# Phytobiomes Research for Enhancing the Sustainable Production of Food, Feed, and Fiber

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Exploring Phytobiomes Workshop

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PAG XXVIII

# Holy Grail for Plant Production

To understand, predict, and control emergent phenotypes within specific sites for the sustainable production of food, feed, and fiber

***How do we get there?***

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# Moving From Simple to Complex

Traditional science approach

- Reductionist
- World is linear and can be understood by focusing on individual components
  - Soils
  - Plant genetics
  - Microbiomes or
  - Weather

Embracing the concept that agriculture is a **complex system**

- non-linear organization
- governed by multiple non-linear interactions and environmental variables
- adaptation via learning or evolution
- it can be influenced

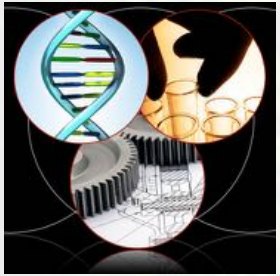
**Paradigm shift to a systems approach**

# Technological Advances

- Omics-enabling technologies and data
- Advances in computational science
  - Machine learning, deep learning
  - Network analyses
  - Predictive analytics
  - Quantum computing
- Precision Agriculture
  - Variable rate technology…seeding & input
  - Unmanned Aerial Systems (UAS)
  - Soil, plant, & weather sensors
  - Robotics
- Convergence science
  - Systems level methods
  - Move from multi- to trans-disciplinarity

➢ **For plants: Phytobiomes approach**

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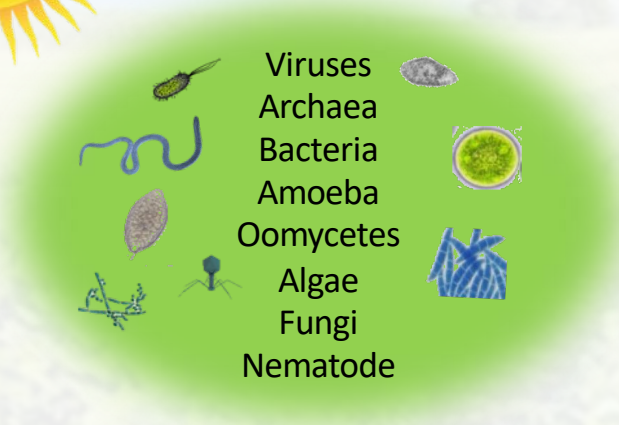
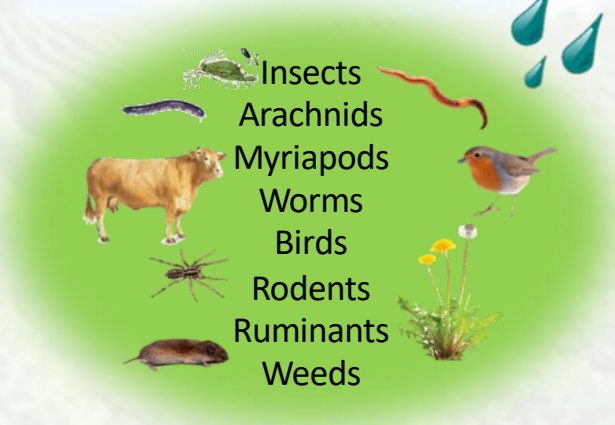
# Phytobiomes: Complex Systems of Plant-based Agriculture

Climate, Weather, Water

## "Biomes": Site specific environments




**Microbiomes and Macroorganisms/Macrofauna**


**Arthropods, Other Animals and Plants**

***How can we facilitate change to the phytobiomes concept?***

**All influenced by Management Practices**

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# INTERNATIONAL ALLIANCE
## FOR PHYTOBIOMES RESEARCH

*A nonprofit consortium of industry, academic, and governmental scientists*

# Phytobiomes Alliance Vision


By 2050, all farmers have the ability to use predictive and prescriptive analytics based on geophysical and biological conditions for determining the best combination of crops, management practices, and inputs for a specific field in a given year.

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# Phytobiomes Alliance

Our **mission** is to establish a science and technology foundation for site-specific, phytobiome-based enhancement of sustainable food, feed, and fiber production

# Phytobiomes: Major Research Gaps


Microbiomes and Macroorganisms/Macrofauna

Climate, Weather, Water

Arthropods, Other Animals and Plants

Management Practices: Precision Agriculture

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# Current Priorities for Research Funding

- Test and develop cost-effective in-field sequencing platforms and moisture/weather sensors for on-farm use
- Evaluate the impacts of long-term crop management on microbiome composition and functional potential
- Characterize the abiotic effects (rain events), sustained soil moisture, and microbial inoculants on microbiome composition and function
- Determine capacities for ambient, landscape-scale weather patterns to predict fine-scale soil moisture dynamics and facilitate prediction and management of microbiome functional dynamics over space and time
- Develop methods for cryopreservation of entire microbial communities
- Build a conceptual and methodological framework that would allow for the introduction of microbial communities to alter agro-ecosystem functioning
- Optimize microbiome for superior hydroponic controlled environment vegetable production

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# Short-term Priorities

- Enhance understanding of the interactions between plants, microbiomes, and other components of phytobiome systems
- Databases that support correlation and network studies of site-specific and temporal geophysical and biological data
- Draft standards, protocols, check-lists (minimum information, sampling, reference datasets, regulatory requirements…)
- Deploy genome sequence-based classification system for microbes
- Census of microbes by state, province, region, and country
- Draft regulatory science roadmap for microbials

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# Areas of Progress

- Genome sequence-based classification system and risk prediction classification system for microbes
- Microbe sequence database that includes phenotypic data
- Draft standards, protocols, check-lists (minimum information, sampling, reference datasets, regulatory requirements…)

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# Alliance LINS Project: Whole Genome Sequence-Based Classification & Identification Platform

Model: *Ralstonia solanacearum*

Database of sequences coupled to pathogenicity data

Precisely circumscribe the strains that should be designated as “Select Agents”

**Objective: Enable rapid and precise taxonomic identification of microbes**

Expand model to other agriculturally relevant bacteria

Expand to include plant-associated fungi

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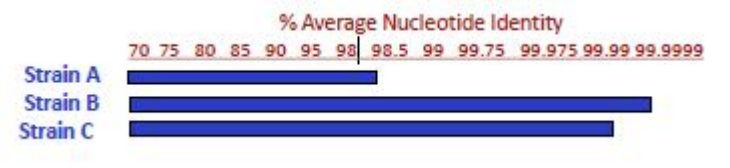
# Life Identification Number® (LIN®)

- Stable and unique codes that are:
  - assigned to individual organisms/genomes (for example, bacterial isolates)
  - based on a measure of genome similarity, such as average nucleotide identity (ANI)
  - informative of the similarity of an organism's genome to the genomes of all other organisms
- Codes consist of a series of positions, each expressing a different threshold of genome similarity
- The more similar the genomes of two organisms are, the more similar the LIN®s of the two organisms

Courtesy of Boris Vinatzer

# Whole Genome-Based Classification & Identification Platform: APHIS LINS Project

- Enable rapid and precise identification of microbes




- Assess rapidly relatedness of new strains to existing strains for which phenotypic and geographic data are available
- Involve government and industry in planning the data, metadata, and user needs and outputs to improve regulatory process for research and commercialization of agricultural microbes
- Embed data privacy options for contributors to the database

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# Risk Prediction Classification (Submitted)

- Develop a “risk prediction” method for beneficial plant bacteria
- Initial focus on *Bacillus, Pseudomonas*, and *Burkholderia* with plant growth promoting activity and biocontrol activity
- Objectives include:
  - ✓ Developing a precise genome sequence-based classification and genome sequence-based phylogenetic trees of the strains
  - ✓ Identifying genetic markers associated with beneficial and pathogenic strains belonging to the genus *Bacillus*
  - ✓ Precisely circumscribe strains that are, and are not, pathogens and plant beneficials

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# Database for rapid assessment of geographic distribution of microbes

- Expand/create database to include WGS, 16S, ITS, metagenomic sequences coupled with geographic metadata
- Controlled vocabulary for phytobiome-associated metadata
- Identify best practices, reference materials, and standards for characterizing phytobiome microbes

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# Proposed Metadata Categories for Future Minimum Information checklist for Agricultural Microbiome Studies (MIxS-Ag)

- Site or location context
- Sample type and description (soil/root associated vs aboveground plant-associated)
- Sample collection
- Sample processing
- Climate
- Management practices history and abiotic characteristics

➢ **Alliance Next Steps: Input from our scientific coordinating committee, industry, EU projects and groups, other interested stakeholders and governmental entities**

Dundore-Arias, et. al. https://doi.org/10.1094/PBIOMES-09-19-0051-P

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# Phytobiomes Conference 2020


**1-4 December 2020**

**Denver, CO, USA**

**www.phytobiomesconference.org**

## Main Scientific topics

- Plant fitness
- Microbial community assembly and function
- Network analyses within the phytobiome system
- Modeling
- Data – framework, tools and resources, big data
- Genetic linkages
- Engineering to improve carbon sequestration
- Interactions within phytobiomes for abiotic stress
- Engineering microbes and microbial communities
- Precision agriculture
- Controlled environment agriculture
- Fertilizer, nutrient, and chemical input efficiency
- Product development
- Regulatory requirements
- Greenhouse & Field trials
- Industry research needs

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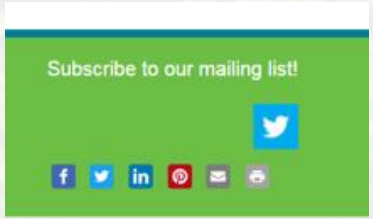


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