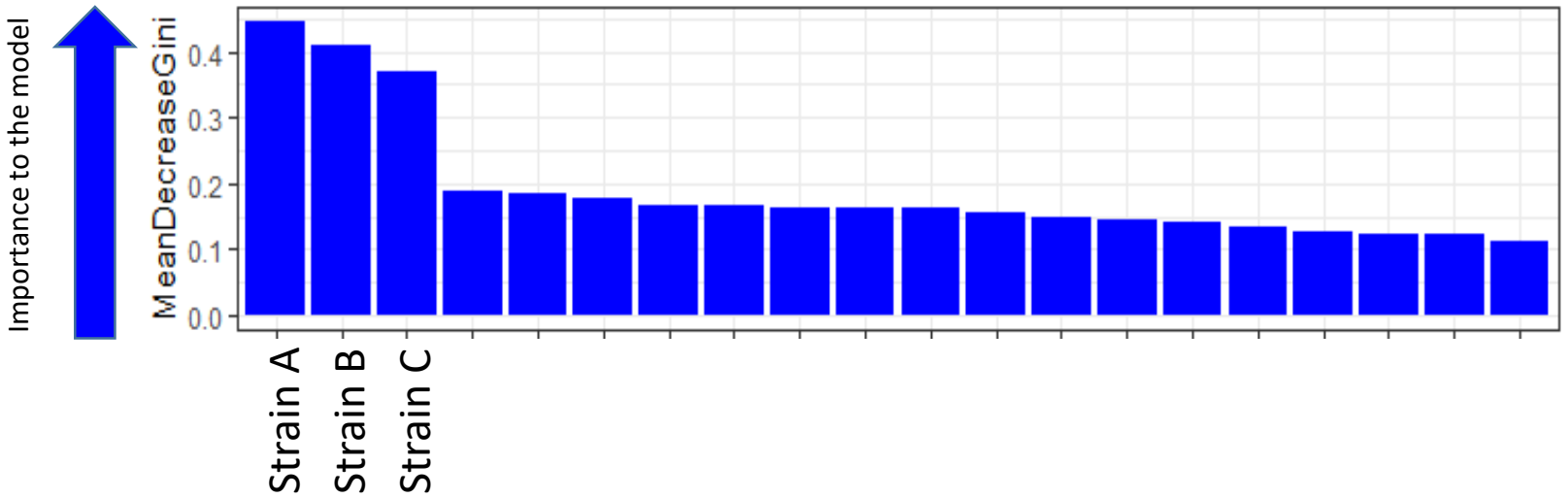


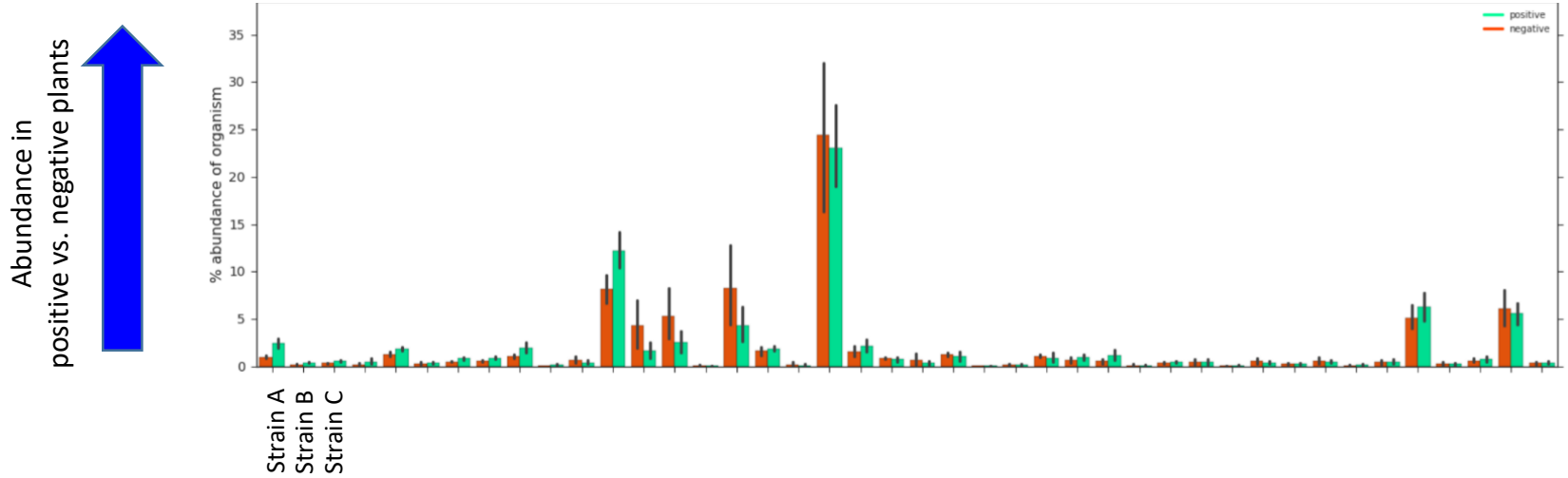
Low Performing Plant: OTU abundance (%)



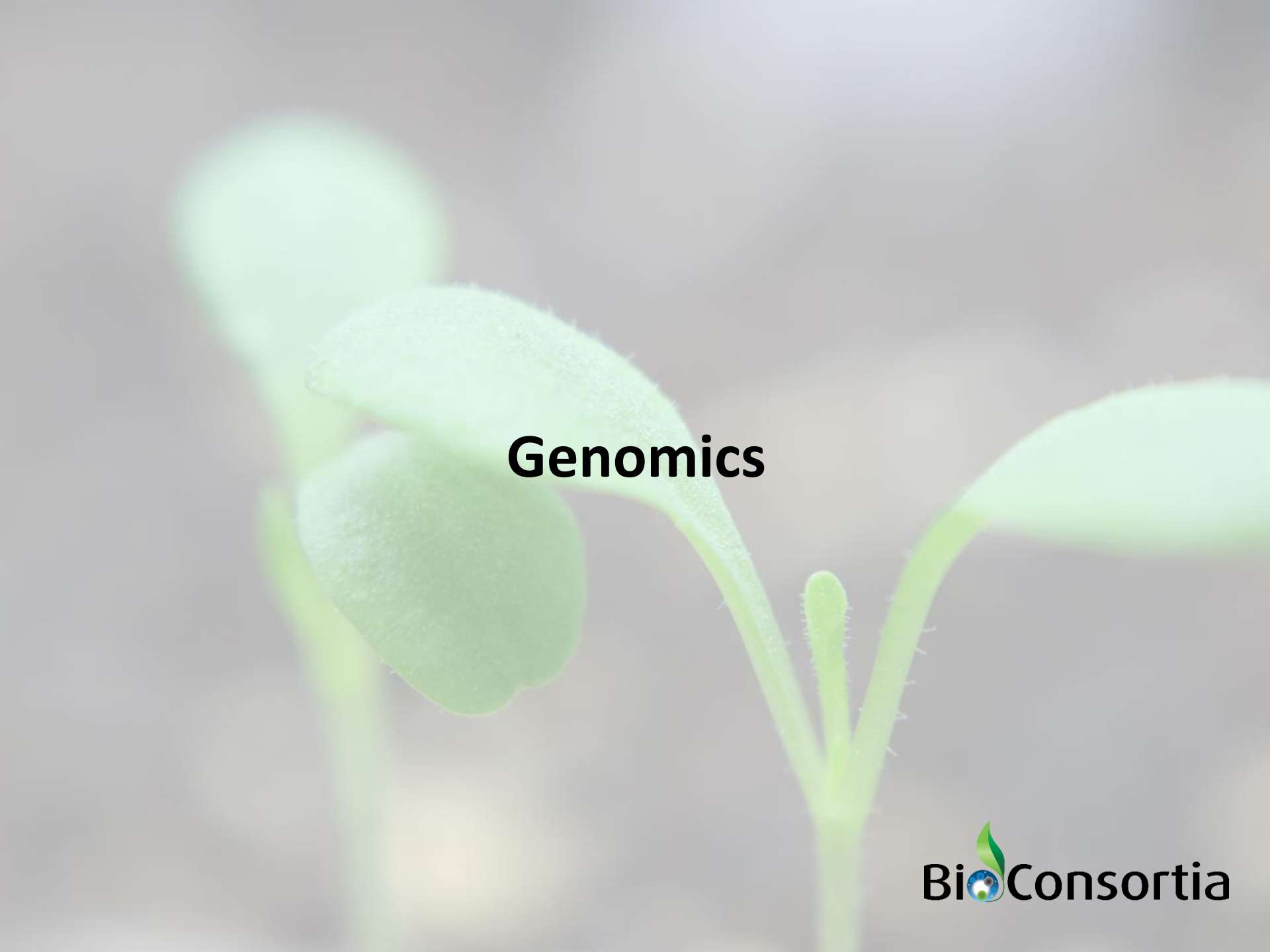
Machine Learning Identifies Key Microbes

-the most important microbes are not always the most abundant



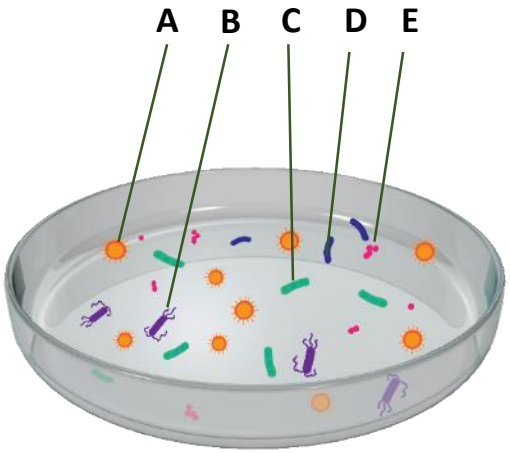


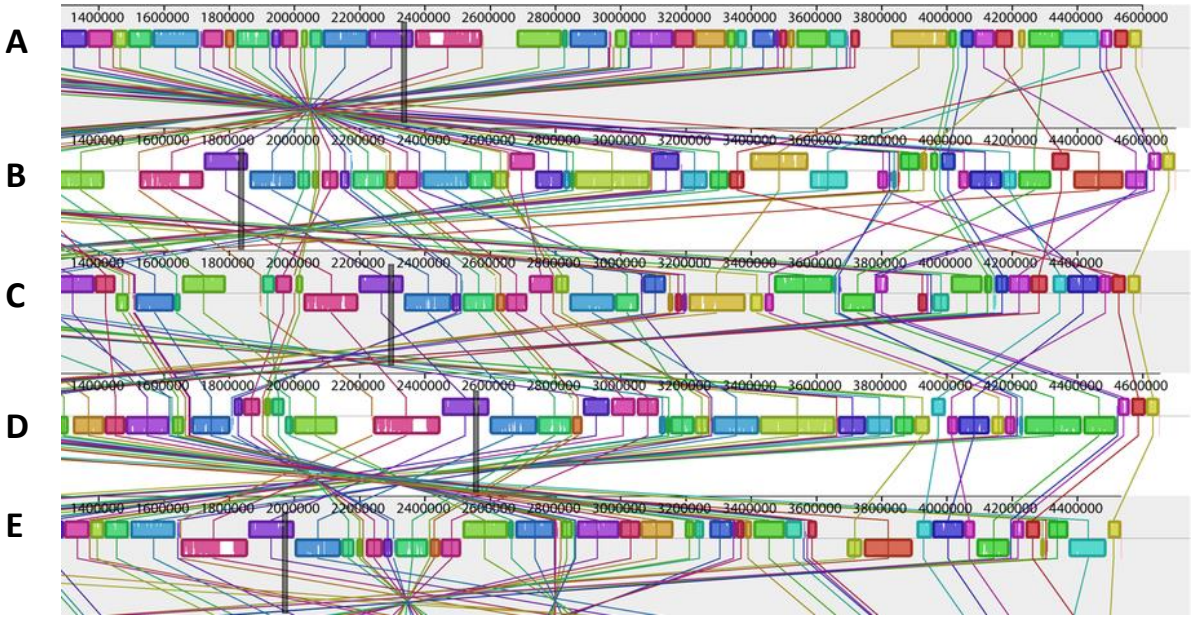
Genomics



Genome Sequencing & Comparative Genomics

- Genomic sequencing and comparative analysis of isolates
- Consolidating the link between community analyses, functional prediction and strain selection





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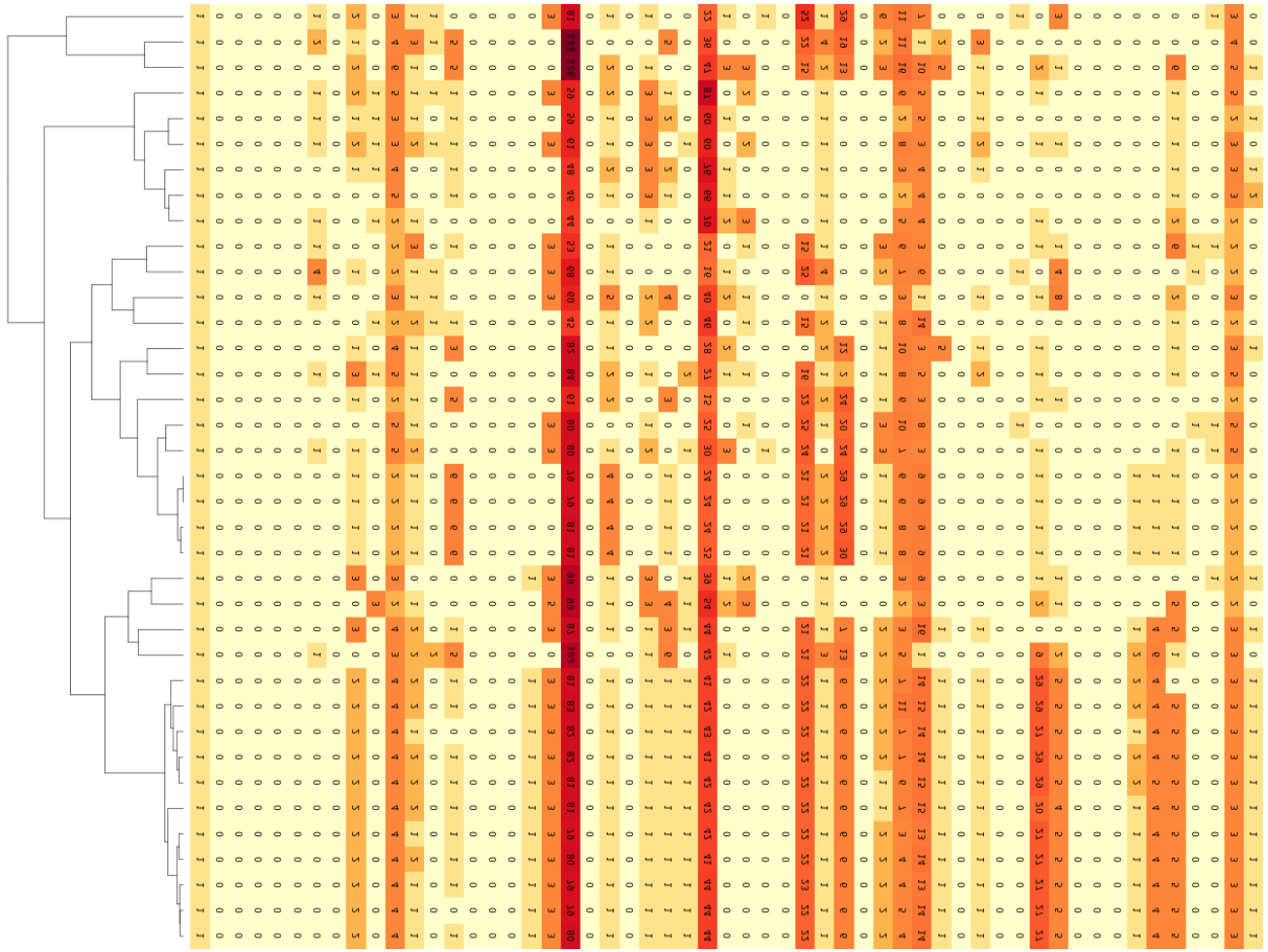
Microbial Potential

Genomic analysis can provide insight into microbial potential

01 Nutrient Acquisition	**02** Root Colonization
03 Biocontrol	**04** Abiotic Stress Resistance
05 Pathogenicity	**06** Discovery

Genomics Platform

Combining data from genomics, microbiome, HTP microbial phenotyping, and in planta assays to build a platform for predicting the best consortia



Isolates

Gene Content

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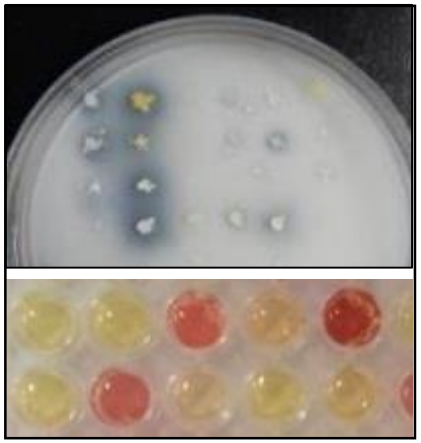
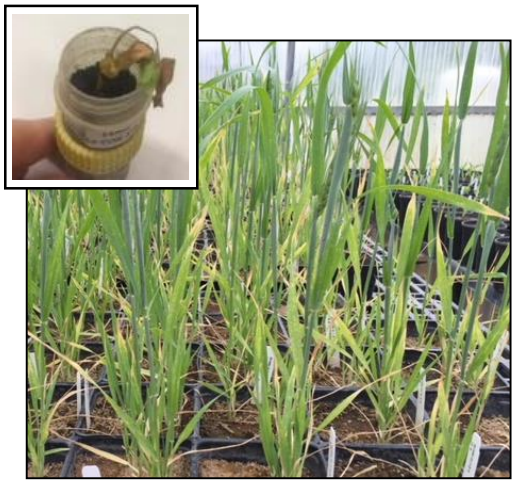
High Throughput Phenotyping (HTP)

HTP microbe phenotyping



- All microbes screened
- Broad spectrum of functions

AMS (focus on easily scored phenotypes)



- Biopesticides
- Abiotic stress

HTP in-planta assays for consortia screening

- Growth room & greenhouse assays
- Digital imaging
- Drone-based field imaging

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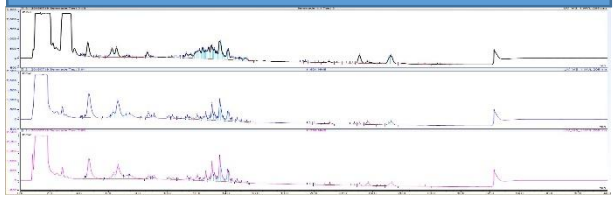
Biofungicide/Biostimulants Leads are Extensively Characterized for Functionality and MoA

Spectrum of control on plant pathogens

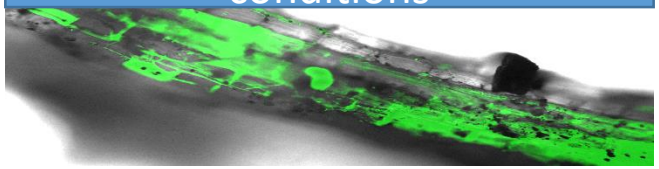
Nutrient solublization ability
N, P, K, Si, Zn, Fe

Bioactive metabolite profiling

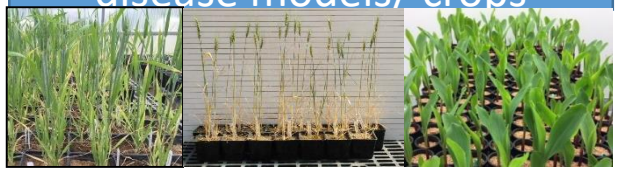


Field
Performance
Consistency
Robustness

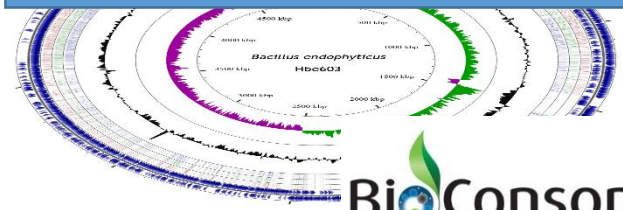
Root colonization robustness under different soils & conditions



Extensive in-planta evaluations with multiple disease models/ crops



Comparative genomics analysis for beneficial traits /safety



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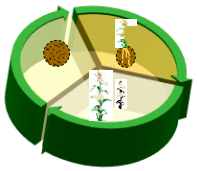
High-Throughput Microbial Screening



One AMS example

150 soil samples

> 10^{13} microbes

> 10^{5} different strains

> Multiple seed chemistries

Selection

60 microbial strains

Lab & Growth Chamber Trials

11 microbial consortia

Pot trial

Field trial

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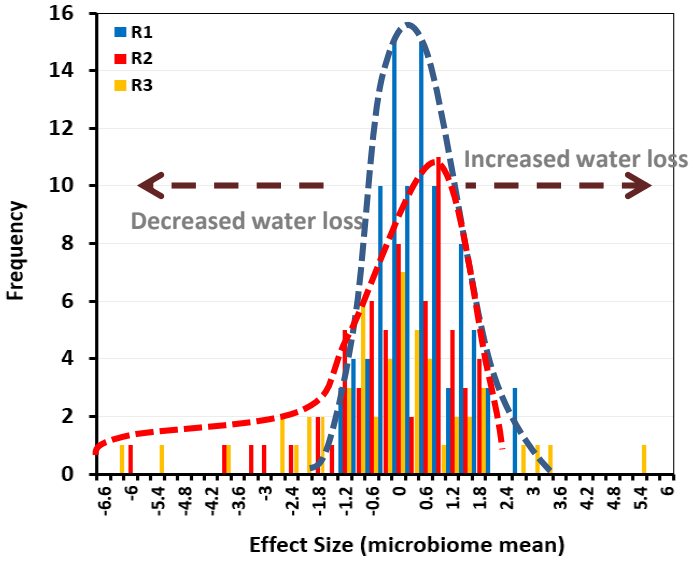
Wheat Water Use Efficiency (WUE)

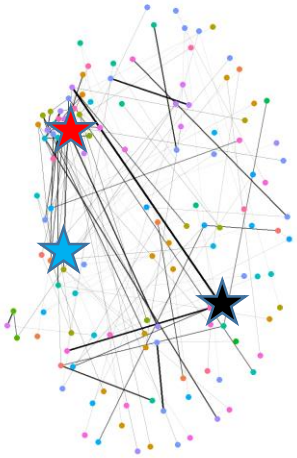
AMS: Wheat Drought Resilience

Multiple positive phenotypes



Consortia Evaluation

Water Use Efficiency (WUE)



Machine learning used to identify key microbes in microbiome

Microplot Trials

Heat and Water Stress

Four consortia (out of 30) showed 15 – 20% yield gain

- Best treatments predicted by microbiome analyses

Initial field trial results

- best lead showed 13.4% yield increase in sub-optimal watering and 8% across all trials

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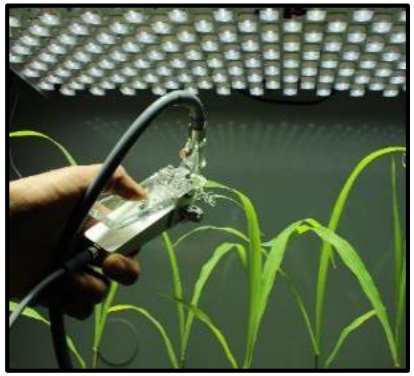
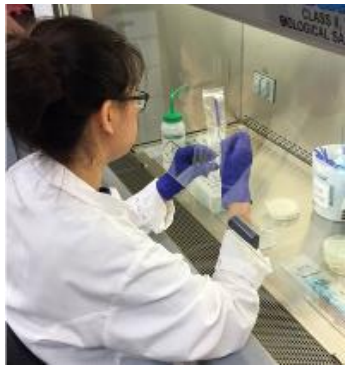
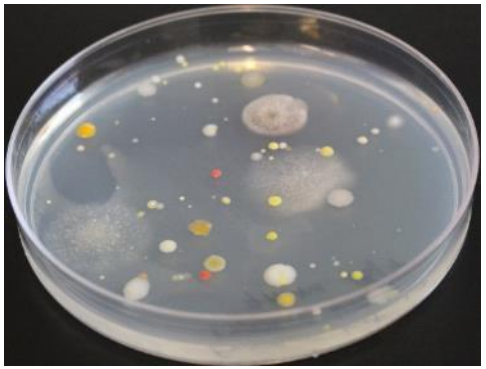
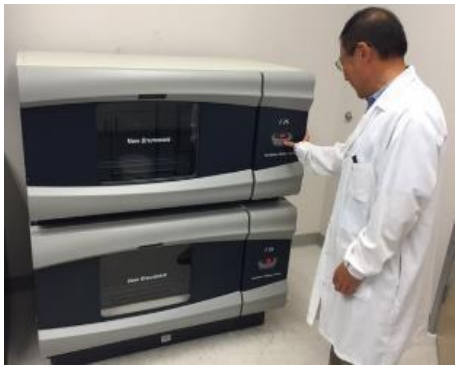

Thank you

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