

BIS 180L

Rice Diversity Lab

April 30, 2019
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Outline

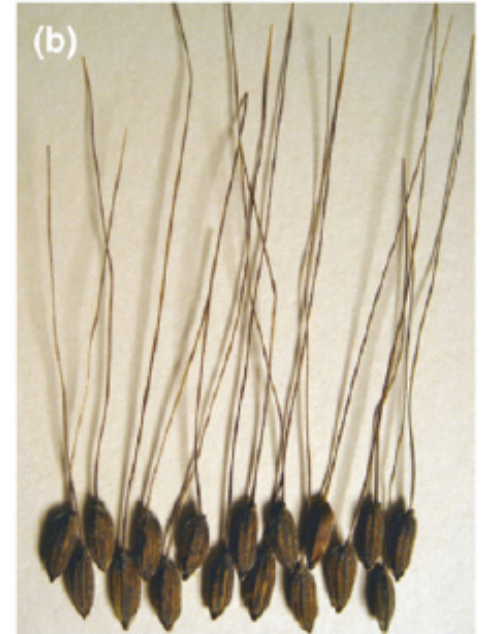
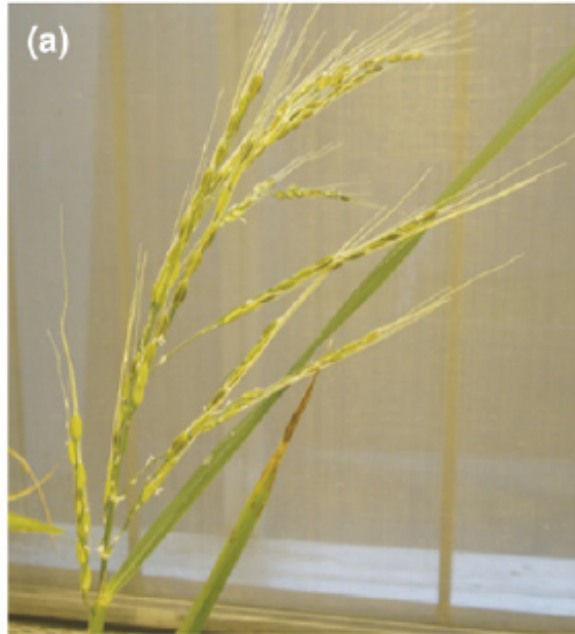
- Today:
 - Intro to rice
 - Review of population structure
- Later today or Thursday
 - Genome Wide Association Mapping (LD)

Study system: Rice

- This Week:
 - Study diversity in ~ 400 rice strains
- Why Rice?

Rice Domestication

Rice progenitor:
Oryza rufipogon



Domesticated rice
Oryza sativa



TRENDS in Genetics

Rice Diversity

- Two main sub populations: *Indica* and *Japonica*
 - Thought to have been domesticated independently from *rufipogon*
 - Estimated divergence time: 100,000 years ago or more.
- *Indica*
 - Grown in lowland tropical areas
 - S. and S.E. Asia and China
 - Further subdivided into *indica* and *aus*
- *Japonica*
 - Grown in lowland and high-elevation upland areas of tropical SE Asia
 - Also grown in colder temperate climates including NE Asia, Europe, Western US, Chile, Australia
 - Subdivided into *tropical japonica*, *temperate japonica*, and *aromatic*

Using natural variation for rice improvement

- Urgent need for crop improvement:
 - World population expected to grow to 9,000,000,000 by 2050
 - Climate change and increasing unpredictability will reduce yield
 - Increasing demand for meat and biofuels put further strains on agriculture
- One path forward is to use the natural genetic diversity (“natural variation”) already present in rice
 - 120,000 different rice strains have been deposited in seed banks
 - These harbor different genetic variants
 - Many are just random
 - some provide adaptation to specific environments/stresses
 - drought, flooding, heat, pathogens, etc
 - some determine specific grain characteristics of consumer interest
 - stickiness
 - grain length
 - aromatic (basmati, jasmine)
 - color
- Identify genes or genomic locations of variants
 - Why?



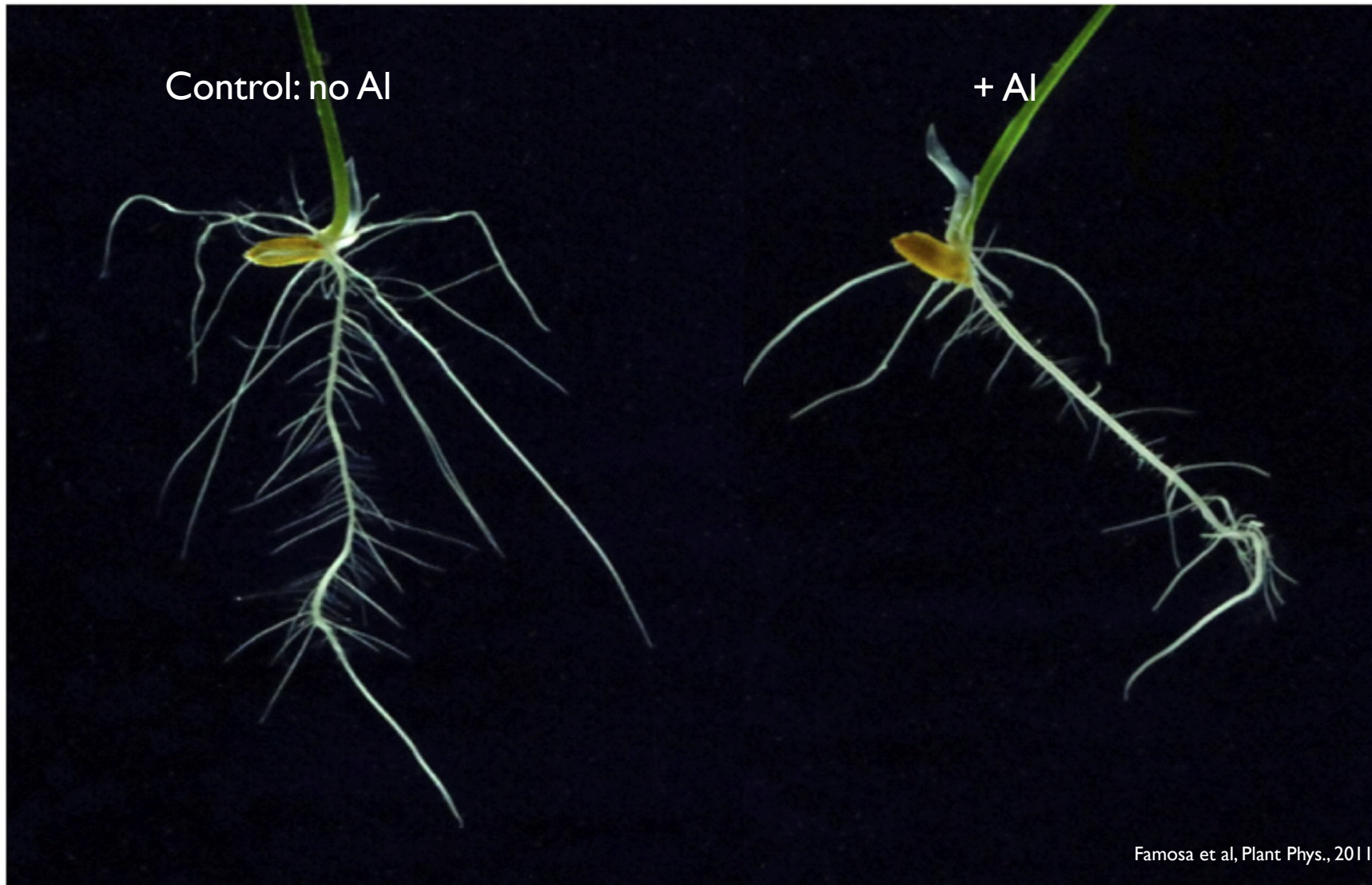
We will focus on root traits

- Why Roots?



Root Aluminum Tolerance

- Aluminum: Most abundant metal in earth's crust.
- Solubilized under highly acidic soil conditions
- Toxic to plant roots
- Can we find variation in resistance to Aluminum among rice varieties?



Study Design

- 413 Rice varieties from 82 countries
- Phenotypes:
 - Roots in control and Al⁺ conditions
 - Grain length
 - Amylose content
 - Flowering time
 - ...
- Genotypes:
 - Sequence 20 strains, find common SNPs
 - Design Affymetrix “SNP chip”
 - Assay 44,000 Single Nucleotide Polymorphisms on each of the 413 varieties
 - Yields ~ 1 SNP per 10kb

Overview of Questions about Rice Data:

- Population Structure:
 - Are these samples from a single randomly mating population or are there sub-populations?
 - Multi-dimensional scaling plot of genotype data to examine diversity and relationships
 - fastStructure to assign varieties to ancestral populations
- Can we find SNPs associated with Aluminum tolerance or other traits?
 - What are the genes underlying these SNPs?

Principal Components Analysis (PCA) and Multi-Dimensional Scaling (MDS)

- SNP Data is multi-dimensional; each SNP site can be considered an axis
- PCA and MDS techniques are ways to visualize this multi-dimensional data in 2D
- PCA:
 - Find the vector through the data that explains the most variance. This is the first principal component
 - Find the vector that explains the most remaining variance. This is the second principal component.
 - repeat...
- MDS
 - Project from multiple dimensions onto 1 or 2 dimensions in a way that preserves distances present in multi-dimensional space
- (Board examples)
- (3D example)

population structure

- Project SNPs in reduced dimensional space.
- Clumps of individuals represent population structure

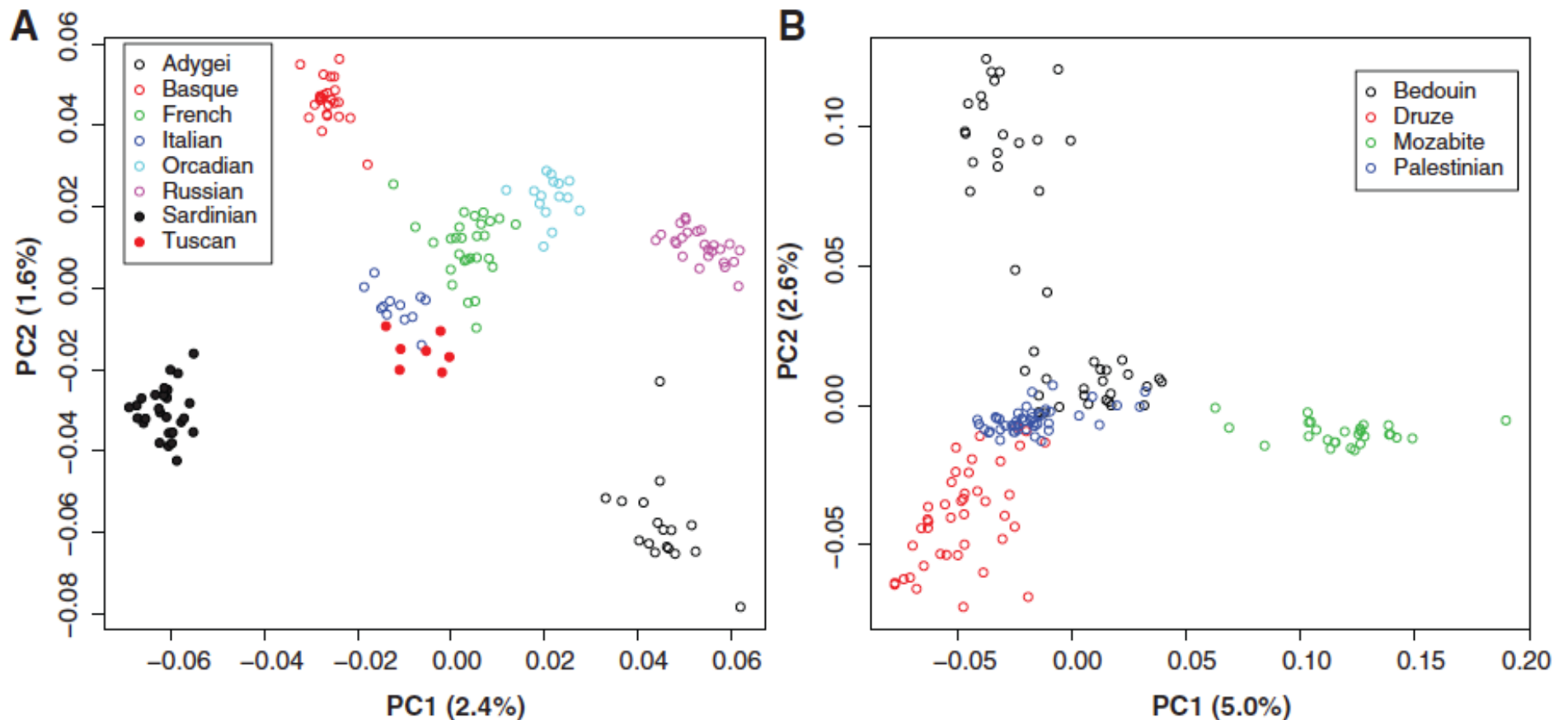
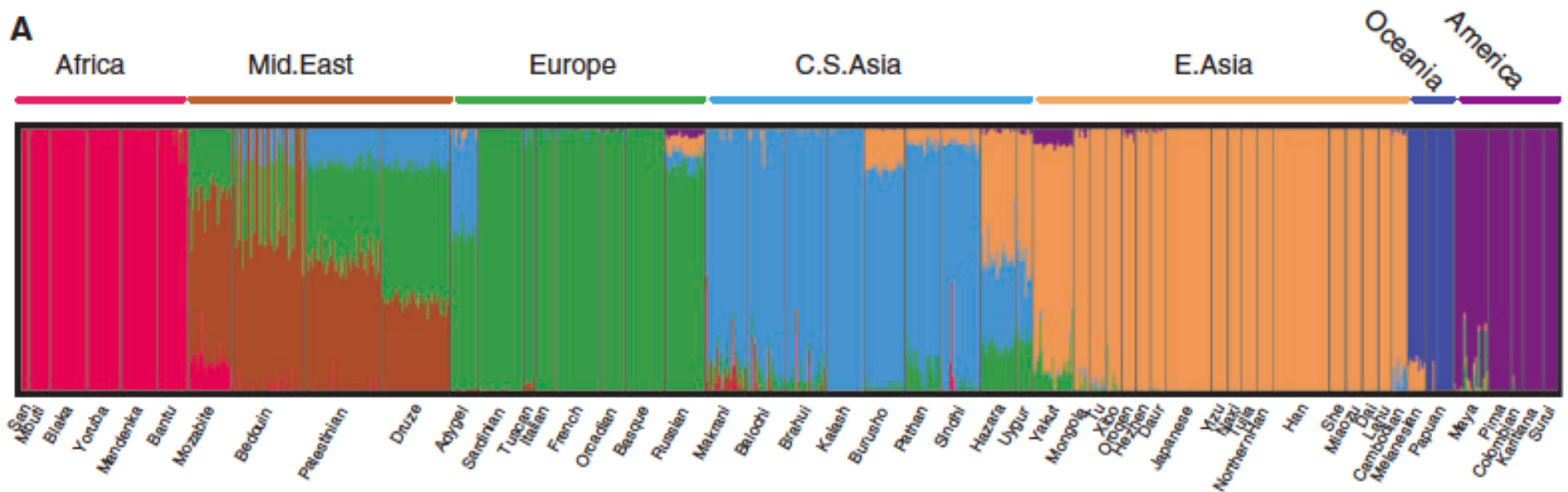


Fig. 2. Fine-scale population structure principal component analyses in two geographic regions, using all autosomal SNPs. (A) Europe. (B) The Middle East.

Model based assignment of individuals to populations



- a priori decide on the number of likely ancestral populations
- use an evolutionary genetics model to assign the most likely ancestry to each individual

Questions to be considered in answering assignment questions:

- Is there population structure?
 - How does structure relate to region of origin?
 - How does structure relate to amylose content?
 - How does structure relate to Aluminum tolerance
- Are there GWAS hits for the trait you are studying (TBD)?
- What are the candidate genes for your GWAS hit?