

Supplementary Information

Genetic structure of *Malus sylvestris* and potential link with preference/performance by the rosy apple aphid pest *Dysaphis plantaginea*

Denoirjean Thomas¹, Doury Géraldine¹, Cornille Amandine², Chen Xilong², Hance Thierry³, Ameline Arnaud^{1*}.

1. UMR CNRS 7058 EDYSAN (Écologie et Dynamique des Systèmes Anthropisés), Université de Picardie Jules Verne, 33 rue St Leu, F-80039 Amiens Cedex, France.

2. GQE– Le Moulon, INRAE, Univ. Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, 91190, Gif-sur-Yvette, France.

3. Earth and Life Institute, Biodiversity Research Centre, UC Louvain, ELIB – Croix du sud 4–5 bte L7.07.04, 1348 Louvain-la-Neuve, Belgium.

1. Supplementary figure related to the population structure of *Malus domestica* and Danish, French and Romanian *Malus sylvestris* seedlings

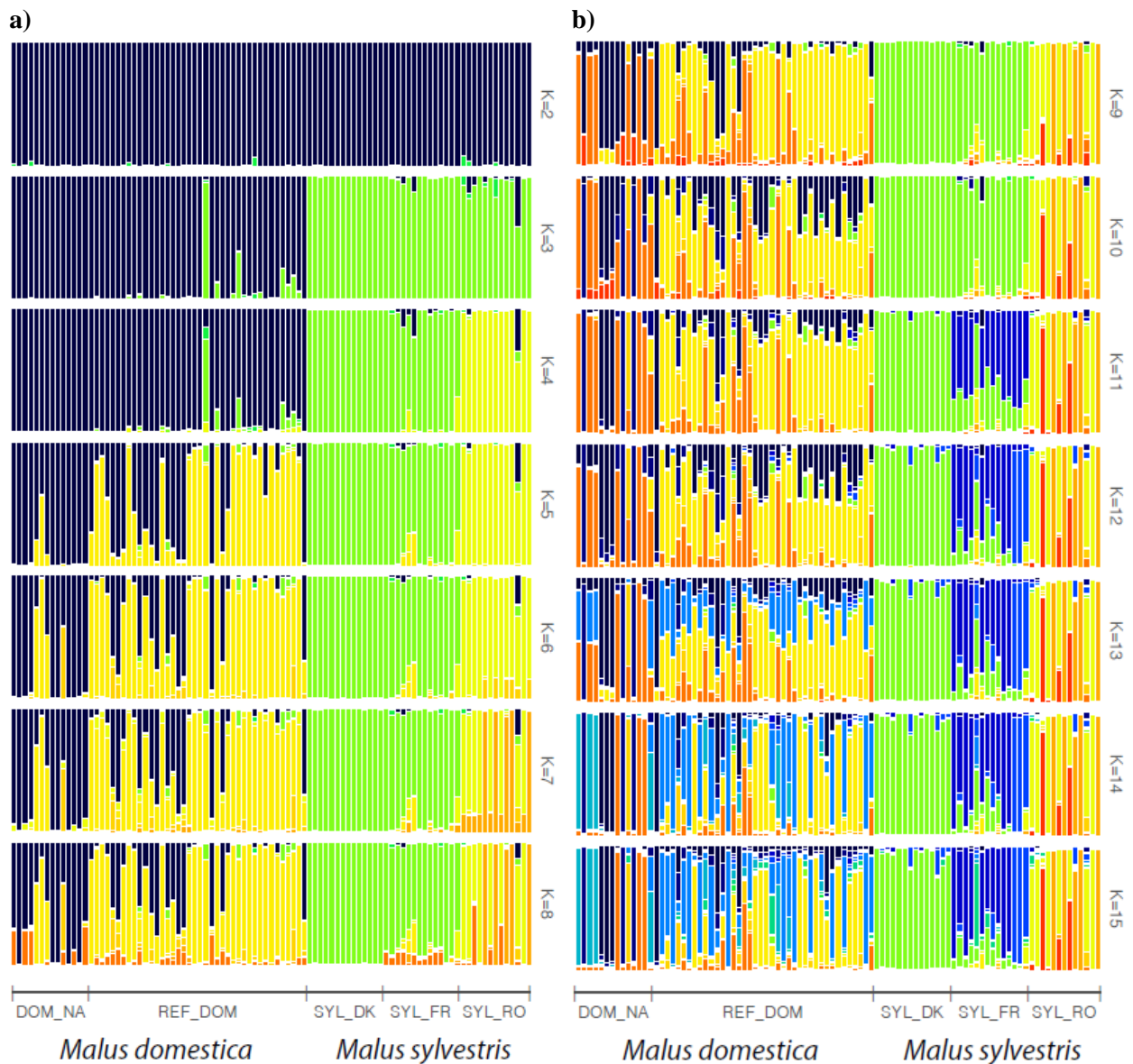


Figure S1. Population structure inferred with STRUCTURE for the Romanian (SYL_RO, $N=13$, one sample could not be genotyped), the French (SYL_FR, $N=14$), the Danish (SYL_DK, $N=14$) *Malus sylvestris* seedlings (green, light blue, yellow, orange colors) and the cultivated *Malus domestica* (dark blue) (DOM_NA, $N=14$, and, REF_DOM, 40 reference *M. domestica*) for a) $K=2$ to $K=8$ and for b) $K=9$ to $K=15$.

2. Supplementary tables related to the genetic diversity and genetic differentiation estimates of *Malus domestica* and Danish, French and Romanian *Malus sylvestris* seedlings

Table S1. Genetic diversity estimates for the three *Malus sylvestris* populations (i.e. individuals assigned to the population with a cumulative membership coefficient of >0.9 to the clusters detected for a group of seedlings from the same geographic origin, i.e. DK, FR, RO) detected with STRUCTURE for $K=14$ (SYL_RO, $N=11$, SYL_DK, $N=12$, SYL_FR, $N=11$) and the cultivated *Malus domestica* (DOM_NA, $N=14$, and, REF_DOM, 40 reference *M. domestica*). *: $0.05 < P\text{-value} < 0.01$; **: $P\text{-value} < 0.001$

Population	Cluster	N	H_O	H_E	F_{IS}
DOM_NA	8 clusters	15	0.737	0.779	0.05
REF_DOM		40	0.813	0.784	-0.04
SYL_DK	1 cluster (green)	12 (2 DK-FR hybrids removed)	0.820	0.801	-0.03
SYL_FR	2 clusters (dark and light blue)	7 (6 samples removed: 3 crop-wild hybrids, and 4 FR-DK wild-wild hybrids)	0.578	0.646	0.11**
SYL_RO	3 clusters (orange, red and yellow)	11 (2 samples removed: 1 crop-wild hybrids, and 1 RO-FR wild-wild hybrid)	0.767	0.784	0.02

N =Number of individuals; H_O : observed heterozygosity; H_E : expected heterozygosity, F_{IS} , inbreeding coefficient, bold values: $P\text{-values} < 0.001$, cluster: cluster(s) detected and used to cumulate membership coefficients for $K=14$ and sort the crop-to-wild hybrids and wild-wild hybrids, total, $N=5$ individuals were removed from the initial dataset (ID).

Table S2. Pairwise F_{ST} (lower diagonal) and Jost's D (upper diagonal) among the three populations (i.e., cluster inferred with STRUCTURE including plants with a membership coefficient of up to 0.90 for the focal cluster, SYL_RO, $N=11$, SYL_DK, $N=2$, SYL_FR, $N=7$) and the cultivated *Malus domestica* (DOM_NA, $N=8$, and, REF_DOM, 40 reference *M. domestica*). All values were significant.

	DOM_NA	REF_DOM	SYL_DA	SYL_FR	SYL_RO
DOM_NA		0.18	0.70	0.57	0.60
REF_DOM	0.05		0.68	0.60	0.52
SYL_DA	0.22	0.20		0.22	0.64
SYL_FR	0.14	0.13	0.08		0.50
SYL_RO	0.11	0.09	0.17	0.09	