#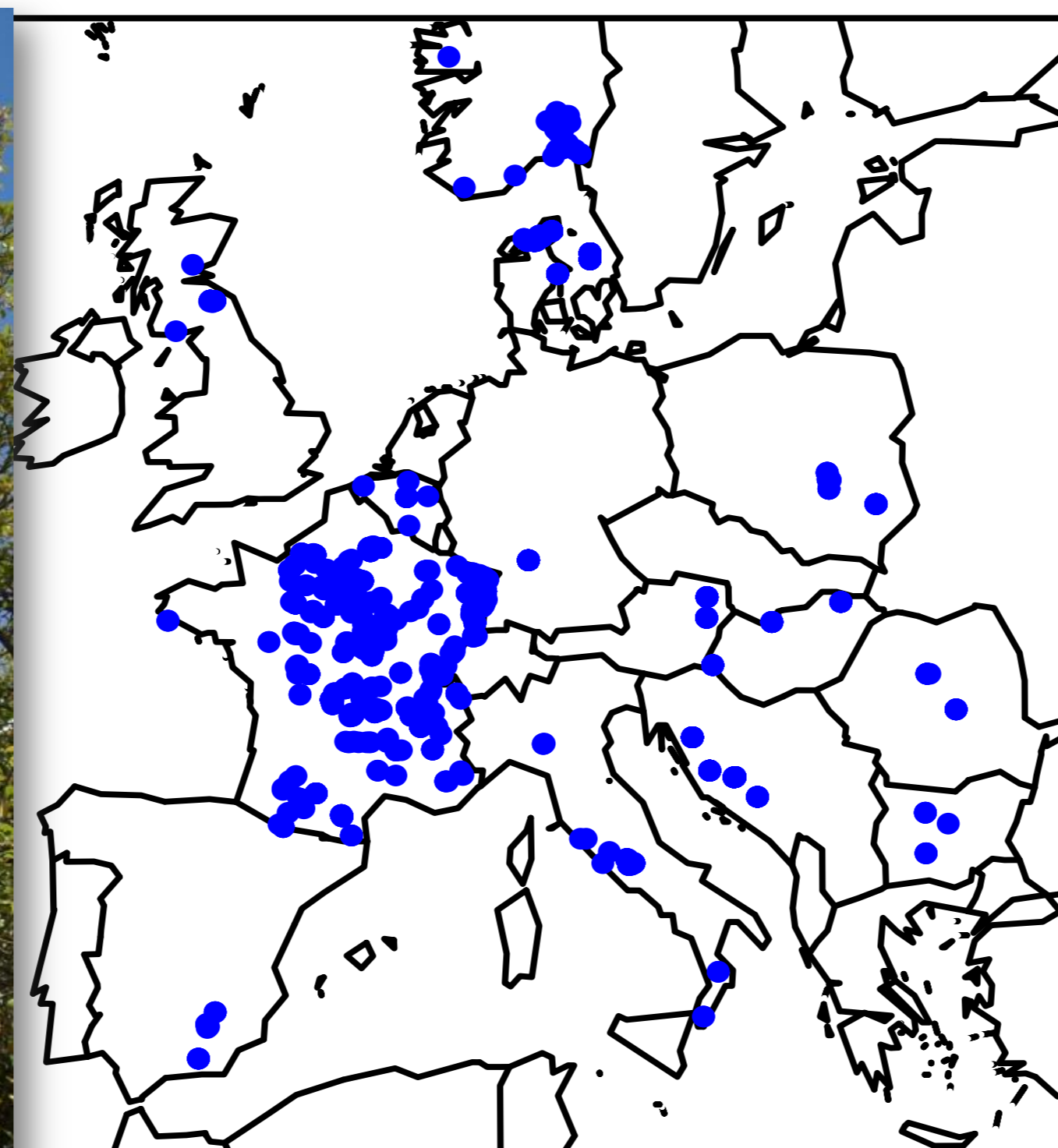 Crop-to-wild gene flow influenced by human activities: insights from the cultivated apple and its wild European relative
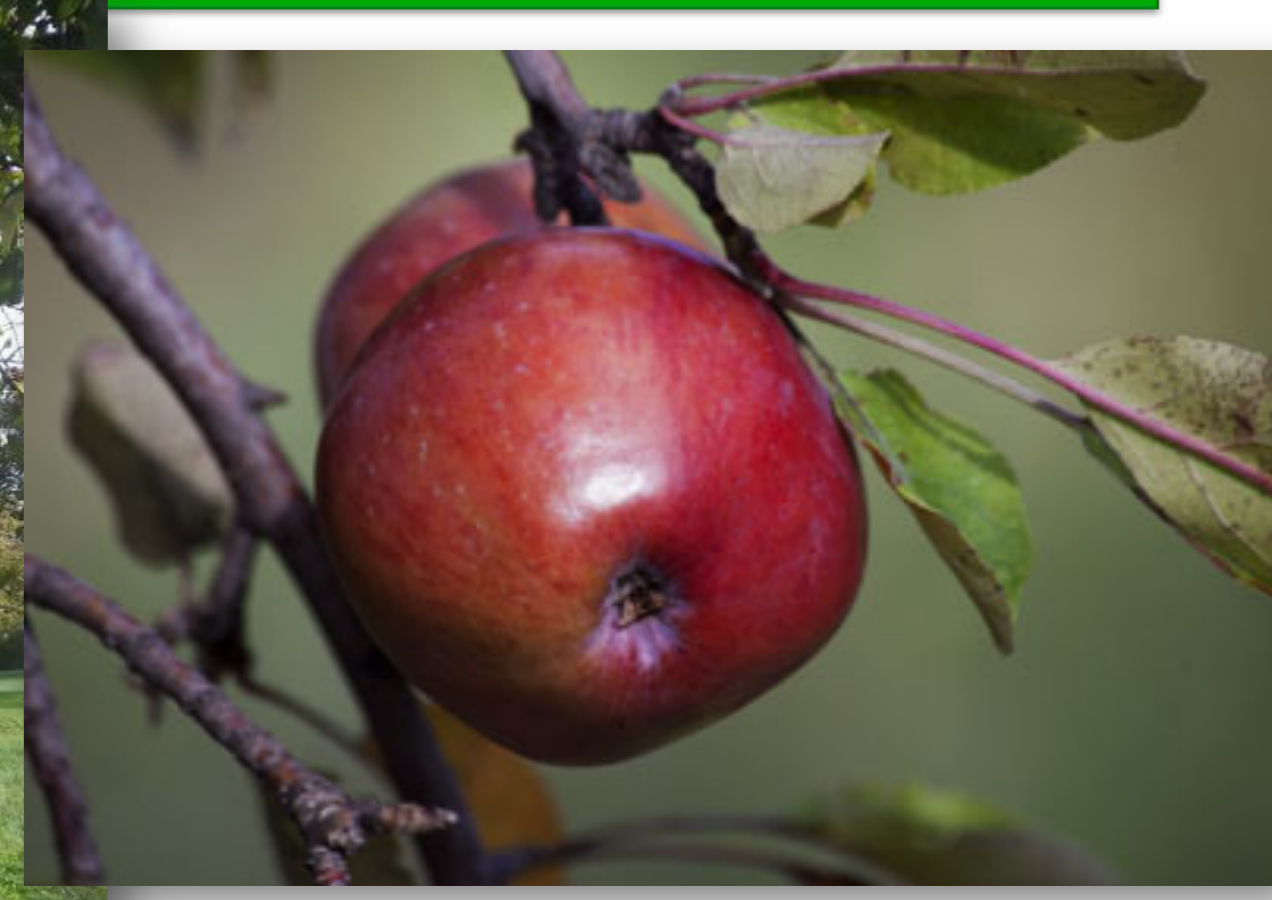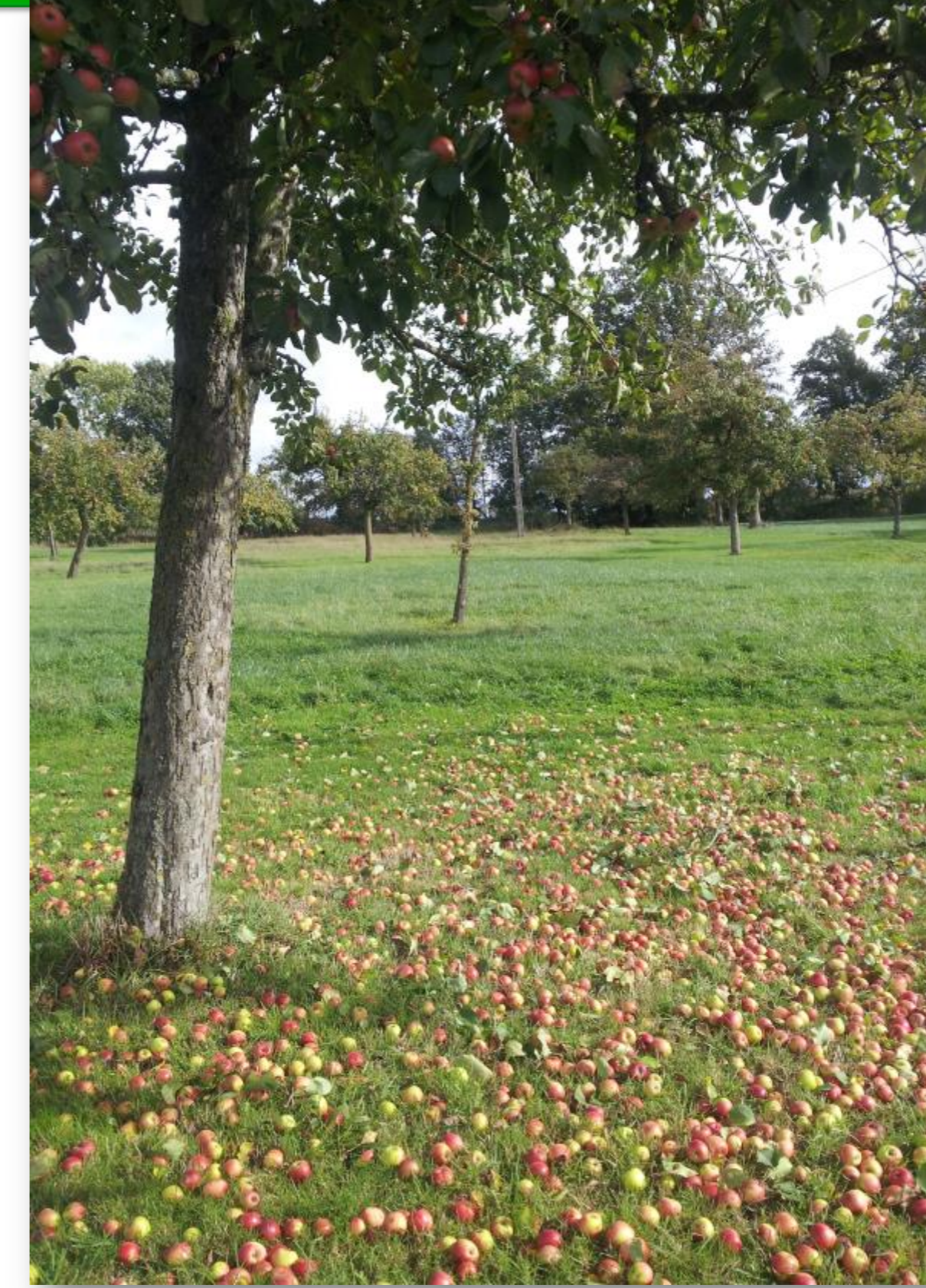
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UNIVERSITÉ PARIS SUD — Comprendre le monde, construire l'avenir®
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Laboratoire Écologie Systématique et Évolution UMR8079

UMR Génétique Quantitative et Évolution - Le Moulon

IDEEV Institut Diversité, Écologie et Évolution du Vivant
LabEx BASC Biodiversité, Agroécosystèmes, Société, Climat

The European wild apple *Malus sylvestris:* secondary major contributor to the cultivated apple genome

What is the extent of crop-to-wild gene flow?
What are the anthropogenic factors affecting them?

Malus sylvestris, the European crabapple **2228 trees**

26 microsatellites

Malus domestica, the cultivated apple 299 varieties (INRA, USDA)

1. Quantification of introgression rate and number of hybrids in the *M. sylvestris* crabapple, from *M. domestica*

a.

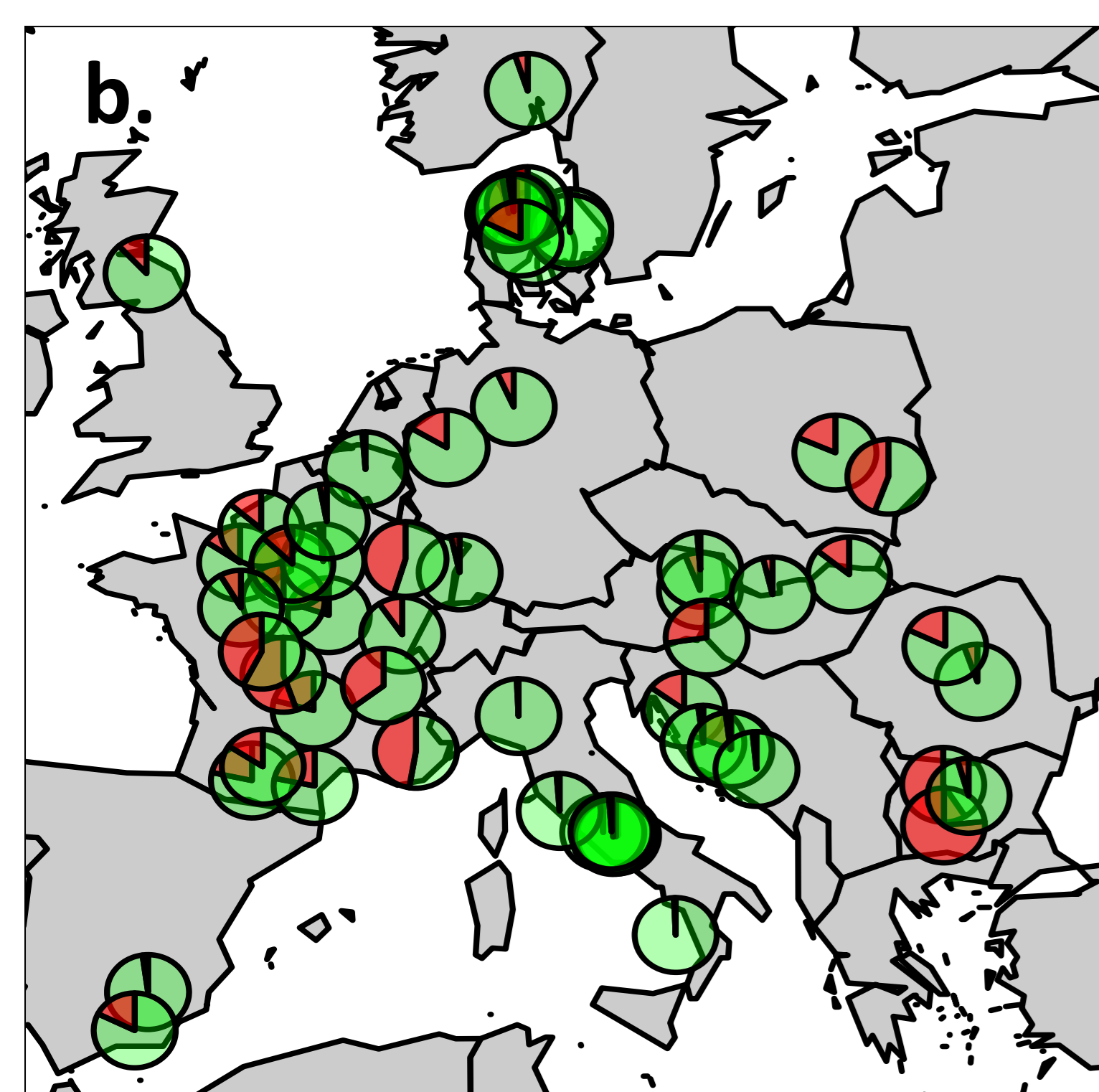**Wild apple** **cultivated apple**

b.

Figure 1. (a) Proportions of ancestry of *M. domestica* genepool (red) into the *M. sylvestis* genepool (green) (STRUCTURE); (b) Map of mean introgression rates (in red) of *M. domestica* into the *M. sylvestris* genepool.

Substantial numbers of hybrids in *M. sylvestris* (23.1%) Spatial variability of introgression rates

2. Direct and indirect anthropogenic factors influencing introgression rates in *M. sylvestris*

a.
Introgression rate
Number of orchards

b.
Number of observations
■ Less cultivated and managed areas
□ Intensively cultivated and managed areas
Araneae Coleoptera Diptera Hemiptera Hymenoptera Lepidoptera ALL
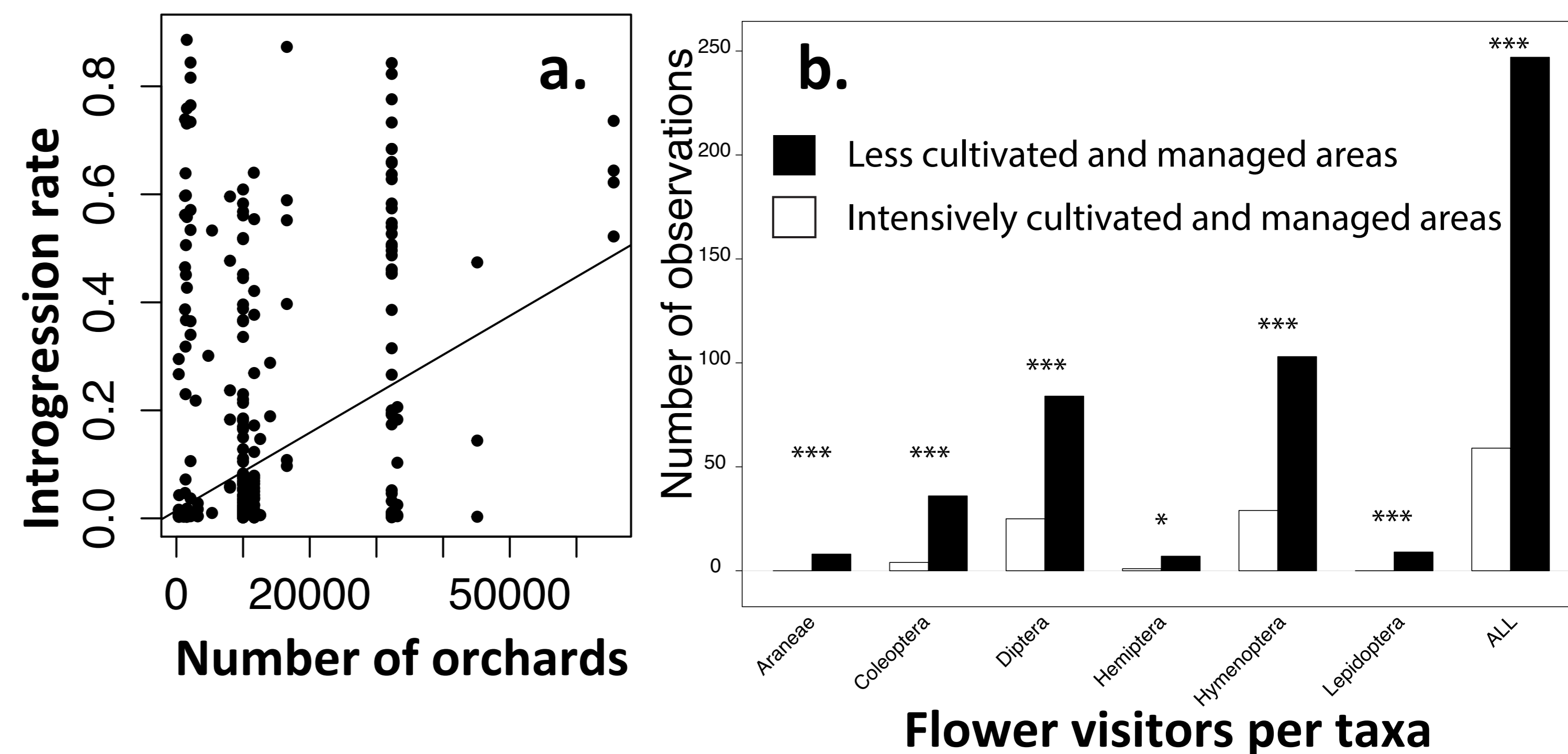**Flower visitors per taxa**

Figure 2. (a) Introgression rates in *M. sylvestris* as a function of the number of orchards in the vicinity (b) Number of observations per order of insect visitors to apple flowers in France, in areas with more intensive (white) and less intensive (black) cultivation and management. **General linear models showed that the number of orchards has a significant effect on introgression rates and that intensity of cultivated and management area decrease apple flower visitors (P<0.001).**

Human activity influence the introgression rate from the cultivated apple to its wild European relative

Next questions :

1-Do the introgressions in *M. domestica* and in *M. sylvestris* occur in particular genomic regions (e.g., coding or non-coding regions, particular genes, near QTL for agronomic traits...)?
→ sequence 10 *M. sylvestris* genomes , to be anaysed with 60 *M. domestica* genomes
2-What is the fitness of hybrids?
→ a) growth of seeds from a forest in greenhouse and genotyping, b) look for selection footprints (positive and negative) around introgressions in genomes
3-Are the trees sold as *M. sylvestris* for reintroduction in agroforestery hybrids?
→ sample trees from nurseries and genotype with microsatellites