

Characterization of Perennial Medicago Germplasm Diversity Using Molecular Markers

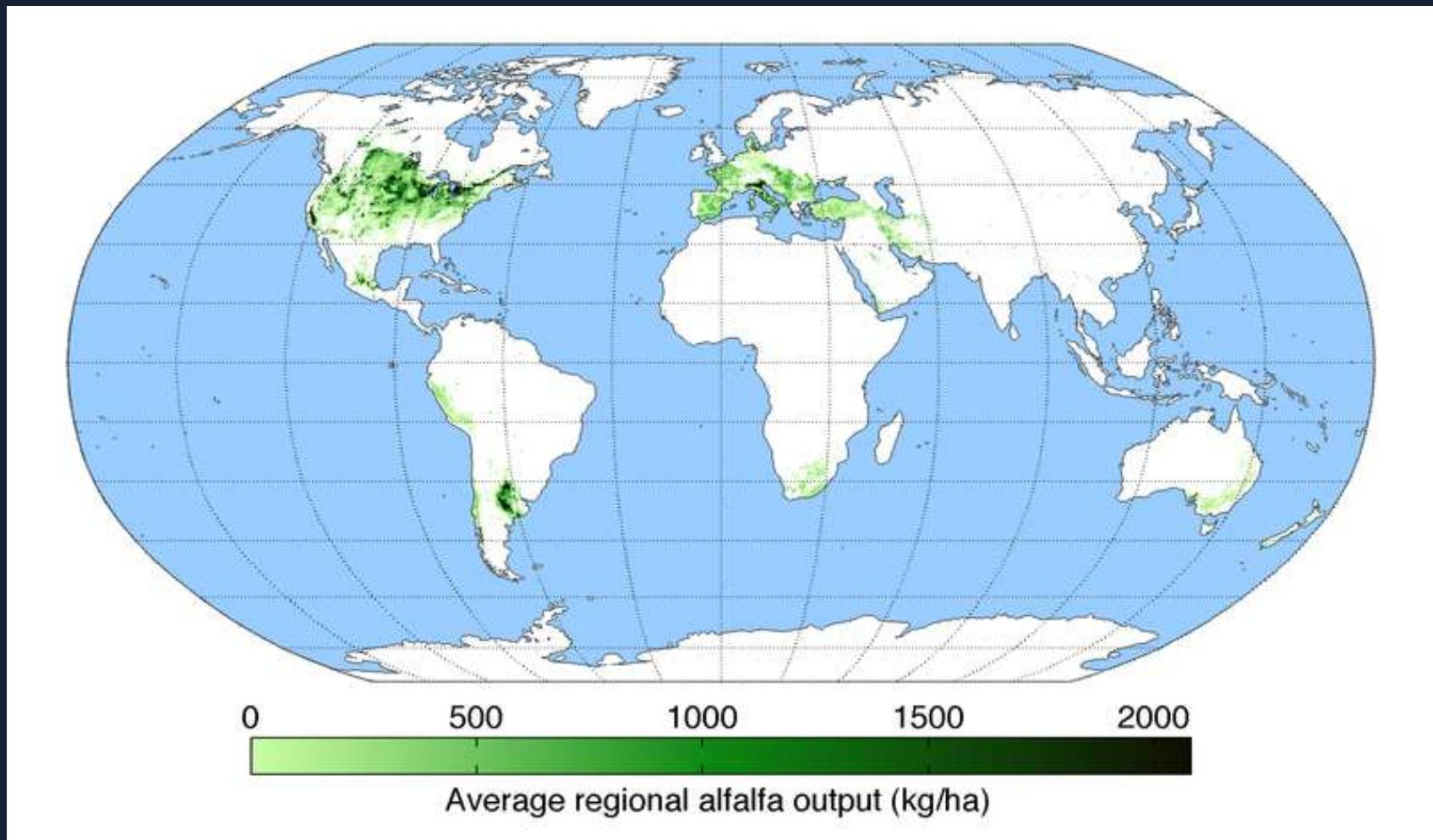
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NAAIC

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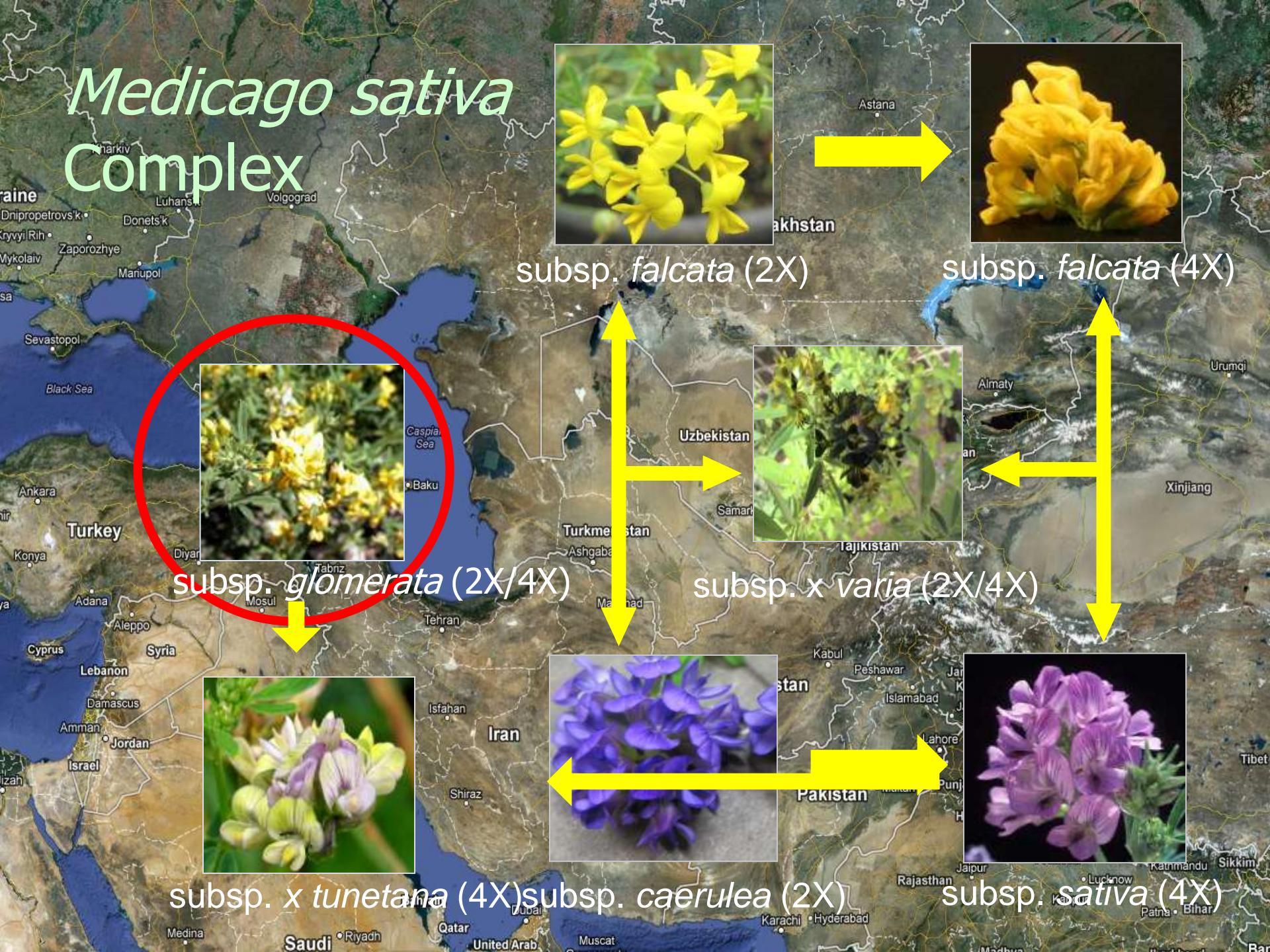


Global Alfalfa Production



Monfreda et al. 2008. Global Biogeochemical Cycles.

Medicago sativa Complex



Value of Genetic Diversity

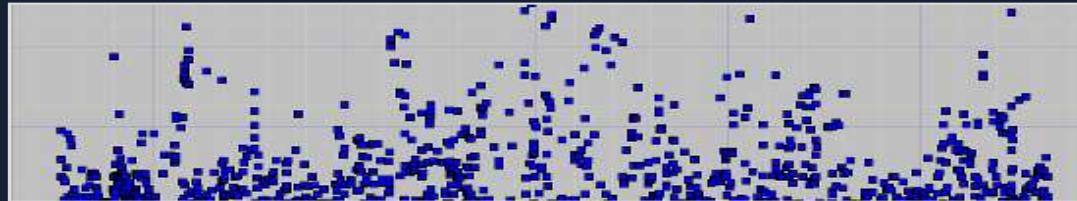
Conservation



Understand the germplasm variation



Identify useful alleles



Use in breeding programs



Objectives

Genetic diversity



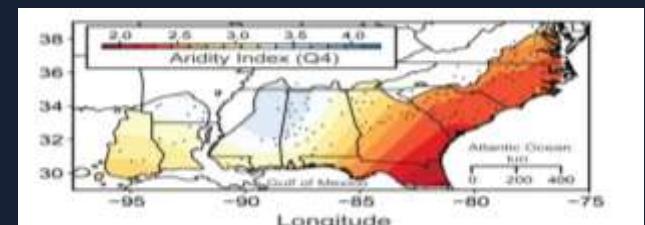
Association mapping

Landscape genetics

Morphological diversity



Ecogeographic data



National Plant Germplasm System

USDA  United States Department Of Agriculture
Agricultural Research Service

Germplasm Resources Information Network

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National Plant Germplasm System

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USDA Alfalfa Germplasm Collection

Subspecies	Accessions
<i>Medicago sativa</i> subsp. <i>sativa</i> (4n)	3331
<i>Medicago sativa</i> subsp. <i>falcata</i> (2n/4n)	488
<i>Medicago sativa</i> subsp. <i>x varia</i> (2n/4n)	328
<i>Medicago sativa</i> subsp. <i>caerulea</i> (2n)	99
<i>Medicago sativa</i> subsp. <i>glomerata</i> (2n/4n)	11
<i>Medicago sativa</i> subsp. <i>x tunetana</i> (4n)	6



USDA Alfalfa Germplasm Collection

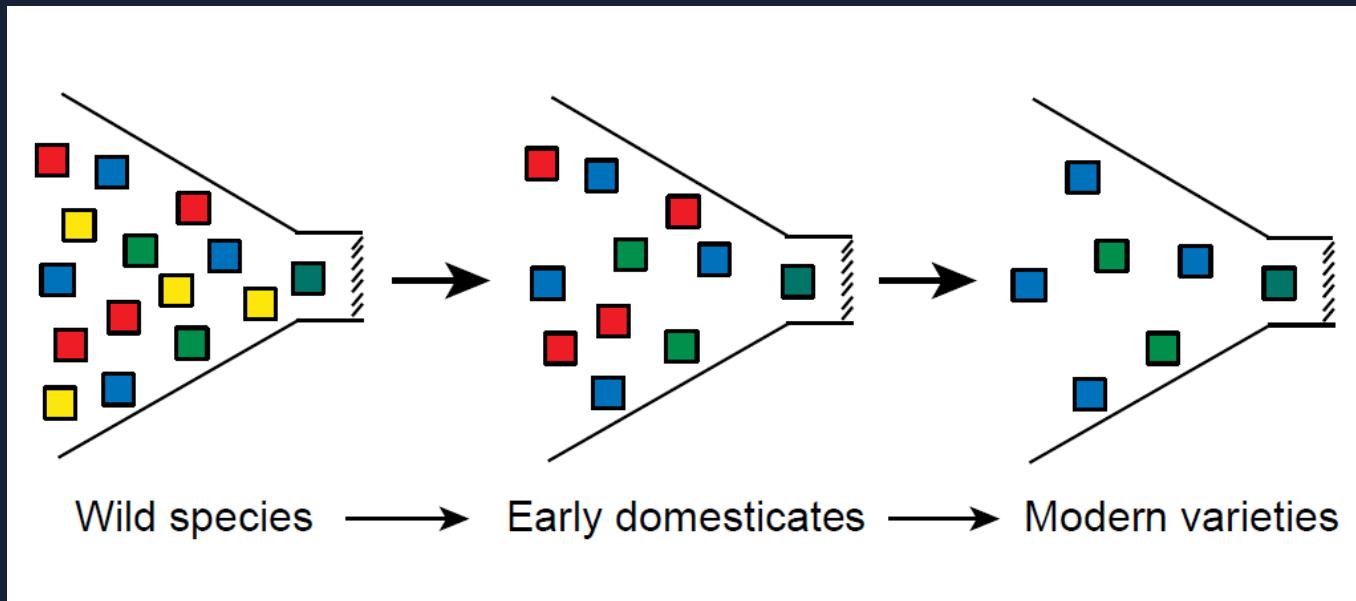


- Cultivated
- Landrace
- Wild

Volenec et al 2000, Report on the Status of *Medicago* Germplasm in the United States



Value of Wild Accessions



Tanksley and McCouch. 1997. Science.

Characterization of USDA Alfalfa Accessions

190 accessions

- Mostly collected from the former Soviet Union area
- 100 from Vavilov Institute, Russia



Species	Accessions
<i>M. sativa</i> subsp. <i>falcata</i>	73
<i>M. sativa</i> subsp. x <i>varia</i>	36
<i>M. sativa</i> subsp. <i>sativa</i>	25
<i>M. sativa</i> subsp. <i>caerulea</i>	24
<i>M. sativa</i> subsp. x <i>tunetana</i>	11
<i>M. sativa</i> subsp. <i>glomerata</i>	6
<i>M. cancellata</i>	2
<i>M. hybrida</i>	1
<i>M. papillosa</i>	2
<i>M. prostrata</i>	2
Winter dormancy controls	8

Geographical Distribution of Alfalfa Accessions



M. sativa ssp. **falcata**

varia

sativa

caerulea

glomerata

tunetana

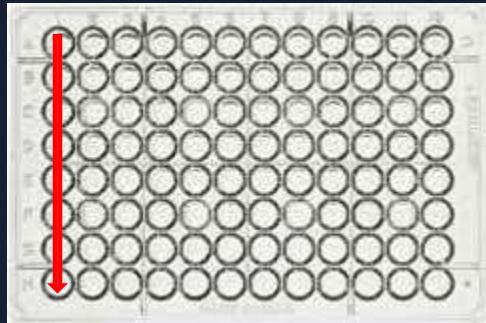


Experimental Design - Genetic Diversity

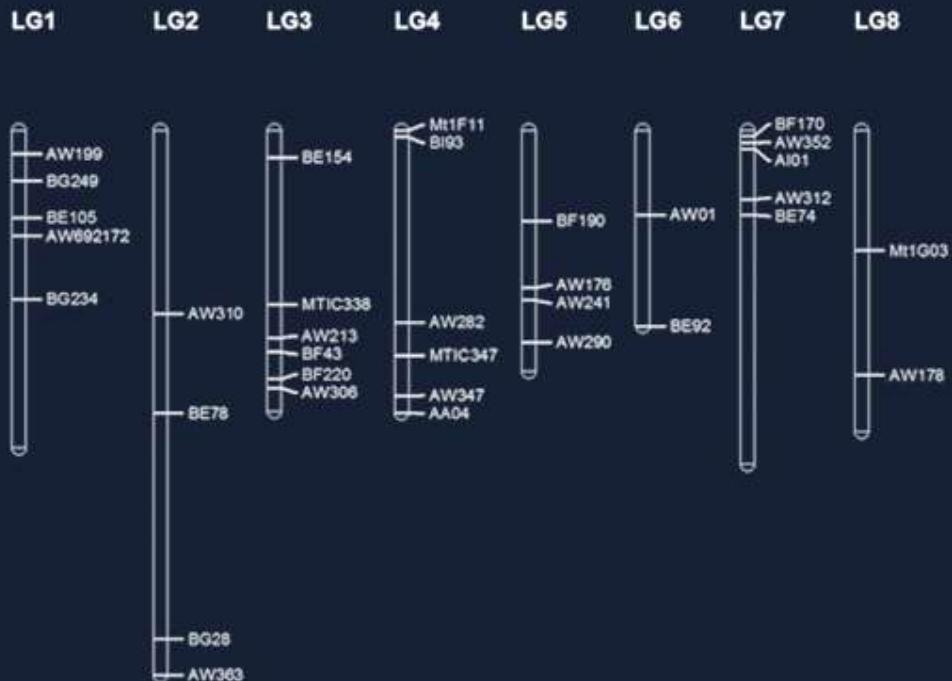
- 190 accessions
- 25 EST SSR markers



- 8 individual/accession



- 1520 samples

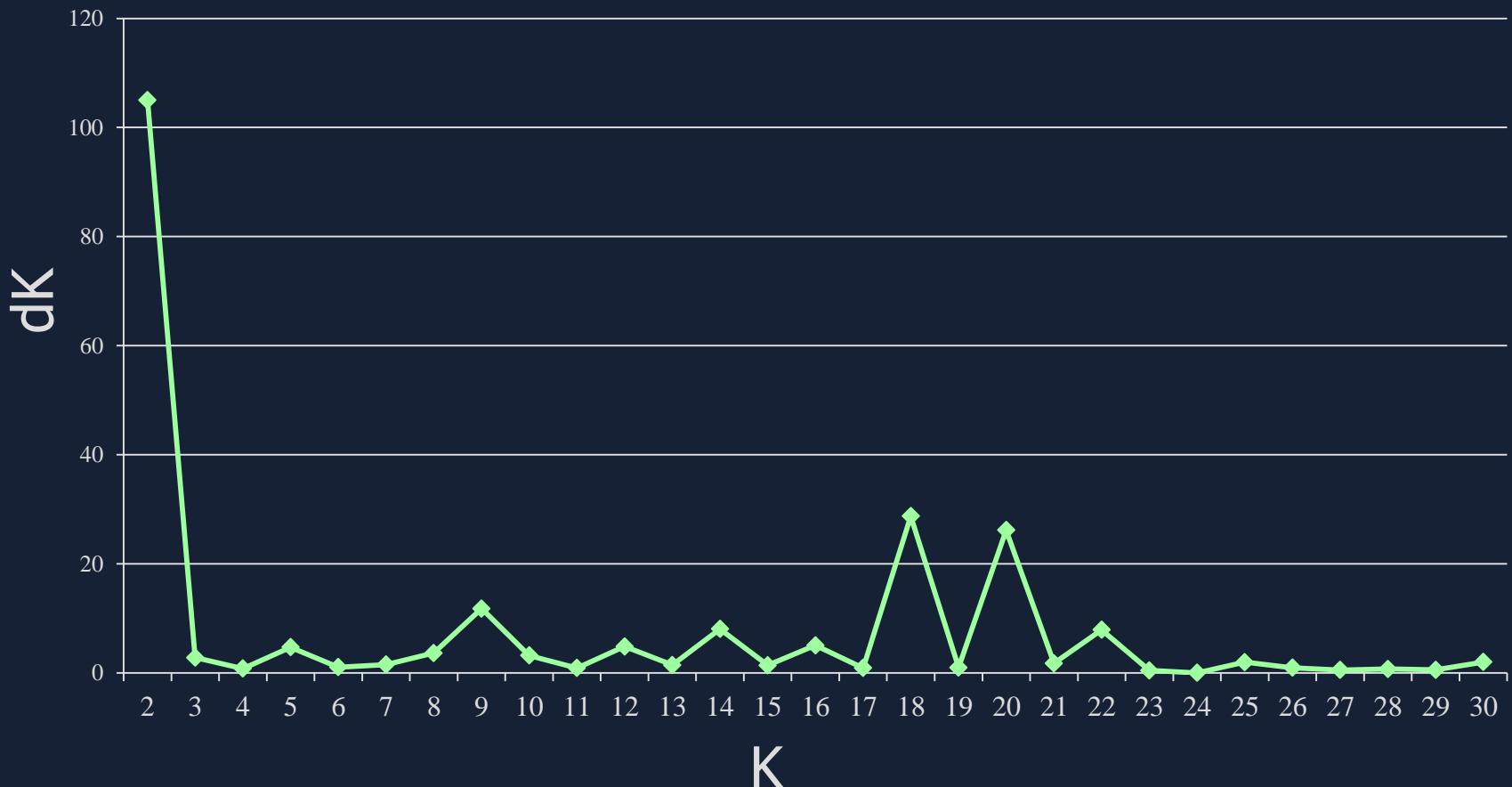


Population STRUCTURE Analysis

- A model-based clustering method (Pritchard et al. 2000)
- Detect the underlying genetic population among a set of individuals genotyped at multiple markers
- Computes the proportion of the genome of an individual originating from each inferred population



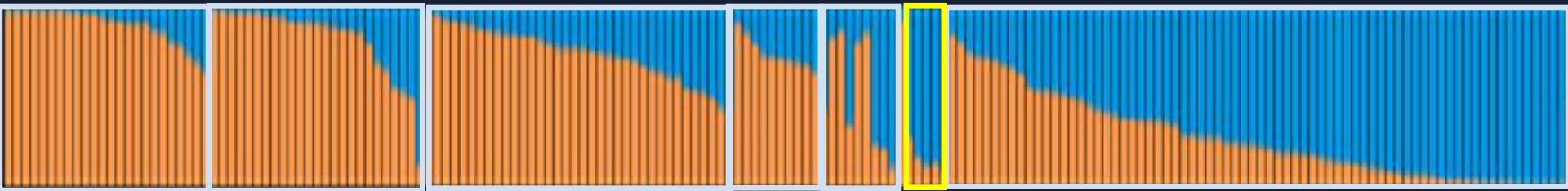
STRUCTURE Analysis of Alfalfa Accessions



STRUCTURE Analysis in Alfalfa

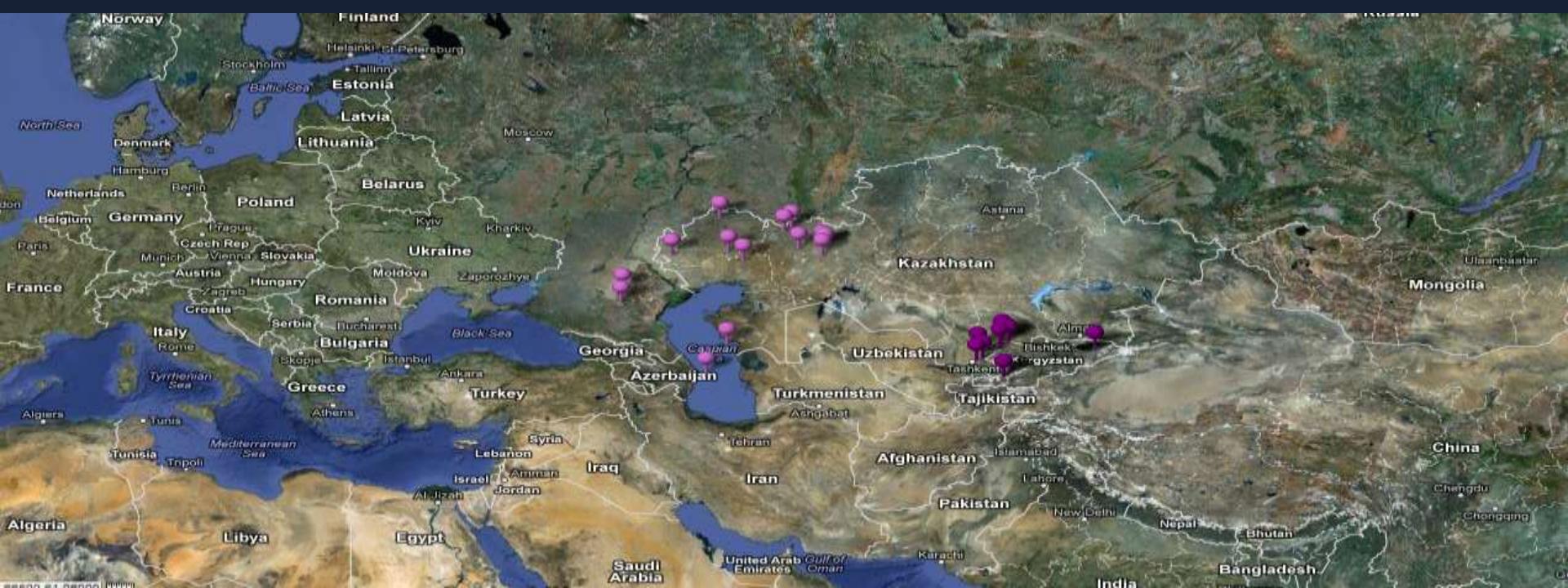
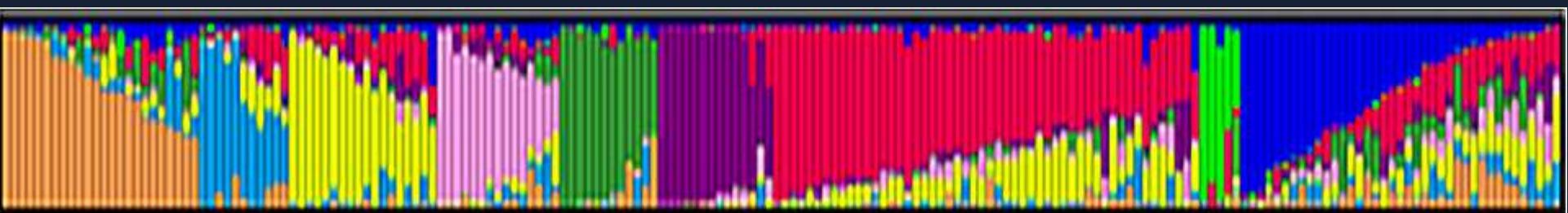
K=2

M. papillosa & *M. prostrata*



STRUCTURE Analysis in Alfalfa

K=9



Summary

- Identified population structure in the alfalfa accessions evaluated
- The sub-populations (K) largely correspond to the division of subspecies
- Detected broad correspondence between sub-populations and their geographical origin

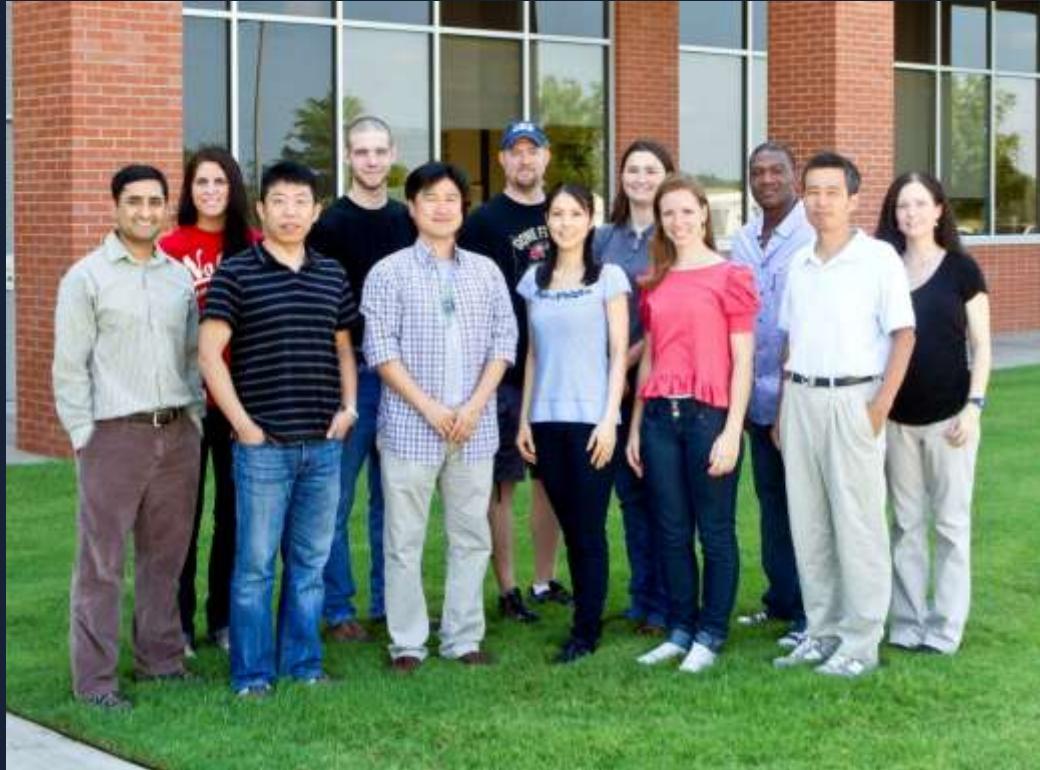


Ongoing Research

- Continue genotyping efforts
- Collect data for target morphological traits
- Identify relationships between marker diversity and phenotype
- Link genotype with environmental data to identify useful alleles for breeding program



Acknowledgments



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Stephanie Greene
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Thank You