

Deciphering the genetic basis of adaptation to environment in *Theobroma cacao* using resequenced genomes

Bénédicte Rhoné

CIRAD, France

Olivier Fouet, CIRAD, France
Rey G. Loor Solorzano, INIAP, Ecuador
Arnaud Lemainque, Génoscope, France
Claire Lanaud, CIRAD, France
Xavier Argout, CIRAD, France

Studying the genomic basis of adaptation of *Theobroma cacao* :



Upper Amazon :
probable center
of origin

- To improve predictions of species' adaptive capacities
- To provide accurate conservation strategies of genetic resources ...

... in the context of **increasing environmental pressures**

Studying the genomic basis of adaptation

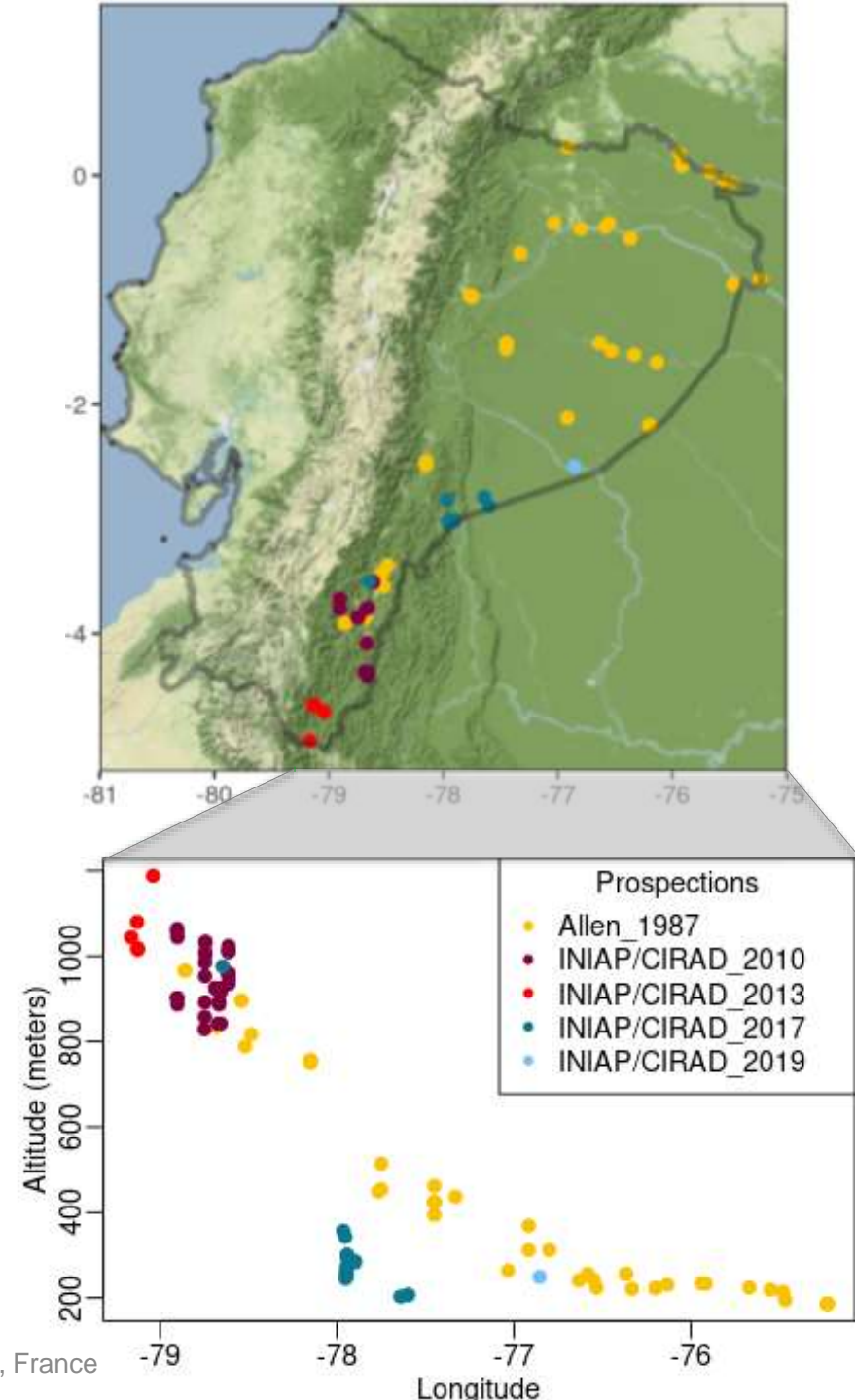
Altitudinal gradient mimics gradual climate change at a restricted geographic scale:

- ↘ temperature
- ↘ CO₂ partial pressure
- ↗ dryness
- ↗ UV radiation

102 accessions from collection expeditions sampled along an altitudinal gradient in Ecuador

Allen 1987, Loor et al 2015, Fouet et al 2022

→ Joint analysis of **genetic** and **environmental** variations to identify functionally important genes contributing to the adaptive potential of the species

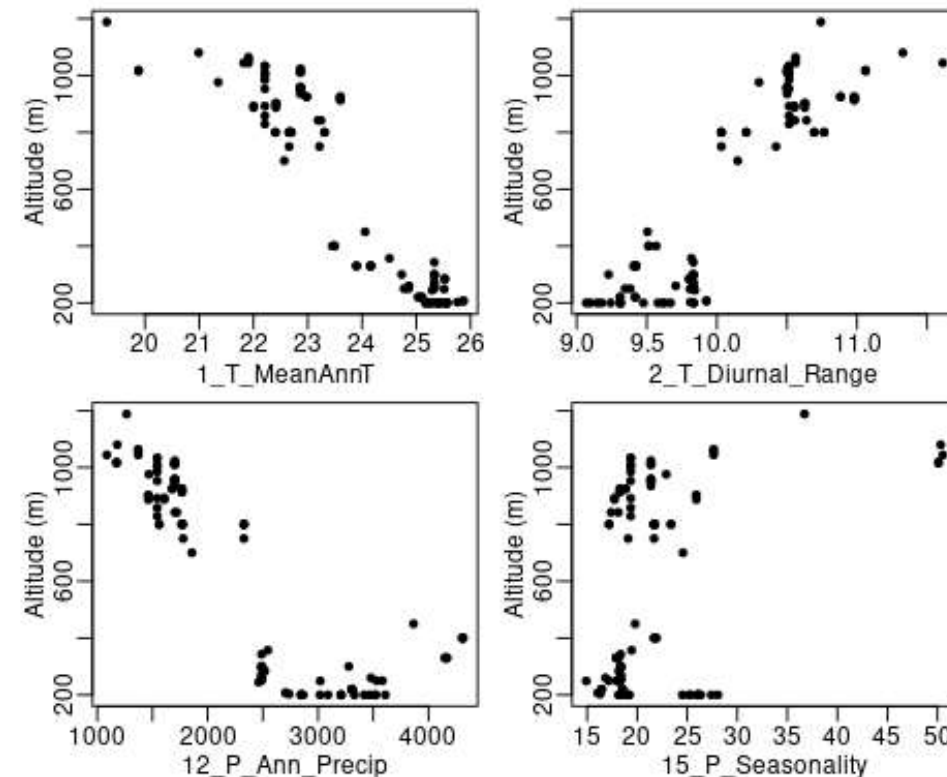
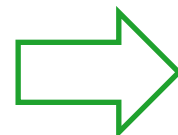
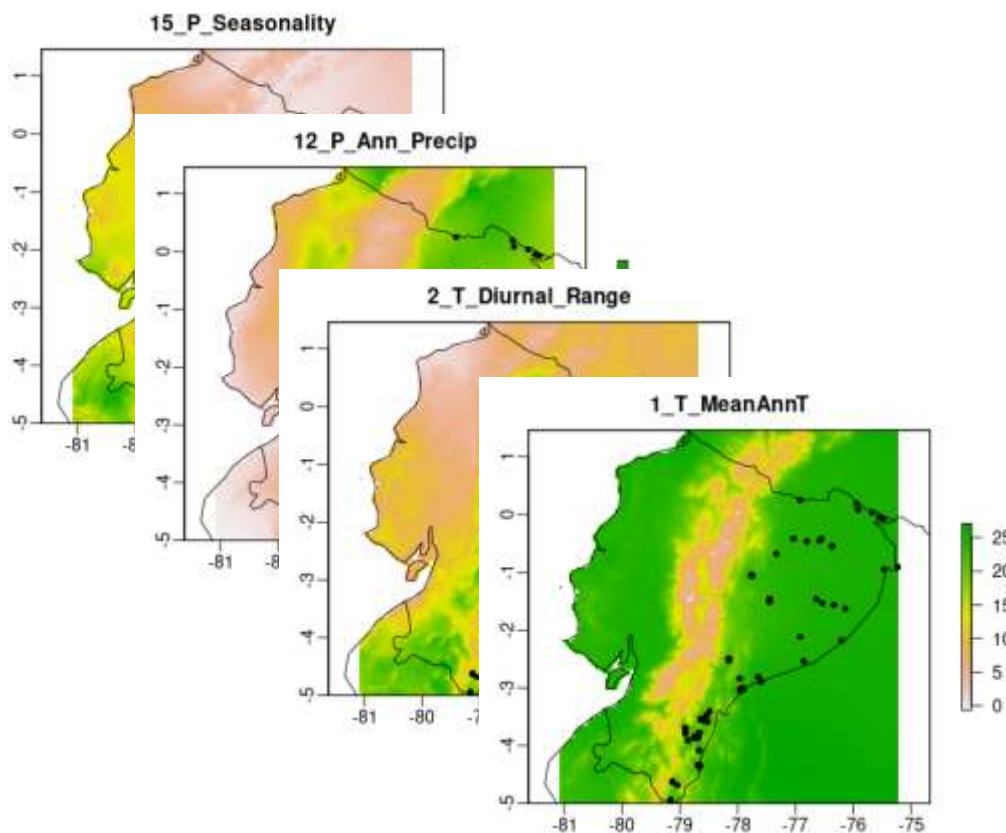


Climate data acquisition

 WorldClim V 2.1 <https://www.worldclim.org/>

Database of high spatial resolution global weather and climate data used for mapping and spatial modeling

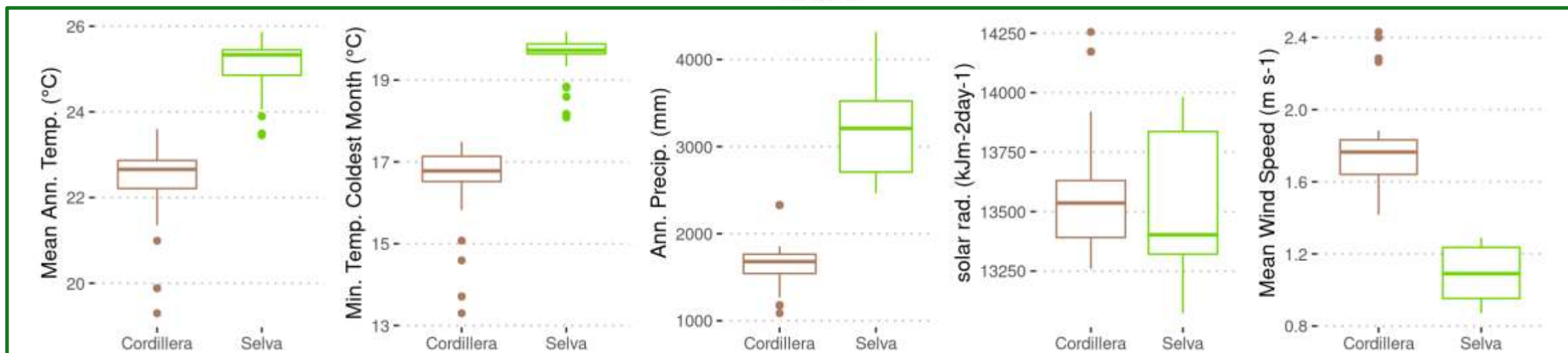
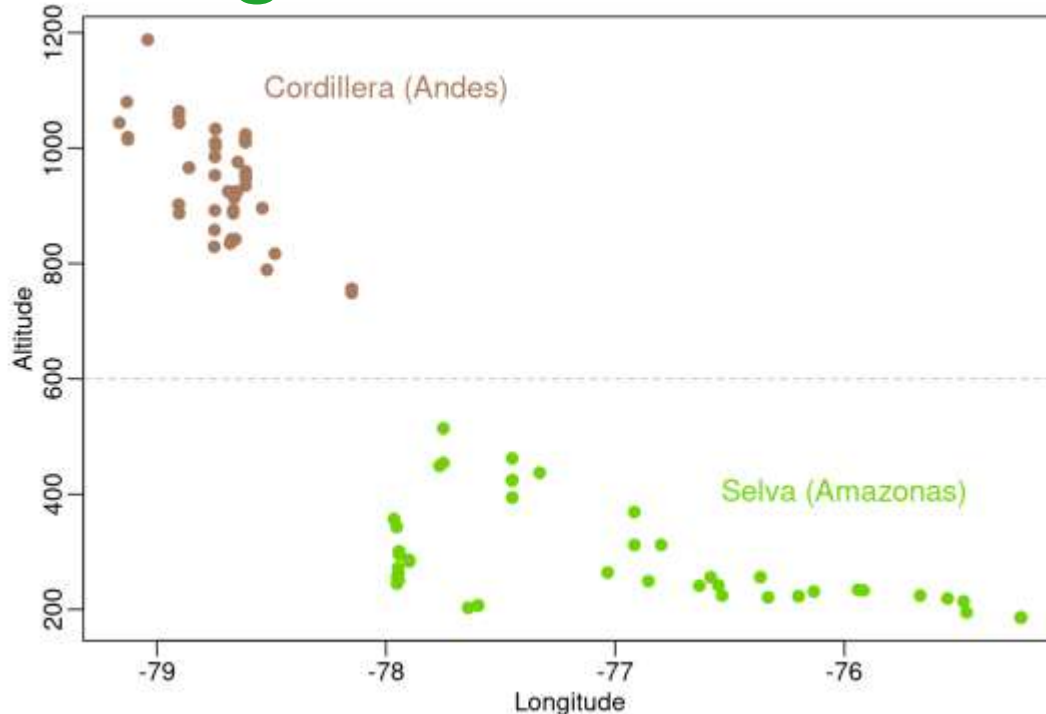
Fick et al 2017



→ **22 climate variables :**

11 linked with temperature, 8 precipitation + Solar radiation + Wind speed + Water vapor pressure

Climate data according to altitude



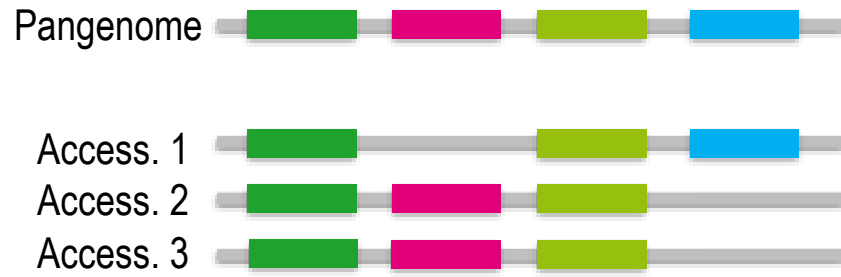
Genomic data

Whole genome shotgun sequencing = Illumina paired-end 150 nt,
Mean sequencing depth \approx 50 X/accession

Pan-genome reconstruction

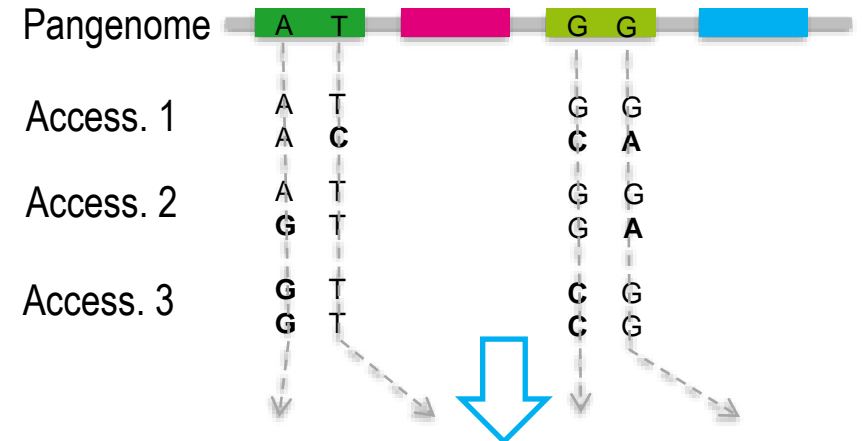
→ cf poster Argout et al S1.29

Gene Presence-Absence Variation (PAV)



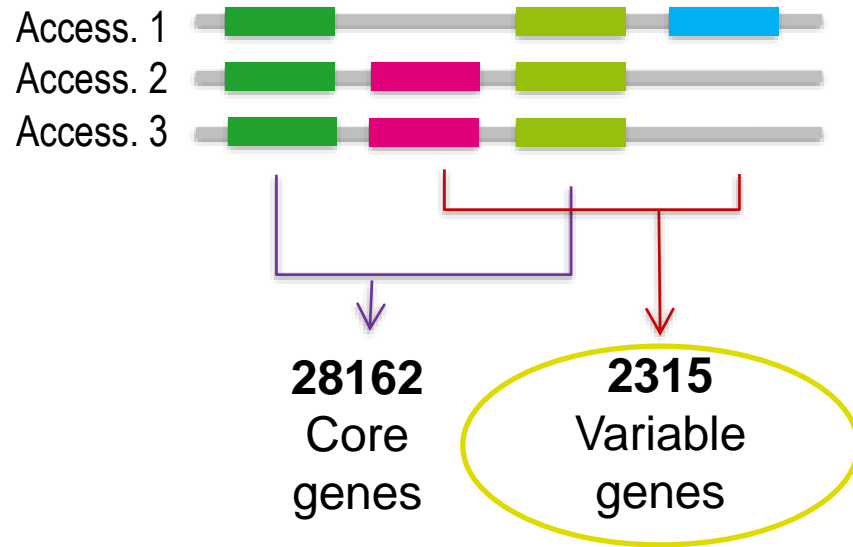
	Gene1	Gene2	Gene3	Gene4
Access. 1	1	0	1	1
Access. 2	1	1	1	0
Access. 3	1	1	1	0

Single Nucleotide Variation (SNP)

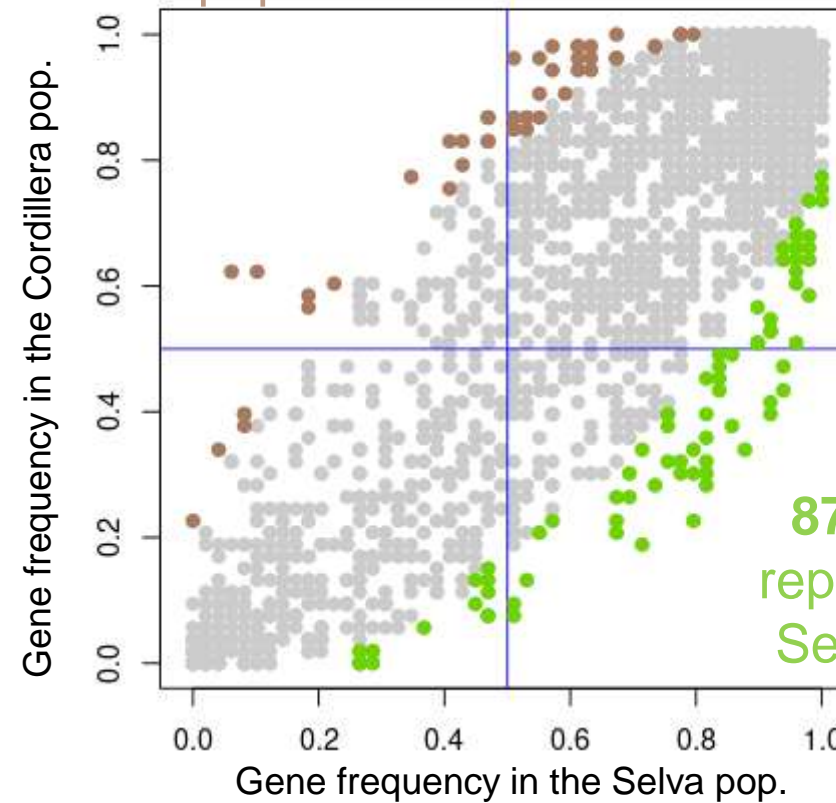


	SNP1	SNP2	SNP3	SNP4
Access. 1	AA	TC	GG	GA
Access. 2	AG	TT	GC	GA
Access. 3	GG	TT	CC	GG

Genomic variation : PAV



47 genes over-represented in the Cordillera population



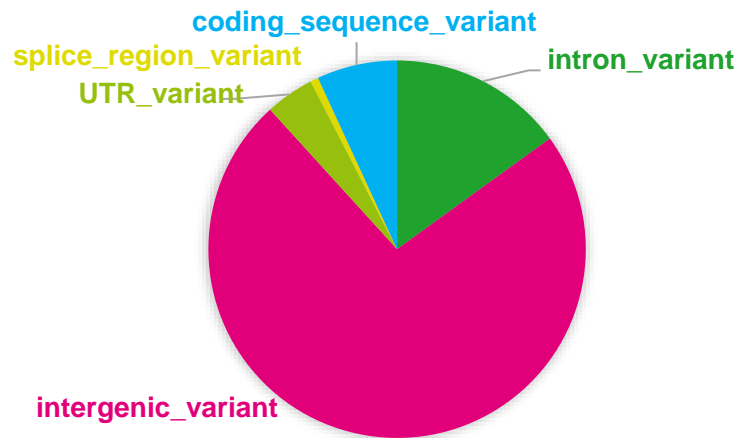
87 genes over-represented in the Selva population

Fisher exact tests, $qVal < 5\%$

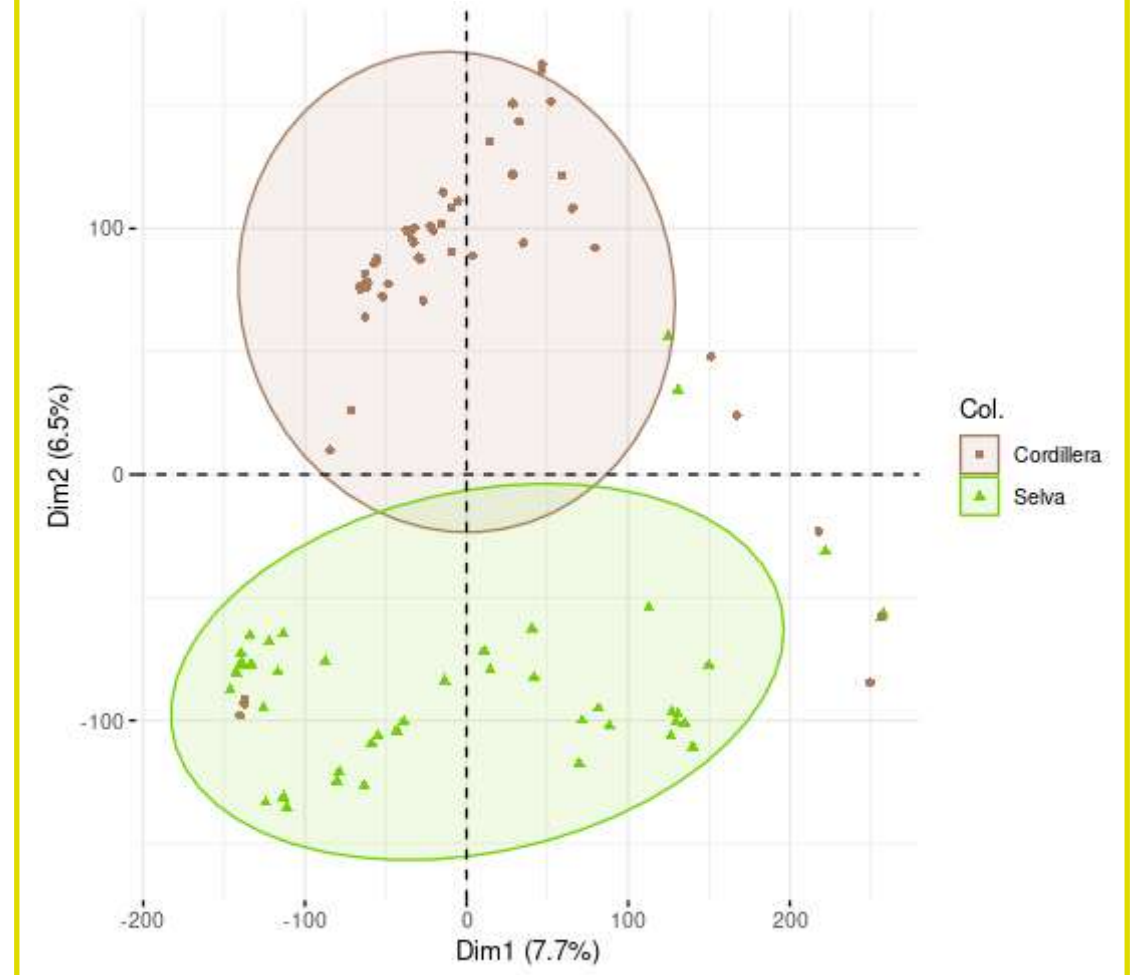
Genomic variation : SNP

Pangenome	A	T	G	G
Access. 1	A	T	G	G
	A	C	C	A
Access. 2	A	T	G	G
	G	T	G	A
Access. 3	G	T	C	G
	G	T	C	G

→ 3 882 106 SNPs (without missing data)

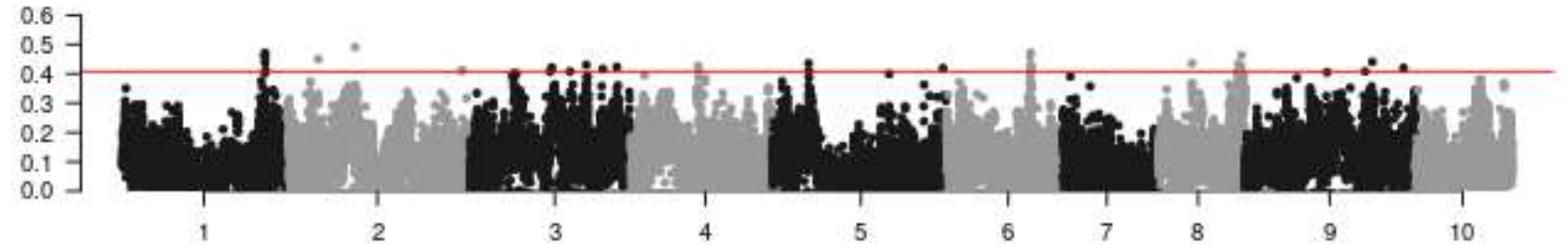


PCA from SNPs data :

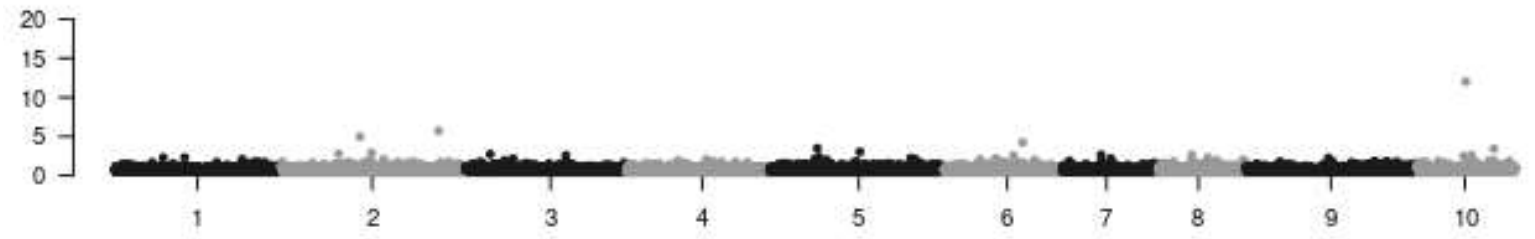


Genomic signatures of selection

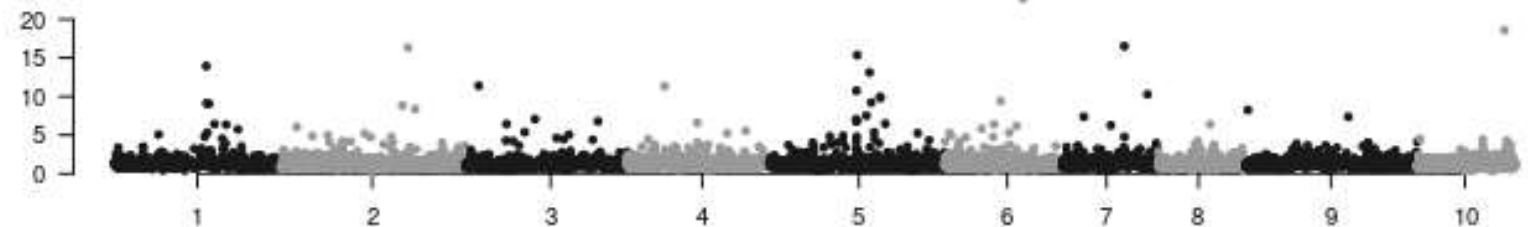
Genetic differentiation, F_{ST}
Selva vs. Cordillera



π ratio
Cordillera / Selva



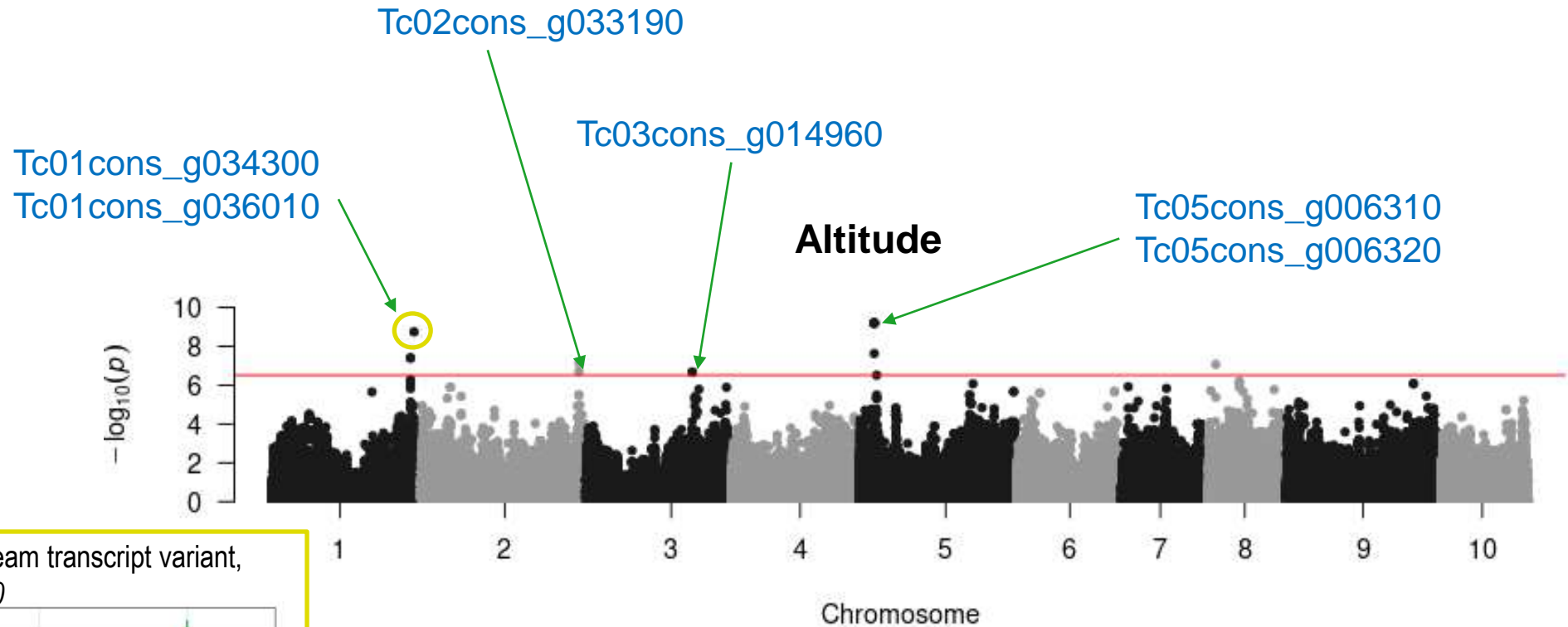
π ratio
Selva / Cordillera



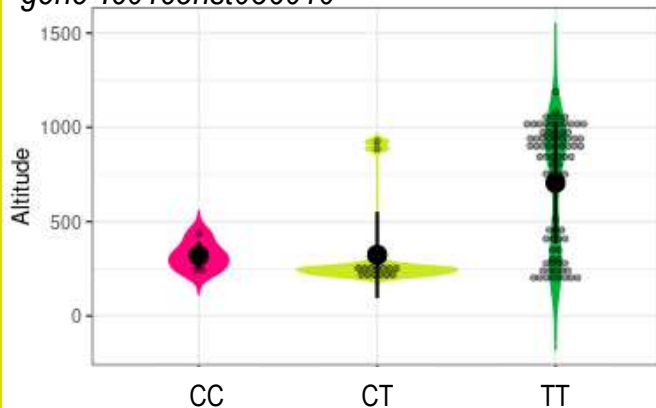
Genomic – Environment association

LFMM (package LEA) : GEA method accounting for population structure

$K=6$, $MAF > 5\%$



Chr1:34456620 Upstream transcript variant,
gene *Tc01const036010*



➔ Identification of candidate genes linked to climate variables

Conclusion

- Evidence of **genomic signatures of local adaptation** to altitude and climate in populations of cacao trees growing in highly contrasted environments
- Identification of candidate genes potentially involved in adaptation

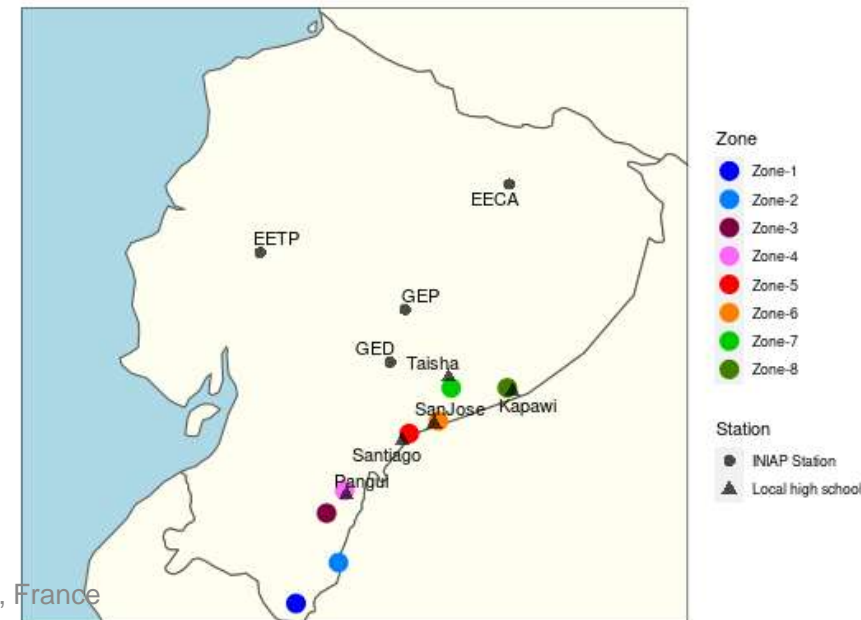
- **Perspectives:**
 - ➔ Consider genetic adaptation to other important environmental variables : soil/pathogens
 - ➔ Use genomic/climate association to assess the vulnerability of cacao production to future climate

Recommendations to farmers & to the ISCR community



- Farmers need **access to varieties adapted to the environmental conditions of their plantations**
- The whole community must **better characterize and preserve adaptive genetic diversity** to face future environmental changes
- We need to promote ***ex-situ*** (experimental stations) and ***in-situ*** (involving farmers, local communities...) **conservation initiatives**

→ cf poster *Fouet et al S2.3*



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benedicte.rhone@cirad.fr