

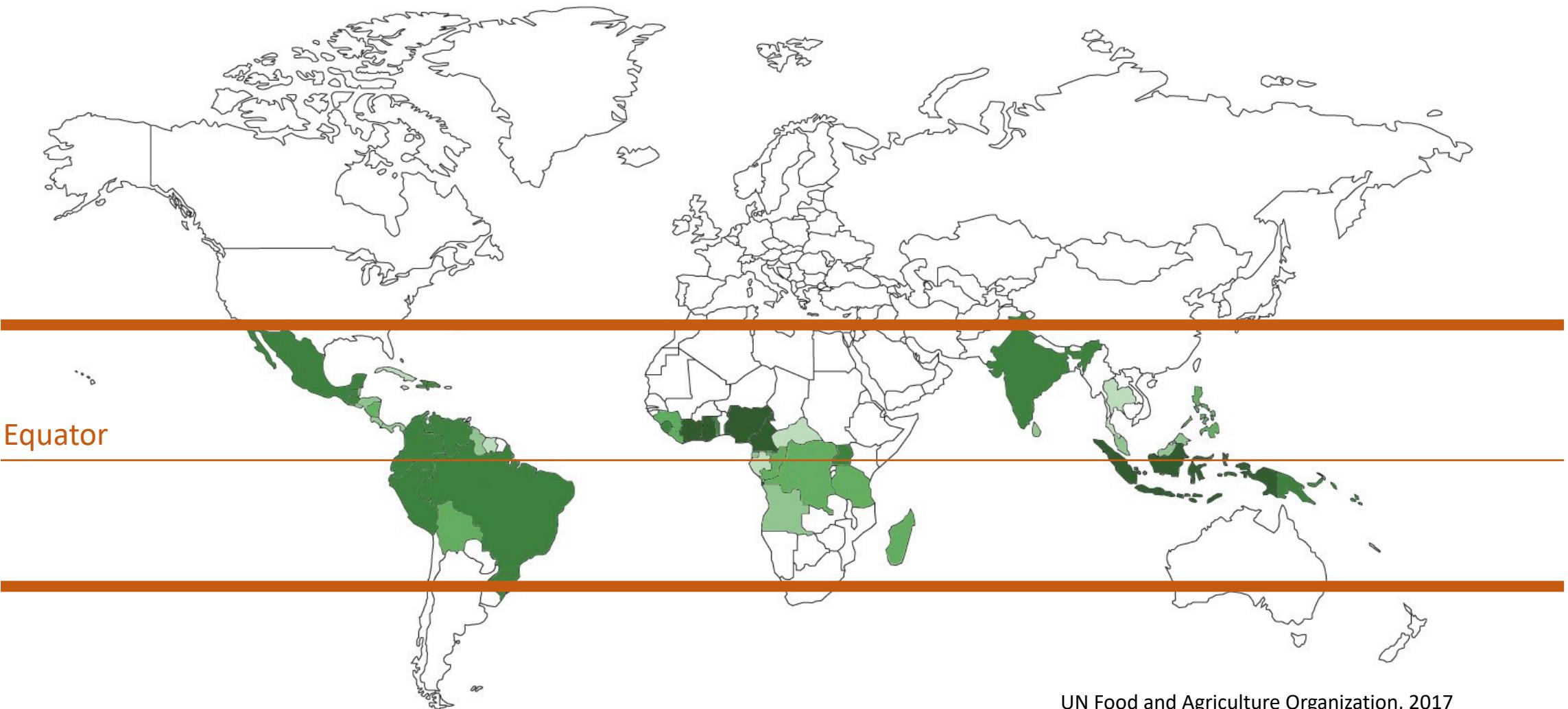
# Variation in leaf microbiomes across several populations of *Theobroma cacao*

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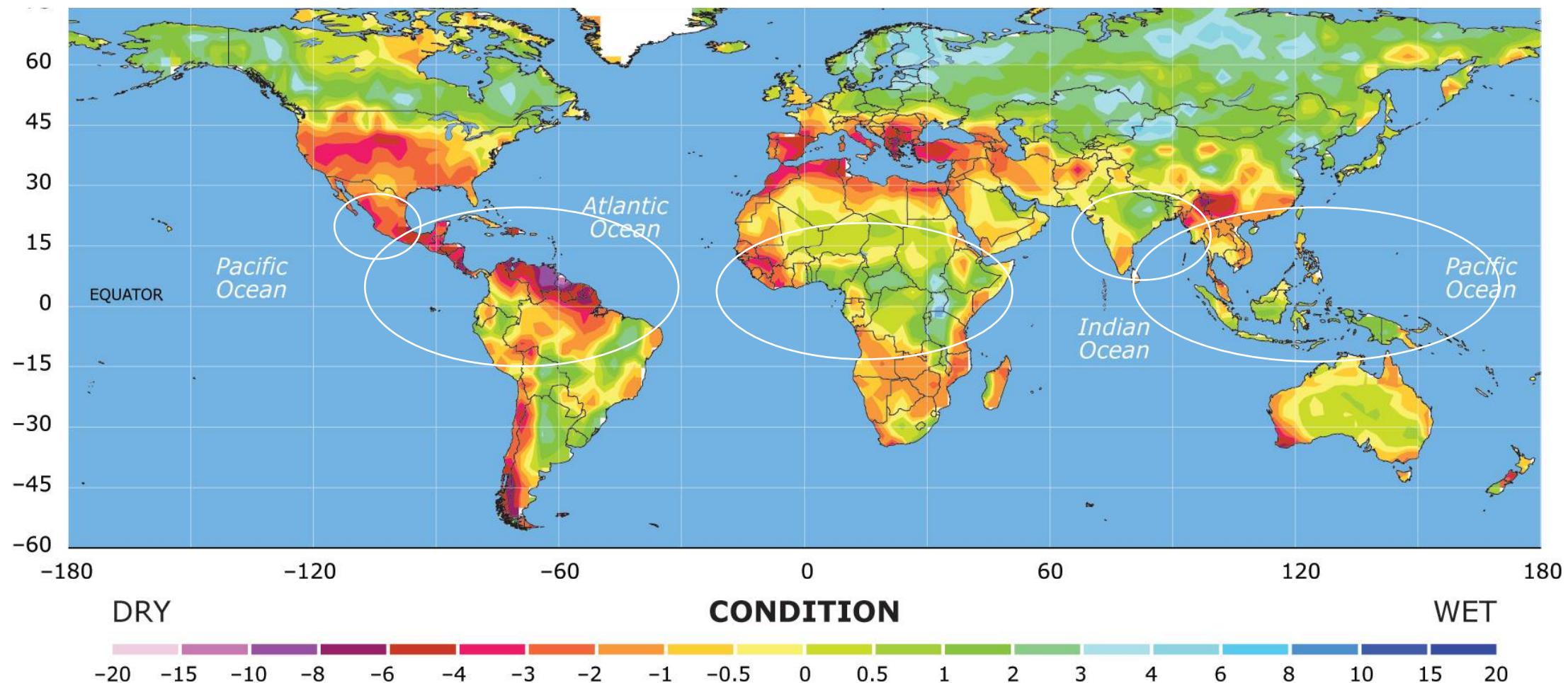
Megan Dolan  
Master's Student – Cornejo Lab  
November 19<sup>th</sup>, 2019

# Global distribution of cocoa bean production

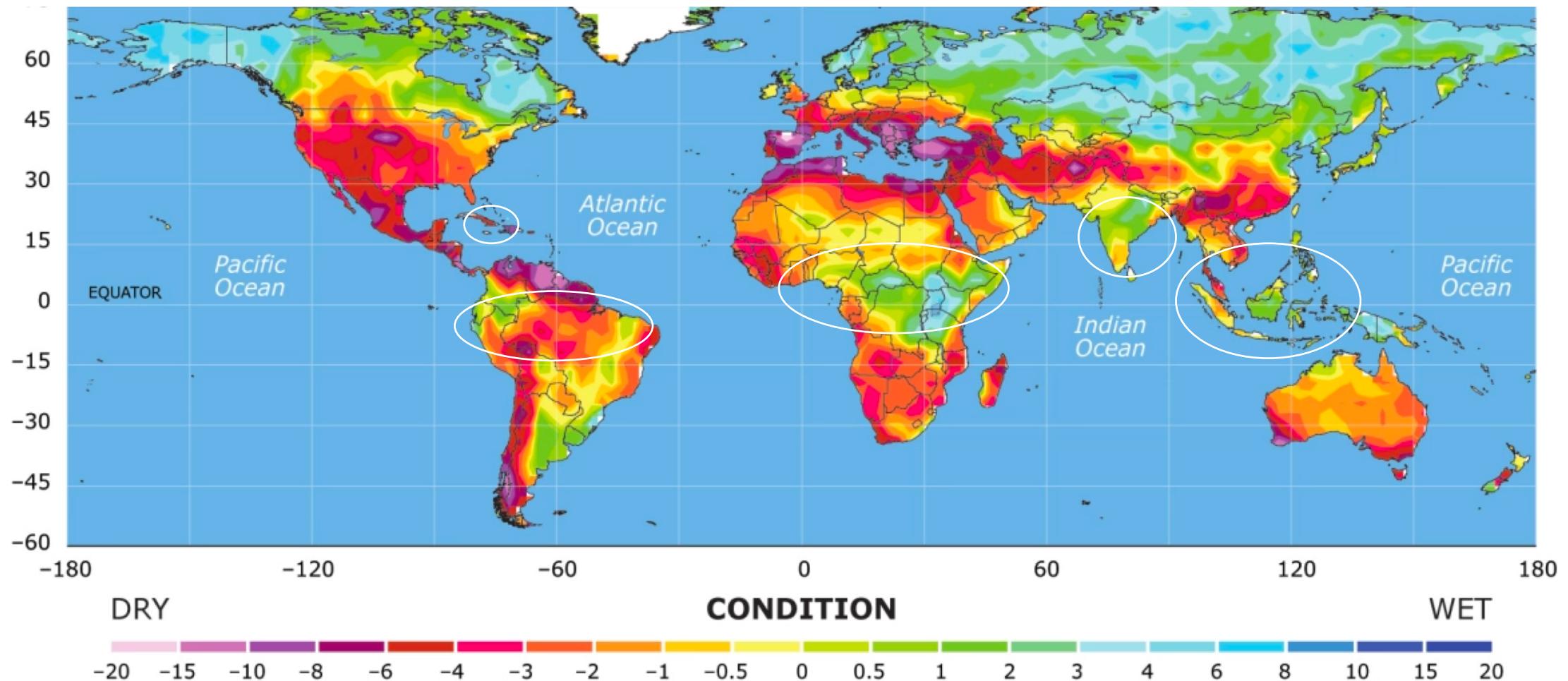
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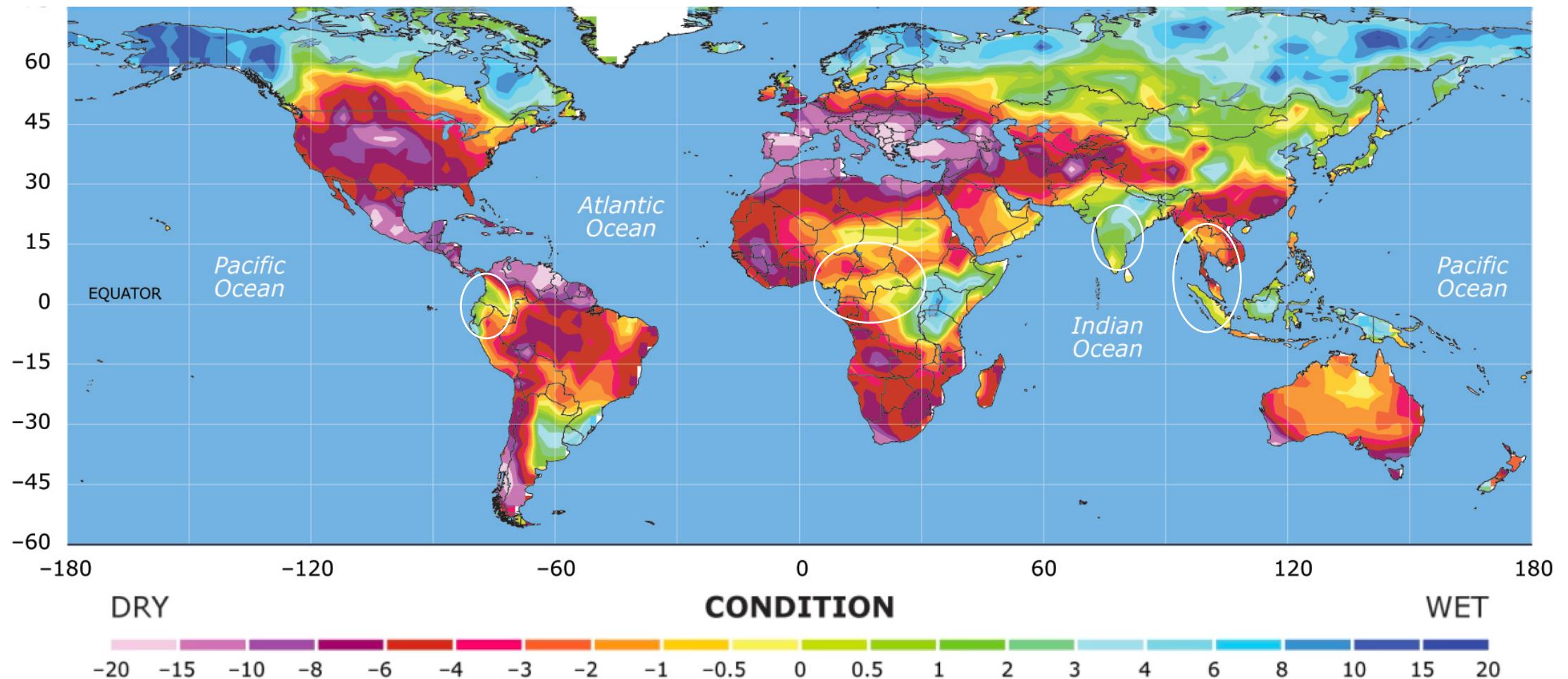
# Drought estimation between 2000-2009



# Drought prediction between 2030-2039



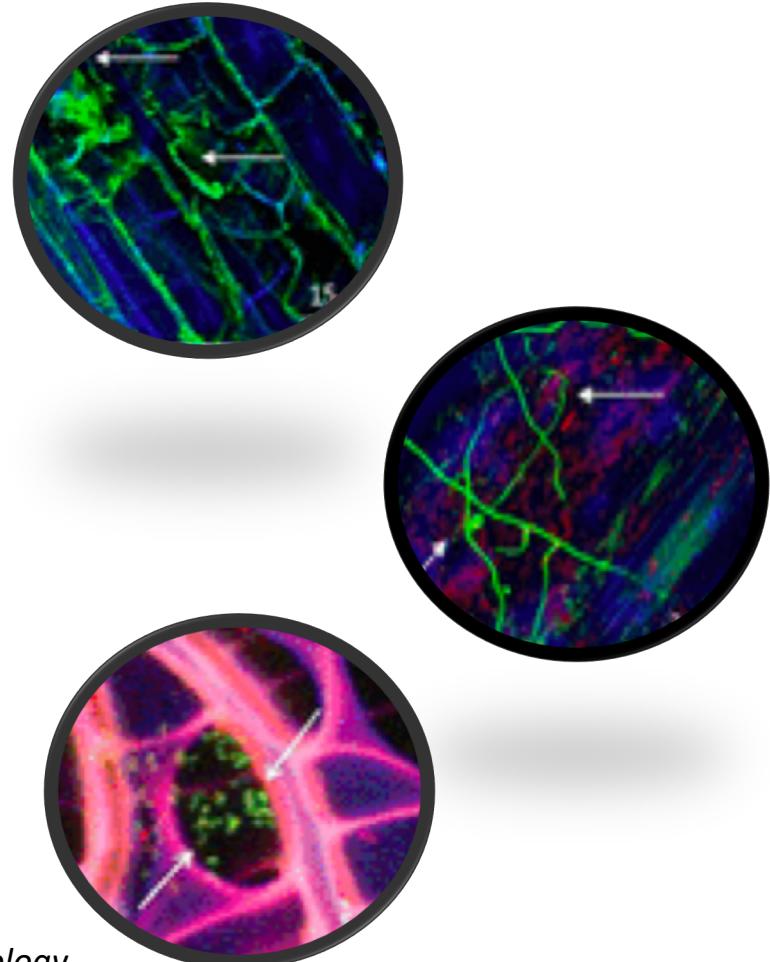
# Drought prediction between 2060-2069



# Benefits of the plant microbiome

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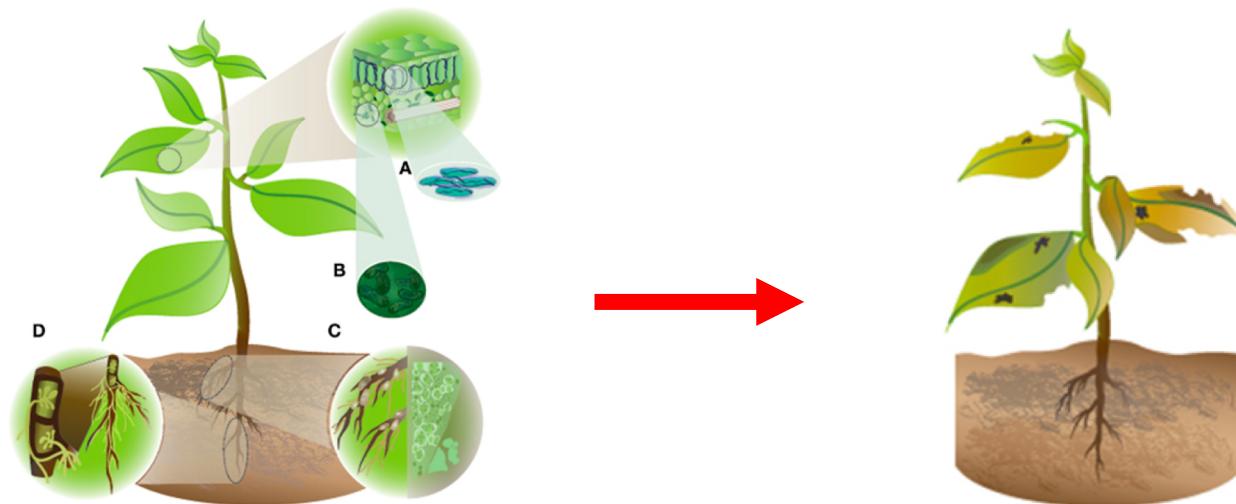
- Promotes plant development/growth
  - (PGPB – plant growth promoting bacteria)
- Aids in plant immunity
- Produces biochemical products essential for creating a survivable environment
  - Alters soil pH
  - Recruits beneficial microbes
  - Deters harmful microbes



Hardoim et al. 2015; American Society for Microbiology

# Importance of the plant microbiome

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Partida-Martínez et al. 2011; *Front. Plant Sci.*

- Without fitness-related benefits that microbes provide, **microbe-free plant would not be fit enough** to survive natural conditions

# What the microbiome can reveal about the host

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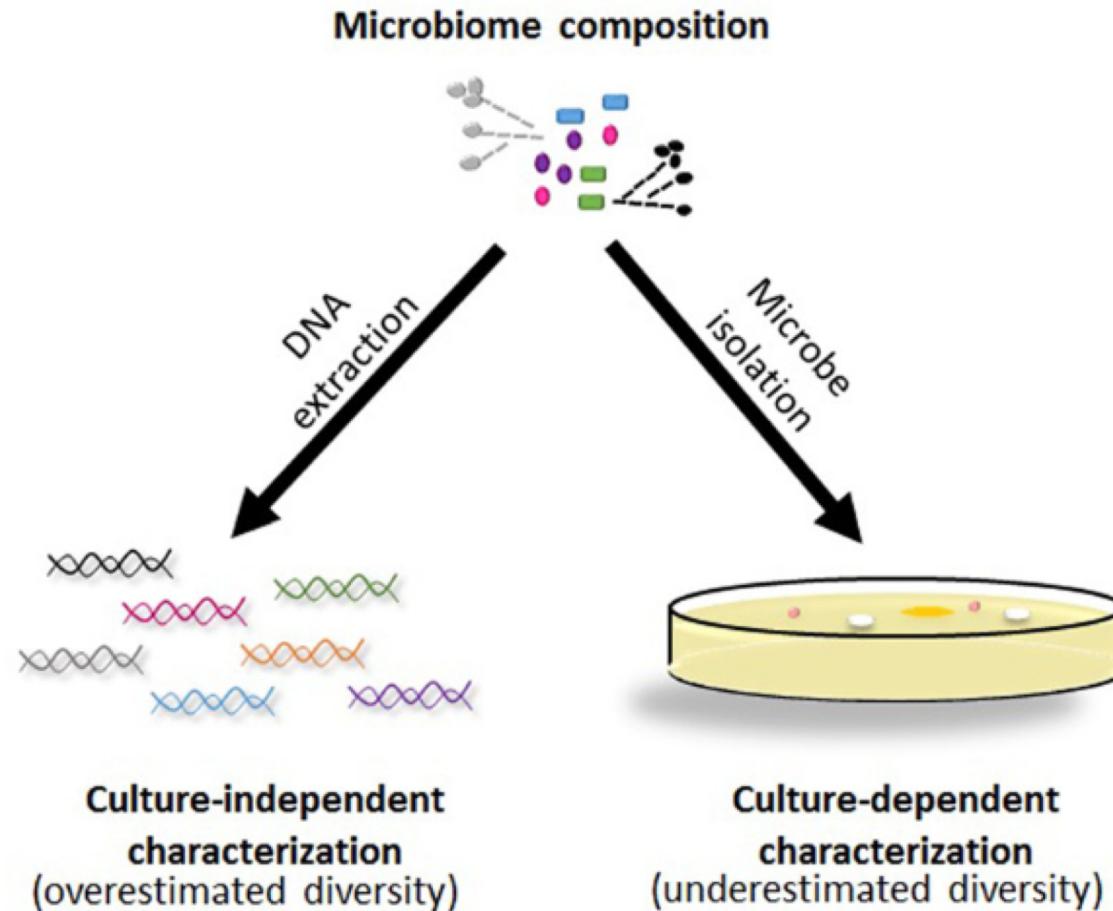
- 1) Acclimation to environmental conditions
- 2) Plant ecology
- 3) Plant and microbe evolution

# The Big Question:

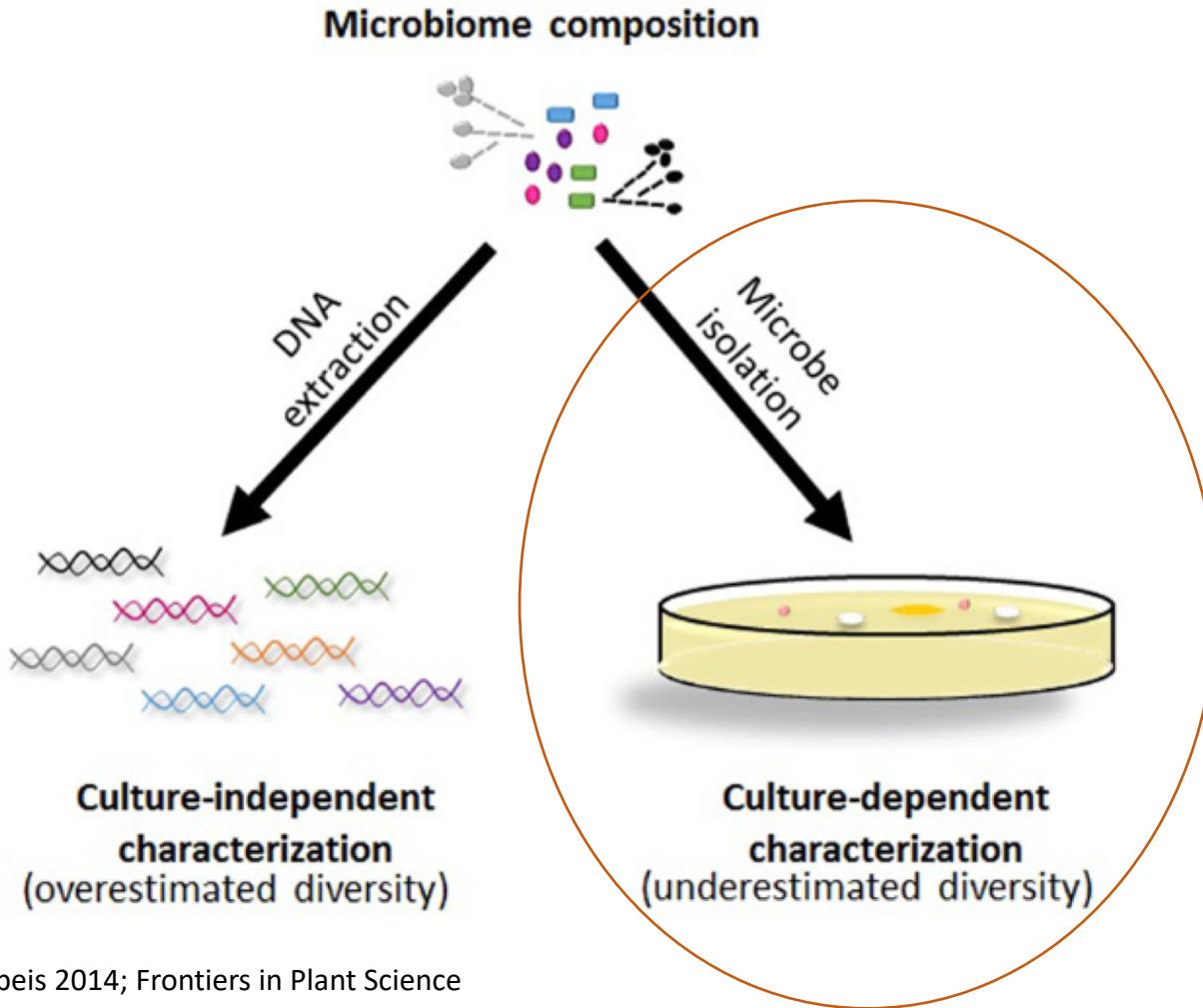
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How do the microbiomes  
differentiate across *T.*  
*cacao* populations?

# Genomic method for taxonomic classification and functional characterization



# Genomic method for taxonomic classification and functional characterization



## Pros:

- Can observe morphology, behavior, and interaction with other microbes

## Cons:

- Very few microbes can be cultured in the lab
- Culturing time and resources

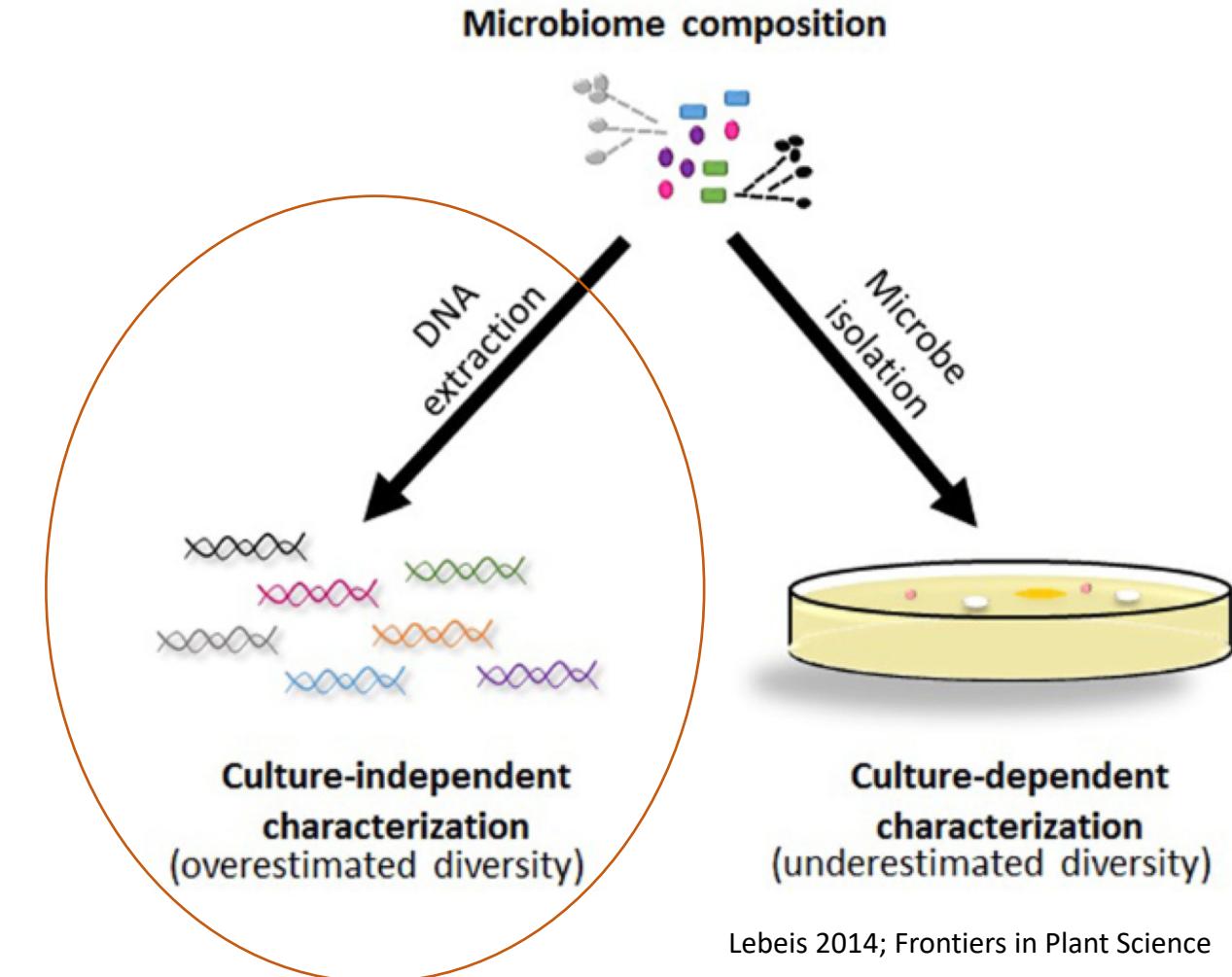
# Genomic method for taxonomic classification and functional characterization

## Pros:

- Captures the breadth of microbe composition
- Requires less resources and laboratory space

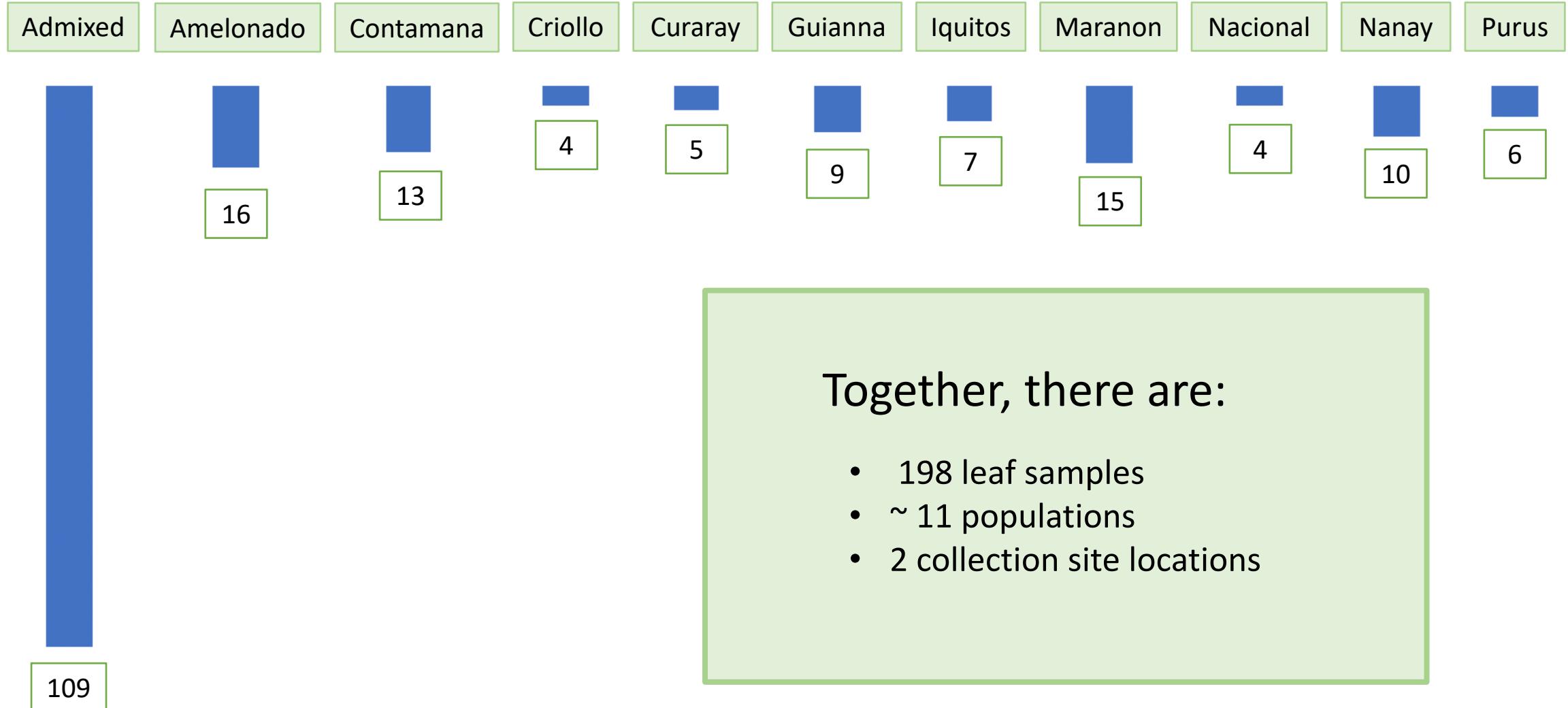
## Cons:

- Limited by genomic data available
  - Potential for inaccurate alignment with sequences less related to the microbes



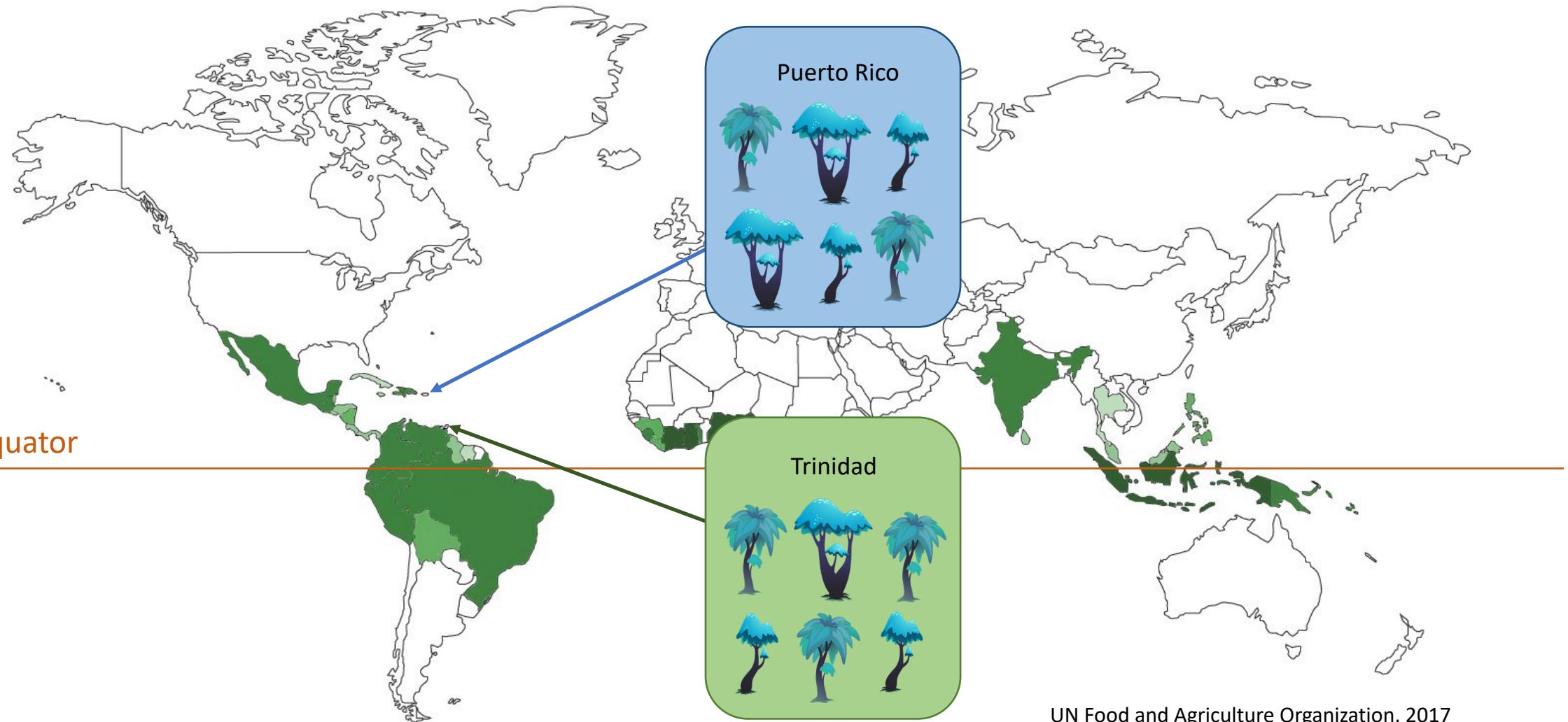
# ~200 individual plants among 11 populations

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# Global distribution of cocoa bean production

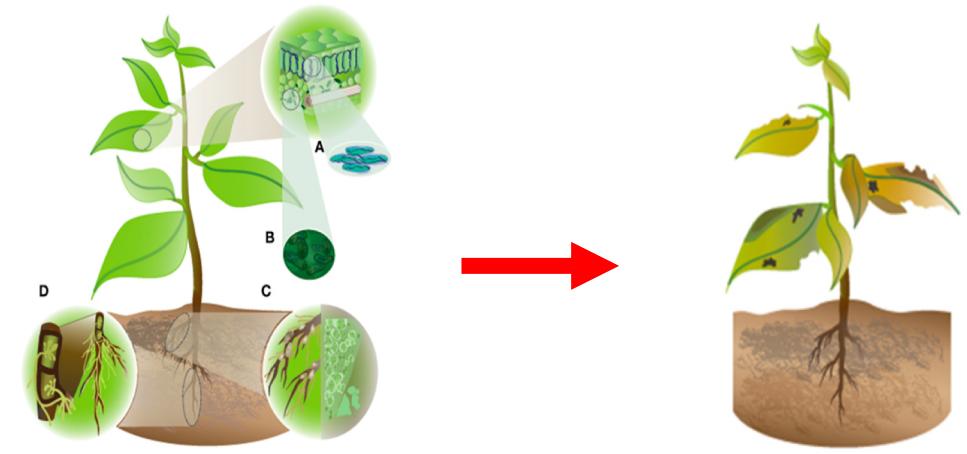
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UN Food and Agriculture Organization, 2017

# Co-evolution of host and microbiome

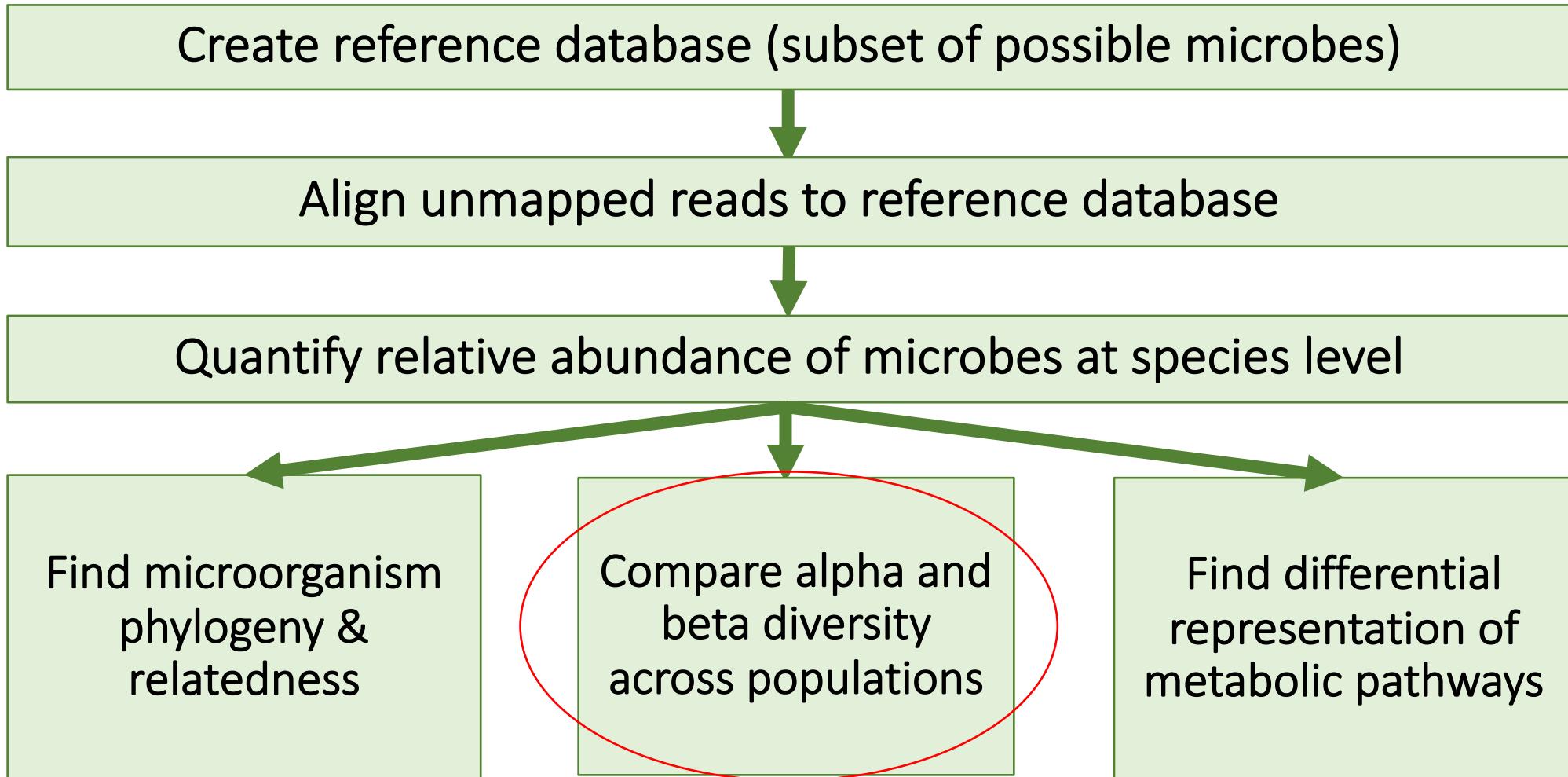
- Introduction of new microbes from the site-specific plots, but similar functional properties
- Co-evolution between plant genomes and microbial genomes due to close interdependency
  - Vertically transmitted endophytes



Partida-Martínez et al. 2011; *Front. Plant Sci.*

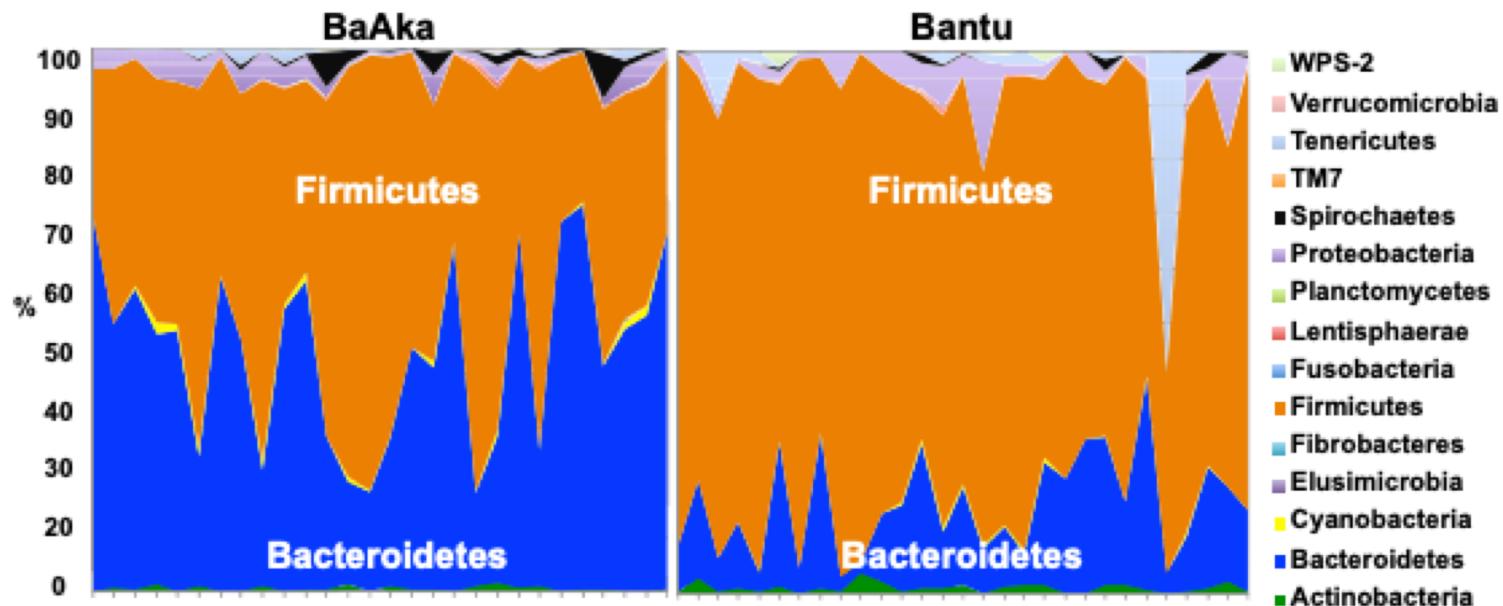
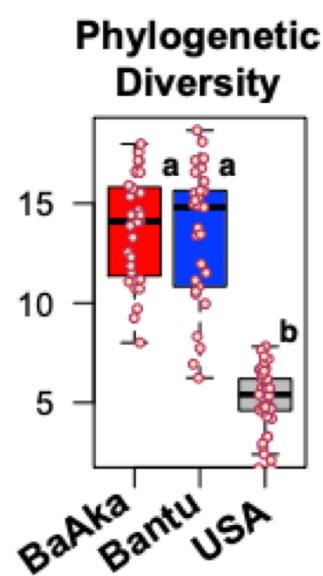
# The general flow of the project

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# Expected outcome: Relative abundance of taxa will differ among populations

- Gut microbiota comparison of different human populations
  - BaAka → Hunter-gatherer community
  - Bantu → Agriculture-based community



Gomez et al. 2016; *CellPress*

# Using microbial composition as a polymorphic trait

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- Nei's Genetic Distance → Developed for markers with many alleles to show genetic distance in proportion to divergence time.

$$D = -\ln\left(\frac{J_{xy}}{\sqrt{J_x J_y}}\right)$$

$J_x = P(\text{two individuals in pop } x \text{ have same allele})$

$J_y = P(\text{two individuals in pop } y \text{ have same allele})$

$J_{xy} = P(\text{an individual in pop } x \text{ and } y \text{ have same allele})$

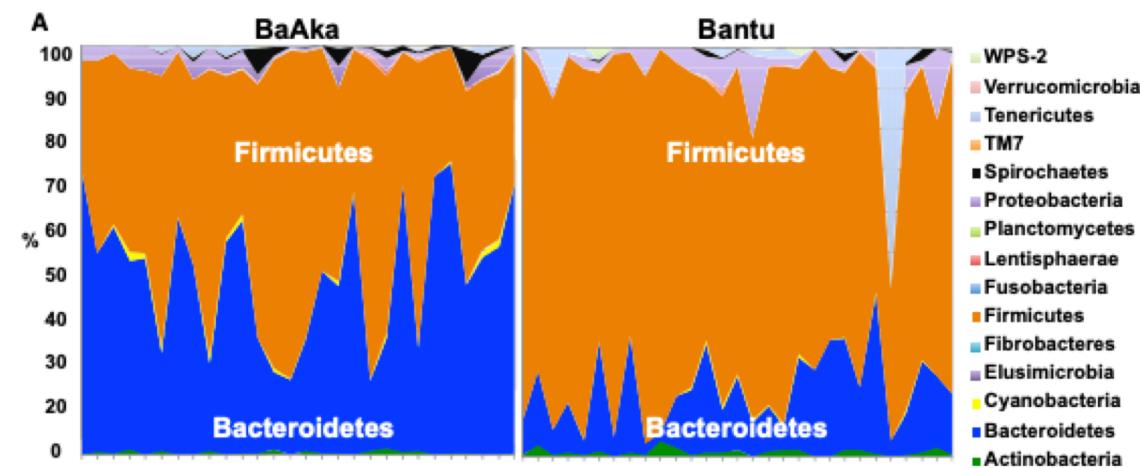
$$J_x = \sum x_i^2 \rightarrow \text{where } x_i \text{ is the ith allele frequency in pop } x$$

$$J_y = \sum y_i^2 \rightarrow \text{where } y_i \text{ is the ith allele frequency in pop } y$$

$$J_{xy} = \sum x_i y_i$$

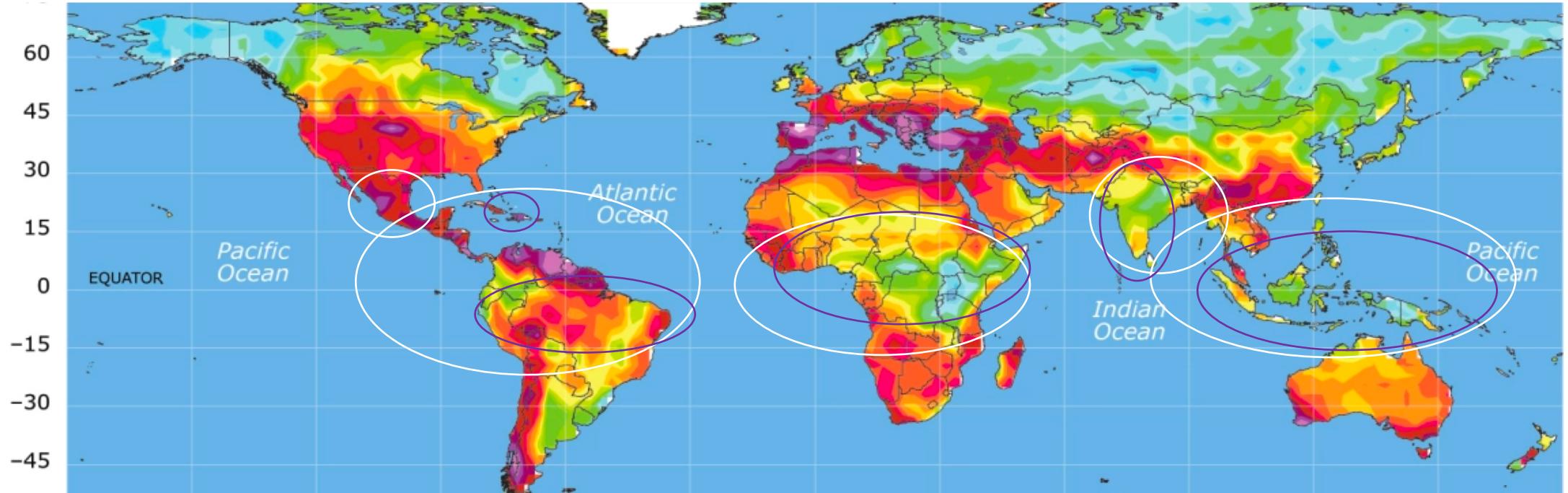
# Using microbial composition as a polymorphic trait

- With the assumption that the host genetic makeup plays a role in microbial selection, then we can..
  - View the whole microbiome as a “locus”
  - Make each taxonomic group an “allele”
  - Swap the allele frequency with the frequency of the microbial taxonomic groups



Gomez et al. 2016; *CellPress*

# Role of the microbiome in host adaptability



Wiley Interdisciplinary Reviews: Climate Change; 2010

- How will the microbiome contribute to the persistence of *T. cacao* in the face of climate change?
- Can the microbiome be exploited to enhance environmental tolerance?

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WASHINGTON STATE  
 UNIVERSITY

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