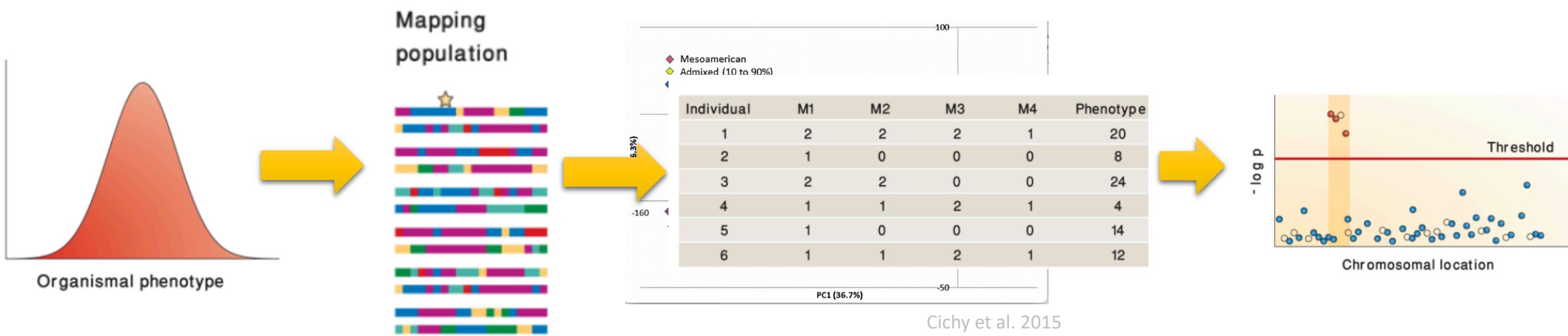


# Association mapping

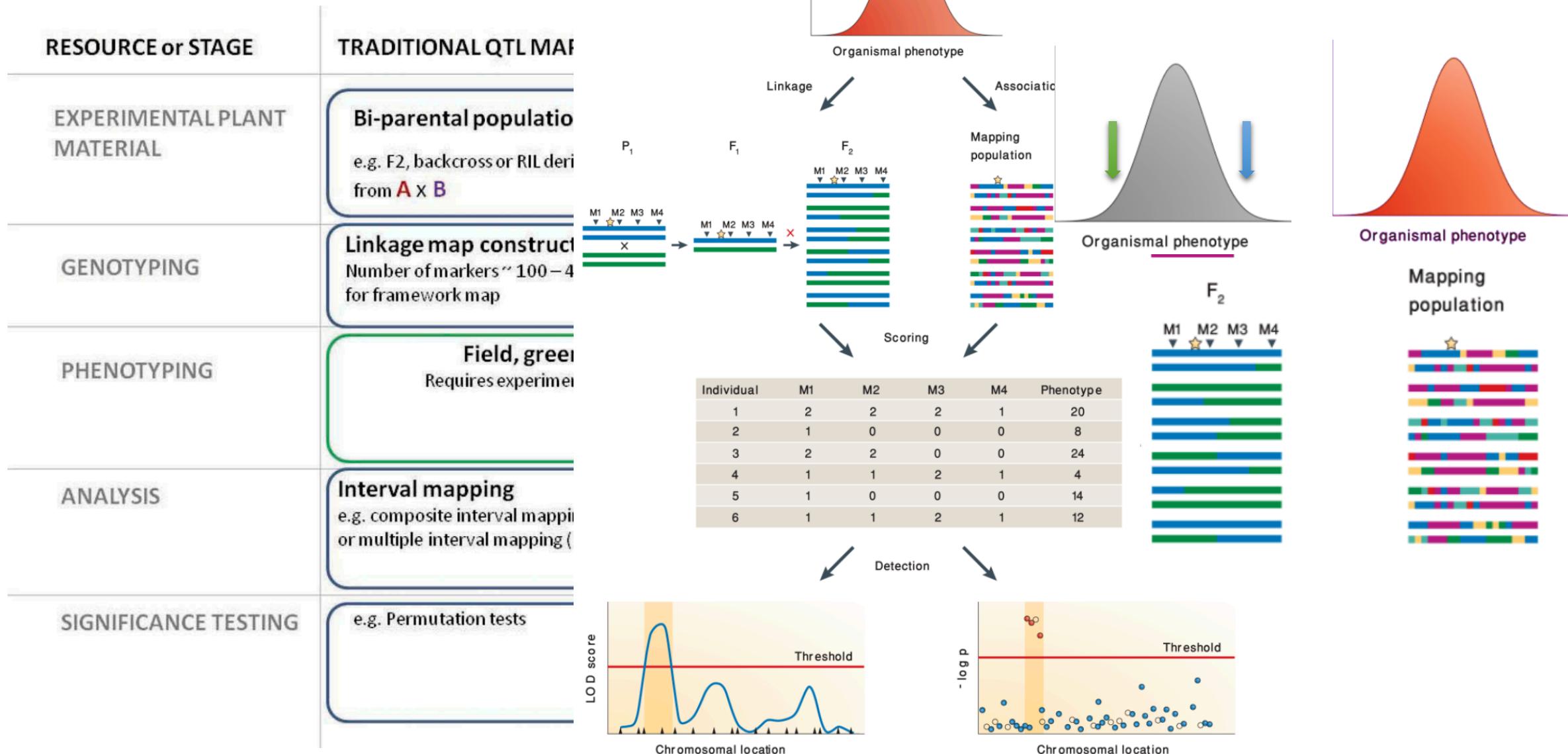
# Association mapping

- Association analysis uses historical recombination events over many generations within a short interval surrounding a trait locus
- The association analysis was advantageous for the identification of relatively small genomic regions, in which only few genes may reside.



Cichy et al. 2015

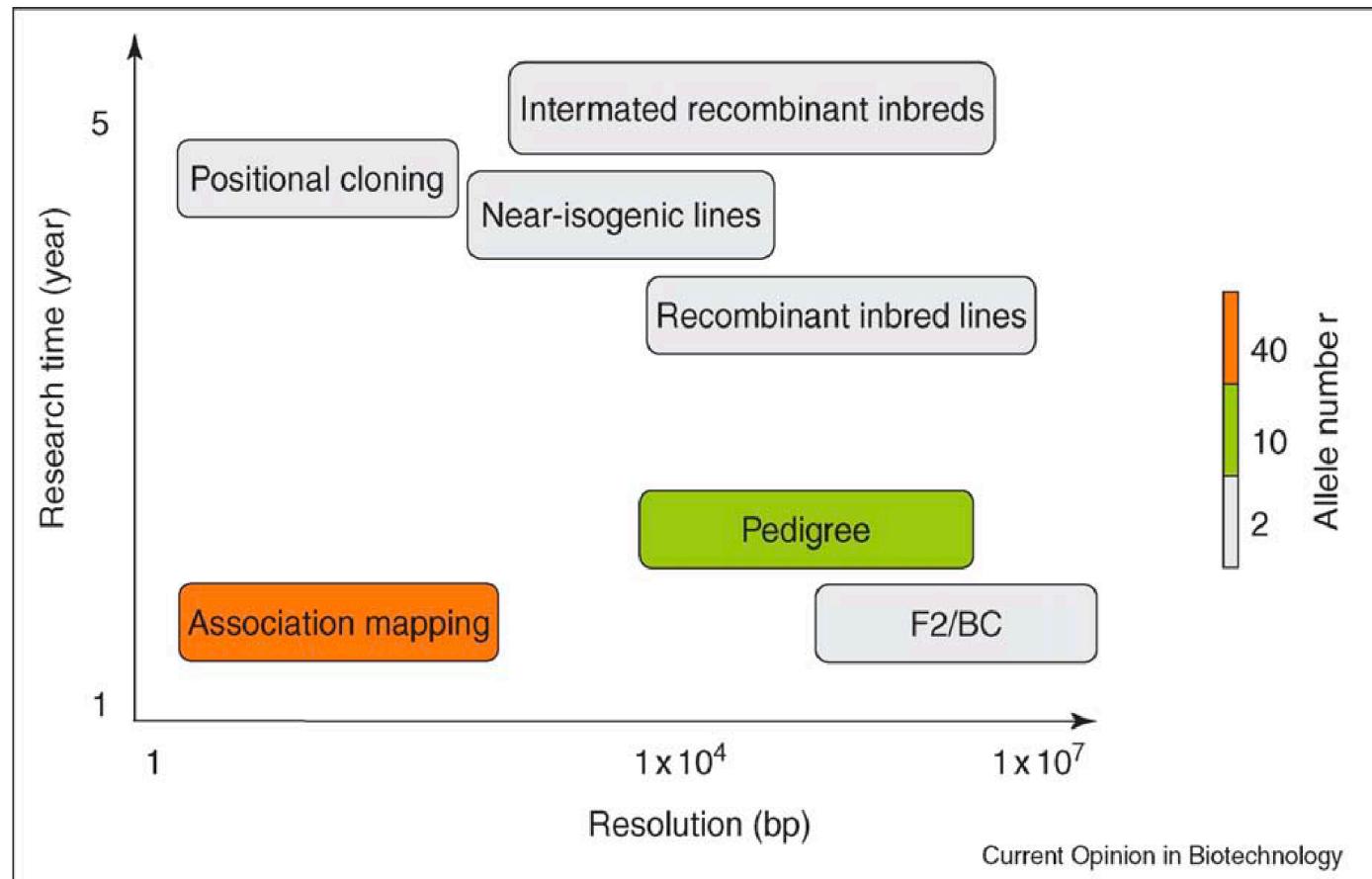
# QTL vs Association mapping



# QTL vs Association mapping

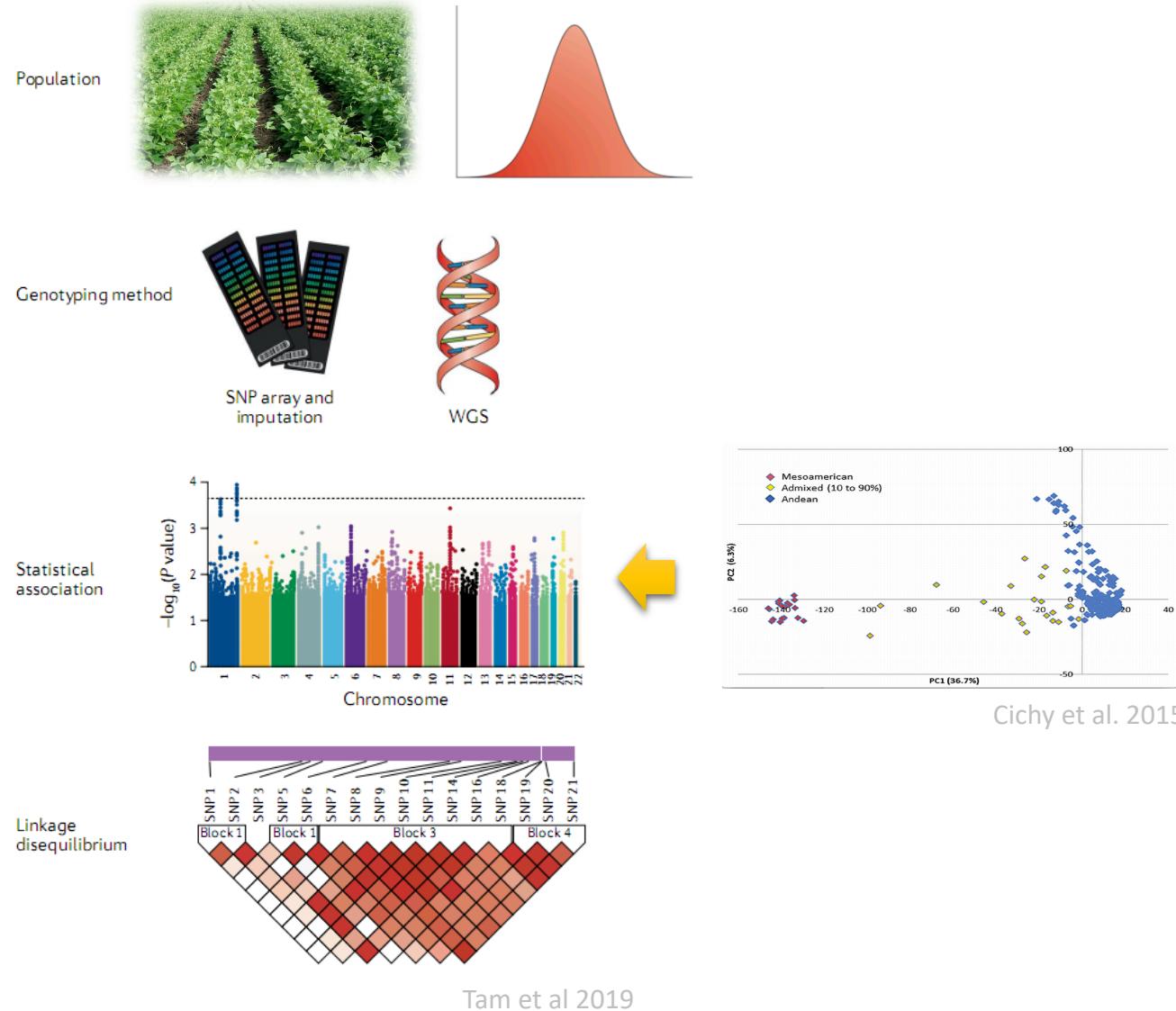
Association mapping offers three advantages over linkage analysis:

- Higher mapping resolution
- Greater allele number
- Broader reference population
- Less research time in establishing an association



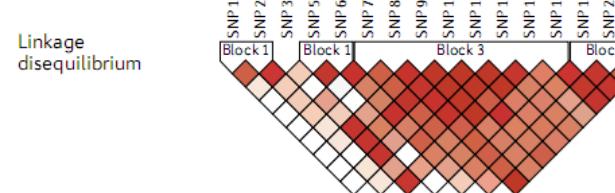
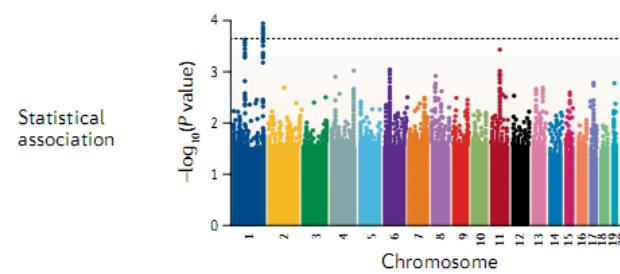
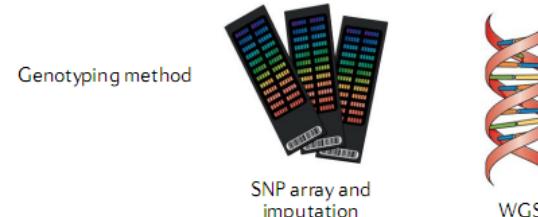
# Association mapping

- Linkage disequilibrium
- Population structure
- Statistical approaches
- QTL vs Association mapping

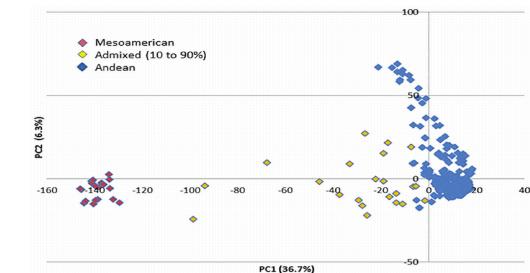


# Association mapping

- Linkage disequilibrium
- Population structure
- Statistical approaches
- QTL vs Association mapping



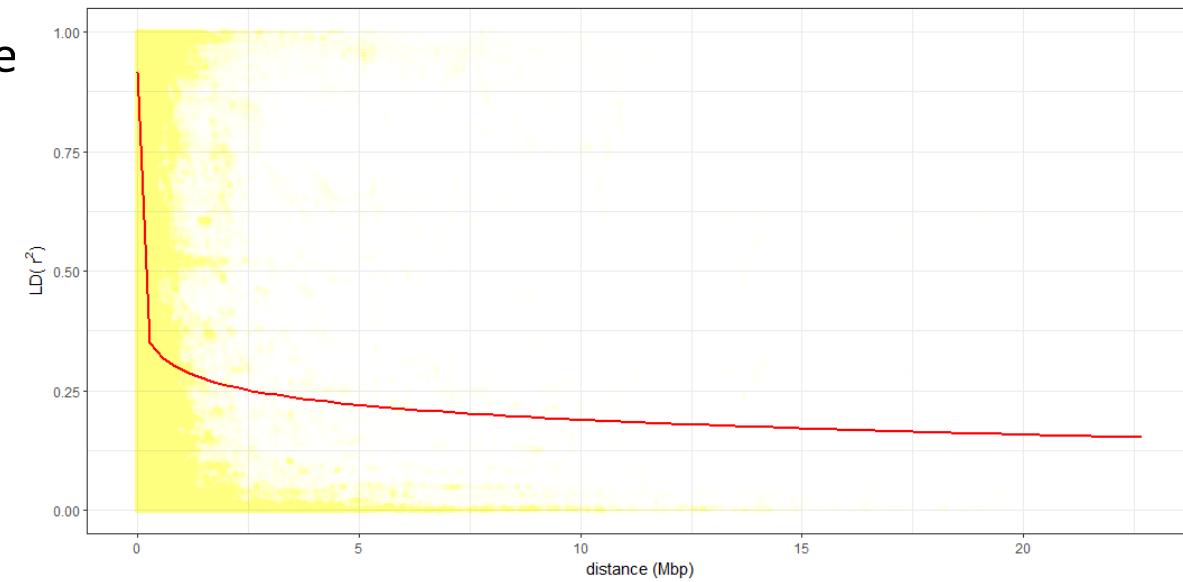
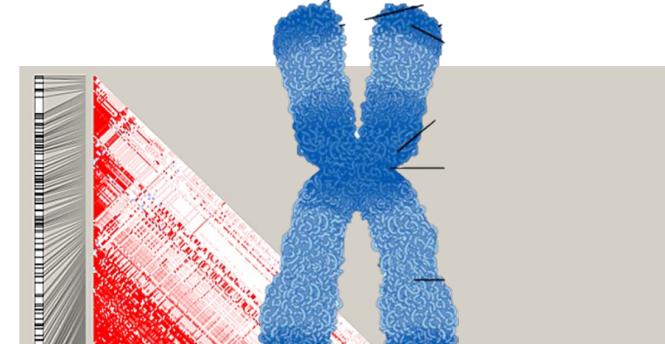
Tam et al 2019



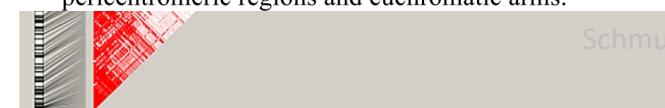
Cichy et al. 2015

# Linkage disequilibrium

- LS is defined as the non-random association of allele between loci.
- The resolution is dependent of the LD.
- LD determines the density of markers needed.



**Supplementary Table 7.** Physical (Kb) and genetic (cM) position of the last marker mapped in each chromosome and recombination rate (Kb/cM) per chromosome and comparison between pericentromeric regions and euchromatic arms.

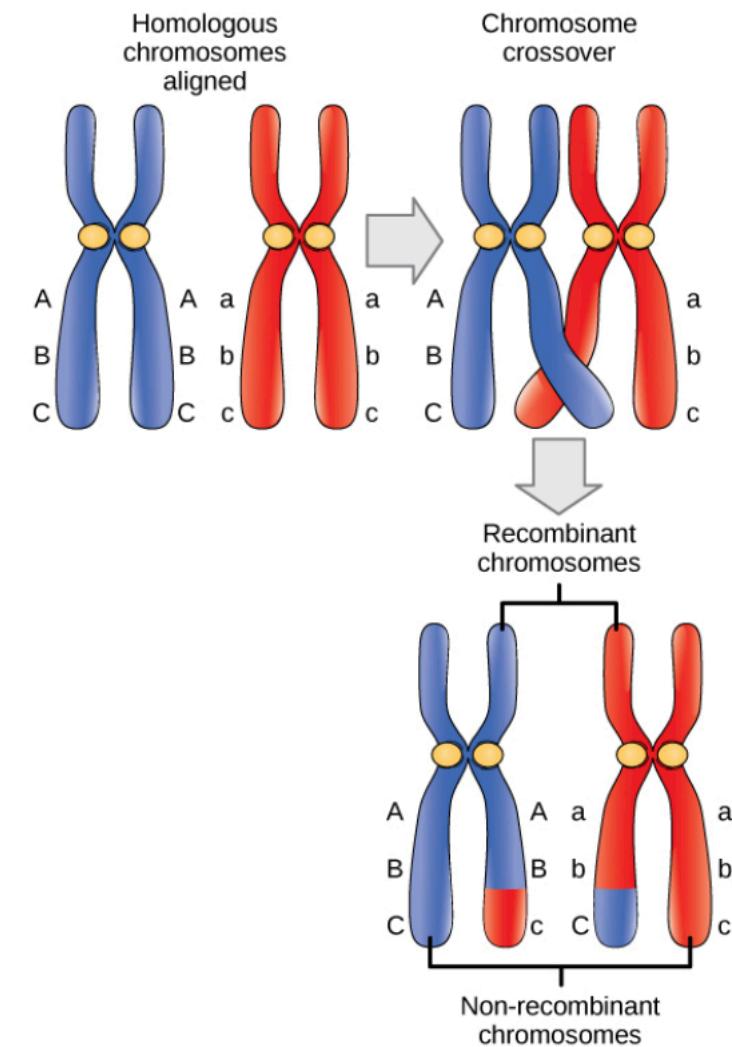
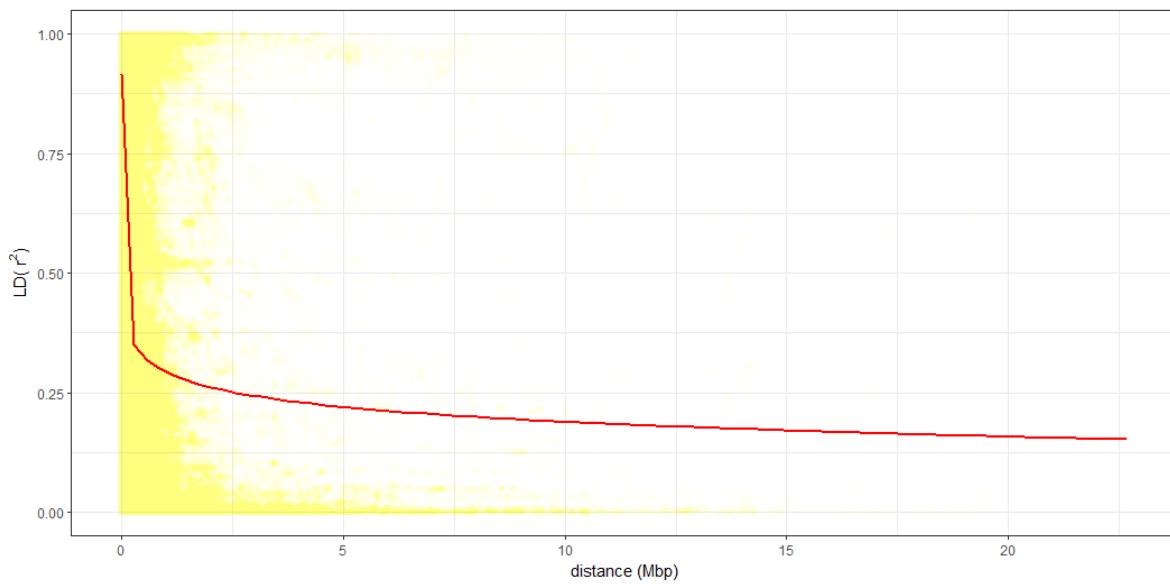


Schmutz et al 2014

Pistis et al. 2013

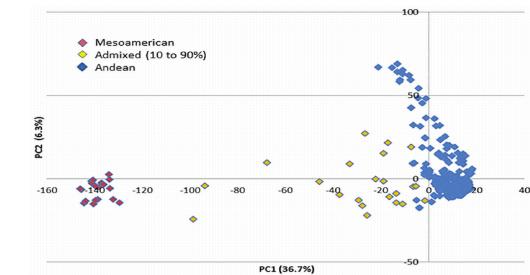
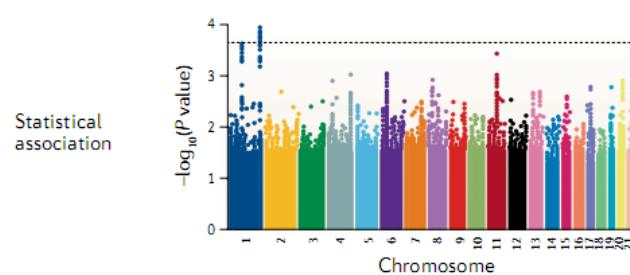
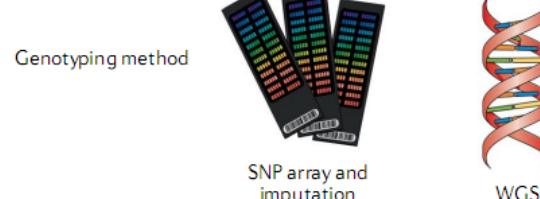
# Linkage disequilibrium

$$r^2 = \frac{p(AB) - p(A)p(B)}{p(A)(a)(B)(b)}$$

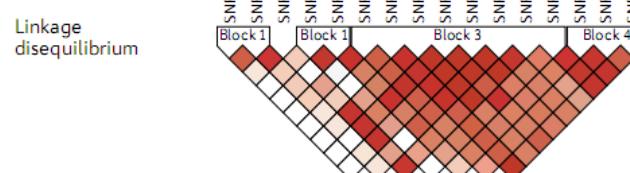


# Association mapping

- Linkage disequilibrium
- Population structure
- Statistical approaches
- QTL vs Association mapping



Cichy et al. 2015

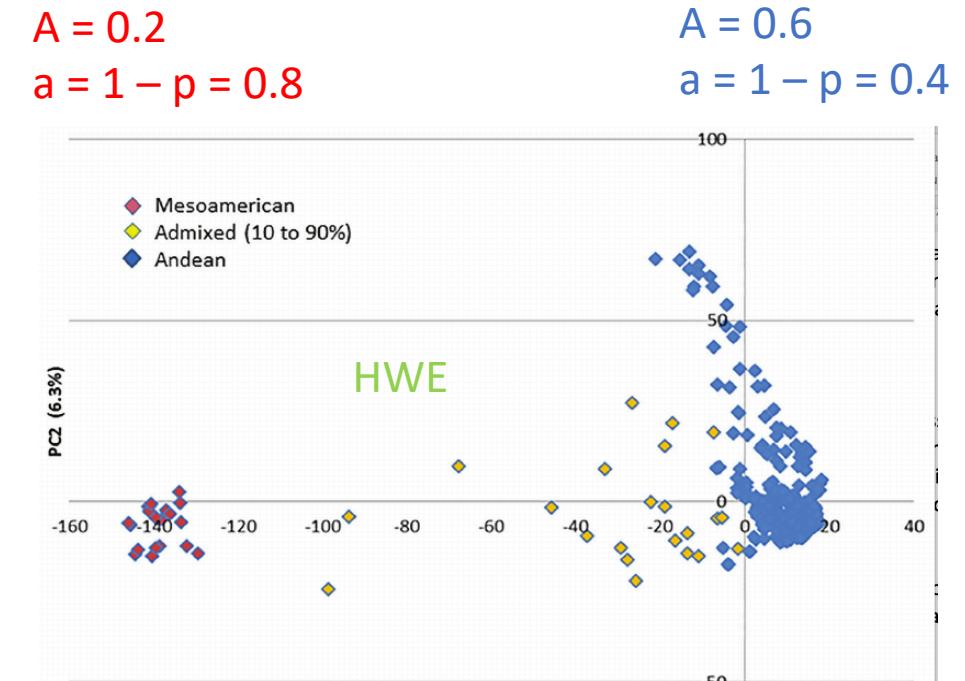


Tam et al 2019

# Population structure

- Population structure can cause false-positive results.

$$r^2 = \frac{p(AB) - p(A)p(B)}{p(A)(a)(B)(b)}$$



Cichy et al. 2015

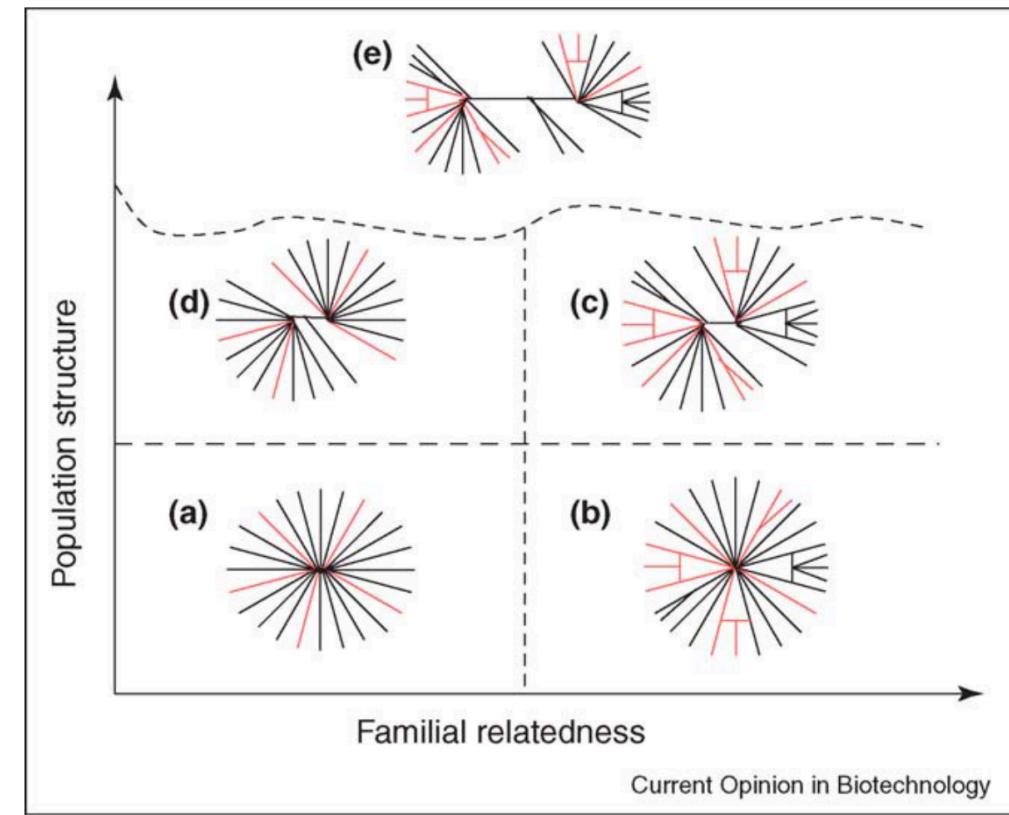
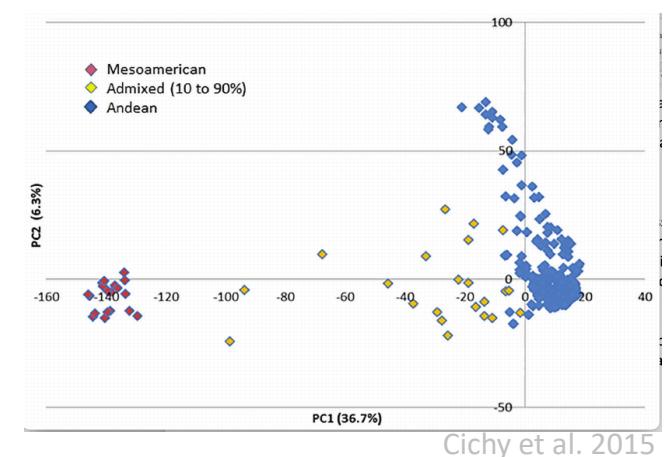
- Statistically controlling for population structure can result in false-negatives, particularly for small sample sizes.

# Population structure

- Population structure can cause false-positive results.

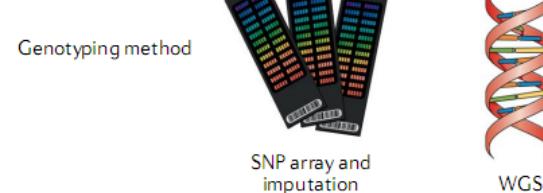
$$r^2 = \frac{p(AB) - p(A)p(B)}{p(A)(a)(B)(b)}$$

- Statistically controlling for population structure can result in false-negatives, particularly for small sample sizes.
- Association studies, therefore, are best carried out in independent populations with a large sample size.

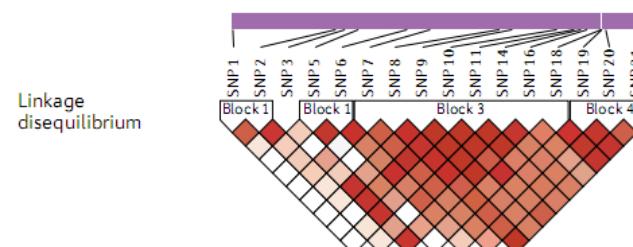
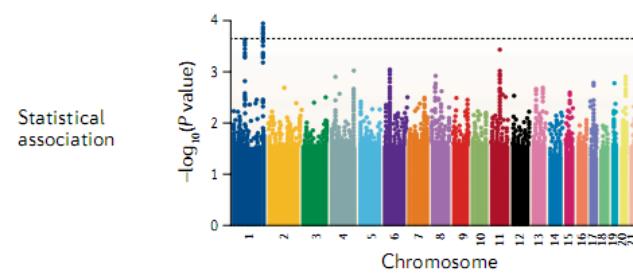


# Association mapping

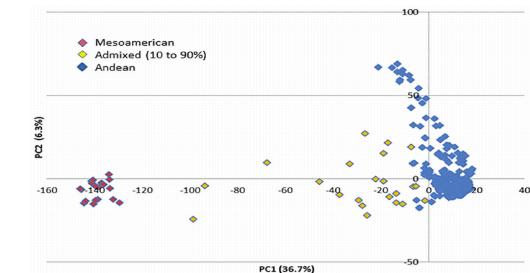
- Linkage disequilibrium
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SNP array and imputation      WGS

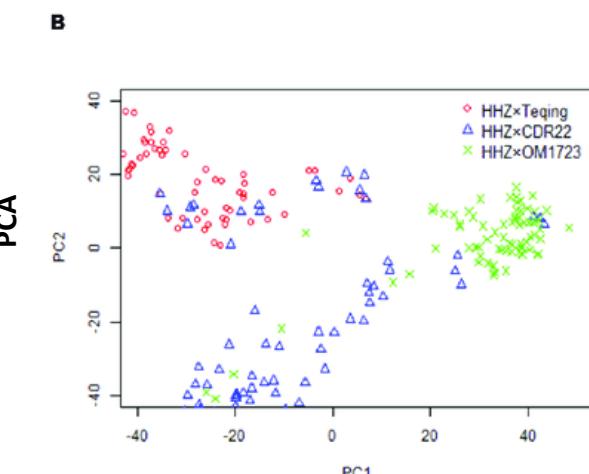
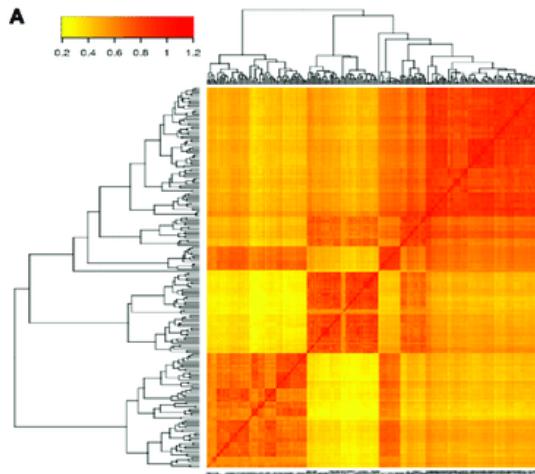


Tam et al 2019



Cichy et al. 2015

# Statistical approaches



Feng et al 2018

$$\Theta_{BC} = F_D = 2\left(\frac{1}{2}\right)^{\varrho} = \left(\frac{1}{2}\right)^{\varrho-1}$$

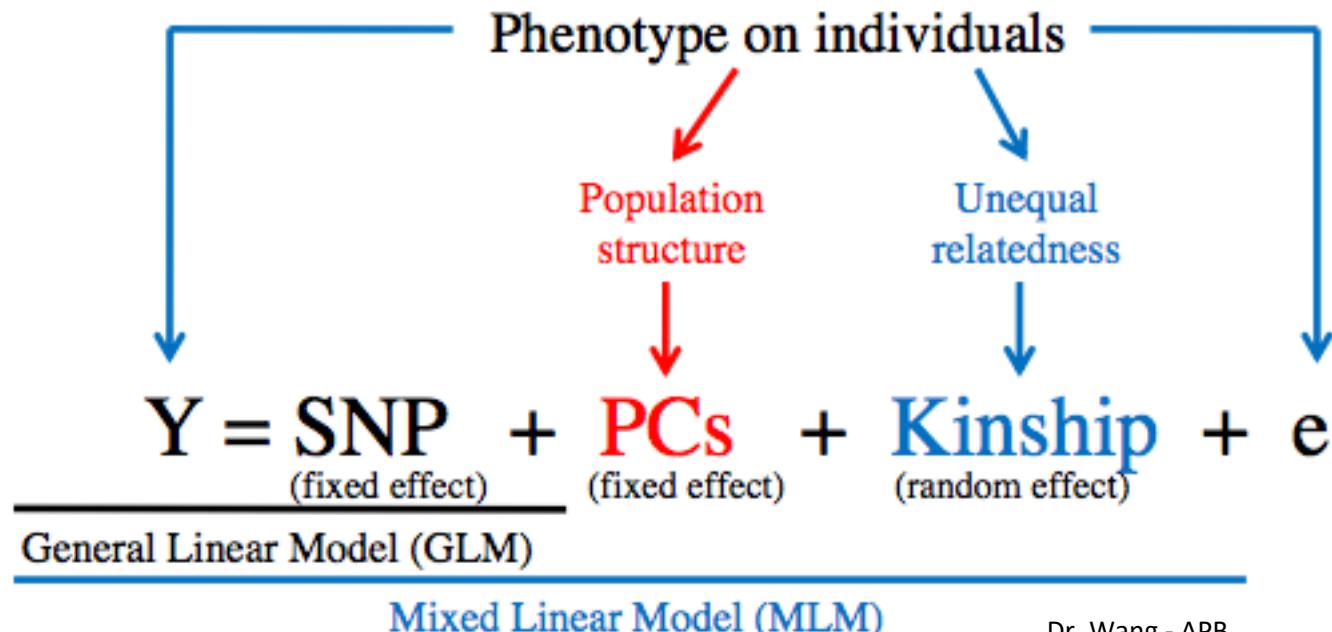
A

B

C

D

Kinship : a measure of genetic similarity between two individuals which is equal to the **inbreeding coefficient** of a hypothetical offspring of the two individuals.



Dr. Wang - APB

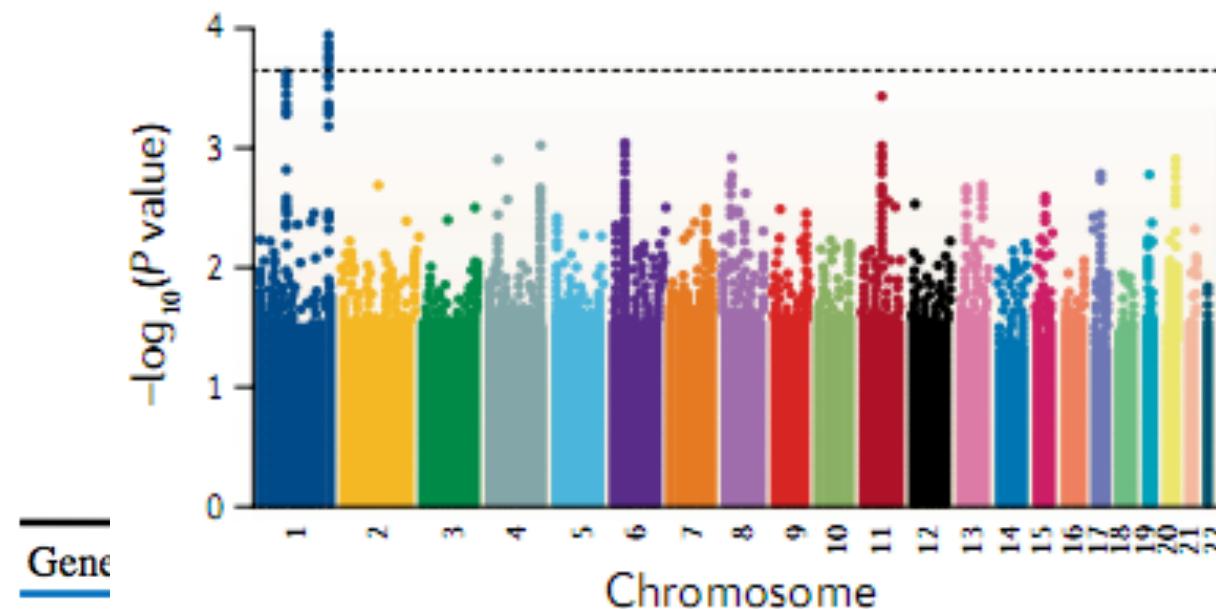
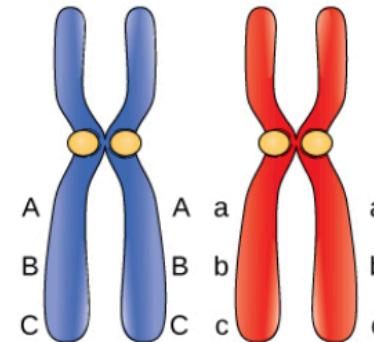
# Statistical approaches



TASSEL Version 5.0 ([Getting Started!](#))  
(Build: February 10, 2021 [Requires: Java 1.8](#))

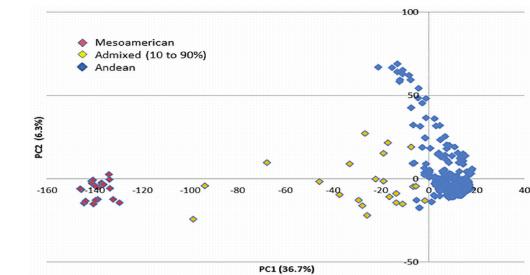
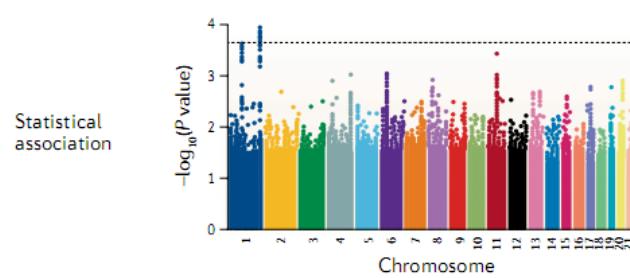
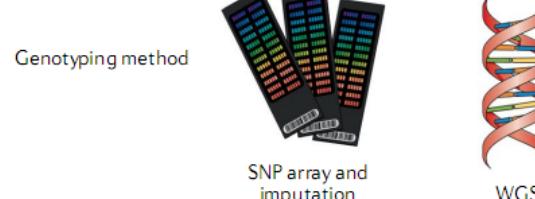
$$F = \frac{\text{variance between treatments}}{\text{variance within treatments}}$$

Large F ratio indicate that there are more variations between groups and likely a difference in the mean



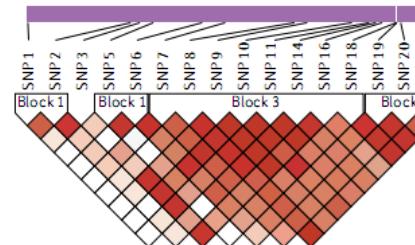
# Association mapping

- Linkage disequilibrium
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Cichy et al. 2015

Linkage disequilibrium



Tam et al 2019

# Bi-parental vs Association mapping

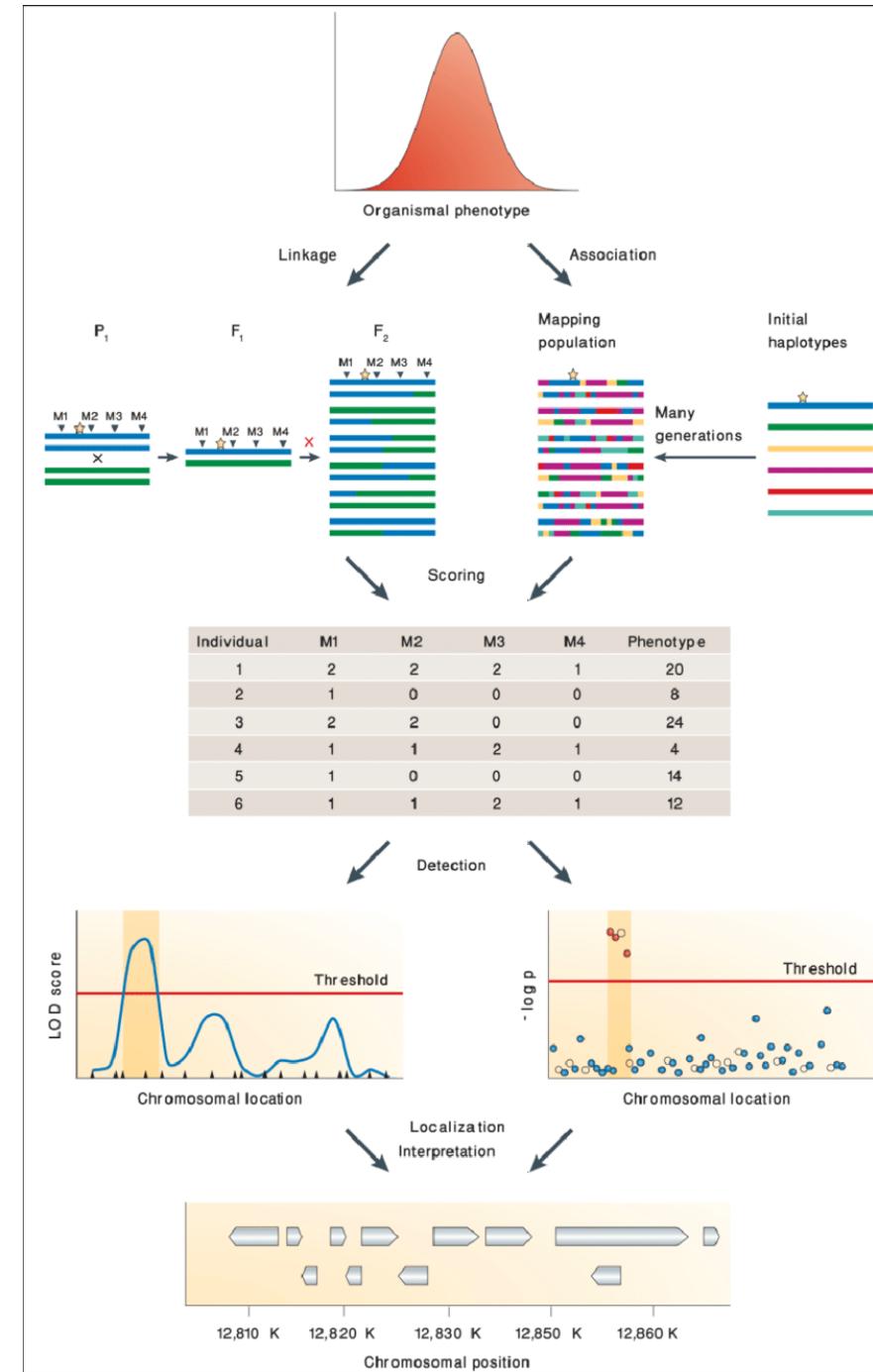
1. Cross required

2. Resolution

3. Alleles tested

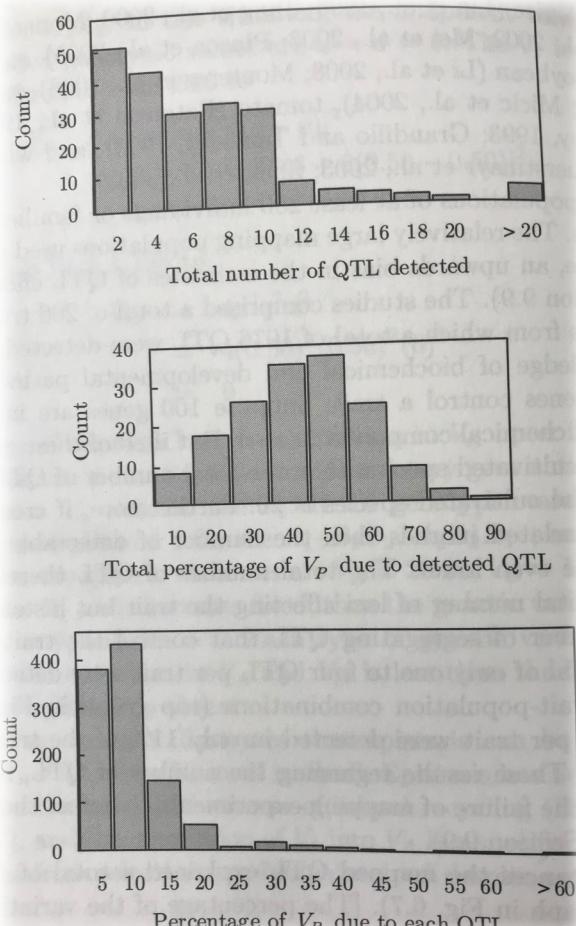
4. Power

$$t = \frac{\overline{MM} - \overline{mm}}{\sqrt{\frac{\hat{V}(MM)}{N} + \frac{\hat{V}(mm)}{N}}}$$

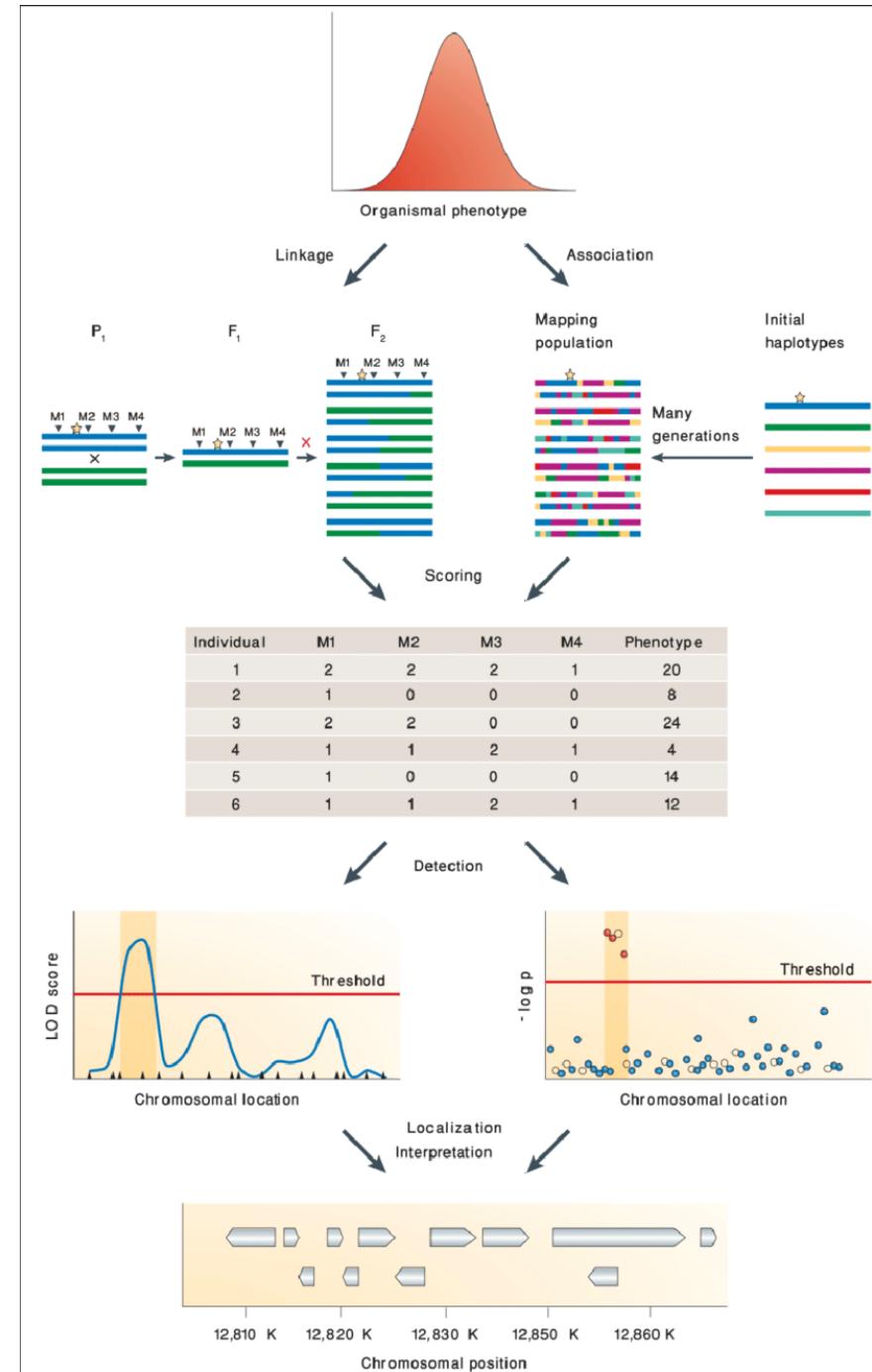


# Bi-parental vs Association mapping

Number of QTL detected for a trait in mapping studies with >250 progeny

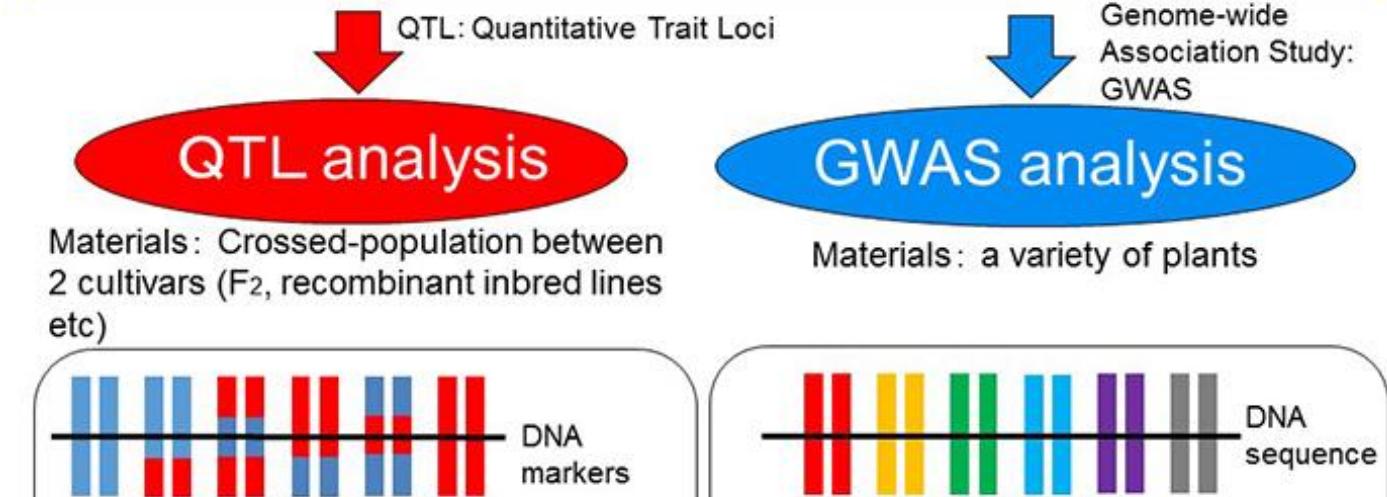


Bernardo 2020, p 152



Mackay et al. 2009

## Identifying genes with significant traits for agriculture



KOBE UNIVERSITY

“When the objective is to detect a rare variant, as is often the case in plant breeding, QTL mapping is therefore preferred over association mapping”

Bernardo 2020