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

Cathy Bouffartigue, Timothée Flutre, Nathalie Couix, Teresa Barreneche, Luc Harvengt, Laurent Hazard

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Introduction

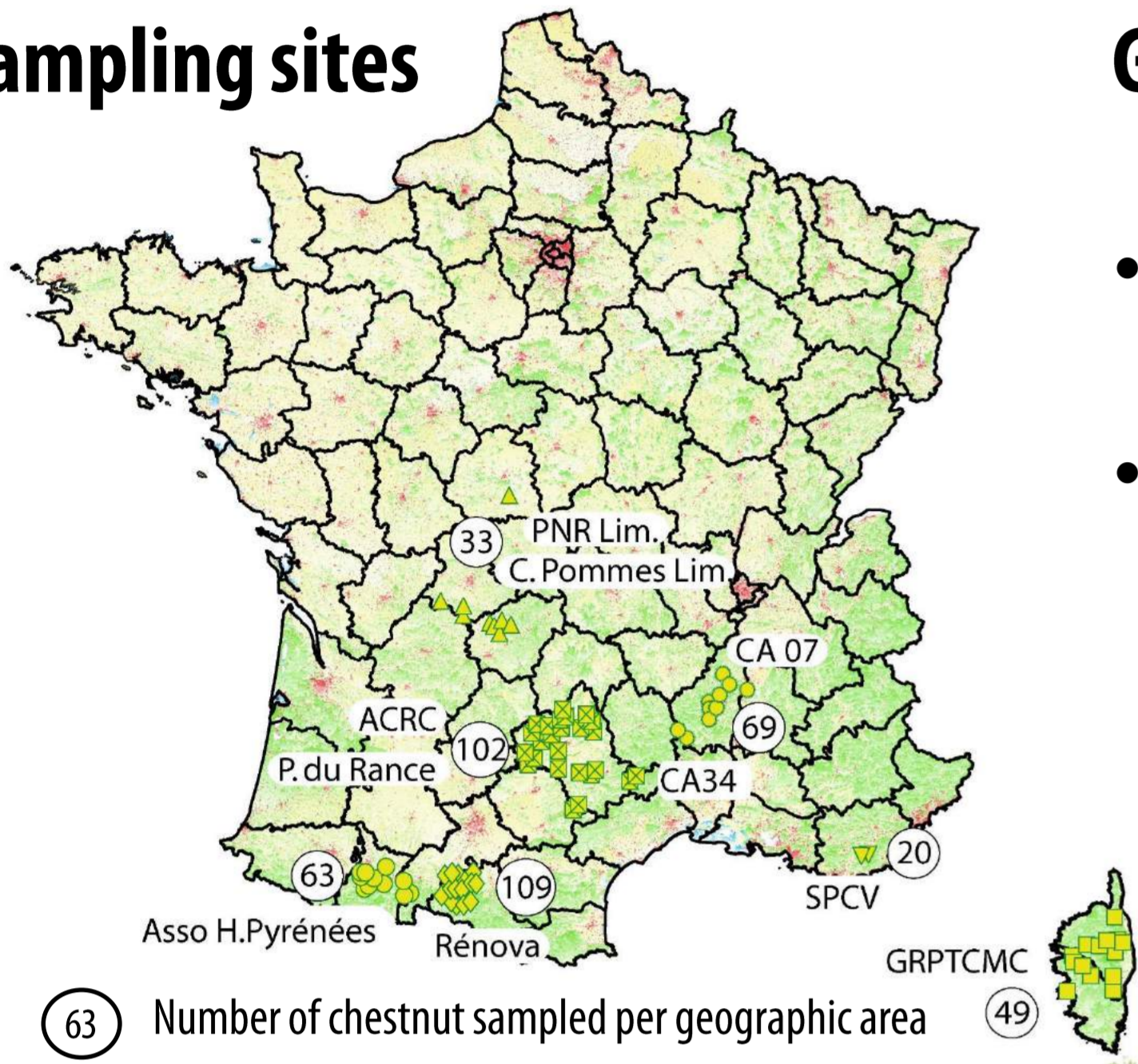
- Management practices of agrobiodiversity (informal plant and know-how exchanges) might play a crucial role in its *in-situ* conservation (Calvet-Mir et al., 2012) but should be further studied for underutilized crops in western countries and for perennials plants overlooked by research funding and 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

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 heterozygotie deficit expected from a crop mainly propagated by grafting

- Hobs = 0.64 / Hexp = 0.72

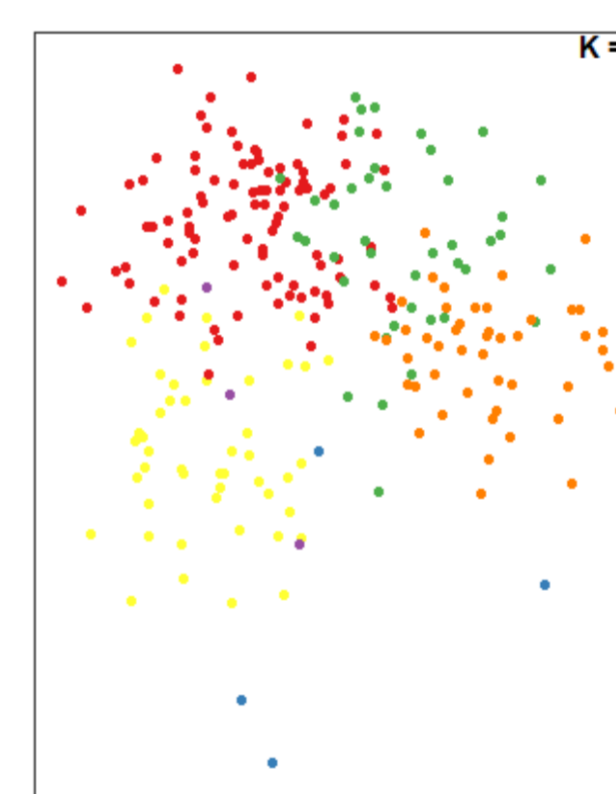
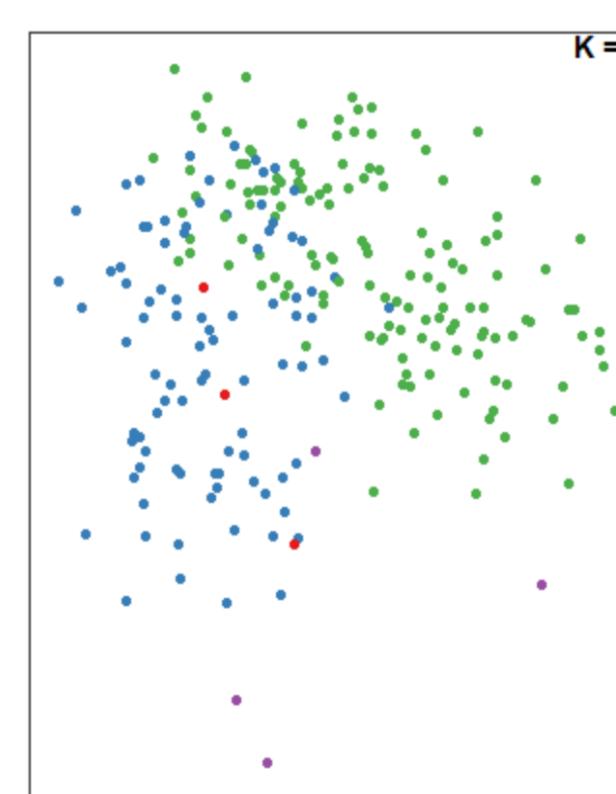
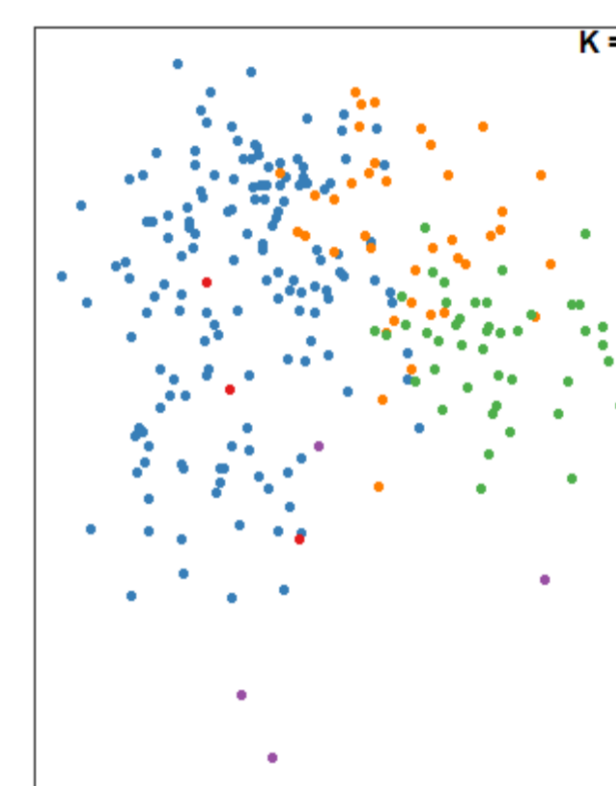
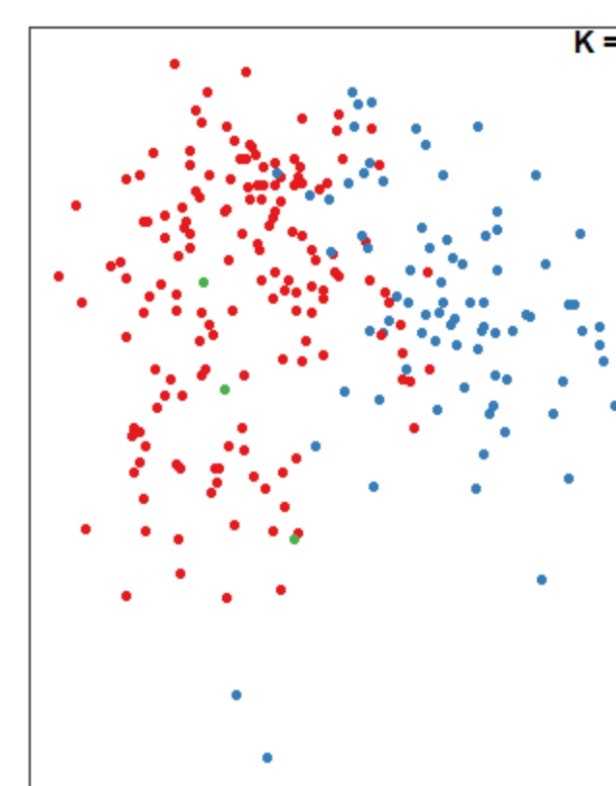
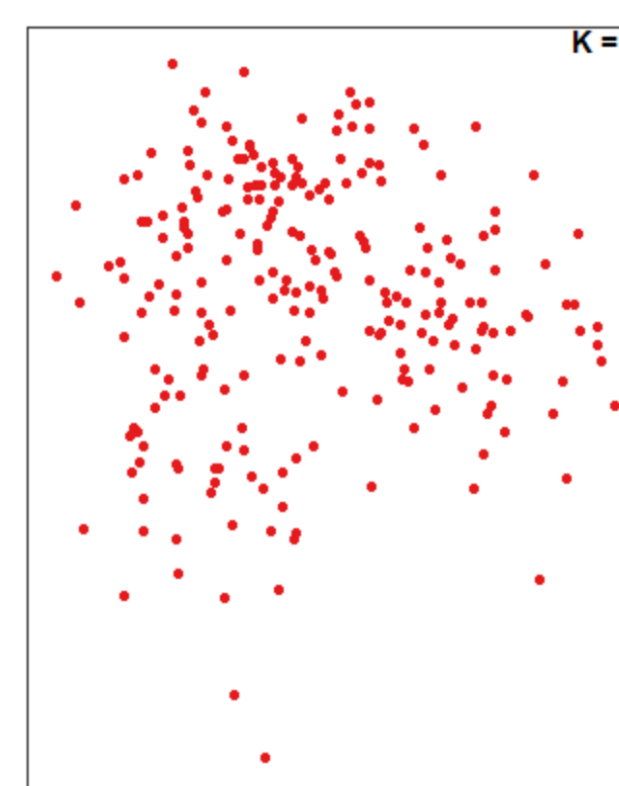
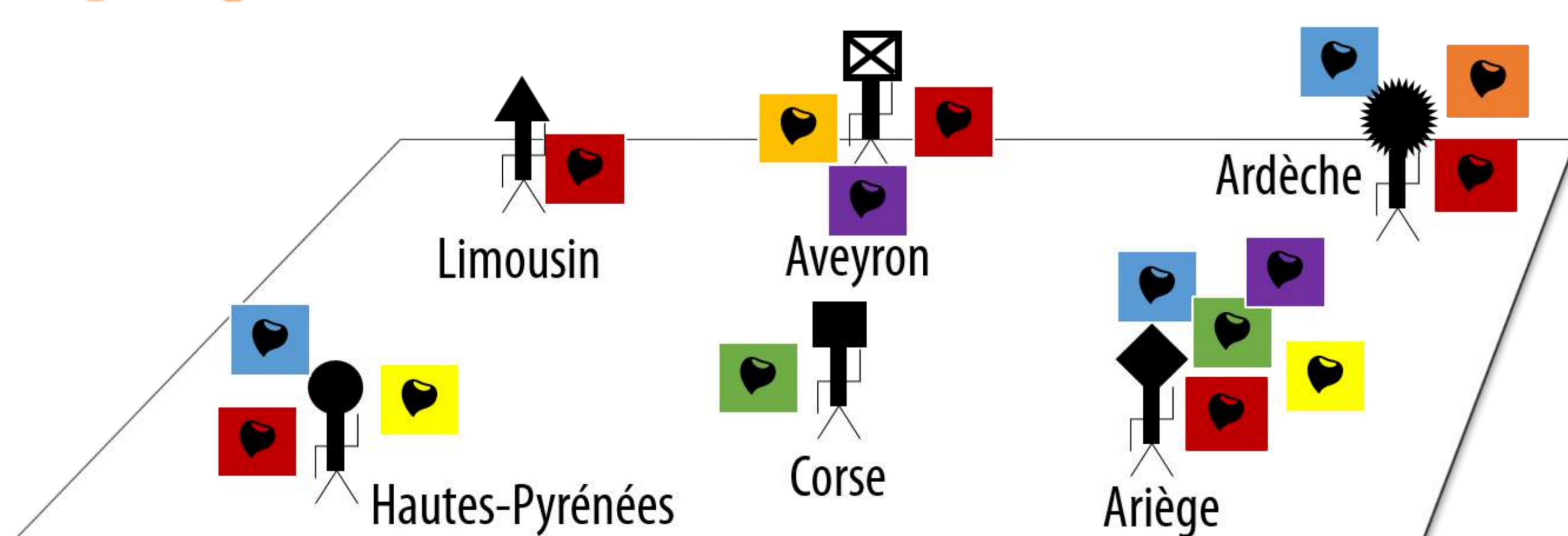
Weak structure cultivated chestnut populations in France

- Total Fst = 0.08
- $0.04 \leq F_{st} \text{ among loci} \leq 0.15$

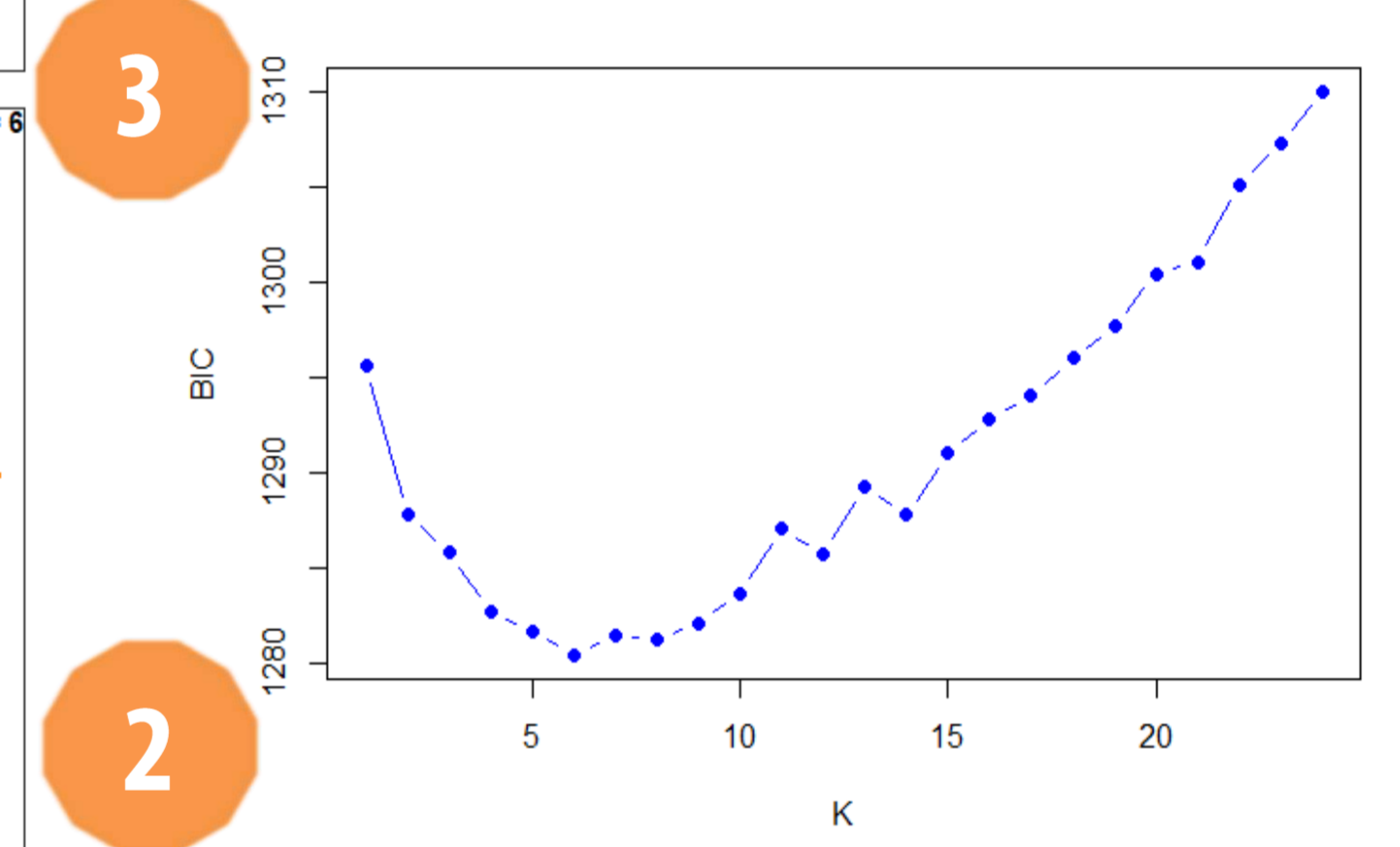
Consistent with comparable studies (for example see Lusini et al., 2014)

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

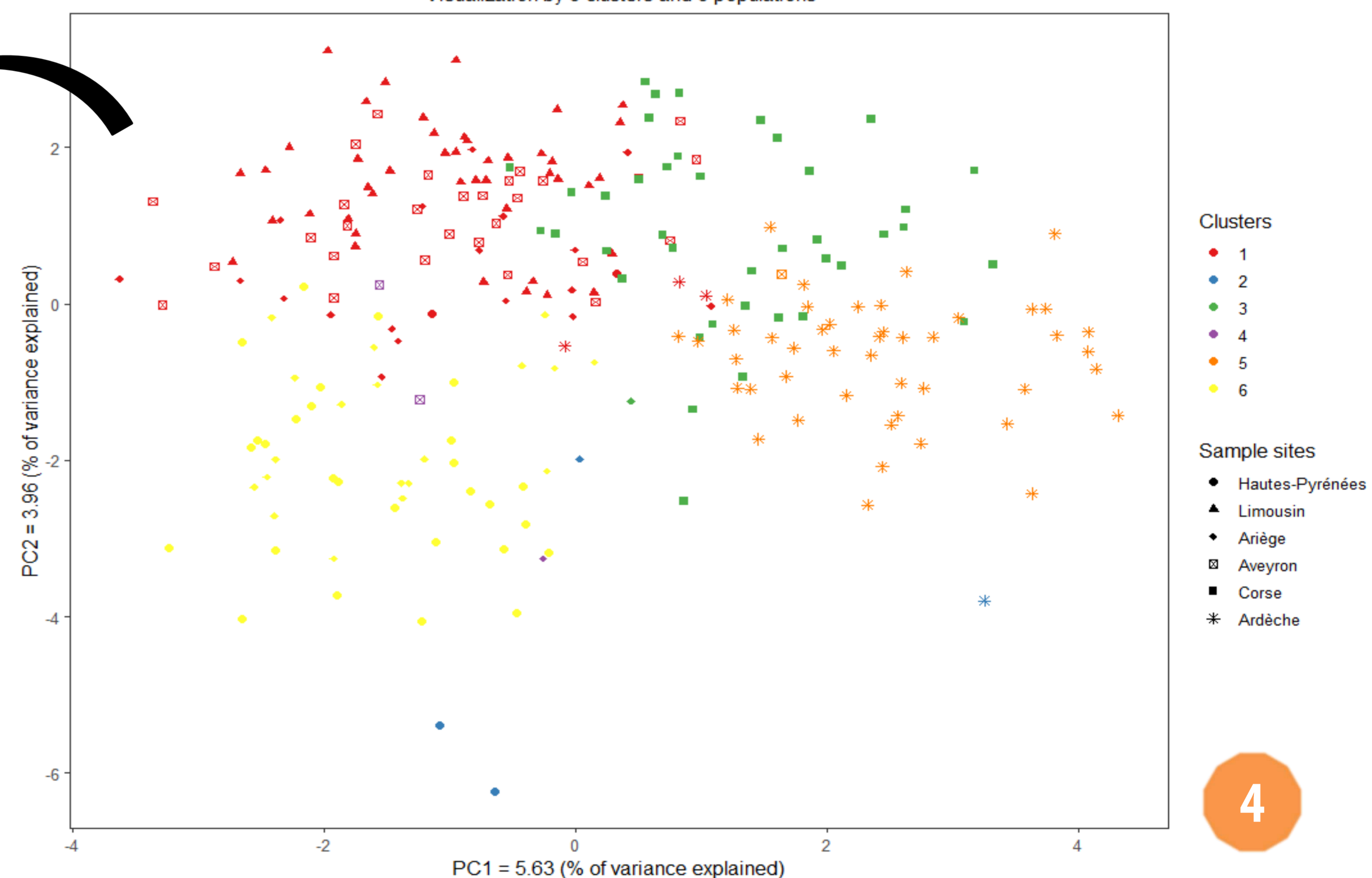
Most sampled sites have genotypes belonging to different clusters (see 3 and 4)



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
Ardèche	3	1	0	0	46	0	50
Sum	96	4	41	3	47	47	238



DAPC of 238 cultivated chestnut genotyped with 22 SSRs
Visualization by 6 clusters and 6 populations



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 ?

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