Evolution of recombination landscape in diverging populations of bread wheat

Danguy des Déserts A. , Bouchet S., Sourdille P., Servin B.
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FLORIMOND DESPREZ

Wheat production faces many challenges

IWGSC **Fact Sheet**

www.wheatgenome.org

Wheat is the most widely grown cereal crop in the world and the staple food for more than 35% of the human population

730 million tons produced

$50 billion of total export value

222 million hectares harvested

60% increase in production needed to feed 9.6 billion by 2050

Wheat FACTS

486 million tons used for human consumption

2.5 billion consumers in **89** countries

19% of our total available calories

67 kilograms consumed on average per person per year

Data year: 2014

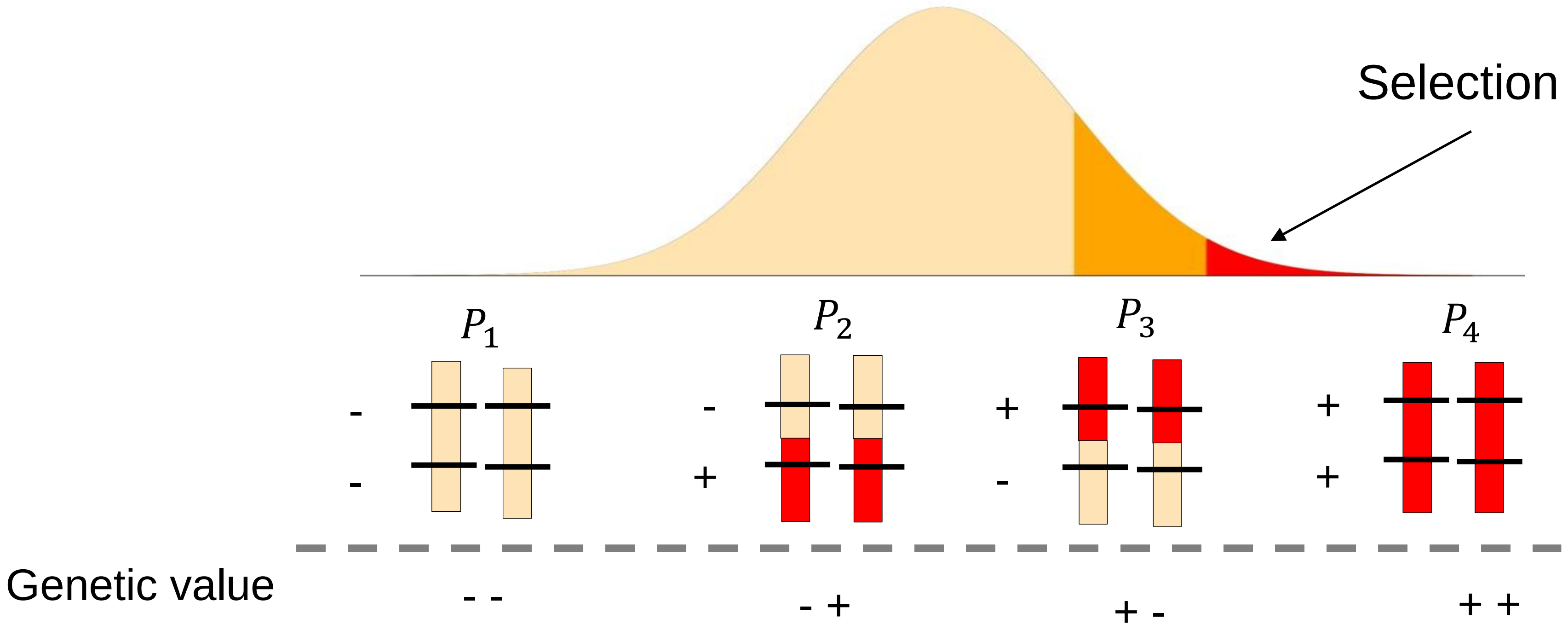
Sources: FAOSTAT www.faostat.fao.org ; CIMMYT www.wheat.org

Updated October 2016

- Demand for yield is increasing
- Reduction of intrants
- Emerging stresses

→ Varietal improvement

Varietal improvement relies on genetic variance

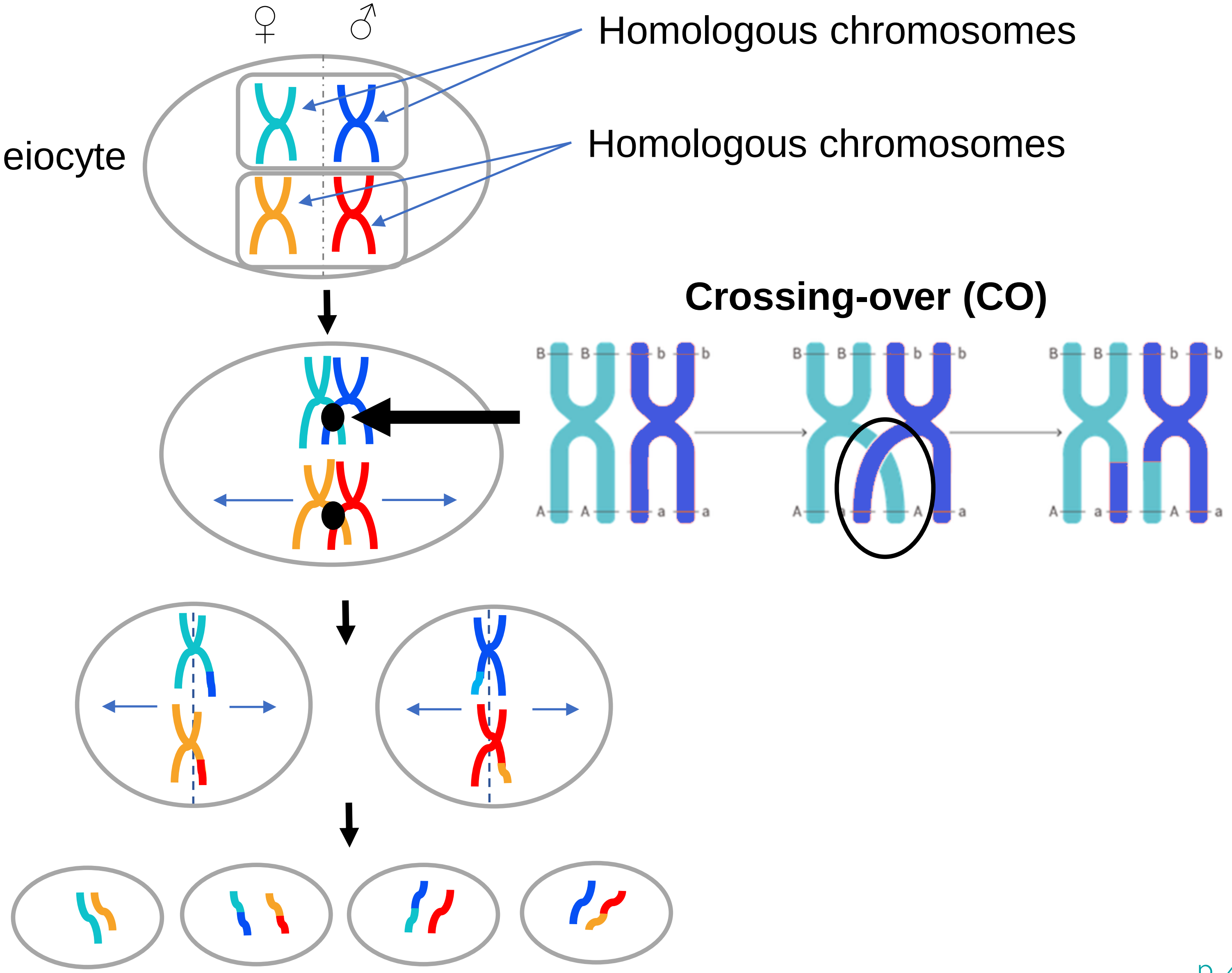


Genetic diversity results from

- Mutation
- Reshuffling of alleles through meiotic recombination

Meiotic recombination

Meiosis = production of gametes



meiocyte

Homologous chromosomes

Homologous chromosomes

1) Metaphase I

Crossing-over (CO)

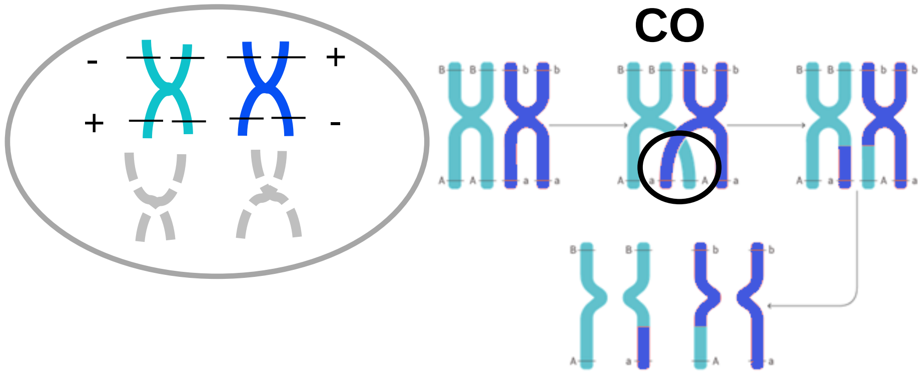
2) First division

3) Second division

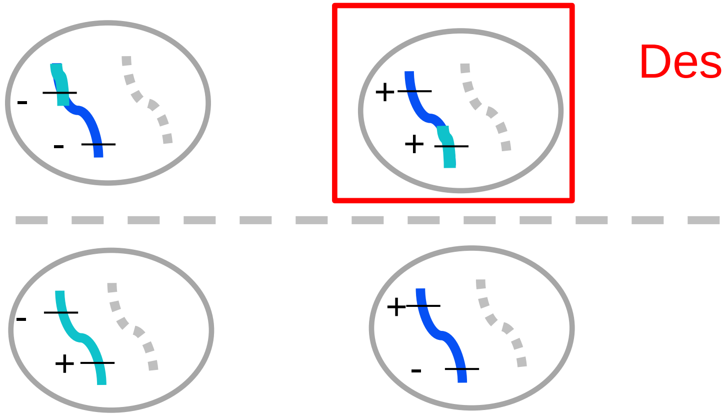
4 gametes

Recombination allows to cumulate desirable alleles in new varieties

If genes are on the same chromosome



Recombined
$f = r$



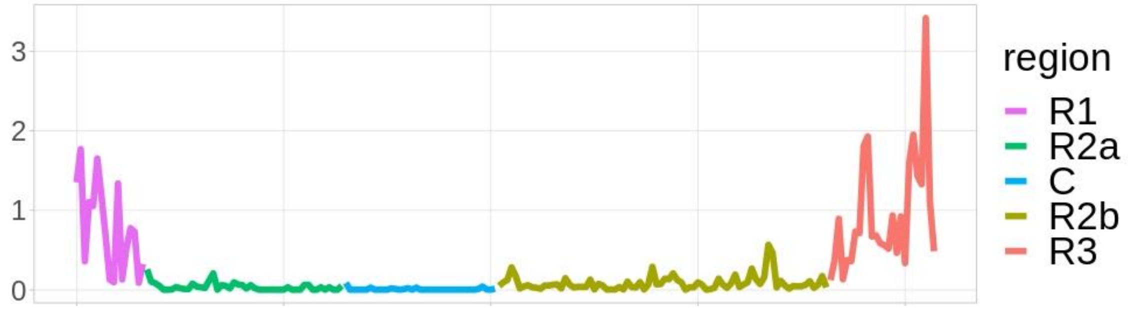
Desirable gamete
$p = r/2$

Not recombined
$f = 1 - r$

Recombination landscape (= repartition of CO along the genome)

Variability along the genome?

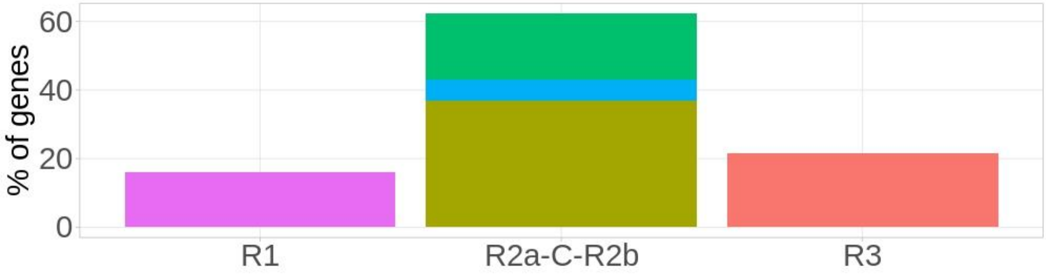
Recombination landscape (bread wheat)



chromosome 3B

Few CO in gene-rich regions
→ CO can be a limiting factor of varietal improvement

Genes count



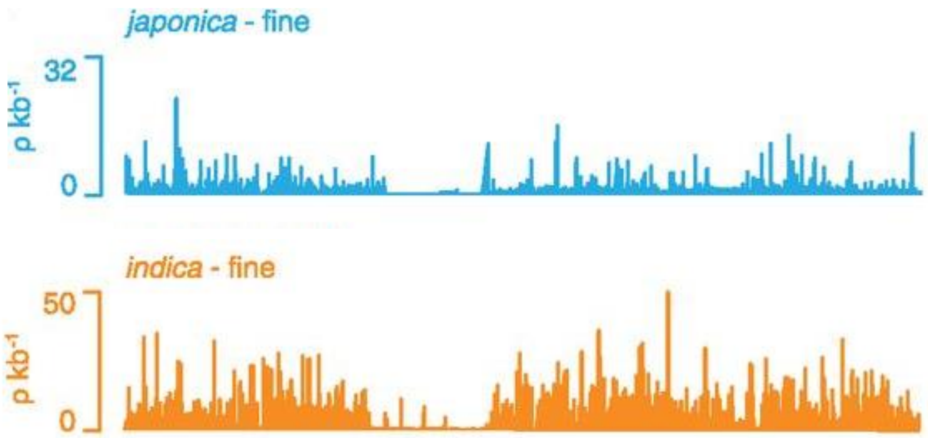
What drives recombination landscape ?

Recombination landscape

Recombination landscape = many mecanisms (interference, DNA compaction…)

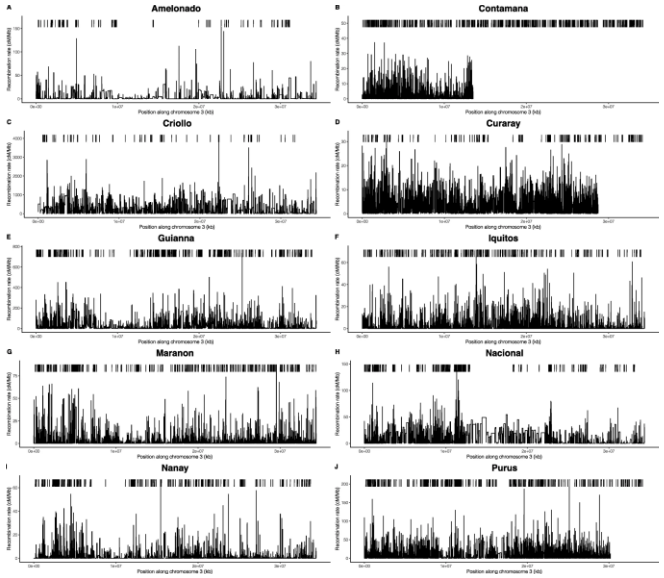
One approach to caracterize the determinism of rec. landscape = variability between populations

Marand et al. 2019 (The Plant Cell):
Comparison of landscapes of two **rice** sub-species



80% of recombination hotspots are **<u>sub-species specific</u>**

Schwarzkopf et al. 2020 (BMC genomics):
Comparison of landscapes of ten **cacao-tree** populations



55% of hotspots are **<u>population specific</u>**

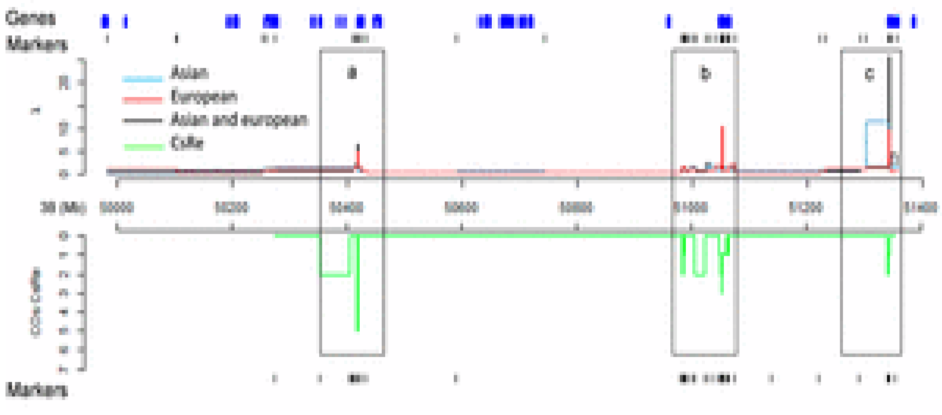
Variability of recombination landscape between populations ?

In bread wheat ?

Gardiner et al. 2019 (Genome Biology):

- Comparison of recombination landscape in 13 NAM families (1 parent x 13 other parents)
- More similar parents have more similar recombination landscapes

Darrier et al. 2017 (Genetics):



🟦 Asian population
🟥 European
⬛ Asian + European
🟩 CsRe

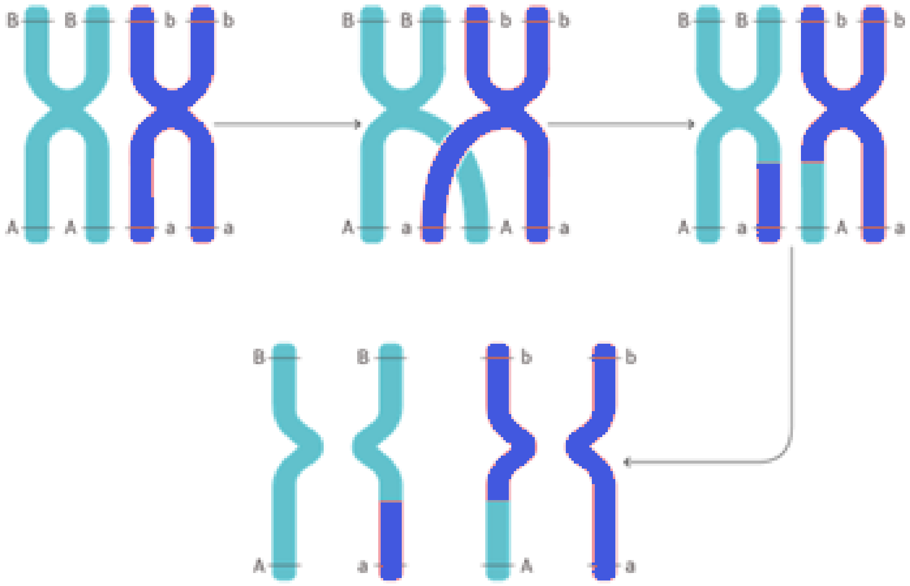
- Recombination landscapes are ~ similar
- But analysed region < 4 Mb

This presentation:
Genome-wide variability of recombination landscape between diverging populations of bread wheat

Methods

Estimate recombination landscape

Method 1: Count recombination within families: « Meiotic landscape »
Ex: Chinese Spring * Renan population (Rimbert et al. 2018, PloS one)



Drawbacks:

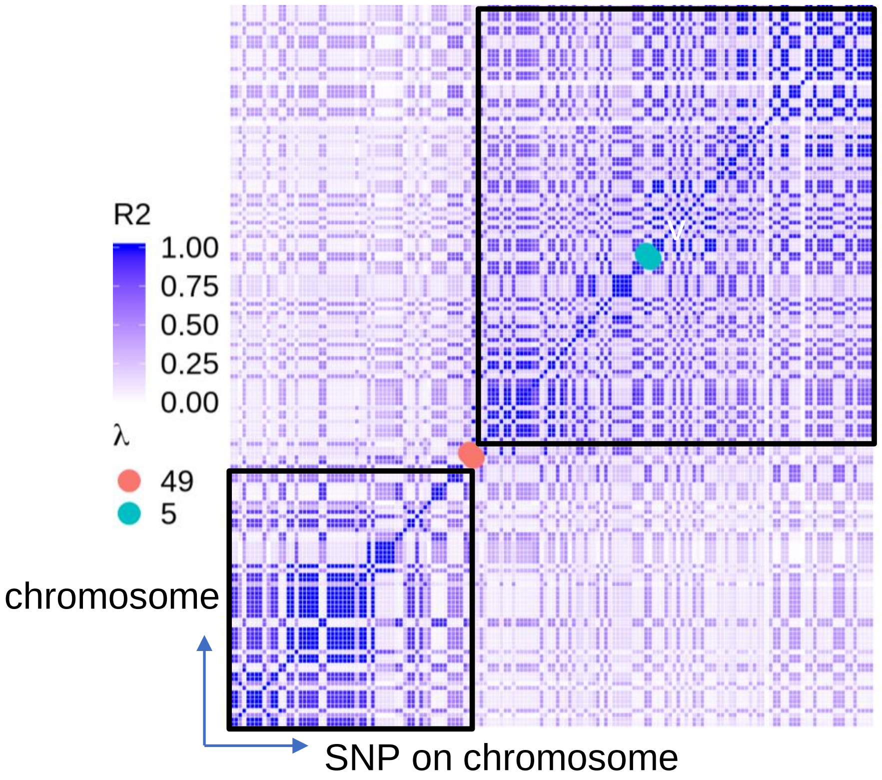
- **Small number of progeny**
- **Specific of parents**

Recombination rate $\hat{c} = f\left(\frac{nb\ recombined\ gametes}{nb\ gametes}\right)$

Estimate recombination landscape

Method 2: linkage disequilibrium of diversity panel: « LD-based landscape »

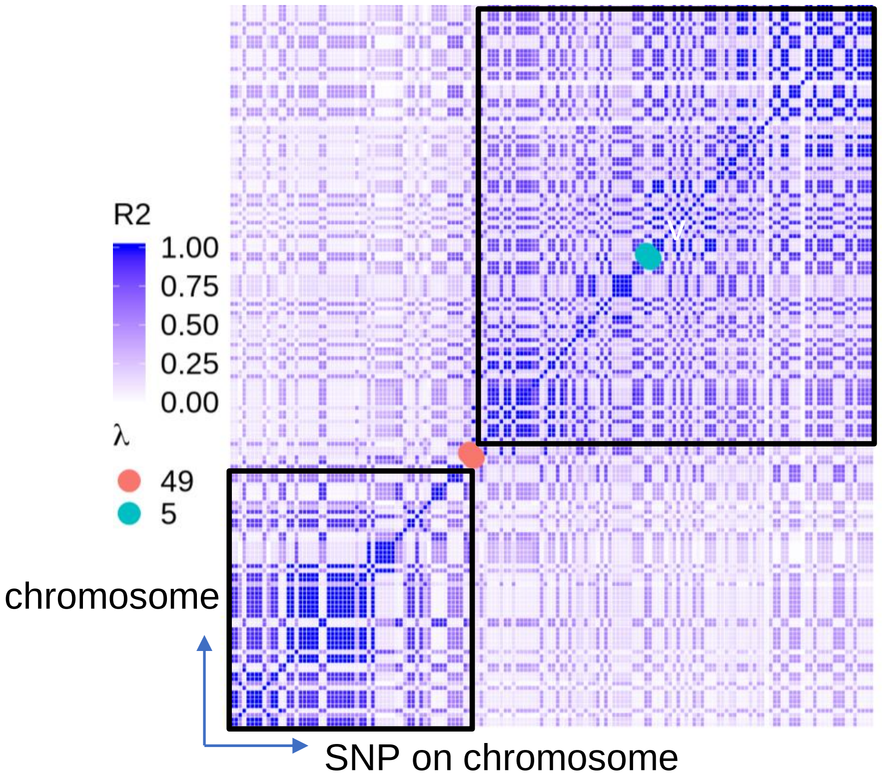
LD patterns



Estimate recombination landscape

Method 2: linkage disequilibrium of diversity panels: « LD-based landscape »

LD patterns

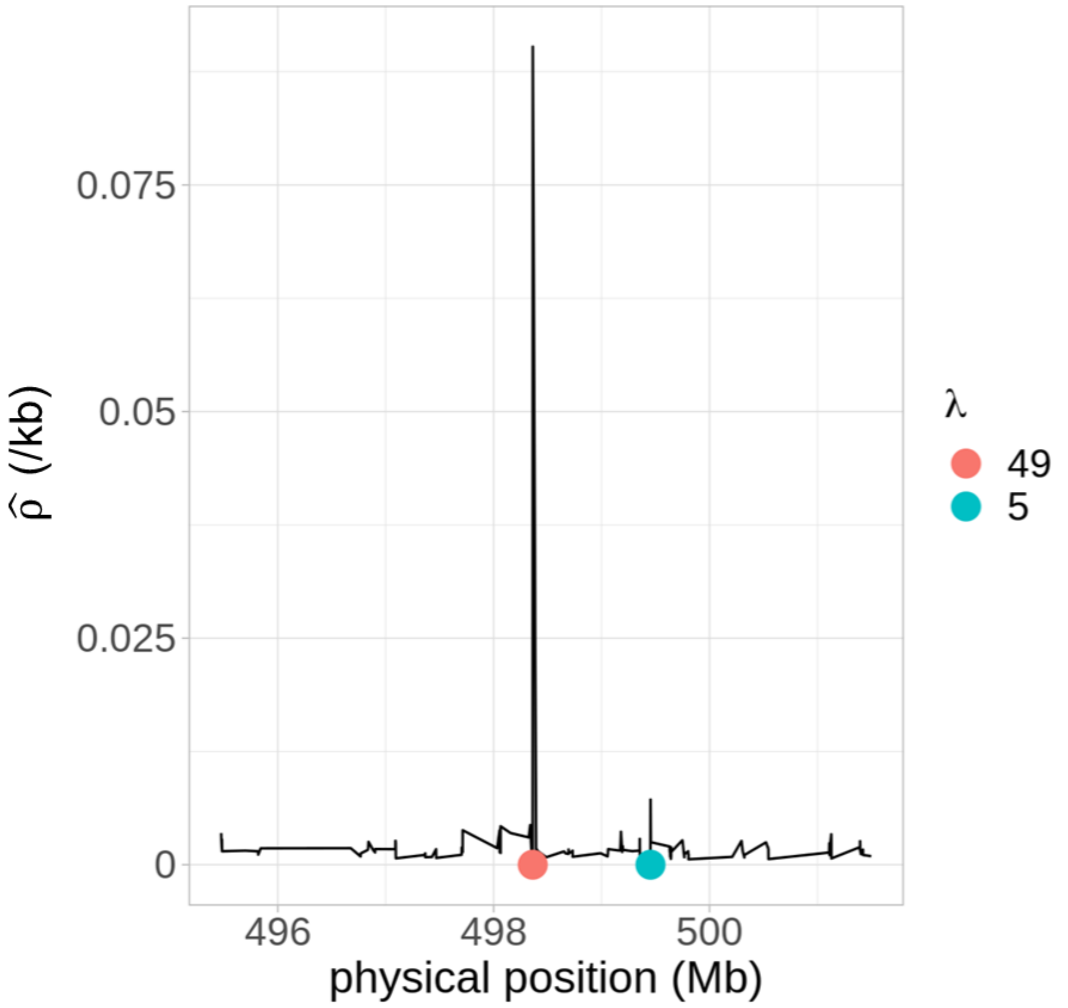


Li et Stephens model (2003, Genetics)

$$\hat{\rho} \approx \rho = K * c$$

with K = f(Ne)

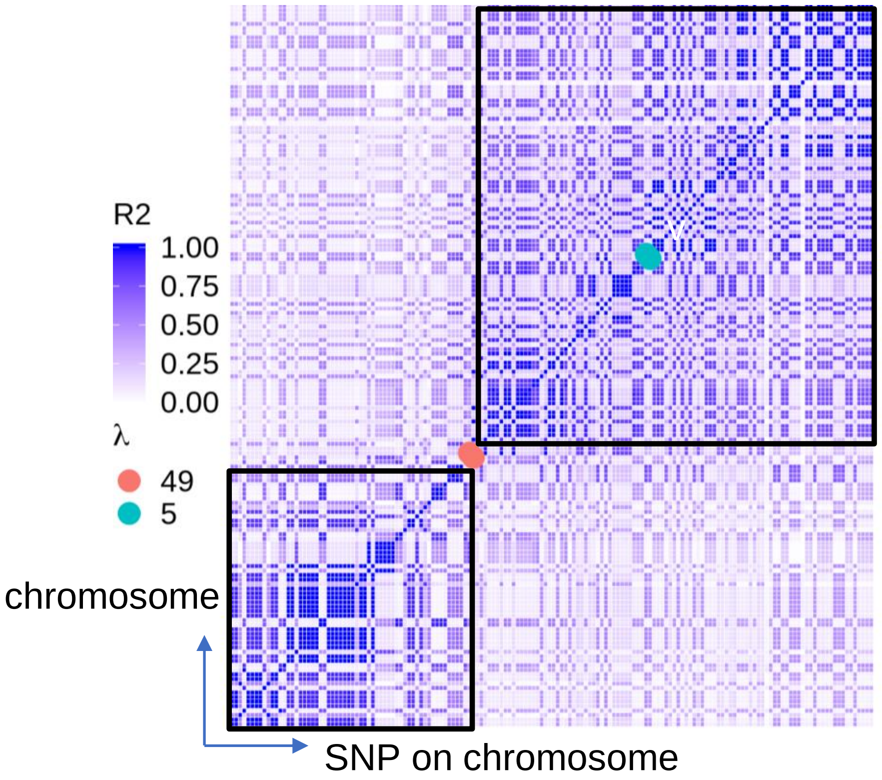
LD-based recombination landscape



Estimate recombination landscape

Method 2: linkage disequilibrium of diversity panels: « LD-based landscape »

LD patterns



Li et Stephens model (2003)

$$\hat{\rho} \approx \rho = K * c$$

with $K = f(Ne)$

Advantages compared to meiotic method:

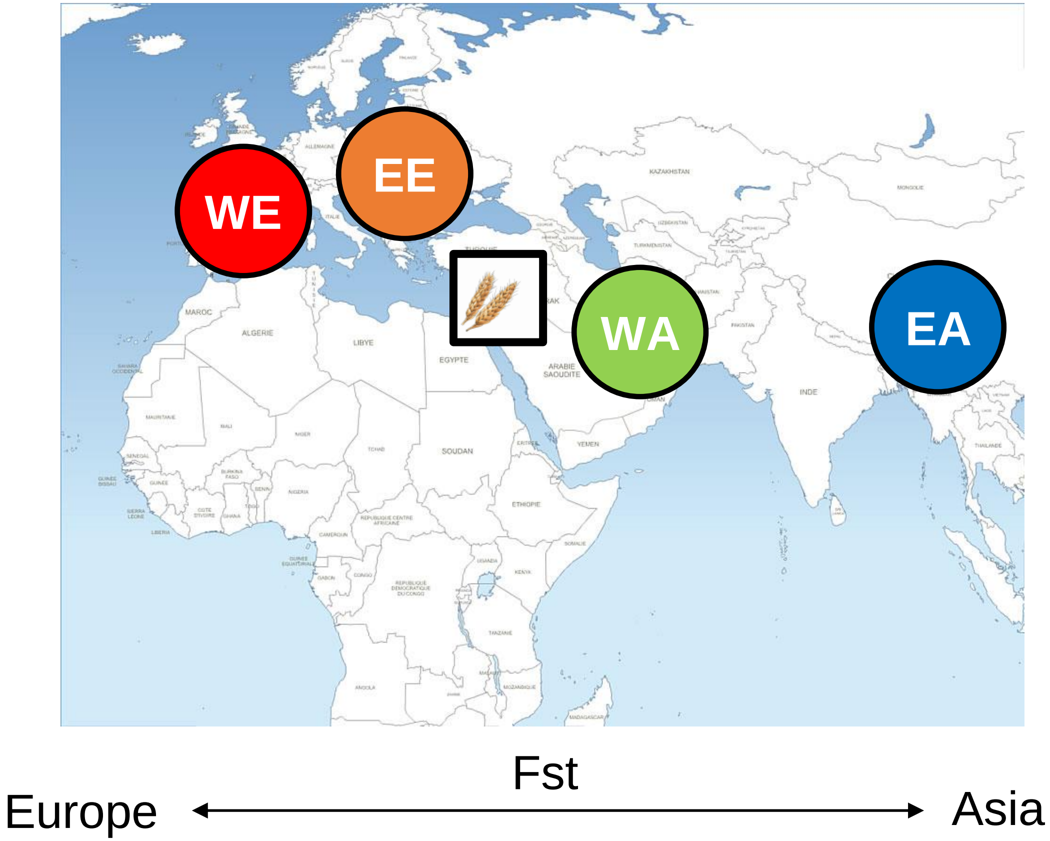
- **Based on many meiosis**
- **Many polymorphic SNP**
- **Representative of the population**

→ Better suited to compare recombination landscapes between populations

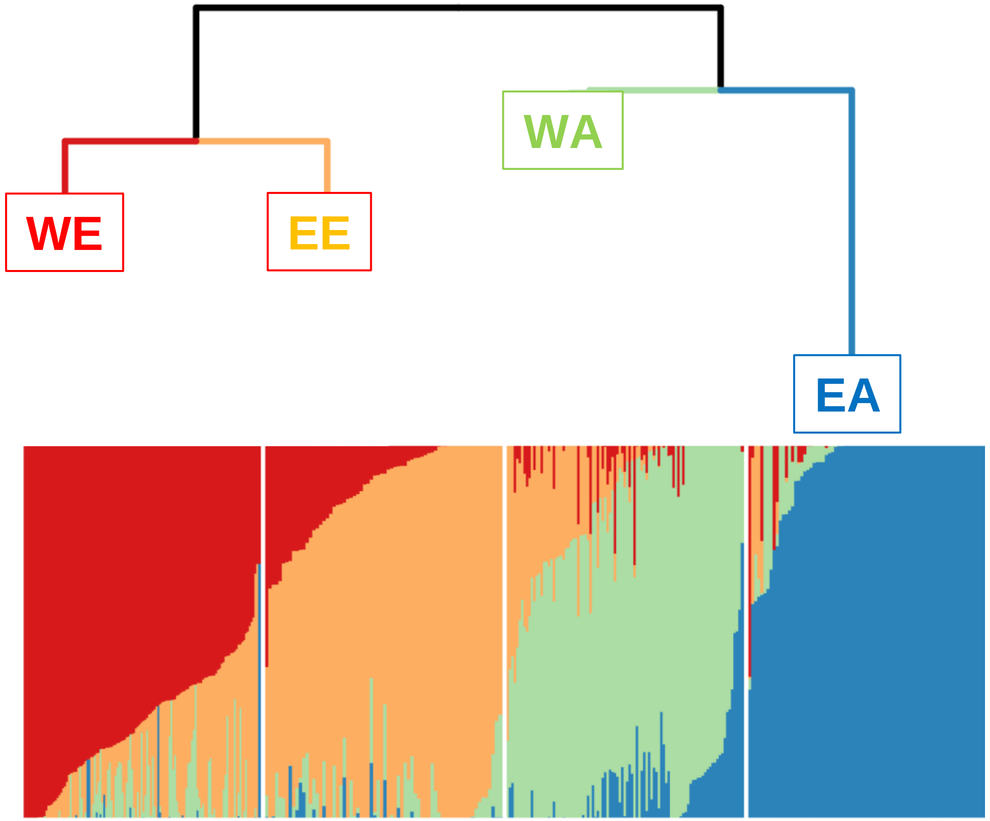
4 different populations of bread wheat

371 bread wheat landraces sampled worldwide (Balfourier et al. 2019, Science Advances)
130k SNP of TABW410k (Kitt et al. 2021, Zenodo)
→ hierarchical clustering K = 4

Populations



Differenciation of populations



- ➢ Do the recombination profiles of these 4 populations vary ?

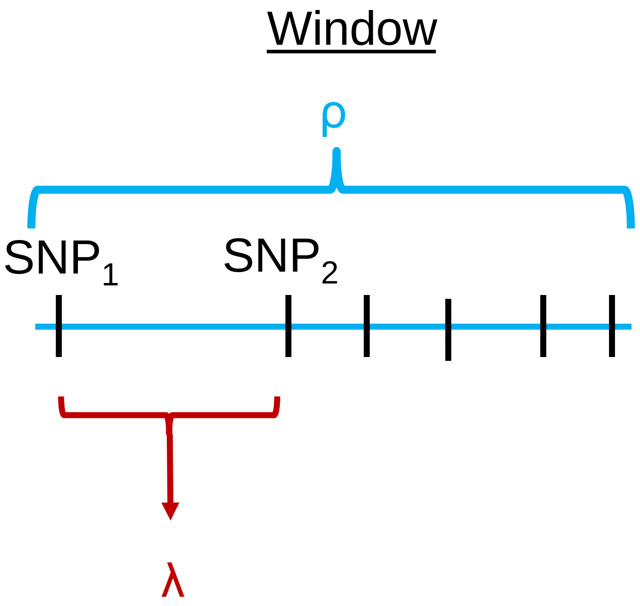
Estimate recombination landscapes

For each population (WE, EE, WA, EA):

- Split the genome into ~ 600 windows of ~ 2 cM length (using CsRe)

- Run PHASE (Li et Stephens 2003, Genetics)

= to obtain joint posterior distributions of ρ and λ



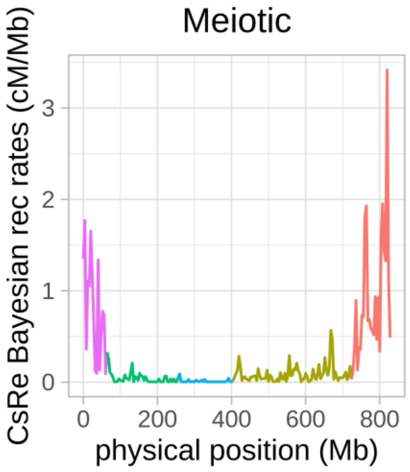
ρ : Background recombination rate

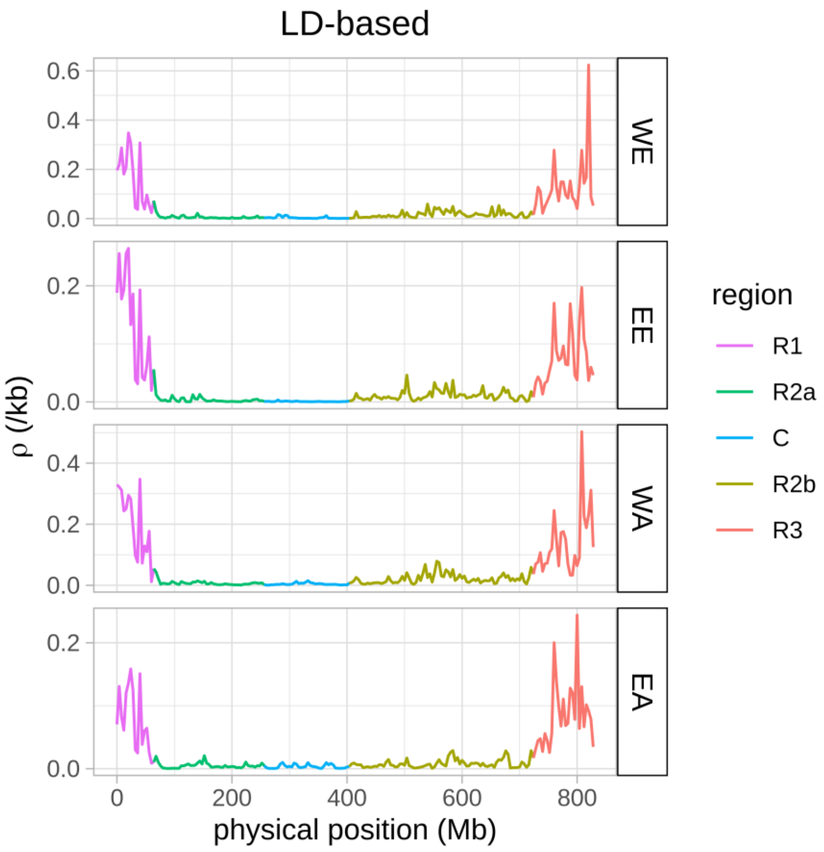
λ : Local inflation of recombination

Results

Validation of LD-based recombination landscapes

3B chromosome



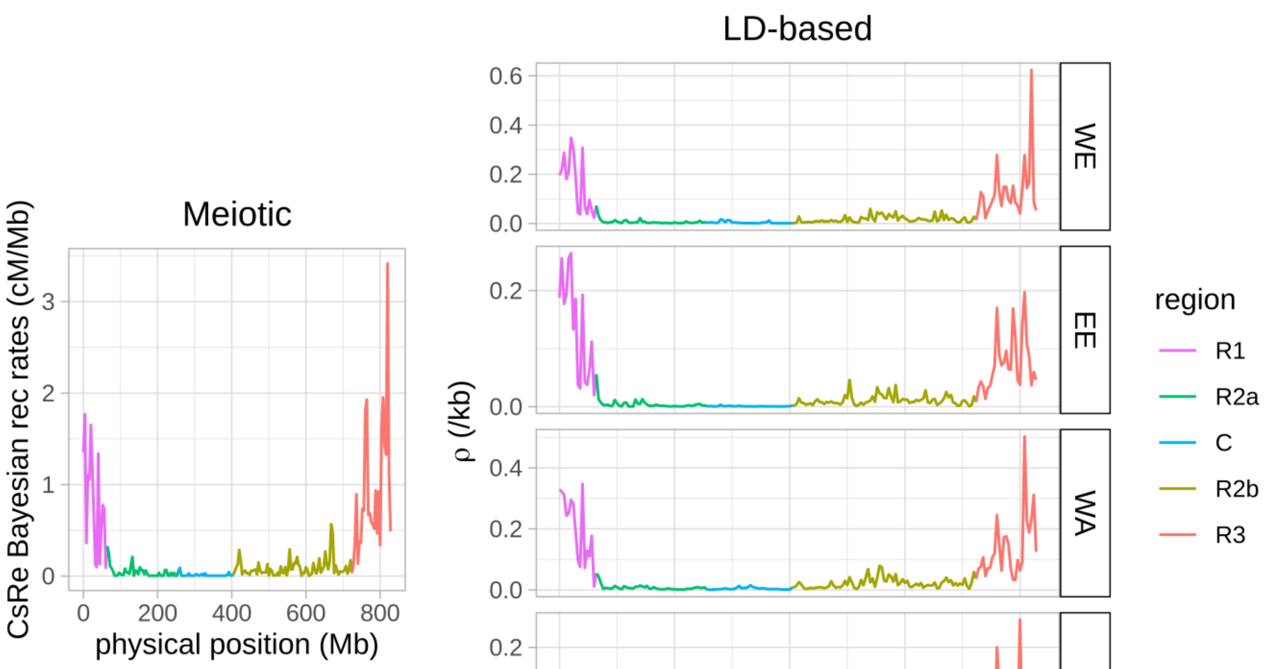


$$\hat{c} = f\left(\frac{nb\ recombined\ progenies}{nb\ progenies}\right)$$

$$\hat{\rho} = K*c$$

Validation of LD-based recombination landscapes

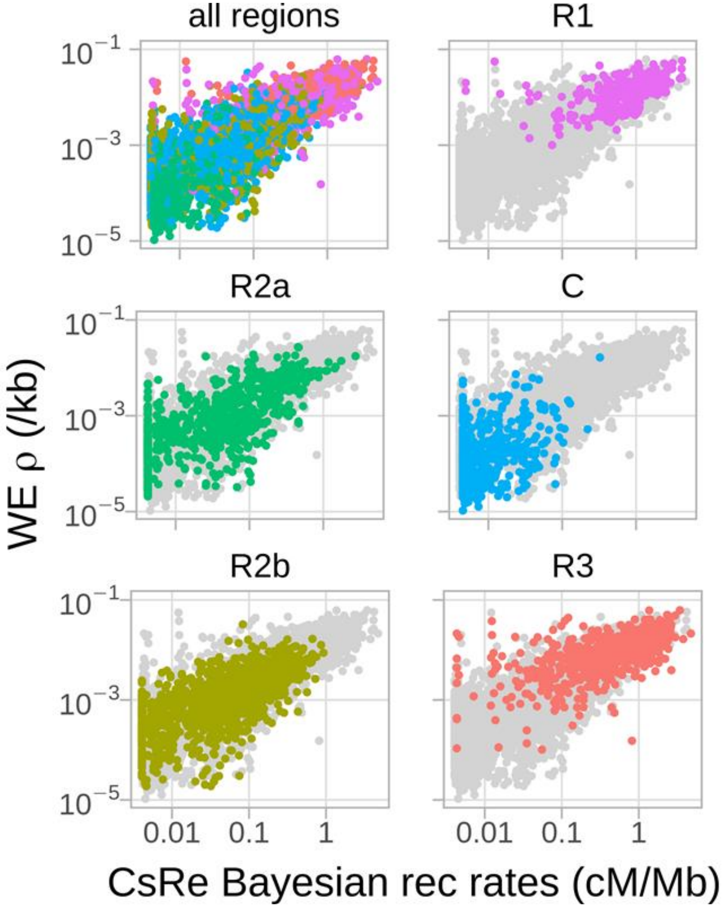
3B chromosome



$$\hat{c} = f\left(\frac{nb\ recombined\ progenies}{nb\ progenies}\right)$$

$$\hat{\rho} = K*c$$

Correlation all genome

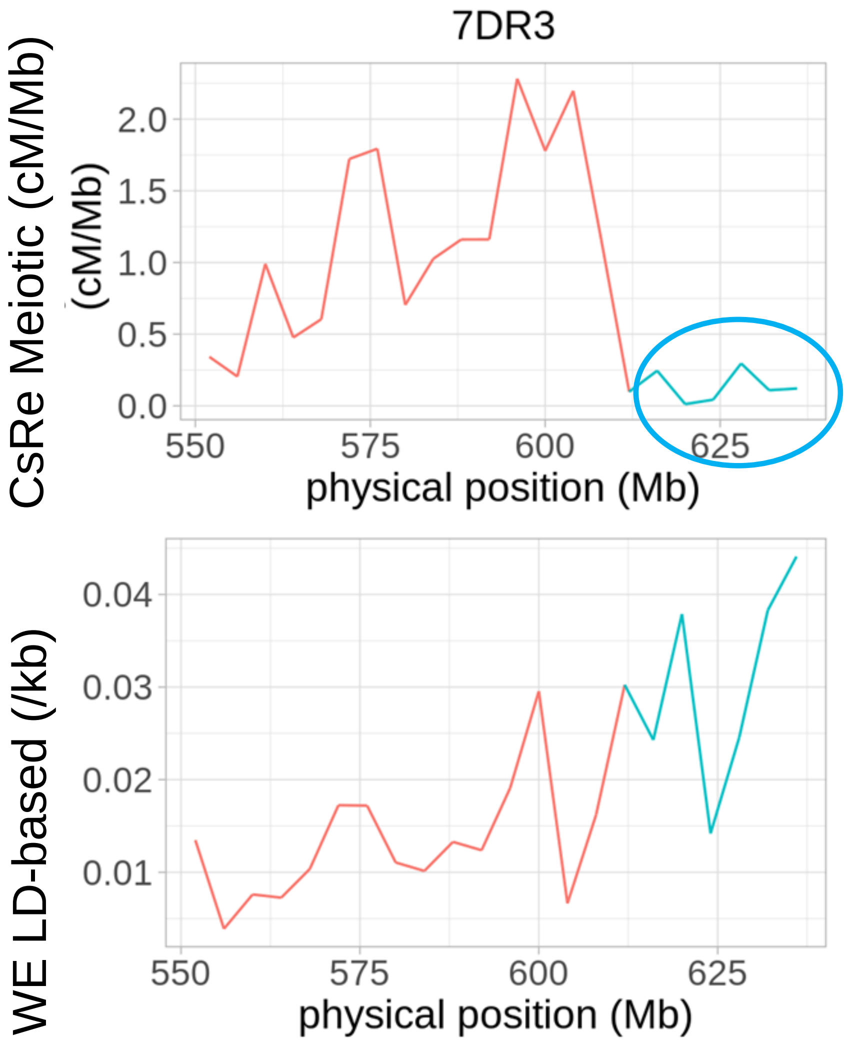


Average correlation within genomic regions (1AR1…7DR3) = 0.6 ± 0.2

Local differences between meiotic and LD-based landscapes

- Low correlation in the 7DR3 region
- Wild introgression in Renan population

→ Meiotic landscapes are sensitiv to individual specific variation

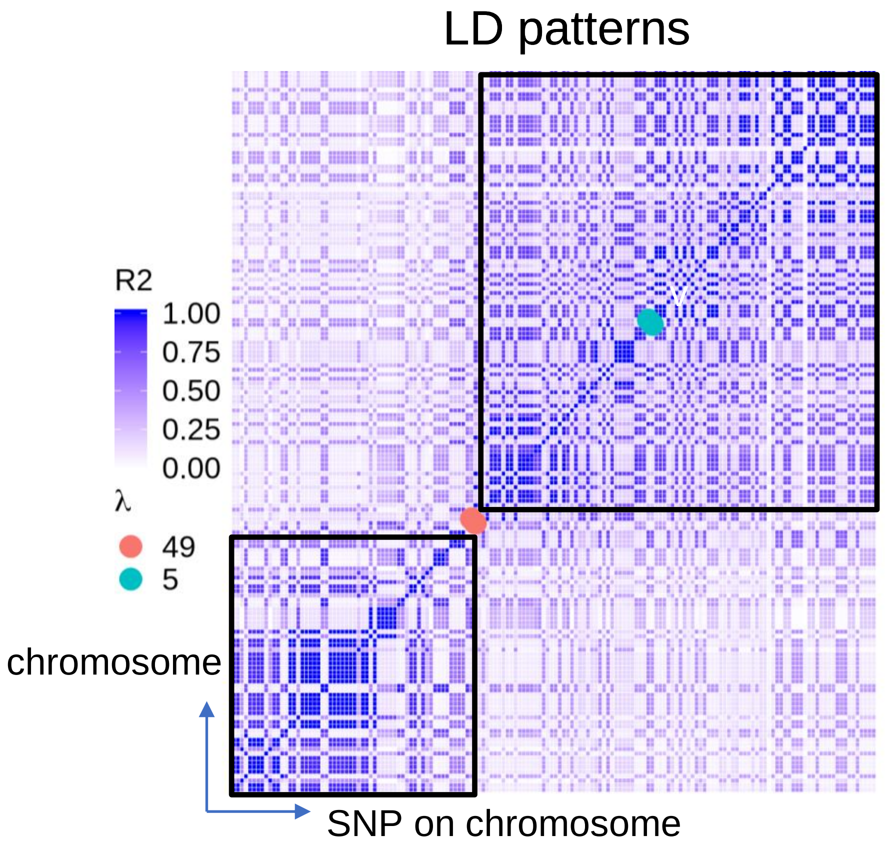


Validation of LD-based recombination landscapes

- Good correlation between LD-based and meiotic landscapes
- But higher resolution in LD-based landscapes

→ LD-based = better suited to study and compare
fine scale variation of recombination between the 4 populations

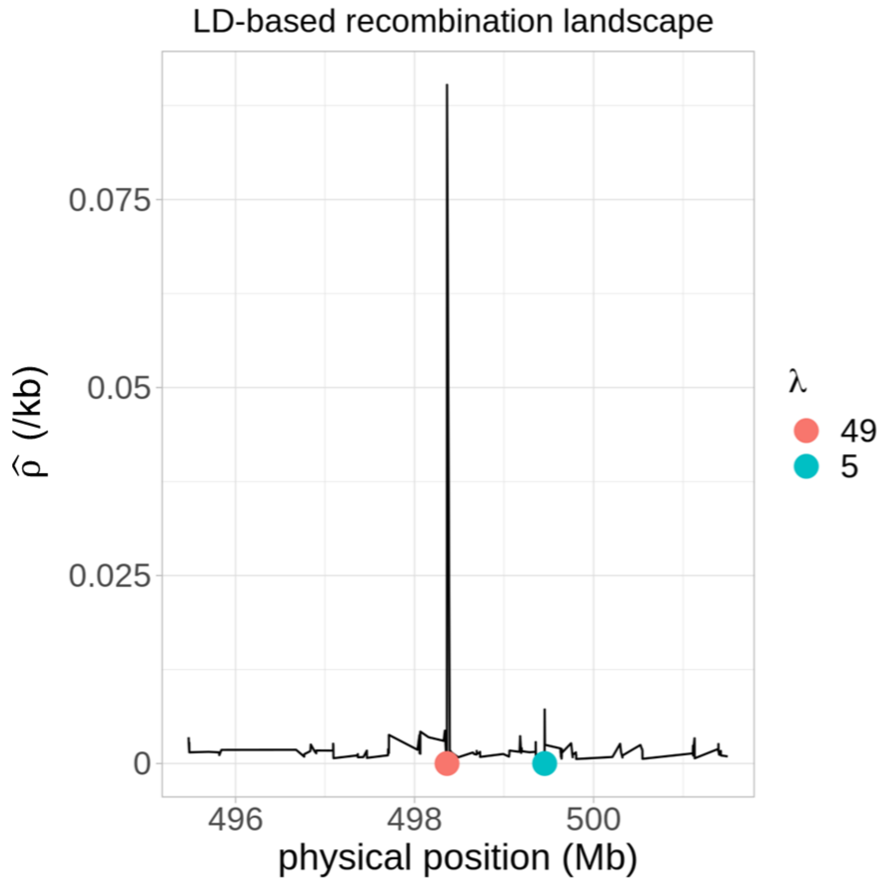
Comparison of fine scale variation of LD-based landscapes



Li et Stephens model (2003)

$\hat{\rho} \approx \rho = K * c$

$\xrightarrow{\text{with } K = f(Ne)}$

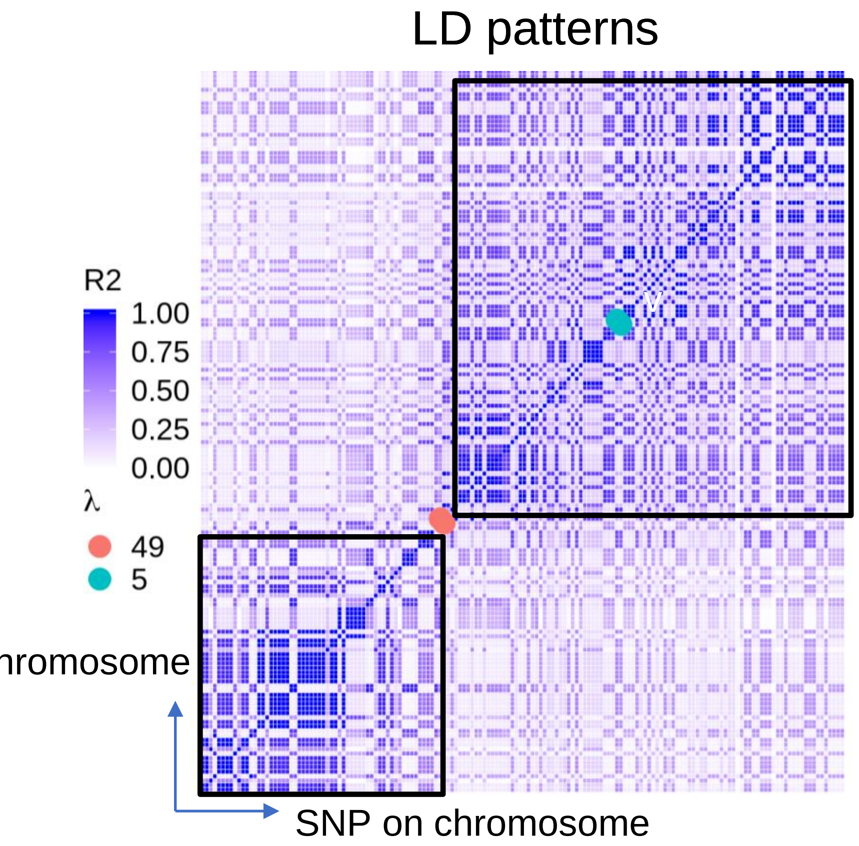


Drawback: $\hat{\rho}$ sensitivity to evolutionary forces K= f(Ne)

Example: selection acts locally

$$\lambda = \frac{\rho_{interval}}{\rho_{larger\ window}} = \frac{K * c_{interval}}{K * c_{window}}$$ = local inflation of recombination

Fine scale variation of LD-based landscapes



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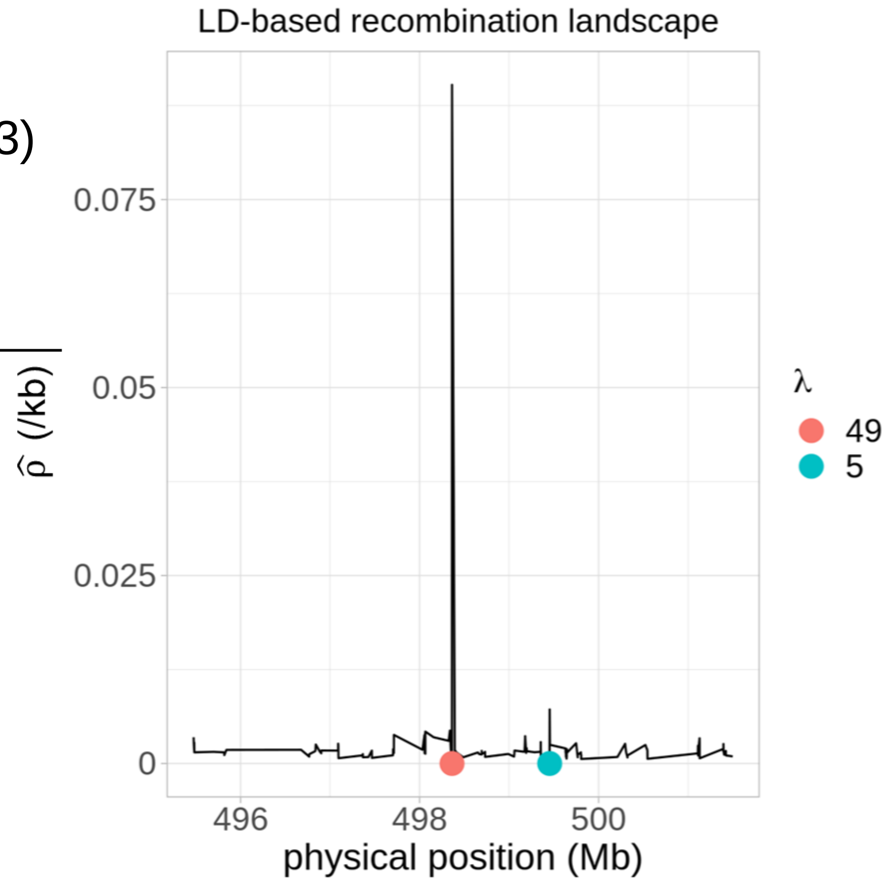


$$\lambda = \frac{\rho_{interval}}{\rho_{larger\ window}} = \frac{K * c_{interval}}{K * c_{window}}$$ = local inflation of recombination

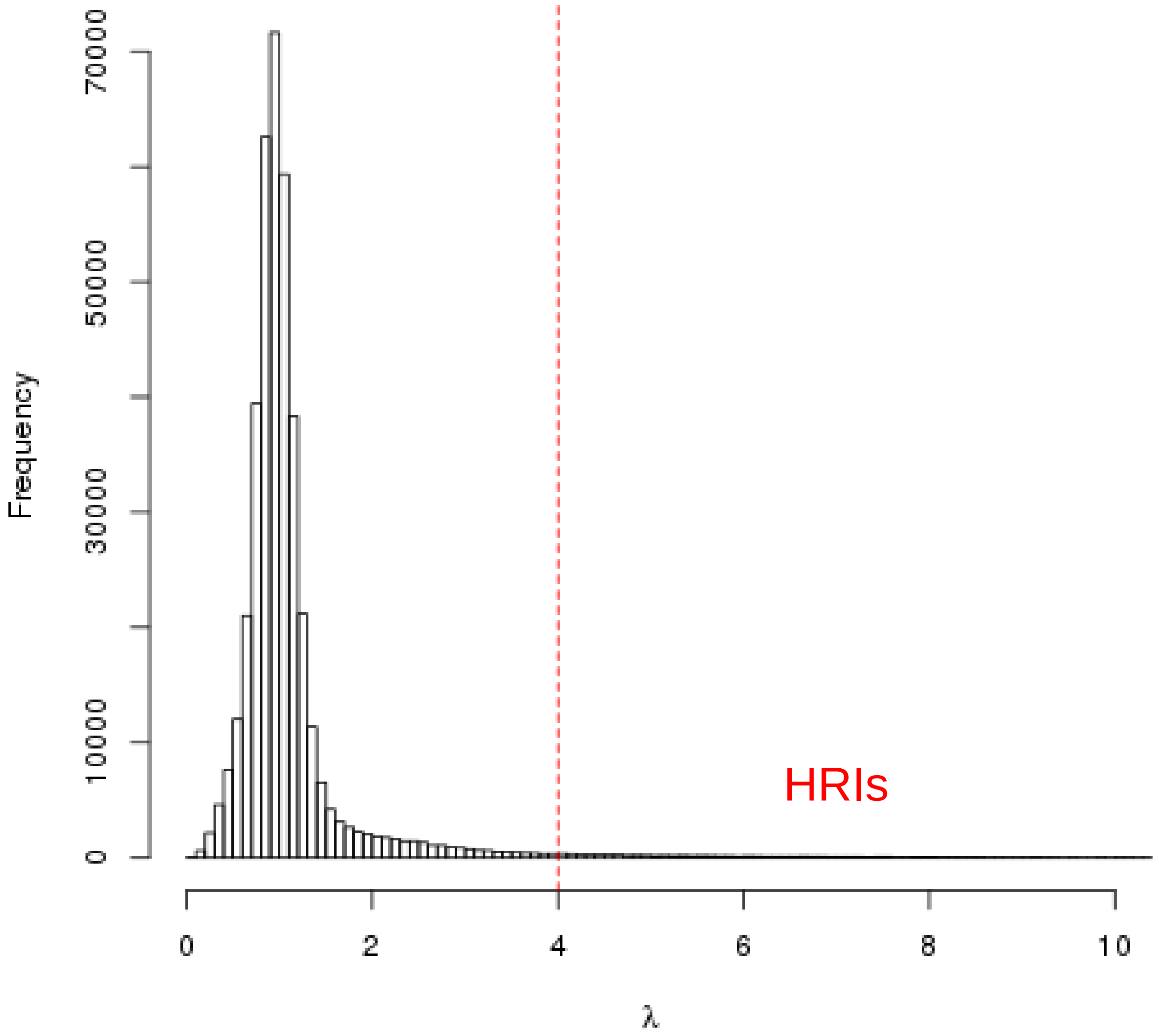
λ landscape = variation of recombination « only »
→ λ = better suited to compare populations

Localization of high recombination rates

Highly Recombining Intervals (HRIs)

HRIs = intervals with high λ

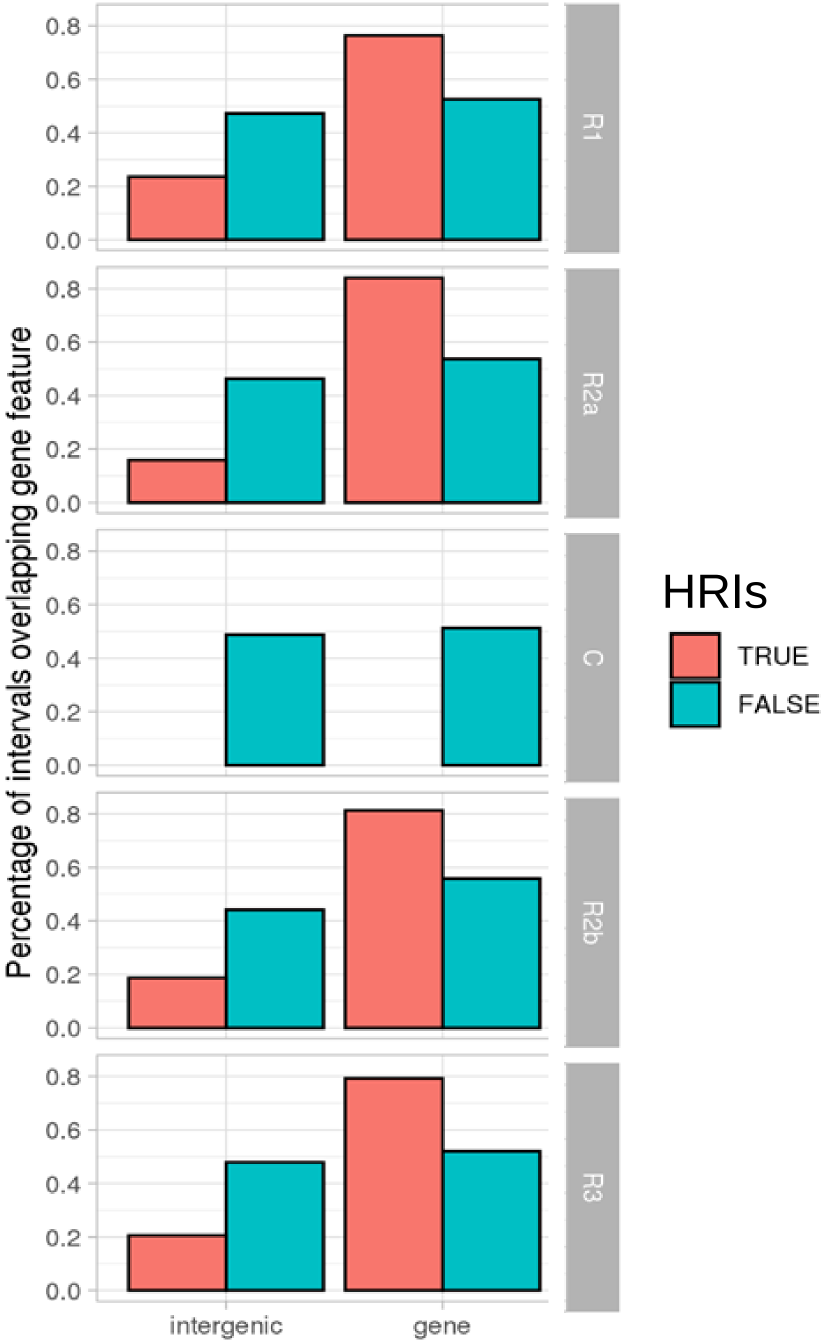
$\lambda = \frac{c_{interval}}{c_{window}}$ = local inflation of recombination



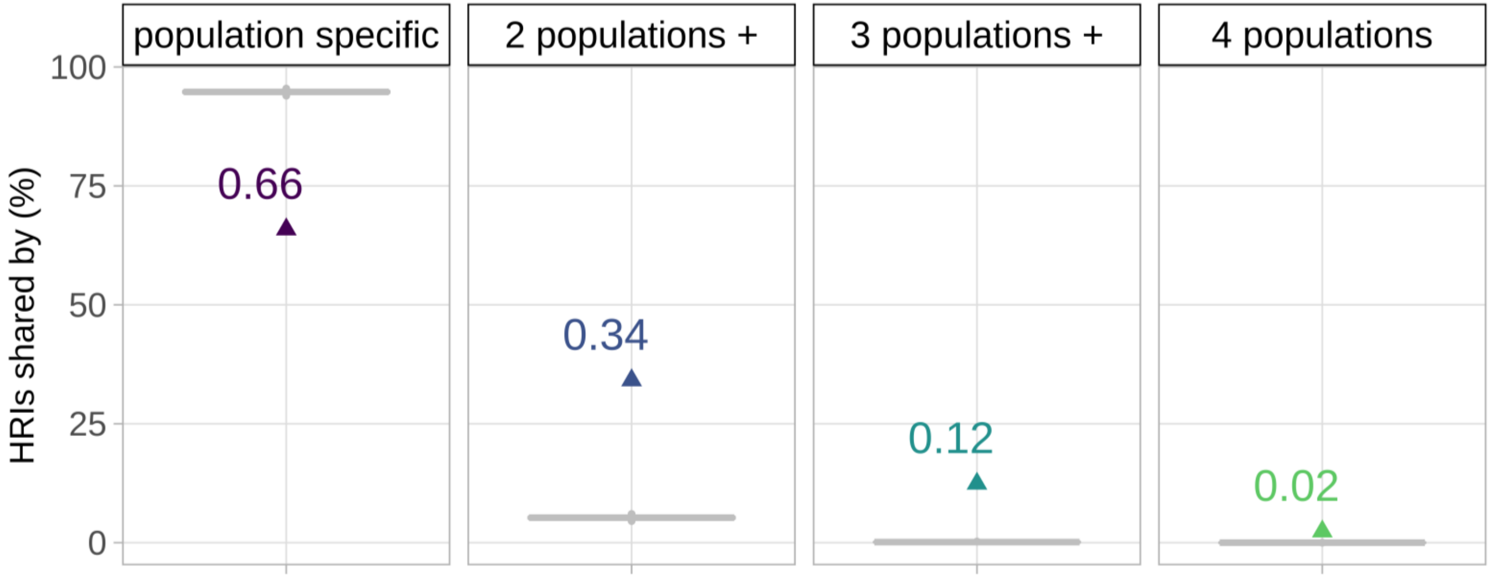
Features associated with HRIs

- ~ 9k HRIs (all populations combined)
- > 70% of HRIs located in regions R1 and R3
- 80% of HRIs overlapped genes

→ HRIs associated with open-chromatine
Consistent with litterature on rec. hotspots



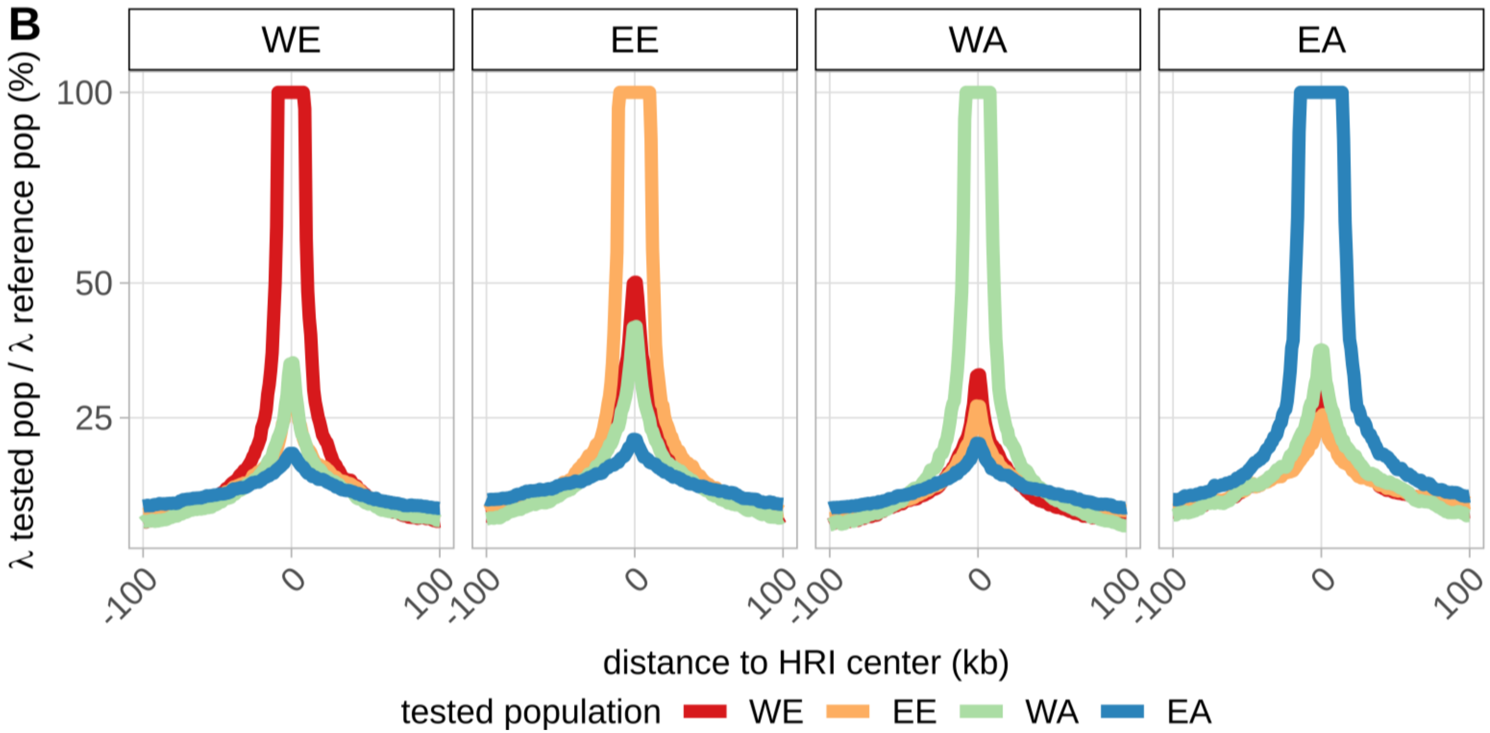
Conservation of HRIs across the 4 populations



- Less population specific intervals than expected
- 34% of HRIs are shared > than expected by chance

Common mechanism driving HRIs positions
but differenciation

Conservation of HRIs across the 4 populations

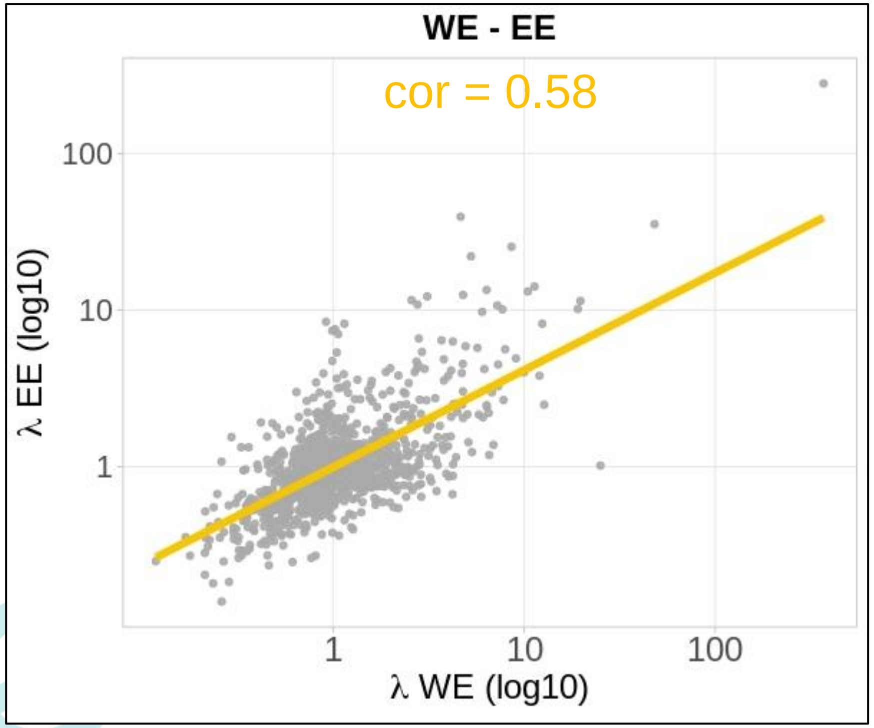


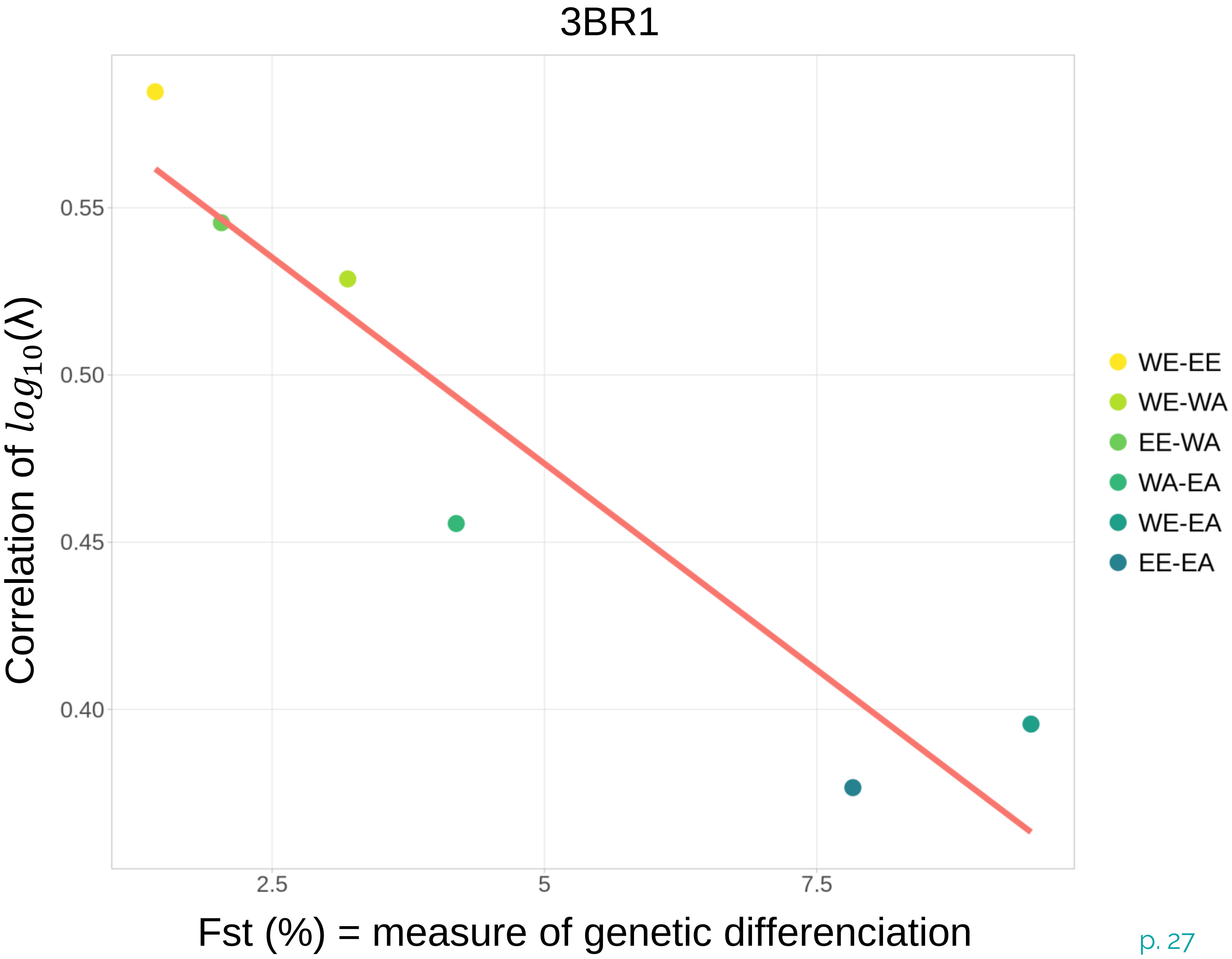
Recombination at HRIs increased in closer populations

Variability of global recombination landscape

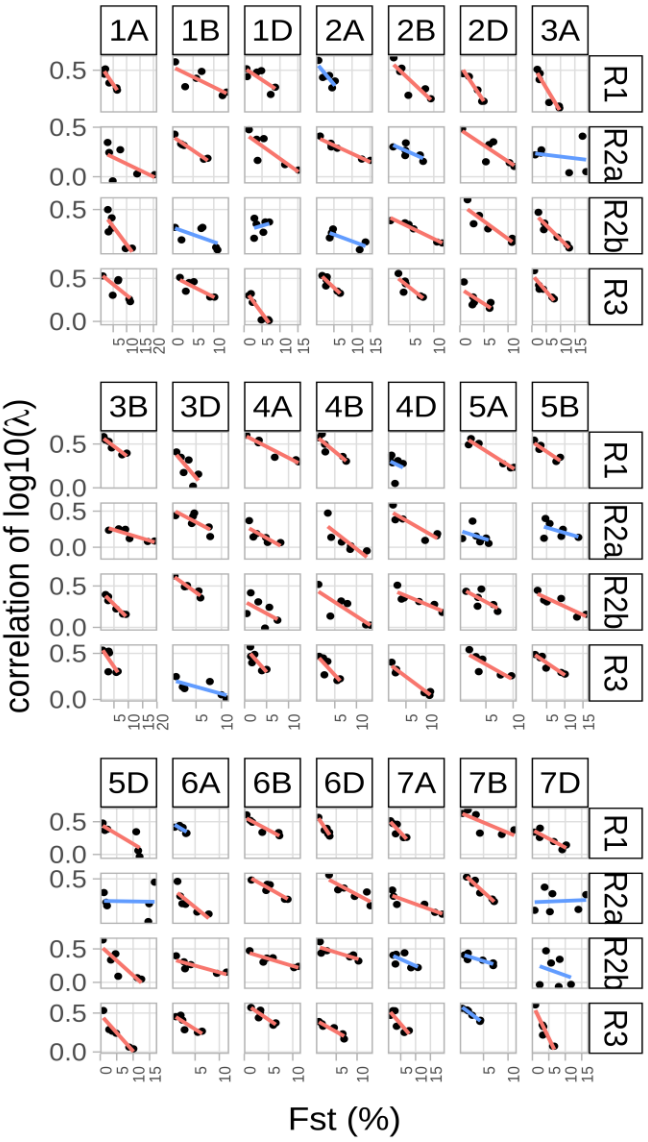
For each genomic region 1AR1 ... 7DR3 and each pair of populations:

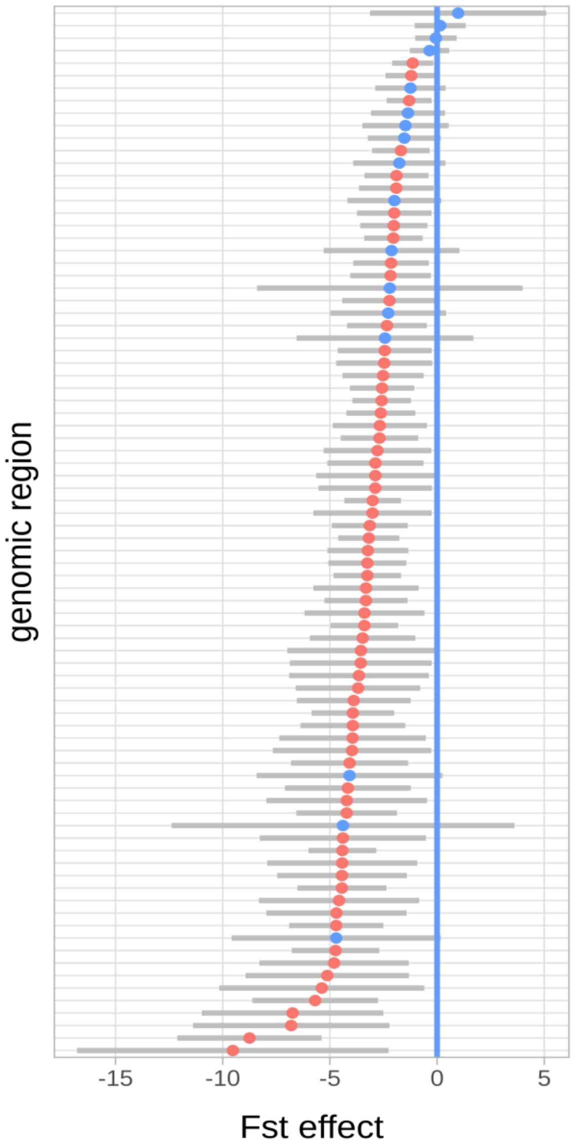
- Compute Fst
- Compute correlation of rec. inflations (λ)





Variability of global recombination landscape





95% confidence interval of slope estimate: 🟥 <0 🟦 include 0

- Negative slopes for most regions
- Most slopes significantly < 0

→ Similary of recombination landscapes decreases with genetic differenciation

Conclusion

Recombination landscape evolved quickly in bread wheat

Genetic divergence associated with increased differenciation of LD patterns

- Among the highest resolutive recombination landscapes of bread wheat
- Very clear signal
- Results likely not biased by evolutionnary forces
- Also observed in other studies on plants:
  - Bread wheat (Gardiner, 2019, Genome Biology)
  - Rice (Marand et al. 2019, The Plant Cell)
  - Cacao (Schwarskops et al. 2020, BMC genomics)

+ Maize (Rodgers-Melnick et al. 2015, PNAS), Poplar (Wang et al. 2016, Genetics), Cotton (Shen et al. 2019, The Plant journal)

→ Evolution of CO repartition along the genome in plants

Discussion: Drivers of the evolution of CO repartition along the genome

→ Might provide some insights about CO position determinism

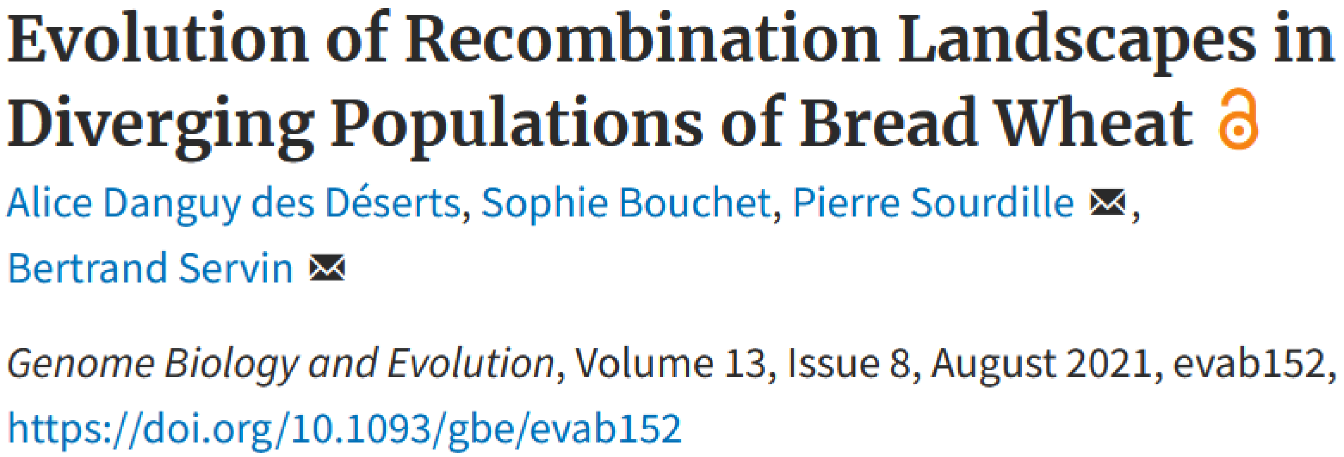
How to explain such variability ?

- Environmental effects: T°C
- (Epi-)Genomic variability: DNA sequence or chromatine landscape
- Genes driving CO position (Ex: PRDM9 in few mammals)

Perspectives:

- Detect recombination hotspots
- Functionnal annotation + chromatine marks at hotspots
- GWAS in segregating families

Thank you for your attention



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