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# Conservation and usage of chestnut diversity : a case study of partnership research

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## Introduction

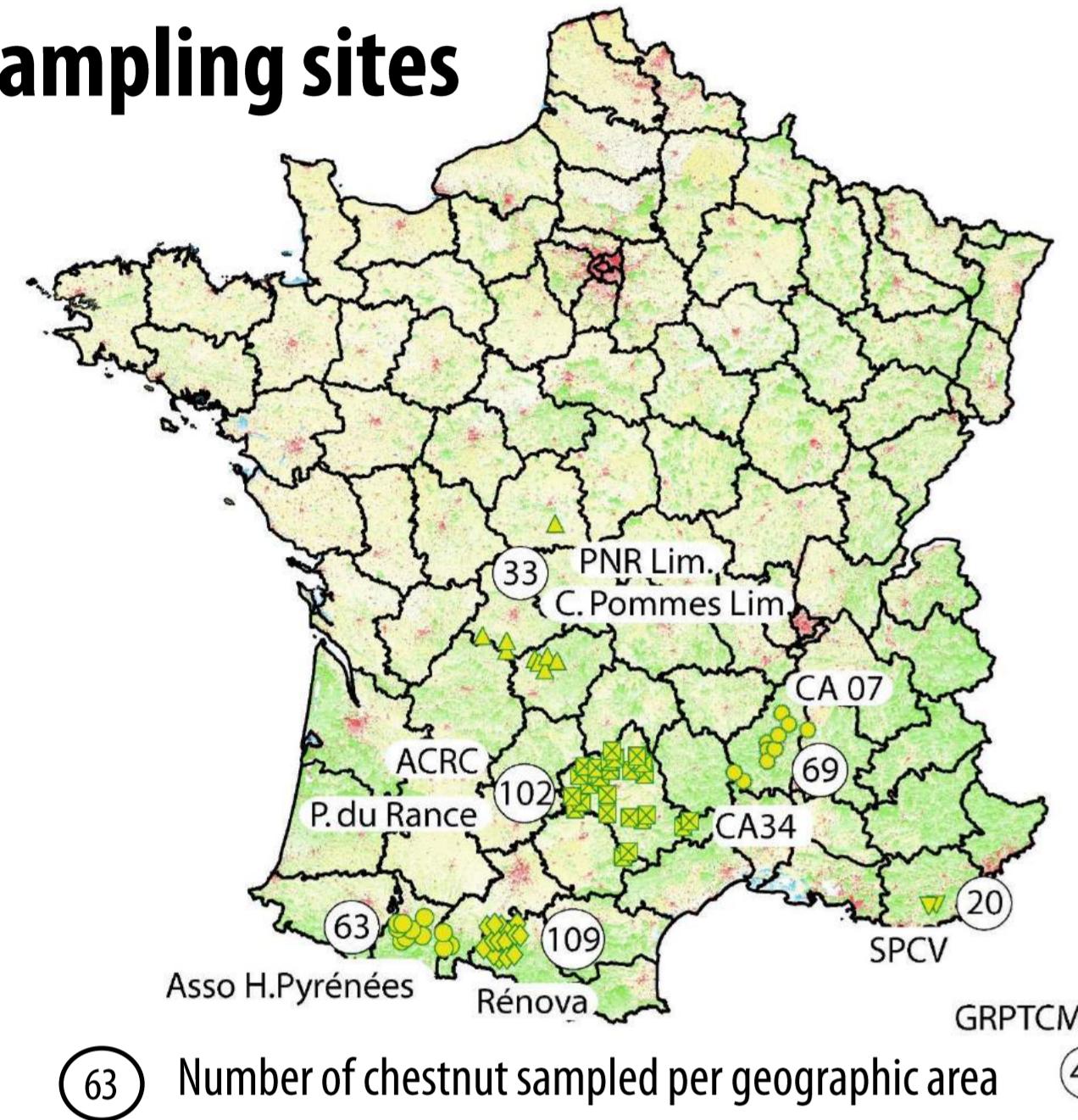
- Management practices of agrobiodiversity (informal plant and know-how exchanges) might play a crucial role in its *in-situ* conservation (Calvet-Mir et al., 2012) but should be further studied for underutilized crops in western countries and for perennials plants overlooked by research funding and whose cultivation fell into disuse.
- Partnerships with local associations is necessary to access local chestnut diversity and knowledge.
- Considering together the social and biological aspects embedded in the diversity of an underutilized fruit tree species is crucial.

## What is the role of amateurs' practices and views on the conservation of chestnut diversity ?

- What is the cultivated chestnut diversity in France ?  See results
- What are the practices and views of amateurs on chestnut diversity ?
- How practices and views of amateurs influence chestnut diversity ?

## Material and methods

### Sampling sites



### Genetic analysis

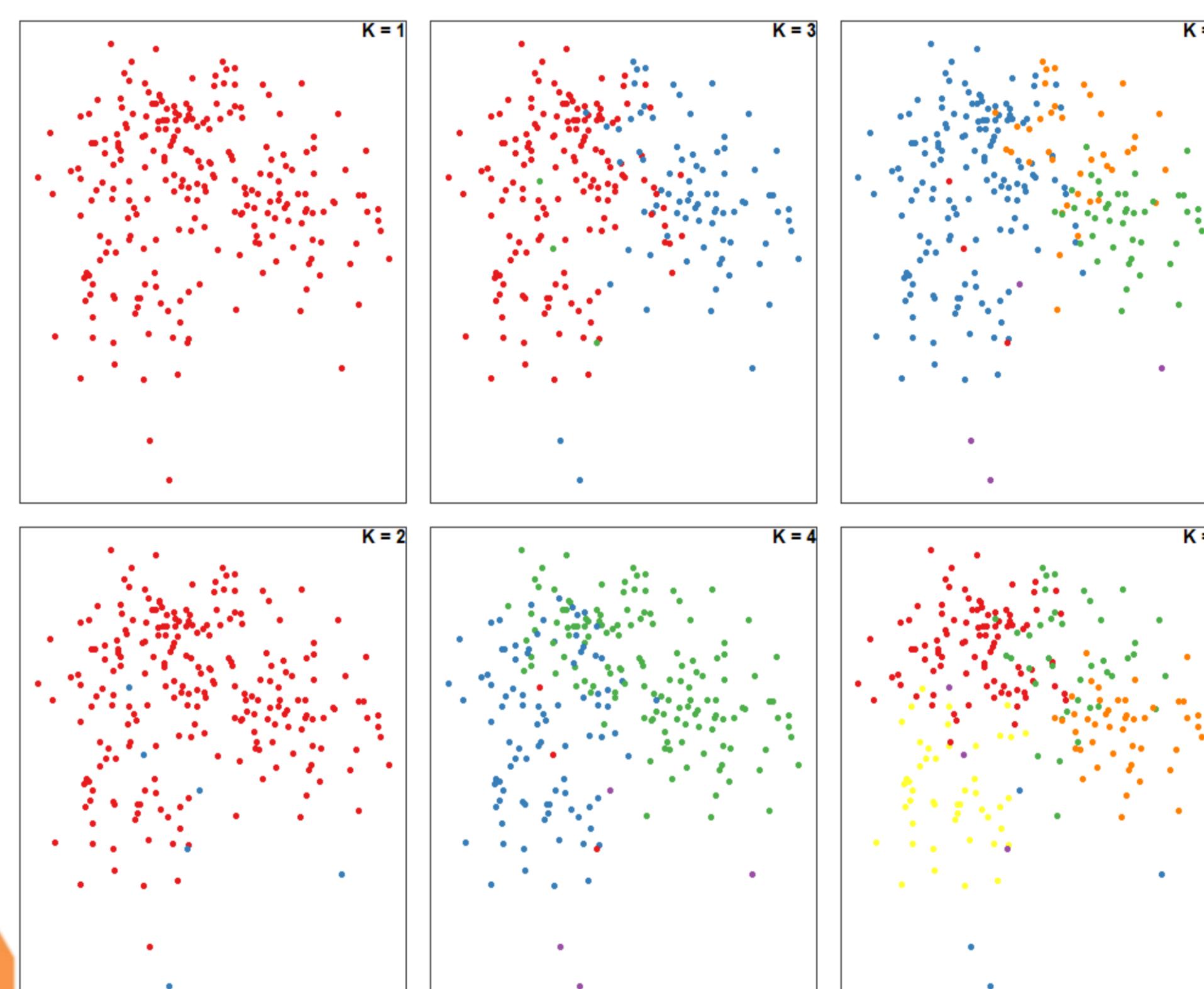
- 450 cultivated chestnut genotyped with 13 or 24 SSRs, 10 partners organisations.
- 238 unique genotypes of cultivated chestnut at 24 SSRs → Only analysis of this dataset are presented



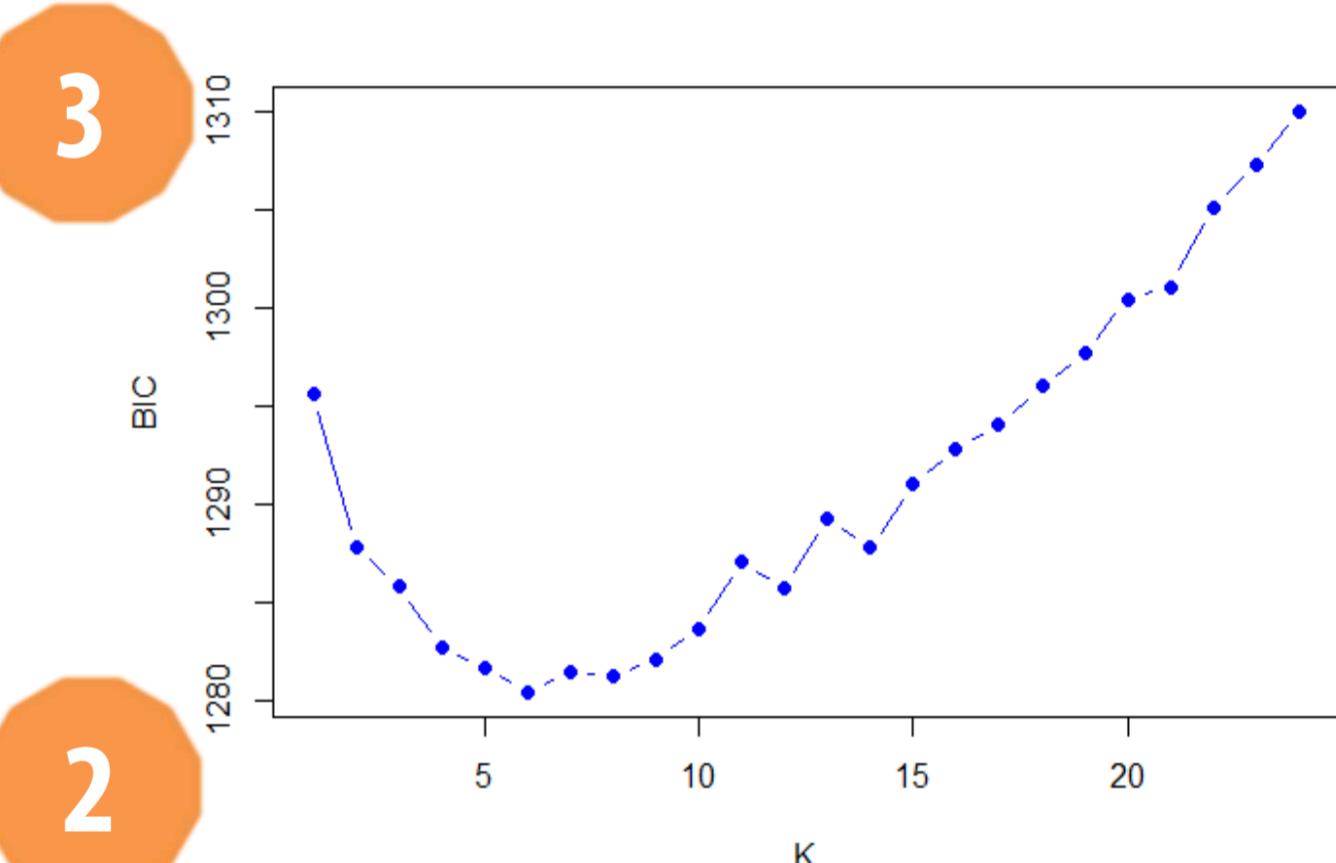
### Workshops and interviews

- 3 days of workshops and visits in 2016
- ≈20 prospective interviews.
- Discussions about the outcomes of genetics analysis and field work in 2019

## Results



Sample sites	Clusters						Sum
	1	2	3	4	5	6	
Haute-Pyrénées	2	2	0	0	0	28	32
Limousin	44	0	0	0	0	0	44
Ariège	18	1	1	1	0	19	40
Aveyron	29	0	0	2	1	0	32
Corsica	0	0	40	0	0	0	40
Ardeche	3	1	0	0	46	0	50
<b>Sum</b>	<b>96</b>	<b>4</b>	<b>41</b>	<b>3</b>	<b>47</b>	<b>47</b>	<b>238</b>



### Cultivated chestnut is quite diverse in France

- Total number of alleles : 227 ,
- Number of alleles by population varies from 128 to 157
- Mean alleles /loci : 10.4

Consistent with comparable studies (for example see Pereira-Lorenzo et al., 2017)

### Slight heterozygote deficit expected from a crop mainly propagated by grafting

- Hobs = 0.64 / Hexp = 0.72

### Weak structure cultivated chestnut populations in France

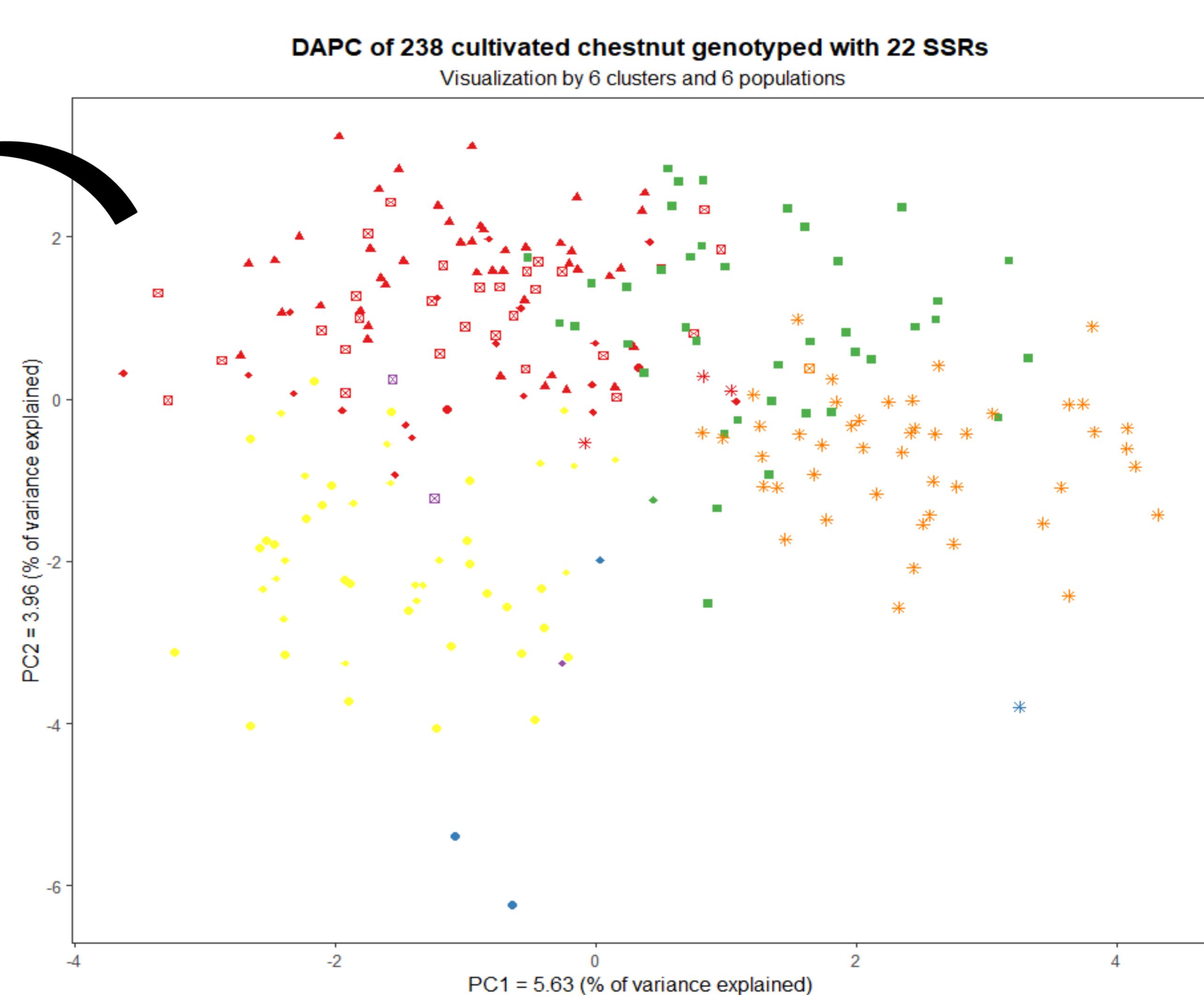
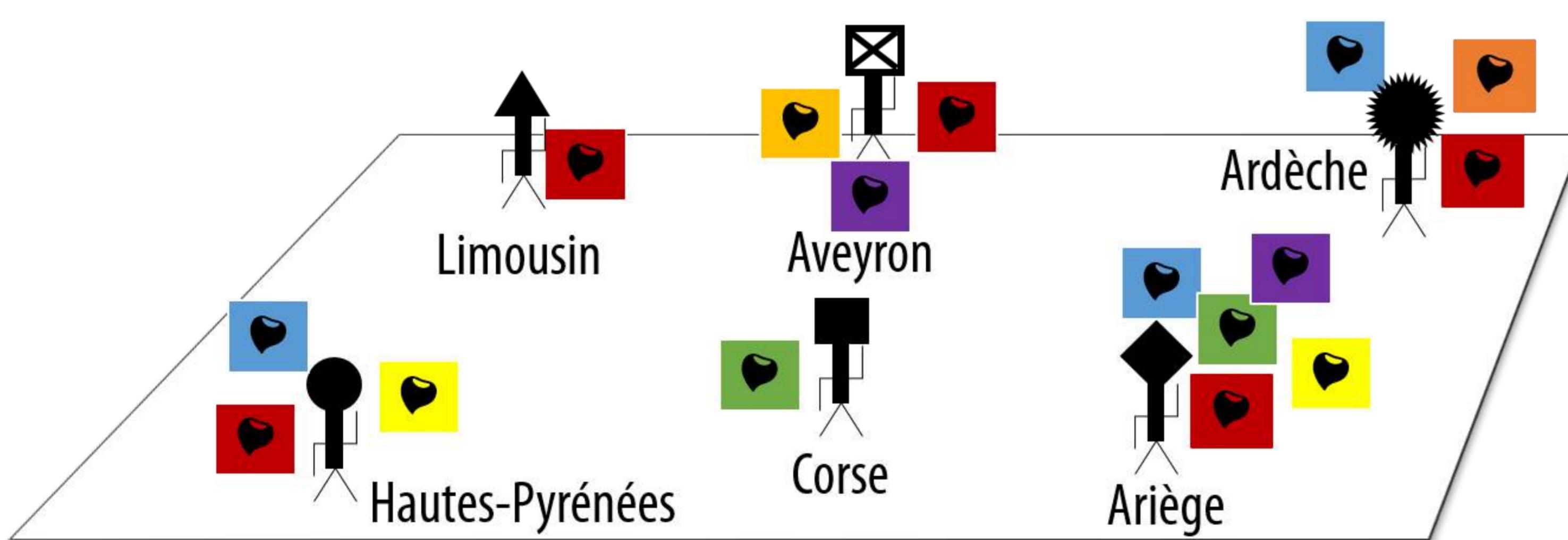
- Total Fst = 0.08

- 0.04 ≤ Fst among loci ≤ 0.15

Consistent with comparable studies (for example see Lusini et al., 2014)

### No clear clustering from SSR analysis (see ① and ②)

### Most sampled sites have genotypes belonging to different clusters (see ③ and ④)



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## Discussion

- Is local chestnut from here ?
- Is chestnut diversity and heritage only genetics ?
- Are genotypes found in different sampling sites the best performing or just the preferred ones? For which reasons ?

## References

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