

Plant & Animal Genome XXV, January 14-18, 2017
Town & Country Hotel, San Diego, CA

A grayscale background image showing a hand holding a microarray chip. The chip is a rectangular grid of small spots, likely representing a DNA microarray. The hand is positioned on the left side, with the thumb and index finger gripping the chip. The background is a light gray gradient.

Statistical Genomics in a World of Complete Genome Sequencing

Huihui LI

lihuihui@caas.cn and h.li@cgiar.org

Institute of Crop Science (ICS) and CIMMYT-China office

Chinese Academy of Agricultural Sciences (CAAS)

Outline

- Background
- Linkage map construction for high density markers
- Uniting the world's popcorn diversity for the dissection of complex traits and accelerating breeding



Background

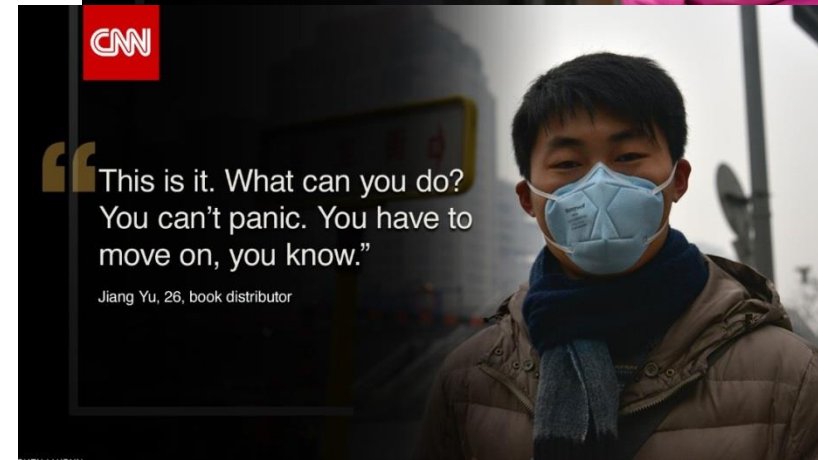
The pressures to increase agricultural production

- The world population is estimated to reach around 9.7 billion by 2050.
- Net investments of US\$83 billion a year will be needed in agriculture in developing countries.



The challenges to increase agricultural production

- Between 20% and 40% of global crop yields are reduced each year due to plant pests and diseases.
- Plant breeding is imperative to meet global challenges such as population growth and climate change.



Achieving food security in view of population growth & climate change



“I challenge the next generation to use **new scientific tools and techniques** to address the problems of the world’s poor.”

1970 Nobel Peace Prize Laureate

Current breeding materials contain only a fraction of the useful genetic variation available.

- Much of the needed diversity exists, like needles in a haystack, on the shelves of gene banks.
- Genomic tools enable us to search for useful diversity much more effectively.



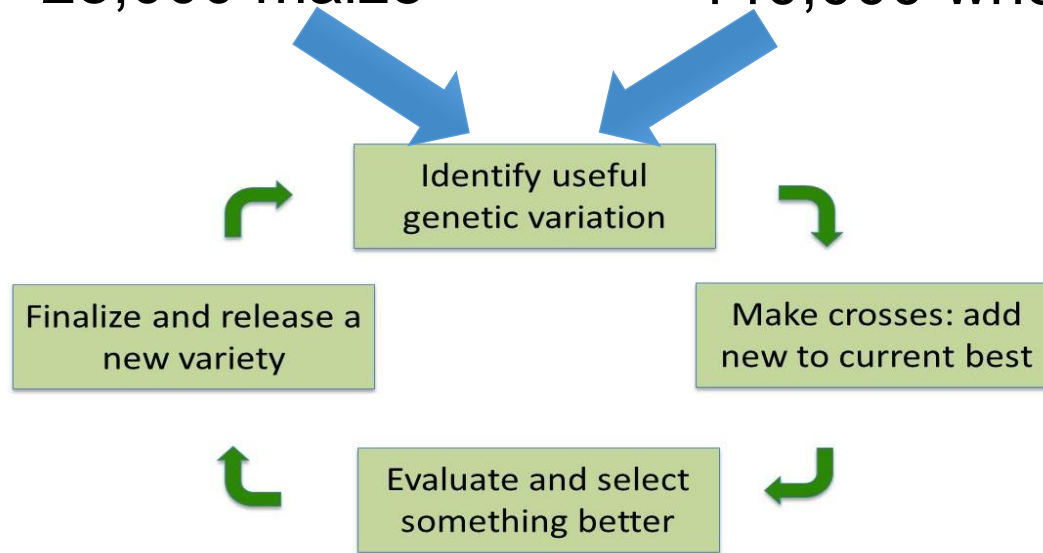
The wealth contained in the world's genetic resources is 'unlocked' for breeders globally to make new varieties



≈ 28,000 maize



≈ 140,000 wheat



High-density genetic profiles

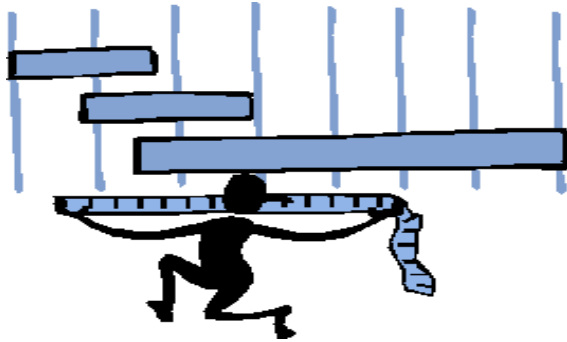


High-density phenotypic profiles

- ✓ Wheat: 1.4 million data points from 30 trials
- ✓ Maize: 0.7 million from 34 trials

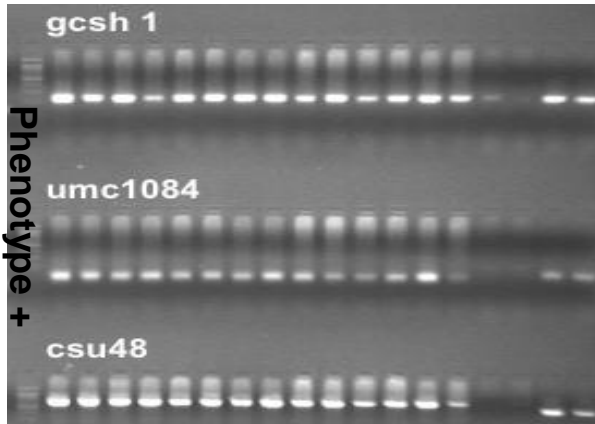
1900s'

Phenotype



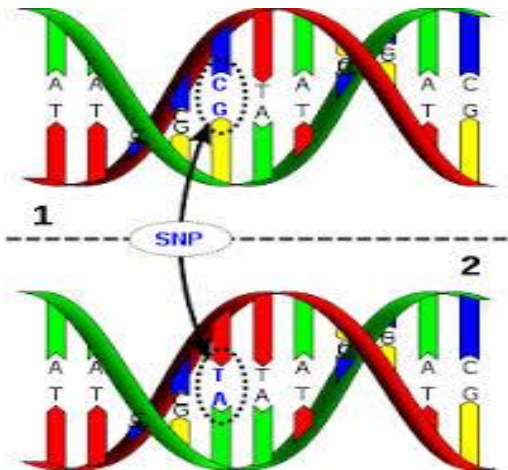
1980s'

Genotype + Phenotype



2010s'

Phenotype + Genotyping by sequencing



Genetics

- Classic quantitative genetics
- Analysis of phenotypic variance by experimental designs

- Linkage map by hundreds of markers
- QTL mapping
- Association mapping on candidate genomic region

- Linkage map by ten thousands of markers
- QTL mapping
- Genome-wide association mapping

Breeding

- Conventional breeding

- Conventional breeding
- Marker assistant breeding (MAS)

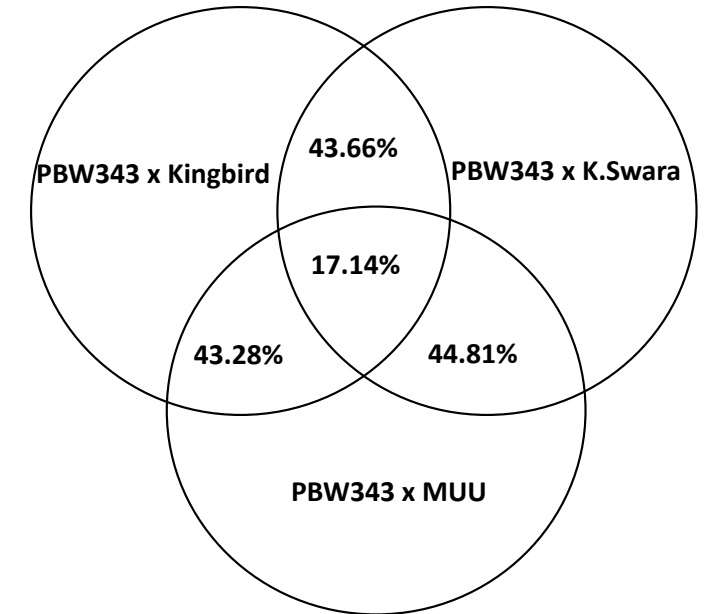
- Conventional breeding
- MAS
- Genomic selection



Linkage map construction for high density markers

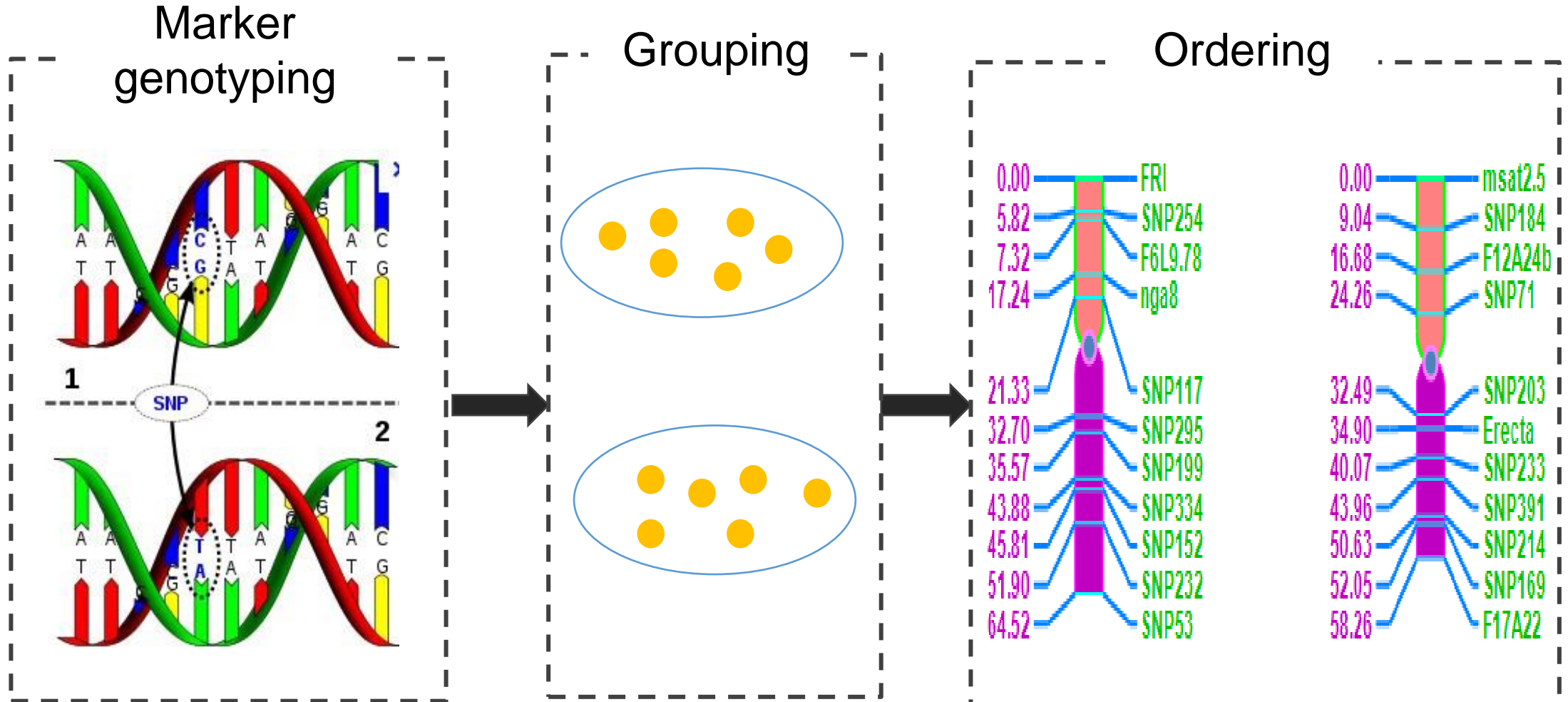
Three bi-parental RIL populations in wheat

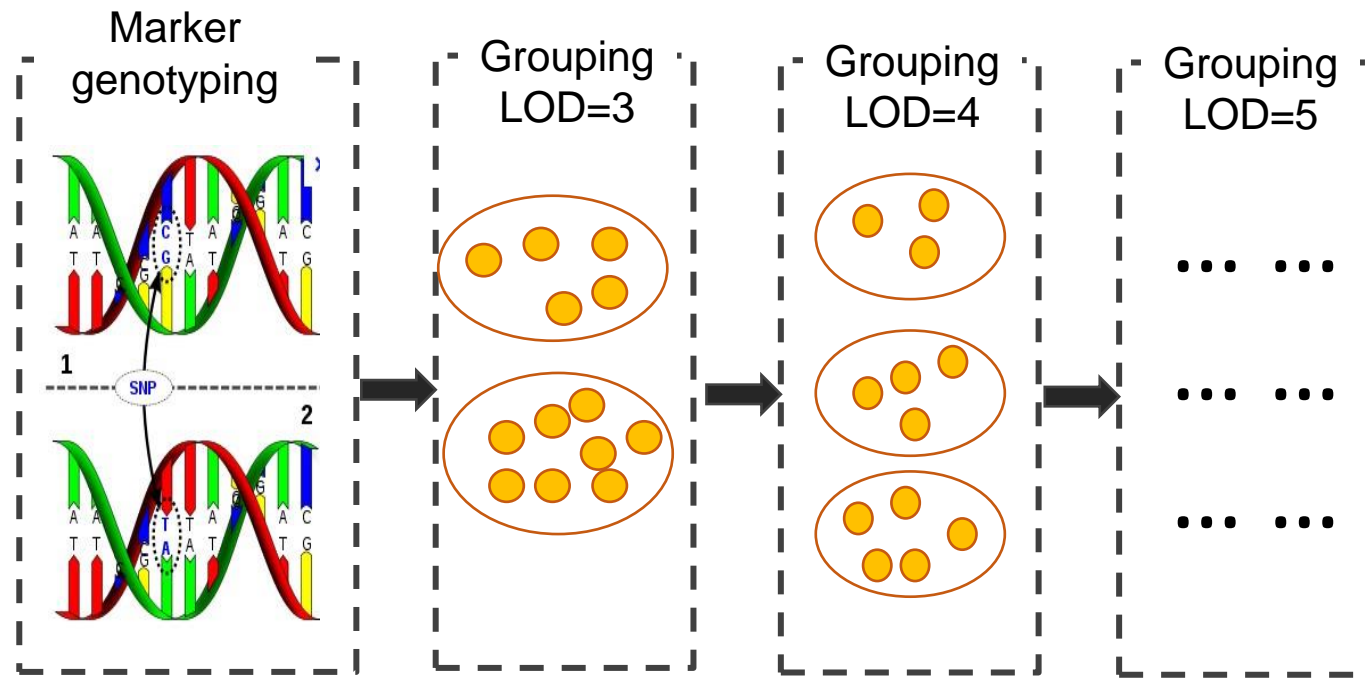
Population	Number of markers	Number of individuals
PBW343 x Kingbird	13123	198
PBW343 x Muu	6936	148
PBW343 x KSwara	18612	109



- PBW343, a major variety in India, is a selection (GID2430154) from CIMMYT line 'Attila' .
- Kingbird and KSwara have maintained high levels of adult plant resistance (APR) to complex disease.
- Muu was found to be susceptible at seedling stage but adult plants showed low disease severity to Ug99 during multiple years of field trials in Kenya (Njau et al. 2010)

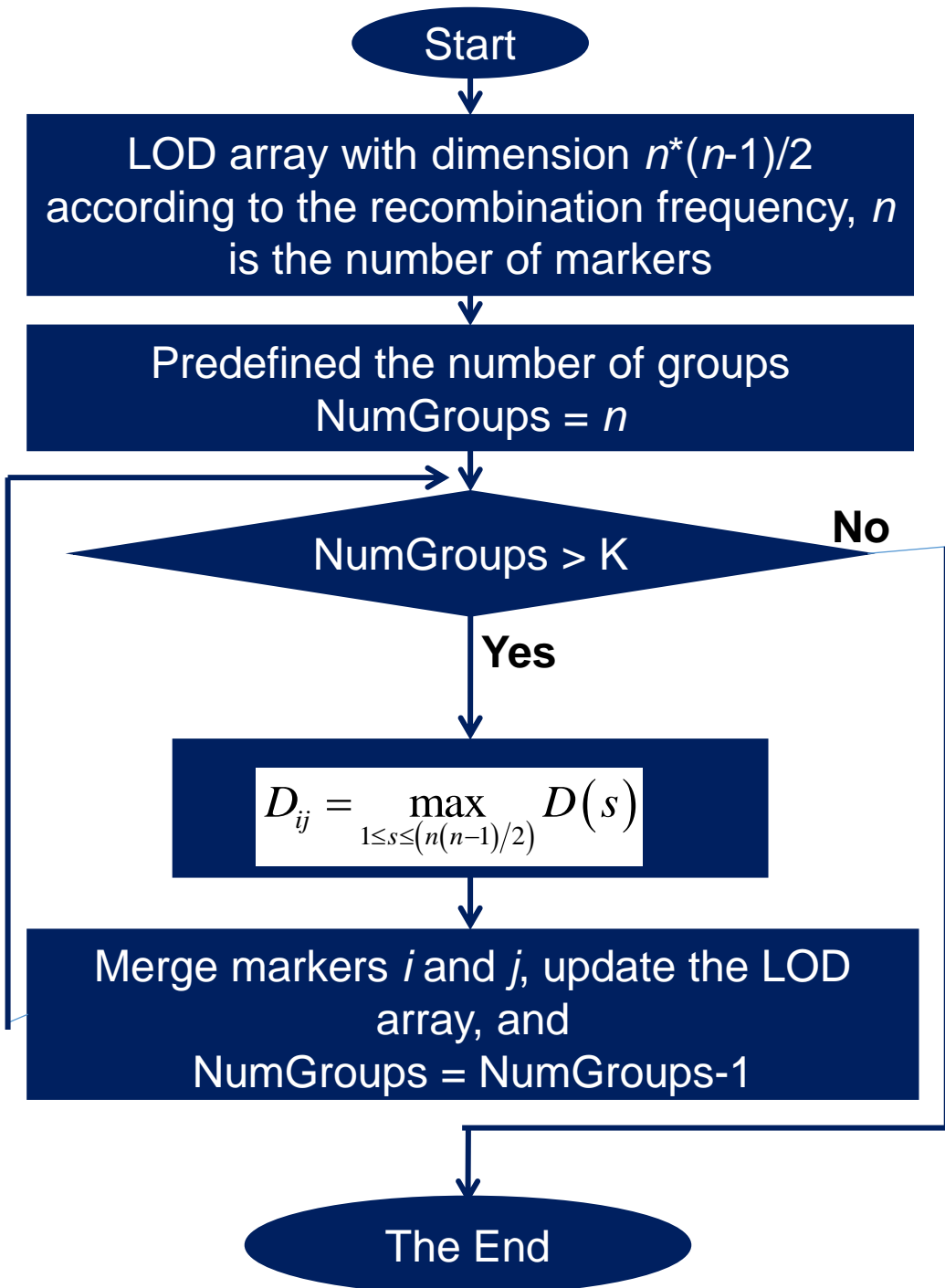
General steps for linkage map construction



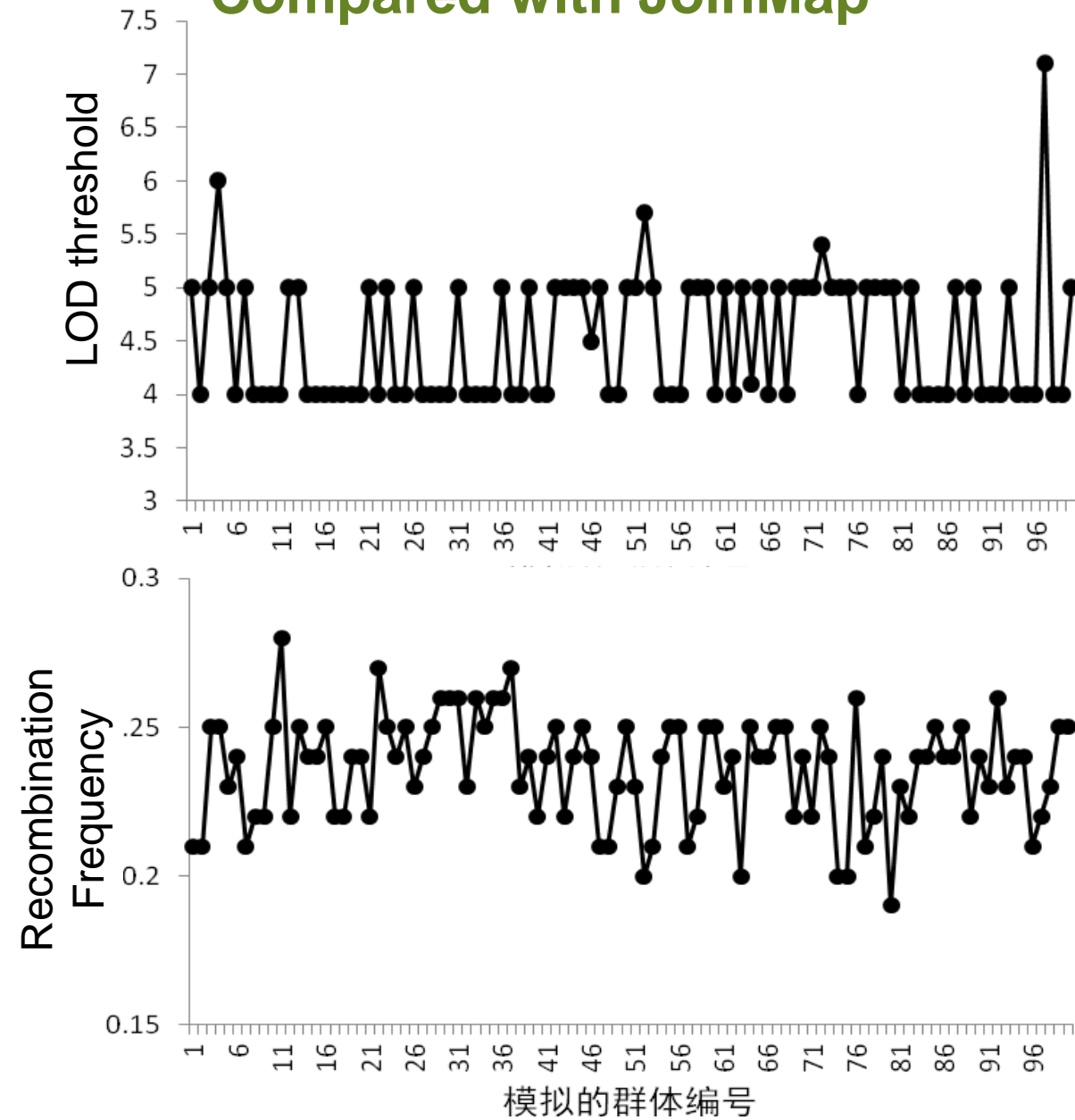


How to make the number of linkage groups more close to the number of chromosomes?

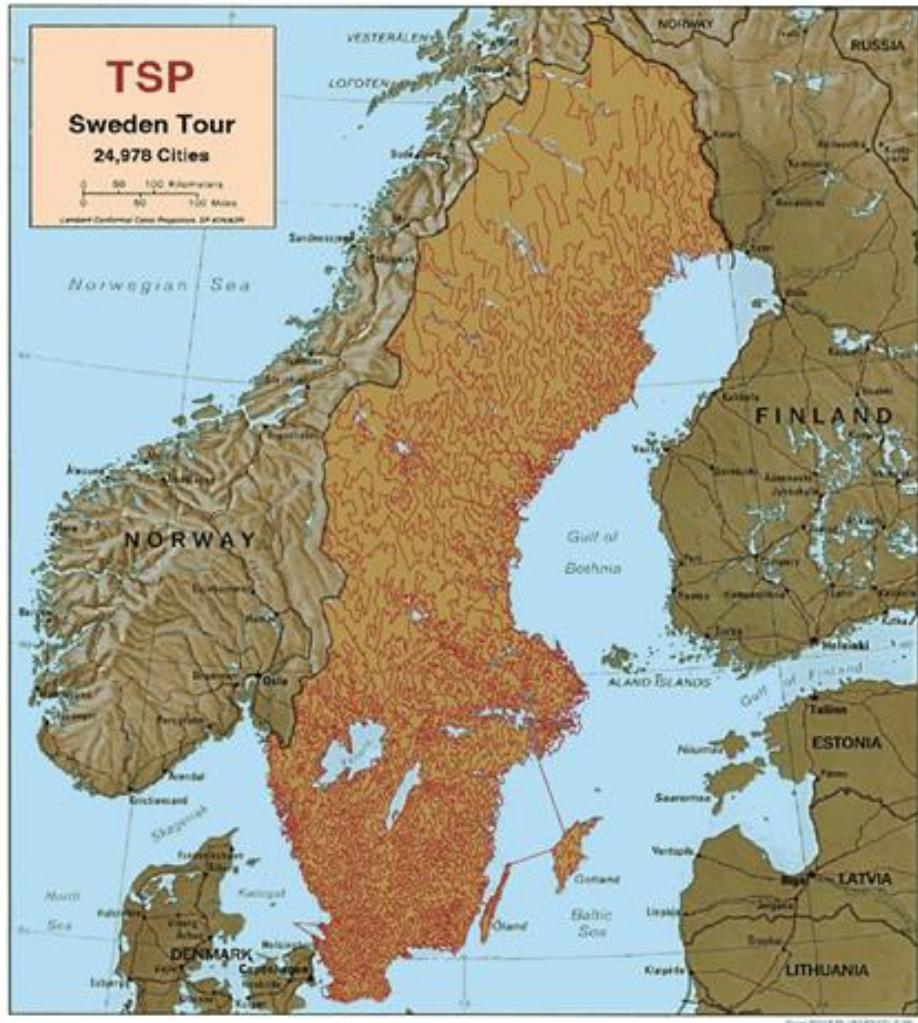
Agglomerative hierarchical clustering algorithm (Kettani et al. 2014, *International Journal of Computer Applications*)



Compared with JoinMap

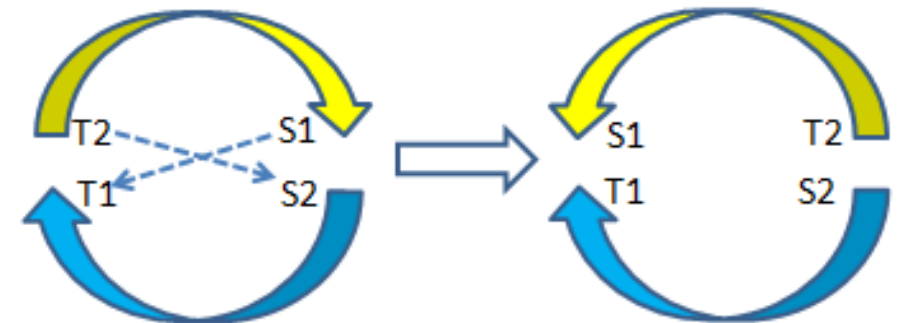


How to make the ordering more fast and accurate?

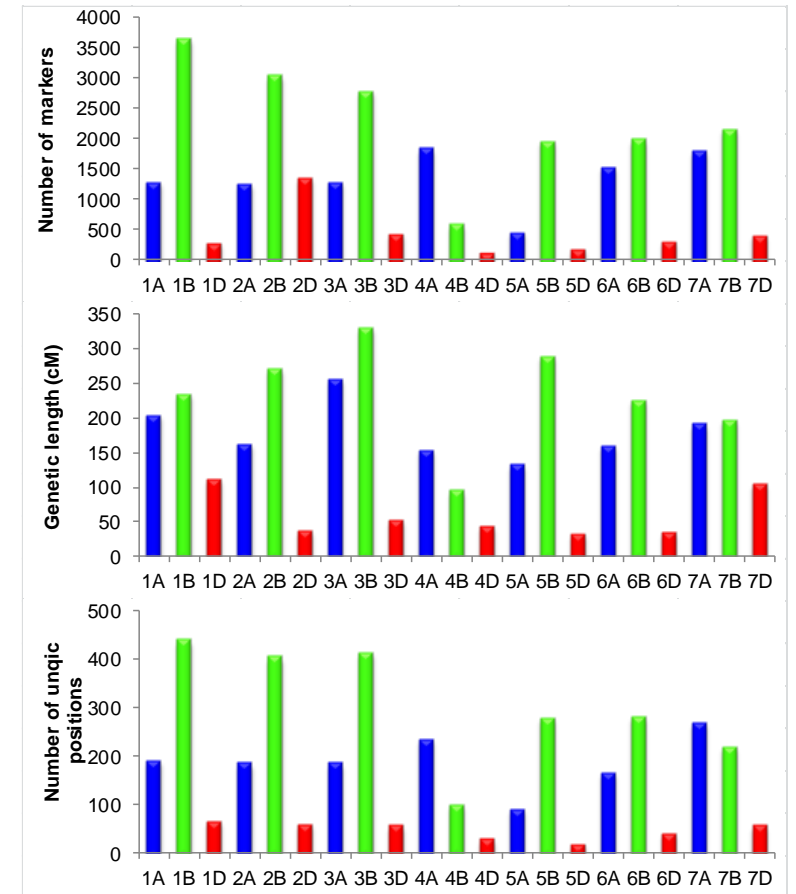
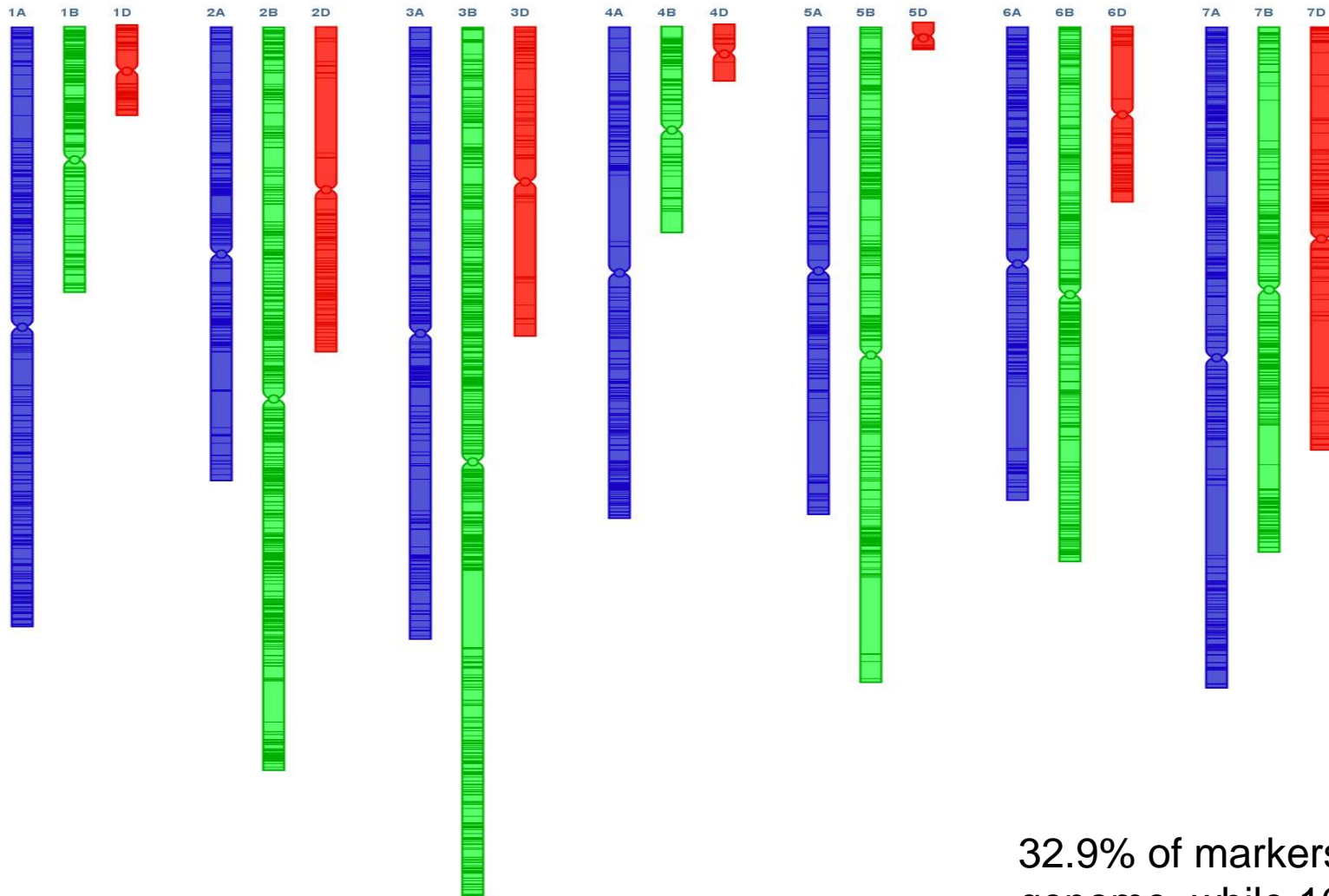


Nearest-neighbor (nn) algorithm for tour construction to solve *traveling salesman problems*.

Two-Opt algorithm for tour improvement (Lin and Kernighan, 1973)



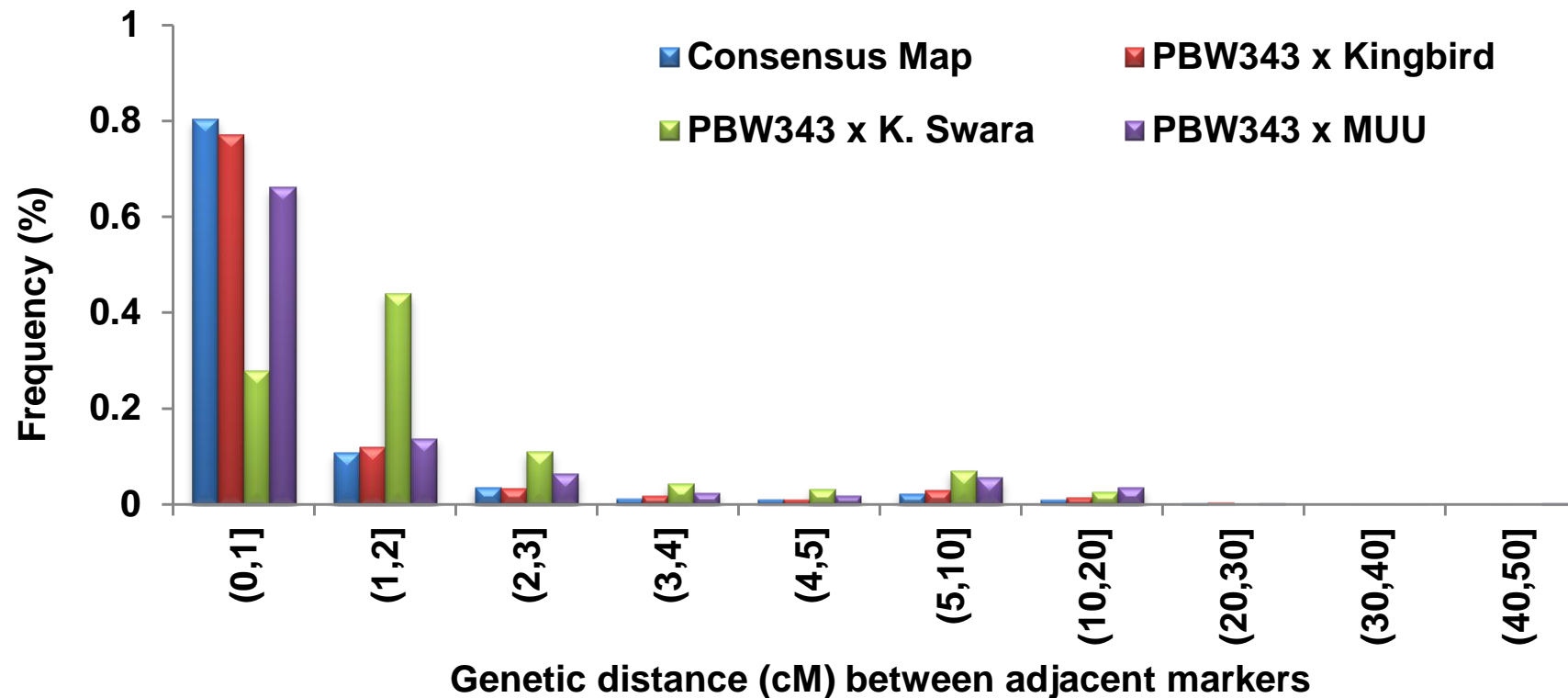
A high density linkage map with 28644 GBSed markers in wheat



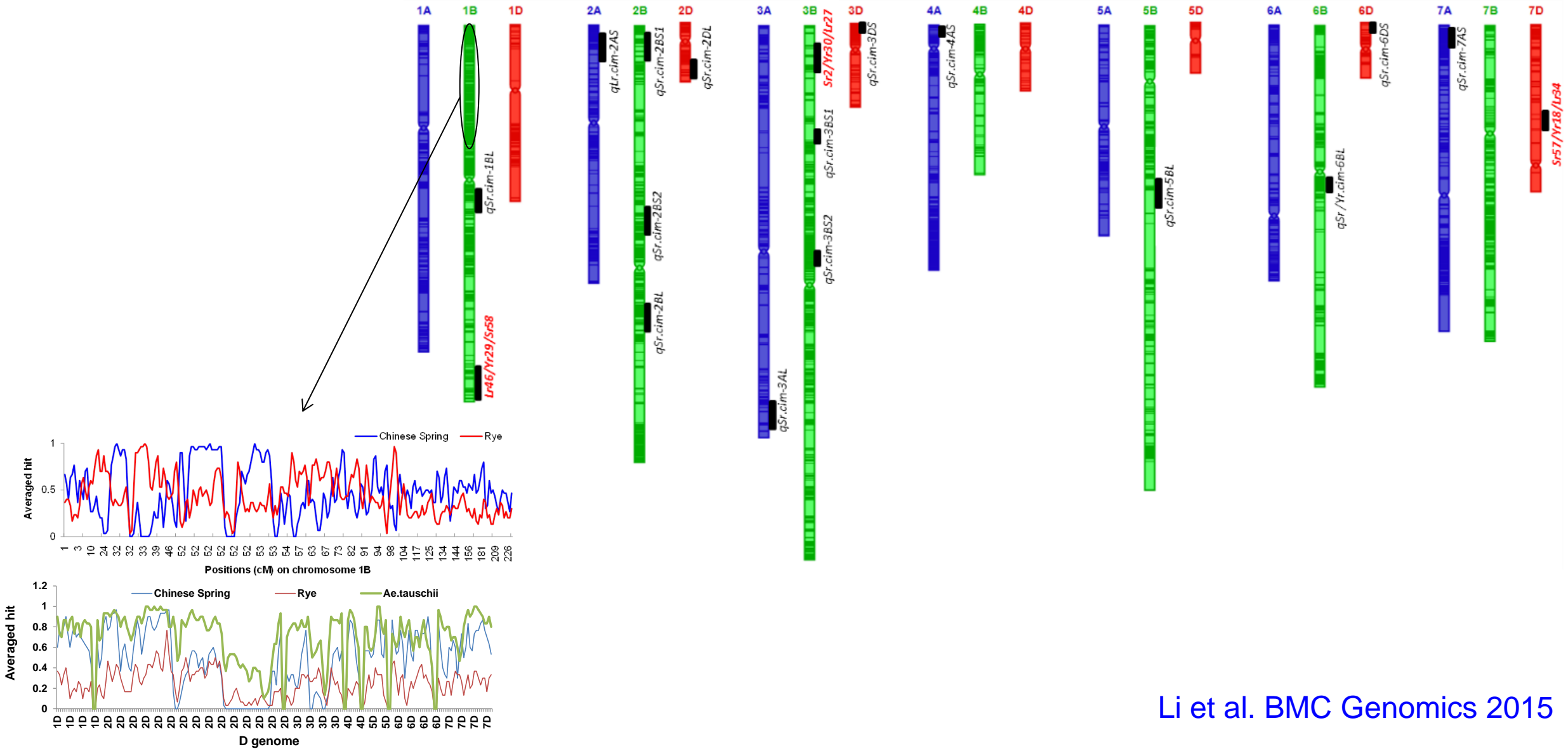
32.9% of markers on A genome, 56.3% of markers on B genome, while 10.8% markers on D genome.

Marker distribution across three populations...

- The averaged marker distance was 0.88 cM;
- Genetic length of the adjacent marker intervals ranged from 0 to 28.3 cM.



QTLs identified for rust resistance





**Uniting the world's popcorn diversity
for the dissection of complex traits
and accelerating breeding**

Why popcorn? --- the most ancient types of maize

- The ancient man noticed that maize was a useful food when grains were accidentally exposed to fire, transforming the hard grain in portions of food.
- The main feature of those races is that all of them pop and they are maintained mainly by indigenous groups: The ceremonial use of those races constitutes an important reason for preservation.



Teosinte

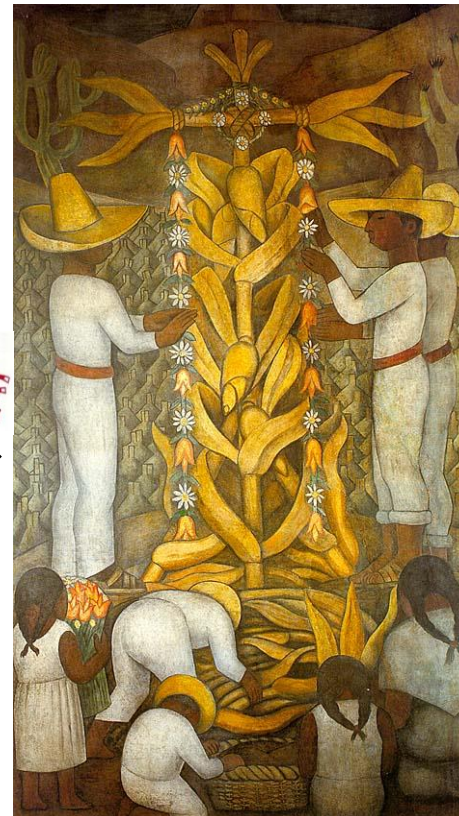


Palomero
Toluqueño

Arrocillo
Amarillo

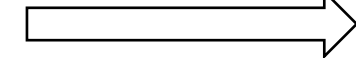
Chapalote

Nal-Tel



Teosinte

Domestication



Tropical
popcorn



Improvement



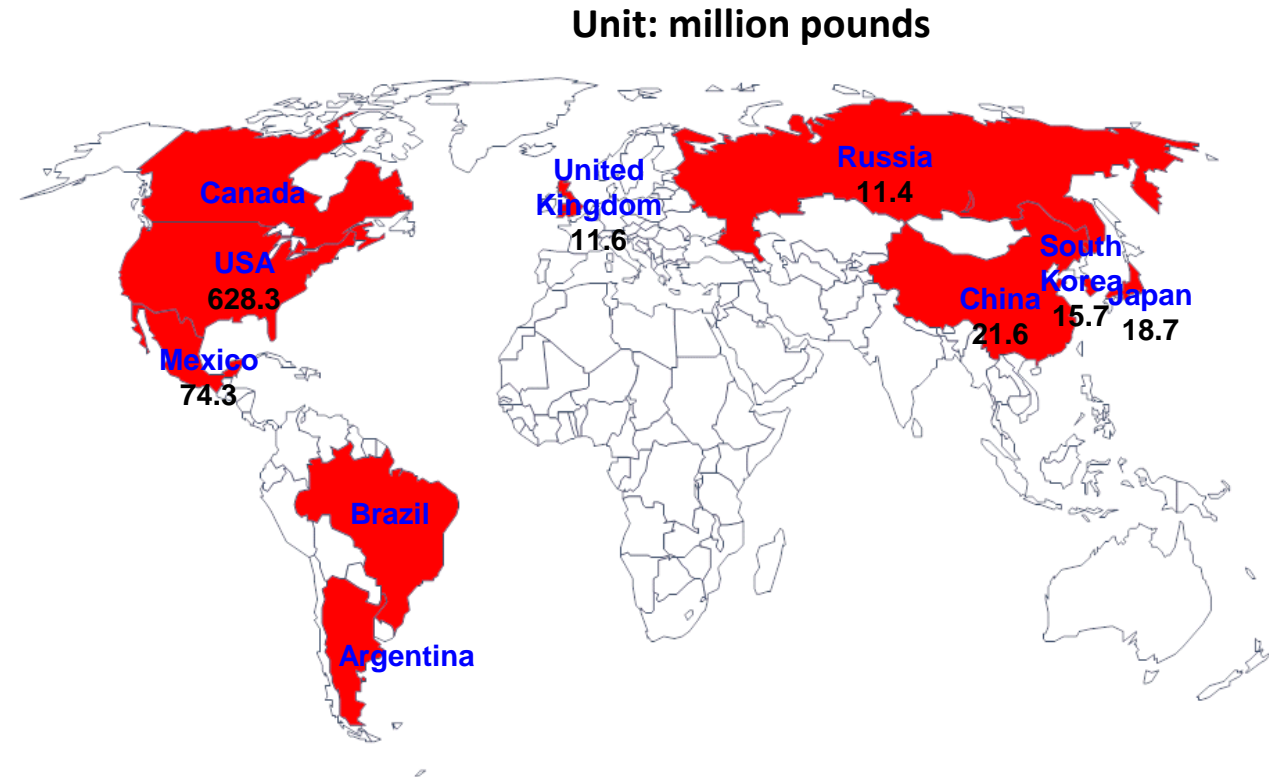
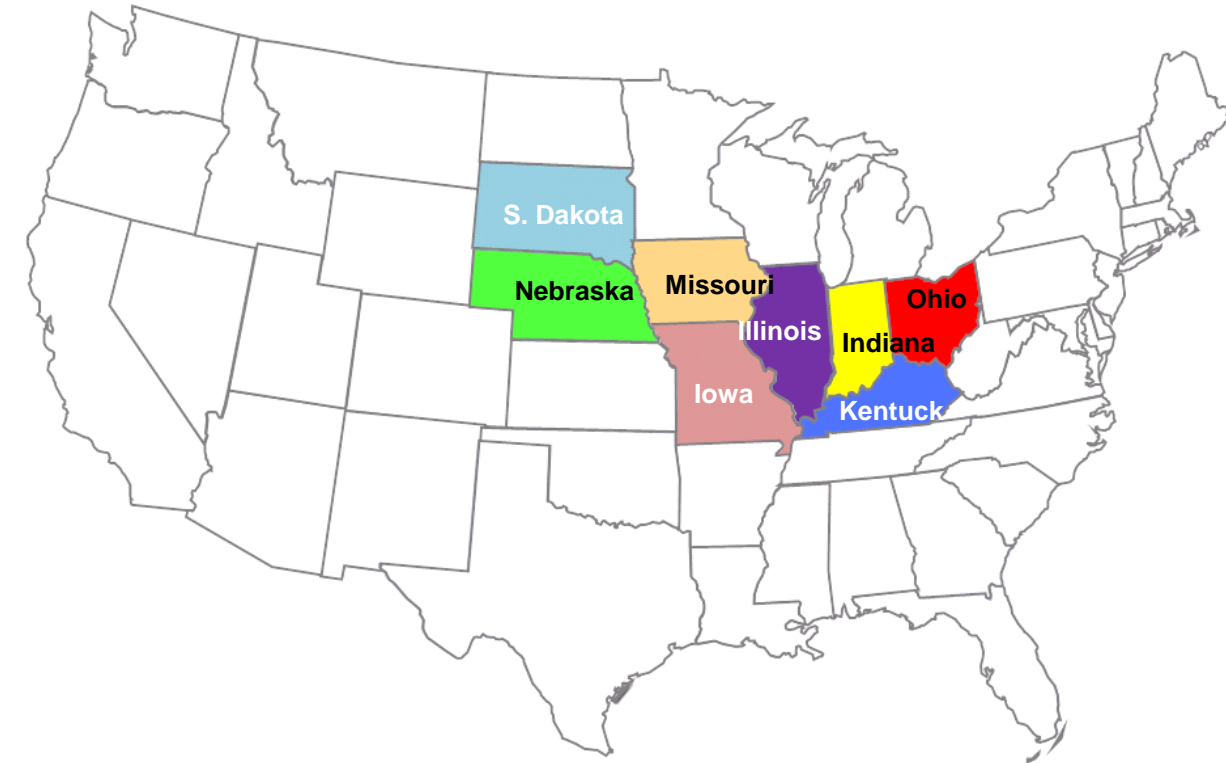
Temperate
Maize

Improvement



Tropical
Maize

Nearly all of the world's popcorn production is in the US. While consumers of popcorn are worldwide!



Sources:

Global Agricultural Trade System, Foreign Ag Service, USDA.

Popcorn, Field Crops: 2007 and 2002, National Ag Statistics Service, USDA.

Popcorn, National Agricultural Library, USDA.

Popcorn Promotion, Research and Consumer Information Order, Ag Marketing Service, USDA.

Why?

- ❖ Mexican landrace popcorns generally show reduced expansion volume (an important market trait)
 - North American Yellow Pearl -- **1,166** cm³ 30 g^{-1*}
 - Mexican landraces (mean) -- **48.8** cm³ 30 g^{-1*}



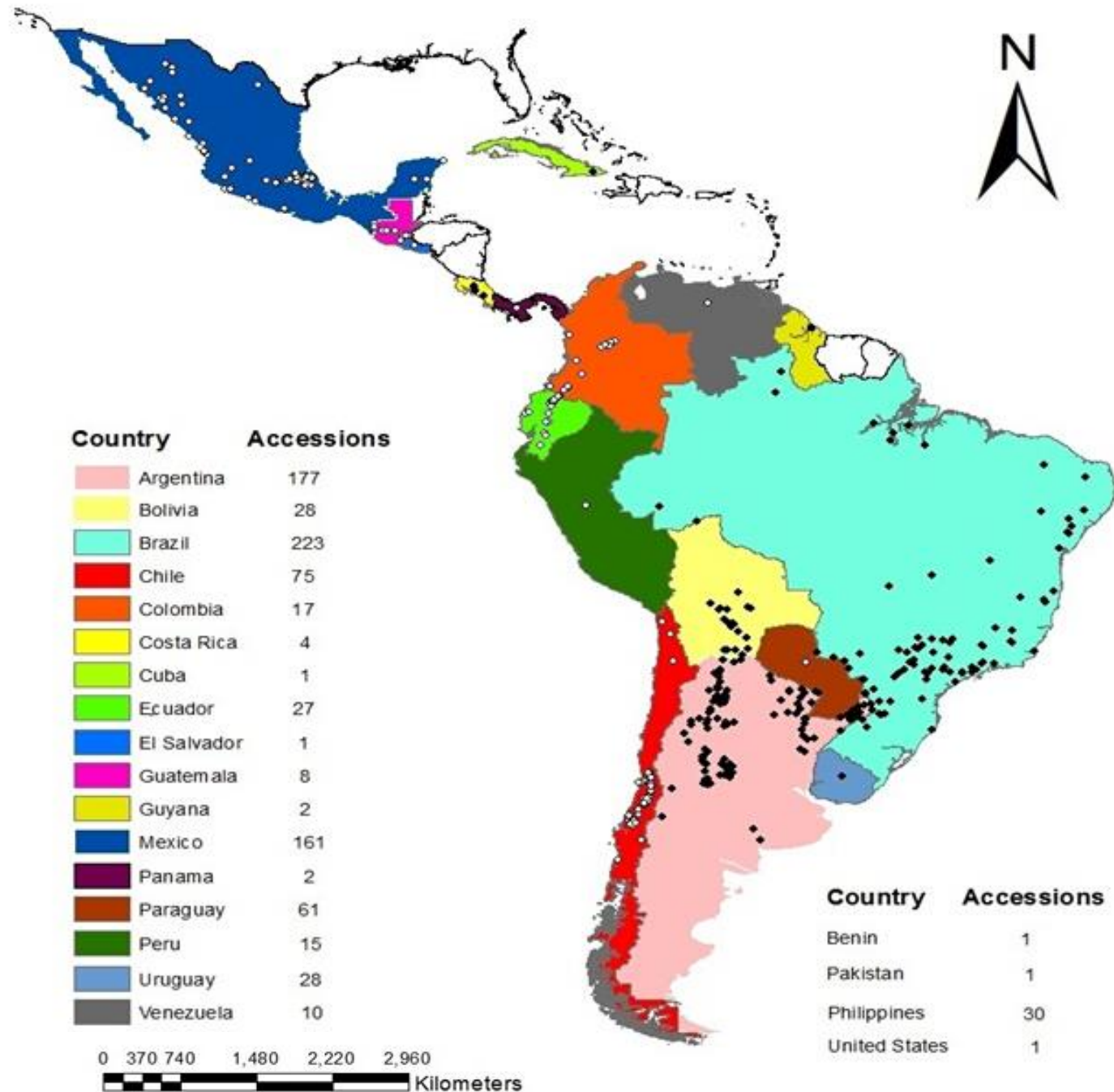
24 : 1 Ratio

- ❖ Decline in use of popcorn as a specialty maize:
Often the grain is mixed with other types for tortillas...

* Data from our collaborator, Dr. Amalio Santacruz Varela (Colegio de Posgraduados)

CIMMYT Maize Gene Bank has a global collection of popcorns

873 popcorn accessions in total



Objectives

- To find the sources for the best genetic diversity for popcorn traits;
- To determine the genetic basis for these traits;
- To validate the role of tropical popcorn in maize evolution history;
- To provide the germplasm to accelerate breeding programs for popcorn in Mexico and other countries with market potential and interest in self-sufficiency.

Popcorn Phenotyping Team in Action!

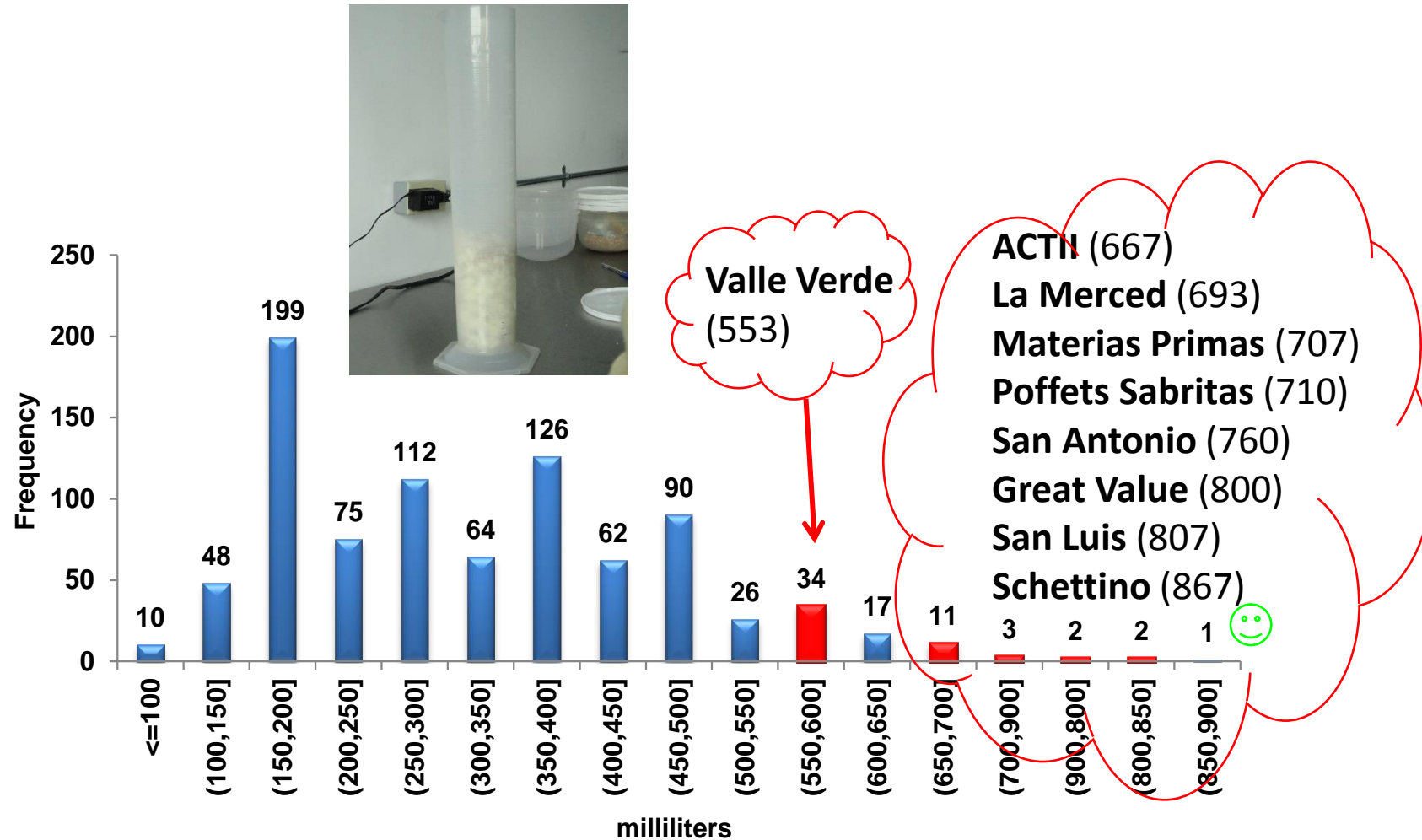
873 landrace accessions, 537+ CMLs, and 9 commercial checks measured for 7 traits



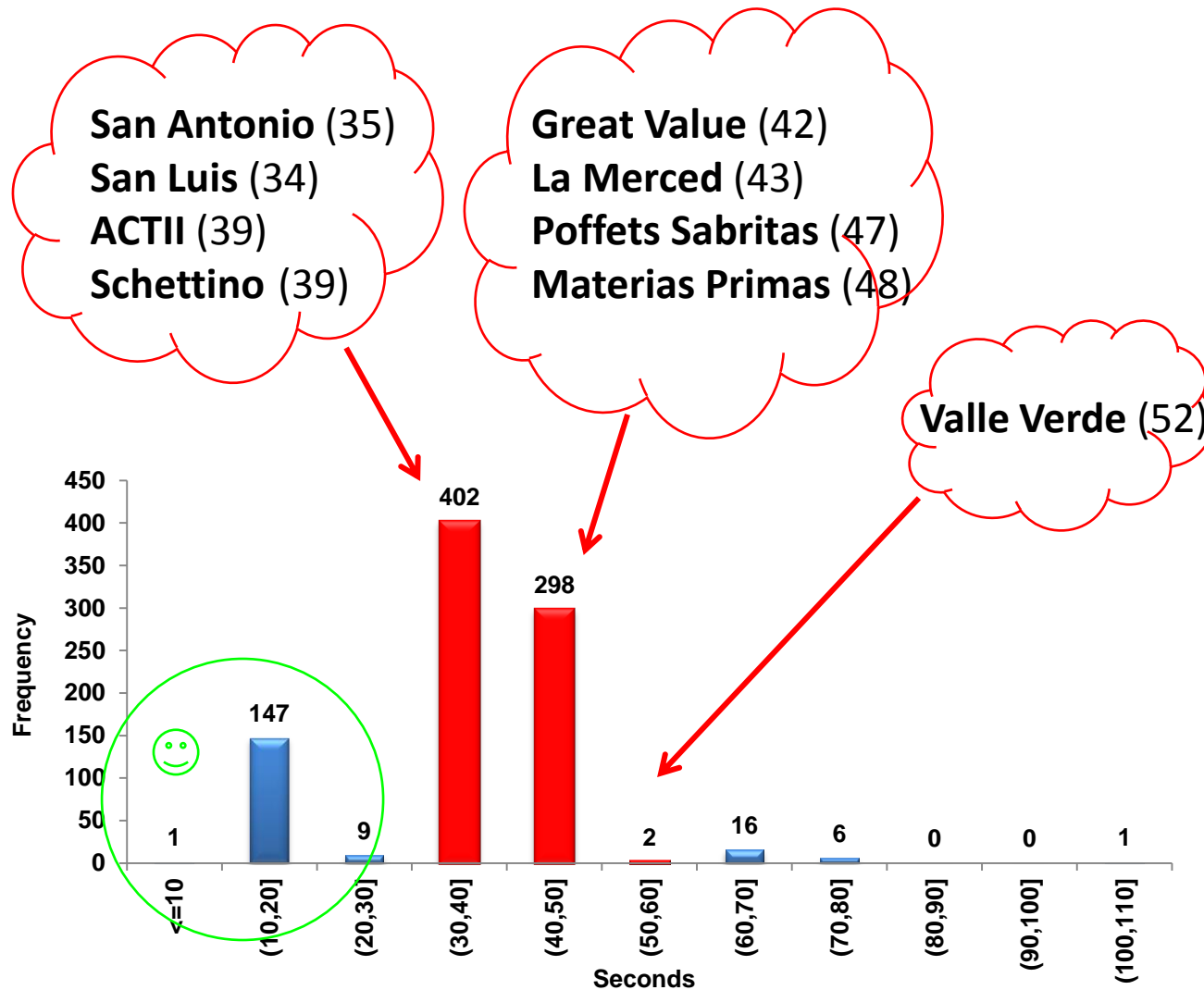
[Place link here for
vide](#)



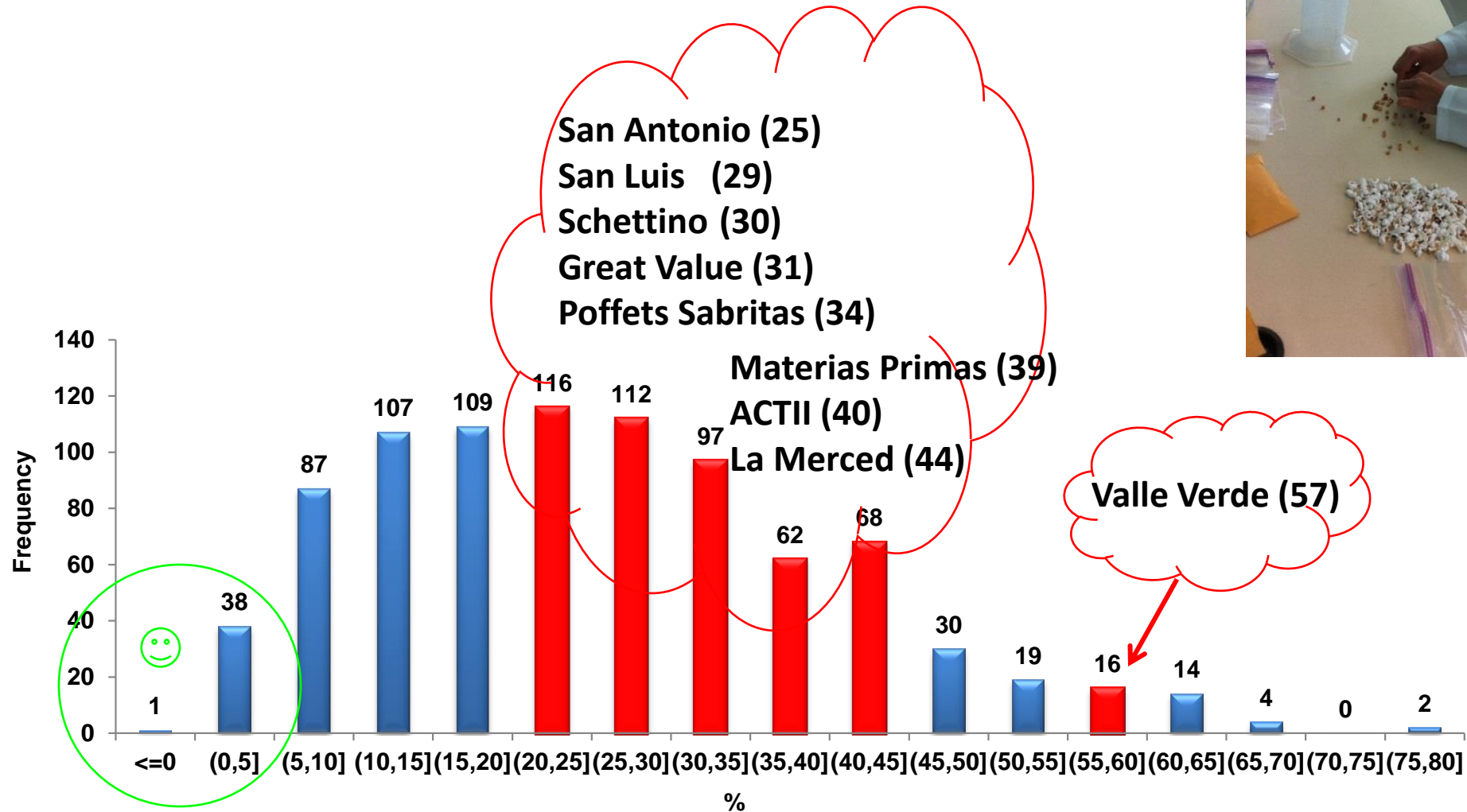
The expansion volume (milliliters) of 30 grams of popped kernels



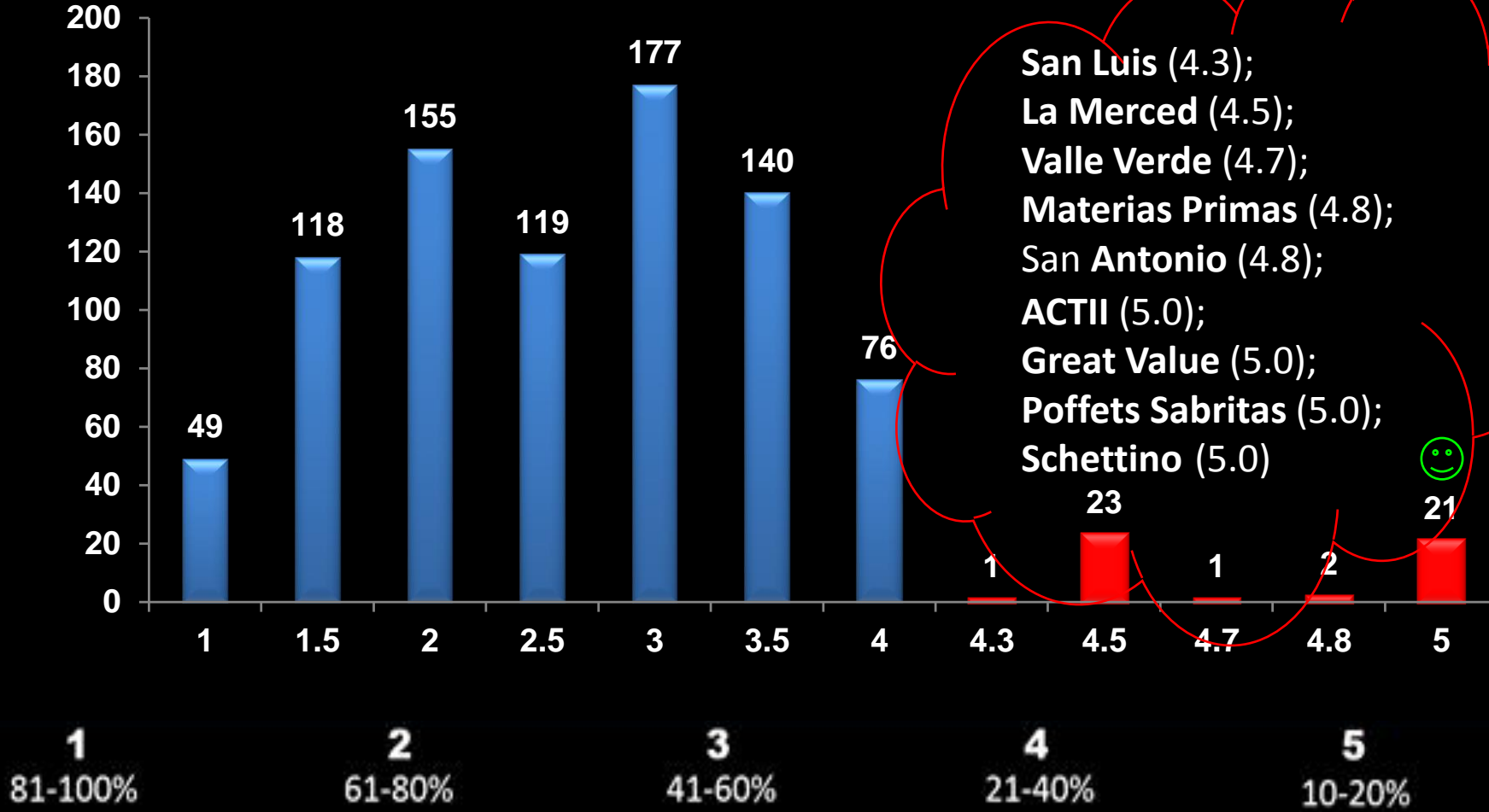
Elapsed time (seconds) to first popping event in microwave



Percent (%) of unpopped kernels after microwaving for 2:45 min at 70% power

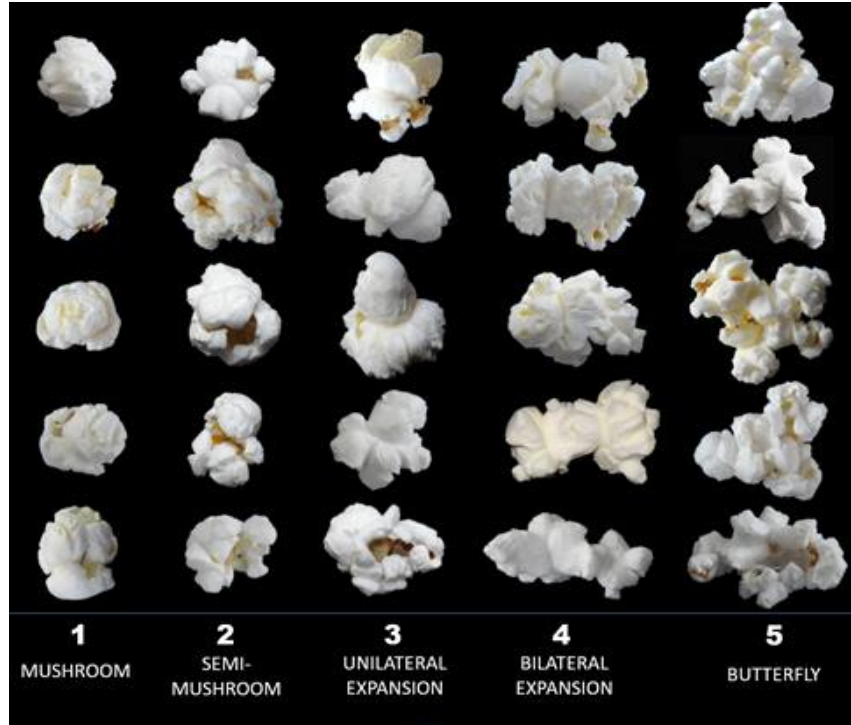


Rating of presence of pericarp after popping



More traits we are phenotyping... ..

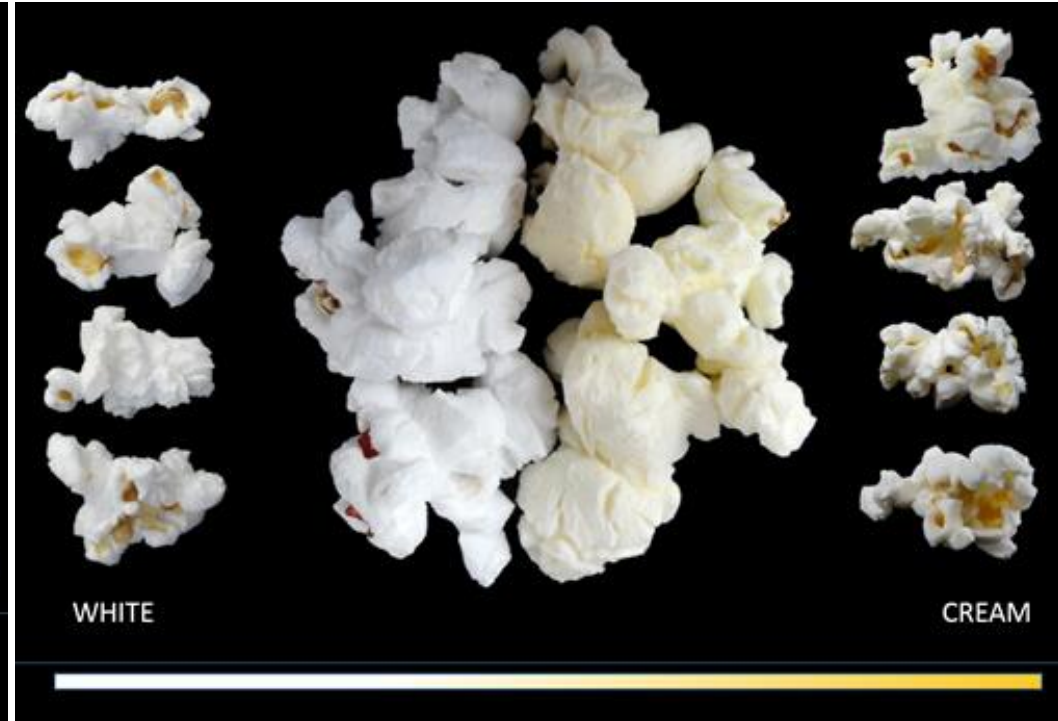
Scale for popcorn flake morphology



Frequency

0 2 54 151 126 303 38 150 49

Popcorn flake color

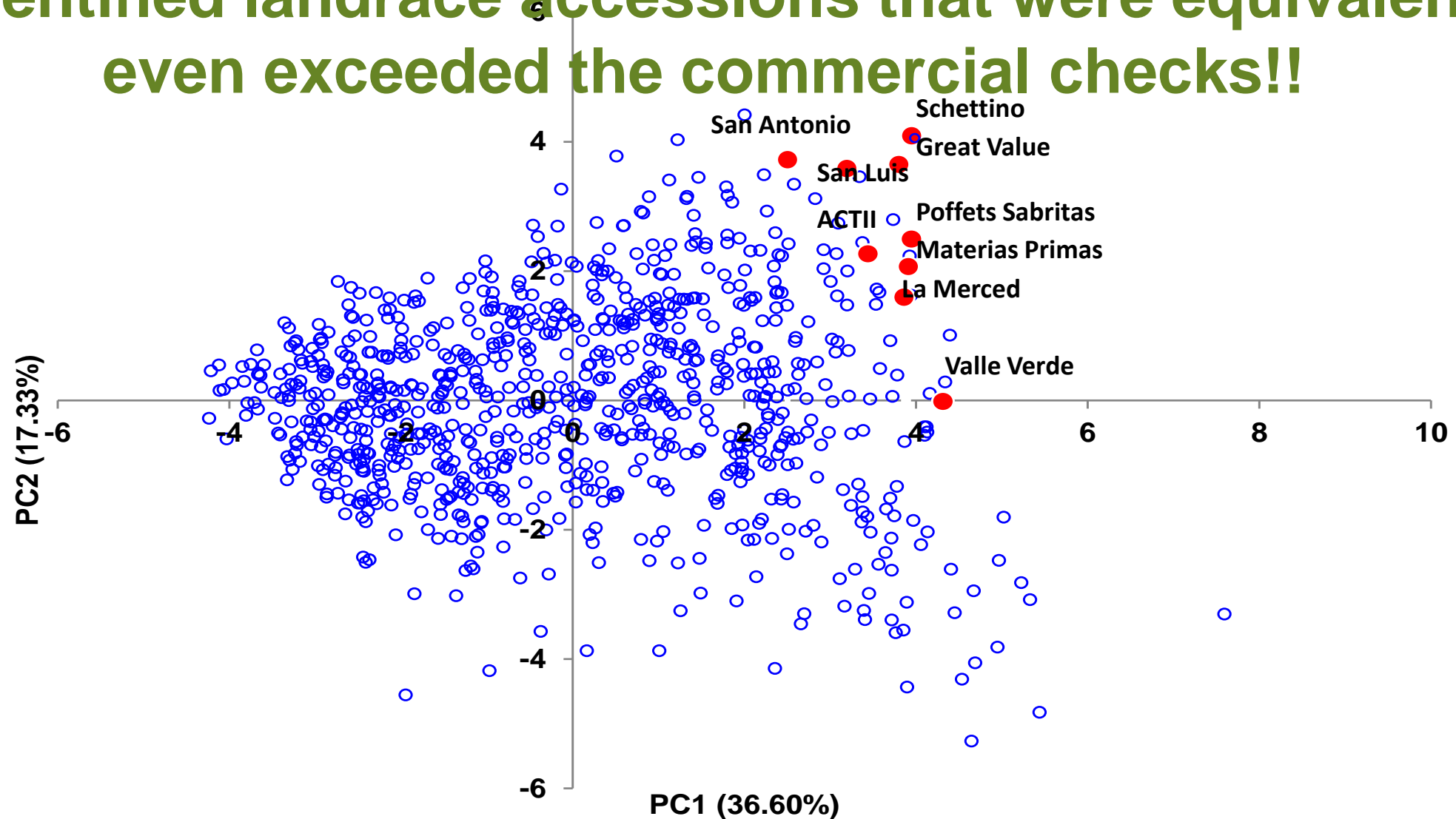


Frequency

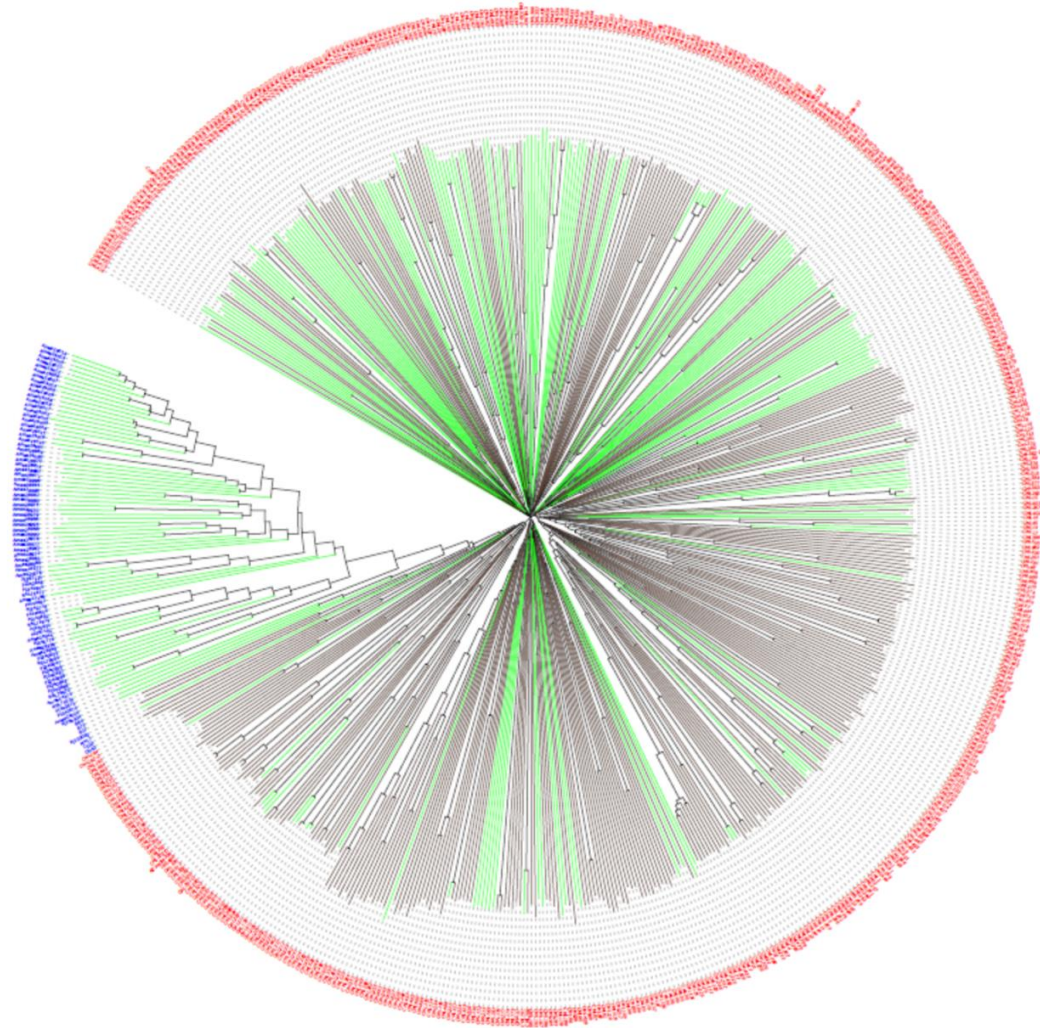
663 14 193 12

Exciting Phenotyping Results

For every important market trait we measured, we identified landrace accessions that were equivalent or even exceeded the commercial checks!!



Surprised Phenotyping Results for CMLs



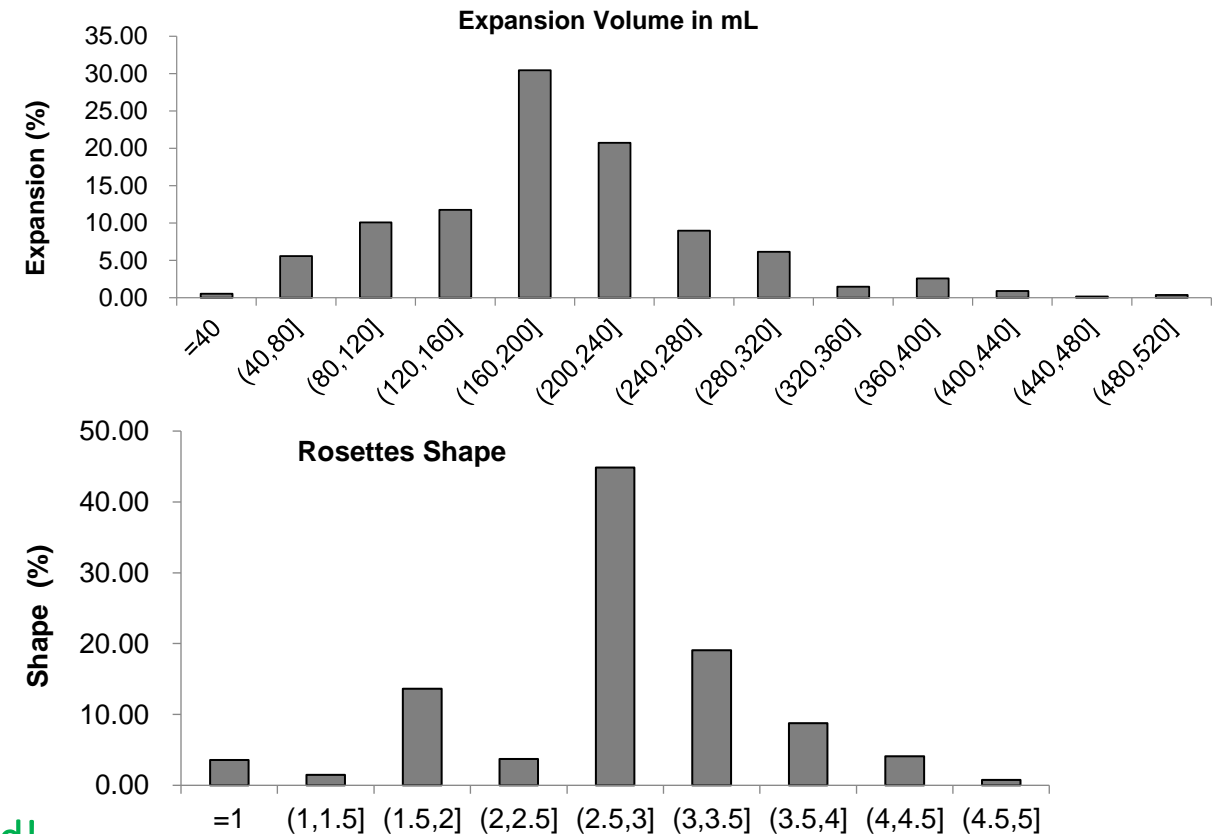
538 CMLs, 85 temperate maize, 257 of them can be popped!



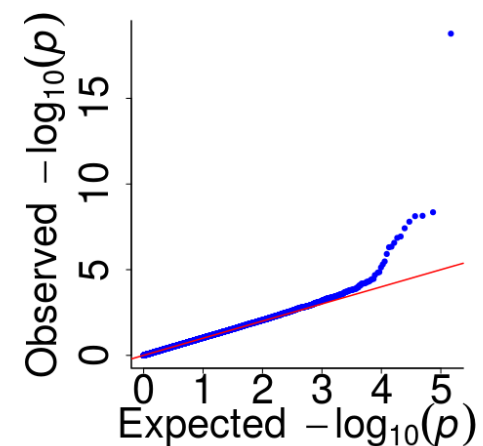
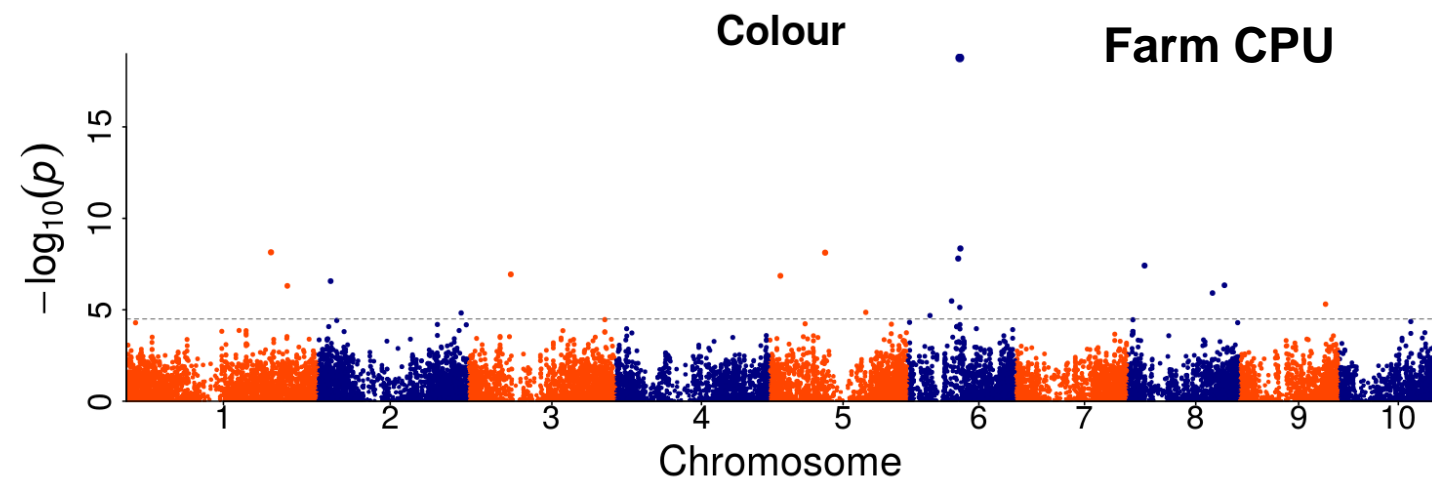
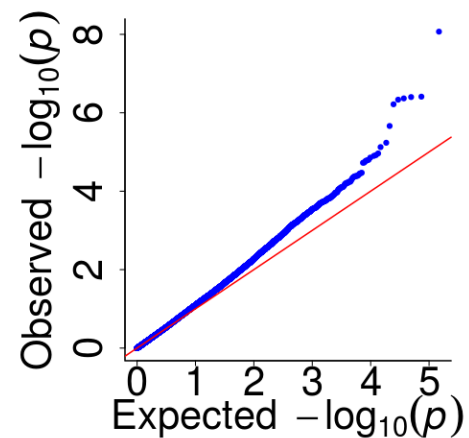
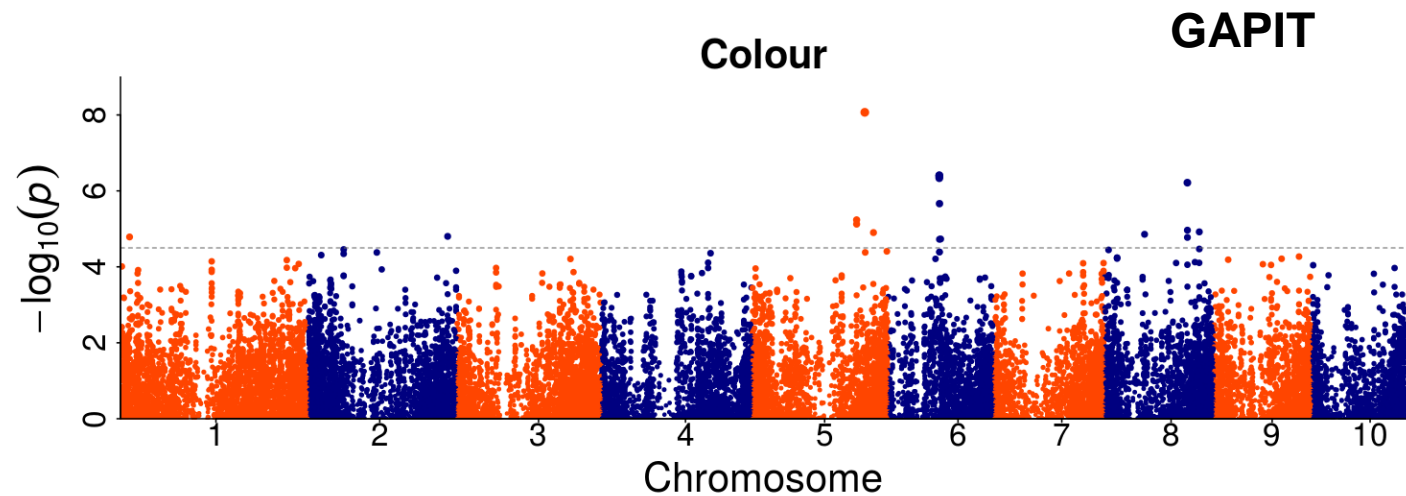
Viridiana Trejo Pastor
COLPOS, Mexico, PhD



Jing Li
CAAS, China, PhD



Preliminary GWAS Results for CMLs



Delin Li
CAU, China, PhD

Fieldwork at Toluca Station

- ❖ Seed increases of highland popcorns
- ❖ Self pollinations to produce inbred lines for genetic studies and breeding program

**Every bag represents
a self pollination
in this popcorn accession**



We are looking forward to having more results come out soon to unlock the science of popcorn.





Thanks for your attention!

谢谢!

Muchas Gracias!