

1 **Ecological and evolutionary drivers of phenotypic and genetic variation in the European**
2 **crabapple (*Malus sylvestris* (L.) Mill.), a wild relative of the cultivated apple**

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28 **Abstract (250 words max with bullet points)**

- 29 ● Characterizing the phenotypic and genetic variation among populations of crop wild relatives
30 help understanding the ecological and evolutionary processes involved in population
31 divergence, and better harness their diversity to mitigate the impact of climate change on crops.
32 We assessed genetic and phenotypic diversity of the European crabapple, *Malus sylvestris*, a
33 main contributor to the cultivated apple genome (*Malus domestica*), and investigated for
34 ecological divergence.
- 35 ● We assessed variation in growth rate and traits related to carbon uptake between seedlings
36 measured in a common garden, and related it to the genetic ancestry of the seedlings, assessed
37 using 13 microsatellite loci and Bayesian clustering method. The occurrence of patterns of
38 isolation-by-distance, -by-climate and -by-adaptation that might have caused genetic and
39 phenotypic differentiation among *M. sylvestris* populations was also tested.
- 40 ● Seedlings belonged to seven *M. sylvestris* populations in Europe, with 11.6% of seedlings
41 introgressed by *M. domestica*. Significant trait variation among *M. sylvestris* populations was
42 observed, which for some was of moderate to high heritability. Lack of association between
43 trait and genetic divergence suggests that this significant phenotypic variation is not adaptive,
44 but strong association between genetic variation and the climate during the last glacial
45 maximum suggests local adaptation of *M. sylvestris* to past climates.
- 46 ● This study provides an insight into the ecological and evolutionary drivers of phenotypic and
47 genetic differentiation among populations of a wild apple species and relative of cultivated
48 apples, which is a starting point for future breeding programs.

49 **Keywords:** population structure, isolation-by-distance, isolation-by-ecology, local adaptation,
50 climate change, apple tree, crop wild relatives.

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53 **Societal impact Statement (113 words needs to be reduced to 100)**

54 Apple is a major fruit crop worldwide and a model species for understanding the evolutionary
55 processes underlying perennial crop domestication. Several wild species have contributed to the
56 genetic make-up of the cultivated apple, yet phenotypic and genetic diversity data across their
57 natural distribution is lacking. This study revealed phenotypic variation between populations of the
58 European crabapple, and showed that both geography, and surprisingly, past but not current climate,
59 shaped its genetic structure. We provide a starting point for harnessing wild apple diversity for
60 apple breeding programs to mitigate the impact of climate change on this perennial crop.

61

62 **Introduction**

63 Knowledge of the spatial phenotypic and genetic variation among populations is essential for
64 understanding the ecological (biotic and abiotic) and evolutionary (gene flow, selection, drift, mutation)
65 processes involved in population divergence and adaptation (Savolainen *et al.*, 2013; Sork, 2018). The
66 global biodiversity crisis, and its consequences on ecosystem health and services, makes investigating
67 these questions, and identifying the taxa most vulnerable to anthropogenic change, all the more relevant
68 (Hoffmann *et al.*, 2021).

69 Plant species distributed across climatic gradients typically experience spatial variation in
70 selection, genetic drift and gene flow, processes that drive genetic and phenotypic divergence among
71 populations (Svenning *et al.*, 2015). Climate influence demography such as population expansion and
72 contraction, the extent of gene flow among populations, and ultimately the extent of genetic divergence
73 among populations (Edwards *et al.*, 2022). For instance, changes in the climate since the last glacial
74 maximum (LGM) 20,000 years ago have driven the genetic composition of the European crabapple and
75 many other tree species (Comes & Kadereit, 1998; Kremer *et al.*, 2002; Pyhäjärvi *et al.*, 2008; Cornille
76 *et al.*, 2013a; Gugger *et al.*, 2013; Riordan *et al.*, 2016; Lander *et al.*, 2021; Yamada *et al.*, 2021;
77 Parisod, 2021). Climate can also shape phenotypic variation among populations. Populations occurring
78 under the same climate may share physiological tolerances to climatic conditions, including plant
79 carbon uptake via photosynthesis. Carbon uptake traits condition plant size and growth, reproduction
80 and survival under different climatic conditions (Nicotra *et al.*, 2010; Hartmann *et al.*, 2020). In some
81 cases, local climate can impose divergent selection on carbon uptake traits and lead to long-term
82 reduction in gene flow among populations and local adaptation (Keller *et al.*, 2011; Franks *et al.*, 2014;
83 Aitken & Bemmels, 2015; Ramírez-Valiente *et al.*, 2017; Alexandre *et al.*, 2020). Whether the
84 phenotypic variation observed in species distributed across large climatic ranges results from their
85 demographic or adaptive history remains an intense topic of investigation (Li *et al.*, 2012; Tiffin &
86 Ross-Ibarra, 2014). Furthermore, investigating this question can help predict how plants may respond
87 to climate change and how species adapt to their environment.

88 There are multiple ways to investigate whether the genetic and phenotypic variation among
89 populations distributed across climatic gradients results from selection, genetic drift and/or gene flow.
90 A first step could be to use a common garden experiment to investigate the genetic basis of phenotypic
91 variation among populations. Indeed, different populations occurring across a climatic gradient may
92 display clinal variation, *i.e.*, differences in a trait that may be the result of plasticity or local genetic
93 adaptation (Savolainen *et al.*, 2013; de Villemereuil *et al.*, 2016). Measuring candidate traits for
94 adaptation to climate, *e.g.*, phenology (Brachi *et al.*, 2013) or traits related to plant carbon uptake
95 (Savolainen *et al.*, 2013; de Villemereuil *et al.*, 2016) in individuals from different populations under
96 the same environmental conditions can help elucidate the genetic basis of phenotypic variation across
97 populations without the confounding effects of the environment. Ideally, common garden should
98 include the main genetic groups across the species' distribution (de Villemereuil *et al.*, 2020). The

99 association of neutral genotypic variation with ecological variation can also be used as evidence of
100 adaptive divergence among populations (Shafer & Wolf, 2013; Wang & Bradburd, 2014). The
101 correlation between neutral genetic differentiation and environmental or phenotypic divergence among
102 populations, independent of geographic distance, referred to as isolation-by-ecology (IBE), is an
103 extension of the isolation-by-distance (IBD hereafter) model (Wright, 1943), and has increasingly used
104 as an indicator of adaptive divergence between populations. In the IBE model, natural selection, which
105 results from several factors including climate, can indirectly increase neutral genetic and phenotypic
106 differentiation between populations by promoting general barriers to gene flow (Nosil *et al.*, 2009;
107 Orsini *et al.*, 2013, p. 201; Shafer & Wolf, 2013; Wang & Bradburd, 2014). The IBE pattern is agnostic
108 with respect to the underlying processes that generated it (Wang & Bradburd, 2014); this pattern can be
109 generated by different processes including natural selection against immigrants, sexual selection against
110 immigrants, reduced hybrid fitness and biased dispersal. Although it can be difficult to map one or more
111 processes to this pattern, testing for the IBE pattern is valuable for better understanding the ways in
112 which natural selection shapes neutral genetic and phenotypic variation. Evidence from common garden
113 experiments and IBE patterns can therefore contribute to understanding how genotypes, phenotypes
114 and the environment interact to ultimately influence population divergence and potentially local
115 adaptation.

116 Fruit trees are a major component of terrestrial ecosystems (Petit & Hampe, 2011) and are
117 grown in managed plantations and orchards to provide a variety of economically important products
118 (Boyd *et al.*, 2013). Recent breeding efforts have involved the repeated use of a limited number of
119 cultivars sources of genetic material leading to a reduction in genetic diversity and the loss of valuable
120 alleles at genes that are not directly targeted by human selection (Myles *et al.*, 2011; Warschefsky &
121 von Wettberg, 2019; Migicovsky *et al.*, 2021). Wild relatives of crop fruit trees (or “CWR” for crop
122 wild relative) harbor phenotypic and genetic diversity that are potentially highly valuable for future
123 breeding programs in the context of climate change (Zhang *et al.*, 2017; Hoban *et al.*, 2018; Hübner &
124 Kantar, 2021). However, rare of the studies which thoroughly investigate the phenotypic variation of
125 CWR of fruit trees in relation to response to climate; most studies so far have focused on forest trees
126 (Kremer & Hipp, 2019). Key traits to study in this context are related to plant carbon uptake. Indeed,
127 climate impacts plant carbon uptake (Aubin *et al.*, 2016), which latter known to impact fruit quality
128 characteristics and production (Demestihias *et al.*, 2017). These questions are urgent as native CWRs
129 can be threatened by crop-to-wild gene flow from nearby domesticated trees (Delplancke *et al.*, 2011;
130 Cornille *et al.*, 2015; Diez *et al.*, 2015; Feurtey *et al.*, 2017; Flowers *et al.*, 2019; Liu *et al.*, 2019).
131 Therefore, the study of the genetic and phenotypic variation among populations of CWR fruit tree
132 species is timely to guide future breeding programs; in addition, it may contribute to our understanding
133 of the evolutionary and ecological drivers of population divergence, including climate.

134 The European crabapple, *Malus sylvestris* (L.) Mill, is a CWR and a major contributor to the
135 cultivated apple genome (Cornille *et al.*, 2012, 2014, 2019; Peace *et al.*, 2019). Substantial crop-to-wild

136 gene flow has been observed across *M. sylvestris* populations in Europe (up to 23.1% of natural
137 populations are introgressed by *M. domestica* (Cornille *et al.*, 2015)). Crop-wild hybrids sampled in a
138 forest in France and grown in controlled conditions showed superior fitness compared to wild seedlings
139 (Feurtey *et al.*, 2017). Population genetics analyses also identified five pure (*i.e.*, not introgressed by
140 *M. domestica*) populations in Scandinavia, western France, eastern France, Eastern Europe and Italy
141 (Cornille *et al.*, 2015). These five populations resulted from past contractions and expansions associated
142 with the LGM (Cornille *et al.*, 2013a, 2015). It remains unclear, however, whether these five
143 populations, distributed across a large area with different climatic conditions, present phenotypic
144 variation that could be the result of local adaptation to past and/or present climates.

145 We investigated the spatial phenotypic and genetic variation among populations of a major wild
146 contributor to the cultivated apple, *M. sylvestris*, to test for adaptive divergence. Variation in plant
147 growth and traits related to carbon uptake was measured in 584 *M. sylvestris* seedlings grown under
148 controlled conditions and genotyped for 13 microsatellite markers. We first assessed the genetic status
149 of each seedling (pure *vs.* crop-wild hybrid). Then, we compared growth traits and traits related to plant
150 carbon uptake among seedlings belonging to different European genetic groups. We also formally tested
151 the impact of geography (IBD) and ecology (IBE tested with phenotypic traits and climate) on genetic
152 variation observed from 13 microsatellite markers. We investigated the following questions: 1) Does
153 growth rate and carbon uptake trait vary between populations of the European crabapple? Are those
154 traits heritable, and thus can population history predict seedling phenotype?; 2) Is there any association
155 between phenotypic variation and genetic variation, taking into account geographic distance?; and 3) Is
156 climate associated with neutral genetic diversity of the European crabapple, which could suggest local
157 adaptation (*i.e.*, ecological/adaptive divergence)?

158

159 **Materials and Methods**

160 **Plant material, experimental design and trait measurements**

161 A total of 584 seeds were collected from 90 *M. sylvestris* mother trees (three to 15 seeds per mother
162 tree, Table S1) from six different geographical regions in Europe: Austria ($N = 89$, two sites), Denmark
163 ($N = 91$, three sites), Spain ($N = 39$, one site), France ($N = 220$, eight sites), Italy ($N = 32$, one site),
164 Romania ($N = 117$, seven sites) (Table S1).

165 In mid-April 2019, the 584 seeds were washed, sterilized (in 0.5% chlorine for 20 min), and
166 vernalized for three months at 4°C in the dark in a mix of damp sand and vermiculite. Then, seeds were
167 sowed in jiffy pellets and each pellet was randomly placed in a 20-hole array. Seeds were grown in
168 controlled conditions for two months (from mid-July to mid-September 2019: 22 ±1°C, 60 ±5 %
169 relative humidity, a 16:8 (L:D) photoperiod and a light level of 40–60 μmol m⁻².s⁻¹). Each 20-hole array
170 was rotated daily in the growth chamber to avoid any micro-environmental variation in plant response,
171 and plants were watered weekly.

172 During the course of the two-month experiment, the number of leaves and the height of each seedling
173 were recorded. Some accessions, due to the low germination rate, could not be recorded (*i.e.*, height
174 and number of leaves could not be recorded for 19 seedlings out of 584, $N = 565$, Table 1). Seedlings
175 were measured every two or three days, starting from day 7-11 after the start of the experiment.

176 The last week of the experiment, the superficial flavonol and chlorophyll content and the nitrogen
177 balance index (NBI) were measured in three leaves per seedling. Superficial chlorophyll content is the
178 concentration of chlorophyll in the leaf epidermis ($\mu\text{g}/\text{cm}^2$), and superficial flavonol content is an index
179 of the flavonoid concentration ($\mu\text{g}/\text{cm}^2$) in this upper layer and is related to phenol accumulation and
180 UV protection. Leaf chlorophyll and flavonol content and NBI are parameters correlated with plant
181 carbon uptake via photosynthesis. Flavonol is a phenolic compound that is also known to contribute to
182 plant resistance, acclimation and adaptation to environmental constraints through various mechanisms,
183 including its antioxidant activity. These traits were measured using a portable Dualex device (Force-A,
184 Orsay, France), which uses a combination of fluorescence signals at various excitation bands to quantify
185 pigments and chemical compounds. As carbon uptake related traits must be measured in the same day,
186 a subsample of 257 seedlings out of the 565 seedlings (Table 1, numbers in brackets) was measured
187 because of time limitation in a day. Seedlings measured for carbon uptake related traits were selected
188 based on two criteria: having at least one seedling per mother tree and three seedlings per geographic
189 site.

190

191 **DNA extraction, microsatellite genotyping and genetic ancestry of the seedlings**

192 At the end of the experiment, leaves of each seedling were sampled for microsatellite genotyping.
193 Genomic DNA was extracted with the NucleoSpin plant DNA extraction kit II (Macherey & Nagel,
194 Düren, Germany) according to the manufacturer's instructions. Microsatellites were amplified by
195 multiplex PCR with the Multiplex PCR Kit (QIAGEN, Inc.). We used 13 microsatellite markers,
196 Ch01f02, Ch01f03, Ch01h01, Ch01h10, Ch02c06, Ch02c09, Ch02c11, Ch02d08, Ch03d07, Ch04c07,
197 Ch05f06, GD12 and Hi02c07 in four multiplexes (MP01 to MP04; (Cornille *et al.*, 2012)).

198 PCR was performed in a final reaction volume of 15 ml (7.5 ml of QIAGEN Multiplex Master Mix,
199 10–20 mM of each primer with the forward primer labelled with a fluorescent dye, and 10 ng of template
200 DNA). We used a touch-down PCR program (initial annealing temperature of 60°C, decreasing by 1°C
201 per cycle down to 55°C). Genotyping was performed at the GENTYANE platform (INRAE Clermont-
202 Ferrand) on an ABI PRISM X3730XL, with 2 ml of GS500LIZ size standard (Applied Biosystems).
203 Alleles were scored with the GENEMAPPER 4.0 software (Applied Biosystems). We retained only
204 multilocus genotypes presenting less than 10% missing data.

205 Clones or closely related individuals can bias inferences of population structure. We estimated the
206 kinship coefficient between pairs of individuals (F_{ij}) with SPAGeDI 1.5d (Loiselle *et al.*, 1995; Hardy
207 & Vekemans, 2002), and removed highly genetically related individuals with $F_{ij} > 0.5$.

208 The individual-based Bayesian clustering method implemented in STRUCTURE 2.3.3 (Pritchard *et*
209 *al.*, 2000) was used to estimate the admixture between *M. domestica* and *M. sylvestris*, and the
210 population genetic structure of *M. sylvestris*. STRUCTURE uses Markov Chain Monte Carlo (MCMC)
211 simulations to infer the proportion of ancestry of genotypes from K distinct clusters. The underlying
212 algorithm attempts to minimize deviations from Hardy–Weinberg and linkage disequilibria. K ranged
213 from 1 to 10. Ten independent runs were carried out for each K and 500,000 MCMC iterations after a
214 burn-in of 50,000 steps were used. CLUMPAK (Greedy algorithm) (Kopelman *et al.*, 2015) was used
215 to identify distinct modes in the 10 replicated runs for each K . STRUCTURE analyses were run for the
216 full dataset ($N = 584$), plus 40 *M. domestica* genotypes included as a reference for the cultivated apple
217 gene pool (Cornille *et al.*, 2013b). The R package pophelper v2.3.0 was used (Francis, 2016) to visualize
218 bar plots. The amount of additional information explained by increasing K was determined using the
219 ΔK statistic (Evanno *et al.*, 2005), as implemented in Structure Harvester (Earl & vonHoldt, 2012).
220 However, ΔK provides statistical support for the strongest but not the finest population structure
221 (Puechmaille, 2016). Natural populations can display a hierarchical genetic structure with fine-scale
222 population structure. Visual inspection of the barplots was used to identify the K value for which all
223 clusters have well assigned individuals, and where additional clusters at higher K values do not have
224 well assigned individuals (indicating that we have reached the highest K value for which no new genuine
225 clusters could be delimited). The K value we therefore considered corresponded to the finest one, which
226 can be higher than the K value of the strongest population structure identified by ΔK .

227 Using the best K value inferred with STRUCTURE, we defined P_{dom} , the membership proportion of
228 a seedling to the *M. domestica* gene pool; membership coefficients were used to define the genetic
229 ancestry of each seedling: 1) seedlings with $P_{dom} > 0.9$, whose mother tree was likely misidentified in
230 the field (referred to as “*dom*” hereafter); 2) seedlings with $P_{dom} > 0.1$, *i.e.*, crop-wild hybrids (referred
231 to as “*cw*” hereafter); then 3) seedlings with a membership coefficient > 0.9 to a given wild apple cluster
232 were considered to be « pure » wild seedlings (referred to as “*pure*” hereafter); and 4) seedlings with a
233 membership coefficient < 0.9 to a given wild apple gene pool were considered to be wild-wild hybrids
234 (“*ww*”, hereafter). In addition, “*pure*” seedlings were assigned to different populations (*i.e.*, groups of
235 seedlings with membership coefficient > 0.9 to a given wild gene pool). Two effects were then tested
236 using statistical models below: the genetic status effect (*i.e.*, *dom*, *cw*, *ww*, *pure*), and the wild apple
237 population effect (*i.e.*, corresponding to the “*pure*” populations detected with STRUCTURE).

238

239 **Fitness proxy estimates**

240 The fitness of each seedling was therefore estimated from growth and carbon related trait proxies.

241 The absolute growth rate (*AGR* (Radford, 1967)), relative growth rate (*RGR* (Briggs *et al.*, 1920)),
242 and whole *AGR* were estimated as follows (the traits considered were the height and the number of
243 leaves of the seedling):

244 $AGR(cm/day) = \frac{(trait_{t+1} - trait_t)}{(date_{t+1} - date_t)} (1)$

245 $RGR(cm/day/day) = \frac{AGR}{date_t} (2)$

246 $WholeAGR(cm/day) = \frac{trait_{end} - trait_{beginning}}{date_{end} - date_{beginning}} (3)$

247 Note that for the whole AGR, the beginning of the experiment corresponded to days 7 and 11 for leaf
248 and height measurements, respectively, while the last measurement was done at day 60. The *internode*
249 ratio, which represents the ratio between the number of leaves and the height of the seedling at day 60,
250 was also considered a fitness trait, as this value plays an important role in apple tree architecture (Ripetti
251 *et al.*, 2008).

252 Seven fitness proxies were therefore calculated for the full dataset (565 seedlings, Table 1):
253 *height_AGR*, *height_RGR*, *whole_height_AGR*, *leaf_AGR*, *leaf_RGR*, *whole_leaf_AGR* and *internode*.
254 In addition, chlorophyll (*Chl*) and flavonol (*Flav*) content, and *NBI*, were measured in the subsample
255 (257 seedlings, Table 1). A preliminary exploration of correlation and variation among phenotypic traits
256 was carried out using a principal component analysis (PCA) with the FactoMineR R package (Lê *et al.*,
257 2008).

258

259 **Statistical analyses of fitness variation**

260 A previous study demonstrated that crop-to-wild gene flow has an impact on early-stage growth rate
261 (Feurtey *et al.*, 2017). The effect of the genetic status of seedlings (*i.e.*, *dom*, *cw*, *ww*, *pure*, Table 1) on
262 fitness variation among seedlings was therefore tested. A linear mixed model was fitted to the data as
263 follows:

264

265 $Fitness_{ijkl} \sim \mu + \text{wild population of origin}_i + \text{genetic ancestry status}_j + \text{wild population of origin}_i * \text{genetic}$
266 $\text{ancestry status}_j + \text{mother}_{rk} + e_{ijkl} (4),$

267

268 where μ is the overall mean, “wild population of origin” is the fixed effect of the population of origin
269 of the seedling inferred with STRUCTURE, “status” is the fixed effect of the genetic status of the
270 seedling (*i.e.*, “*pure*”, “*dom*”, “*ww*”, “*cw*”), the interaction between the two fixed effects, and
271 “*mother*” is a normally distributed random effect with its own mean and variance parameters, and e is
272 the residual. The mother tree of each seedling was used as a random factor to avoid pseudo-replication
273 due to the presence of multiple half-siblings (*i.e.*, from the same mother tree). We ran the model (4),
274 but replaced the “status” effect by the “*Pdom*” fixed effect. We gradually removed interactions and
275 effects depending on their significance. In addition, we evaluated the differences in the effect on trait
276 variation using a contrast analysis. We fitted the data to the model using the *lm4e* R package (Bates *et*
277 *al.*, 2015).

278 For fitness proxies defined from the number of leaves (*leaf_AGR*, *leaf_RGR* and
279 *whole_leaf_AGR*), a log link function was used and the residual distribution was fitted to a negative
280 binomial distribution (function *glm.nb* in R package lme4). For fitness proxies defined from the height
281 of the seedling (*height_AGR*, *height_RGR*, *whole_height_AGR*), and for chlorophyll and flavonol
282 content, and *NBI*, a similar linear mixed model was run, but with a residual term that was assumed to
283 be normally distributed.

284

285 **Heritability estimates**

286 Heritability estimates were computed using only pure and wild-wild *M. sylvestris* seedlings detected as
287 above. We fitted each fitness proxy with a linear mixed model as follows: $Y_{ijk} = \mu + F_i + C_j + e_{ijk}$ (5),
288 where Y_{ijk} is the fitness proxy (growth rate or carbon uptake related trait) of the k^{th} seedling belonging
289 to family i , member of the j^{th} genetic cluster, μ the overall fixed mean of the population, F_i the random
290 effect of the i^{th} family, C_j the fixed effect of the j^{th} genetic cluster and e_{ijk} the random error term. The
291 model was fitted using REML (restricted maximum likelihood). Calculations were performed by the
292 *lme*-function of the R-library *nlme* (Pinheiro *et al.*, 2022). The output of *lme* provides estimates for the
293 variance components, the corresponding standard deviations (sd), and the best unbiased linear
294 predictors (BLUP) for random effects. Genetic parameters were then calculated as follows:

295 - the additive genetic variance: $VA = 4\sigma_F^2$ with σ_F^2 representing the between-family variance

296 - the corresponding coefficient of variation: $CVA = \frac{\sqrt{VA}}{\mu}$

297 - the phenotypic variation: $VP = \sigma_F^2 + \sigma_E^2$, with σ_E^2 representing the residual variance

298 - the corresponding coefficient of variation: $CVP = \frac{\sqrt{VP}}{\mu}$

299 - Narrow-sense heritability: $h^2 = \frac{VA}{VP}$

300 - Dickerson's approximation for its standard deviation: $sd(h^2) \approx \frac{4sd(\sigma_F^2)}{VP}$

301

302 **Test for isolation-by-ecology**

303 Only pure and wild-wild hybrid *M. sylvestris* seedlings were selected for IBE analysis ($N = 449$, 21
304 sites, Table 1). The IBE pattern, *i.e.*, the contribution of climate and phenotypic distances to the genetic
305 structure taking into account geographical distance, was evaluated using a distance-based redundancy
306 analysis (db-RDA). db-RDA can be used when the response variable is a distance matrix, here a genetic
307 distance matrix (F_{ST}) across 21 sampled sites, and the explanatory variables are in vector form.
308 Explanatory variables were as follows : (i) the geographical distance between sampled sites which
309 underlies an IBD process, represented by vectors with positive eigenvalues of a principal coordinate of
310 neighbor matrix (*PCNM*) (Borcard & Legendre, 2002), which was applied to the geographical pairwise
311 distance matrix between sampled sites computed with SPAGeDI 1.5d (Hardy & Vekemans, 2002); 19
312 bioclimatic variables downloaded from the Worldclim2 database (30s resolution,

313 <https://www.worldclim.org/data/worldclim21.html>) representing annual and seasonal trends and
314 extremes averaged (ii) over the years 1970-2000 and averaged (iii) for the Pleistocene period (20K
315 years ago) (Gamisch, 2019), which were used to test for an isolation-by-climate pattern (IBC, hereafter);
316 and (iv) growth rate ($N = 551$, Table 1) and carbon uptake related traits ($N = 239$, Table 1) averaged per
317 site, as well as chlorophyll and flavonoid content, which were used to test for an isolation-by-adaptation
318 pattern, referred as to IBA hereafter.

319 To identify the variables that explained the genetic structure of *M. sylvestris*, a db-RDA using the
320 “capscale” function (Oksanen *et al.*, 2014) was run on a full model which included all investigated
321 variables (*i.e.*, PCNM components, growth rates, carbon uptake related traits, 19 bioclimatic variables).
322 The best variables were selected for an optimum model with the function “step” based on the Akaike
323 Information Criterion (AIC). Because db-RDA does not provide information on the relative
324 contribution of each variable of the model, a variance partitioning analysis was run using the “varpart”
325 function from the R-package “vegan” (Peres-Neto *et al.*, 2006).

326

327 **Results**

328 **Genetic ancestry of seedlings**

329 No clones or closely related individuals were detected (Figure S1) and therefore all 584 seedlings were
330 included in the STRUCTURE analyses.

331 STRUCTURE revealed a clear spatial population genetic structure of *M. sylvestris* in Europe as well
332 as crop-wild admixture (Figures 1 and S2). For $K = 2$, the analysis recovered a group that included *M.*
333 *domestica* and the western *M. sylvestris* samples (green) and another group that consisted of the Eastern
334 European samples (red). For $K = 3$, the western group was split into two groups, one comprising *M.*
335 *domestica* and Spanish and Italian *M. sylvestris* seedlings (black), and another comprising the remaining
336 western samples (green); the Central European group was also recovered. For $K = 4$, the Eastern
337 European samples were split into two groups: an Austrian group and a Romanian group. For $K = 5$,
338 there was a clear east/west substructure in France. For $K = 6$, a sixth cluster comprising the Danish
339 individuals was found. For $K = 7$, the Italian population split into two groups. For $K = 8$, the population
340 from one site in eastern France (*Lor*) was identified as a new cluster. When $K > 9$, STRUCTURE did
341 not reveal any further substructures, with only additional cluster with highly admixed individuals
342 (Figure S2). Therefore, although the ΔK indicated that the most likely K value was five (Figure S3), K
343 = 8 was the finest population structure and was therefore retained in subsequent analyses.

344 For $K = 8$, we found that the *M. domestica* reference varieties were admixed with the Italian and
345 Western European *M. sylvestris*. Conversely, we detected 68 *M. sylvestris* seedlings with $P_{dom} > 0.1$
346 (considered as crop-wild hybrids), corresponding to 11.6% of the seedlings ($N = 584$, Figures 1, S4 and
347 S5, Table 1). We also found 21 seedlings with a membership coefficient to the *M. domestica* gene pool
348 > 0.9 , corresponding to 4% of the seedlings. Nearly all Spanish seedlings were assigned to the *M.*
349 *domestica* gene pool with membership coefficients > 0.1 (*i.e.*, 26 crop-wild hybrids and 13 individuals

350 assigned to the *M. domestica* gene pool) and showed admixture only with the wild Italian purple gene
351 pool (Figure S4). 33 individuals could not be assigned to any cluster (*i.e.*, individuals with a membership
352 coefficient < 0.5 to any cluster).

353 We therefore identified 68 “*cw*”, 21 “*dom*”, 167 “*ww*” and 282 “*pure*” seedlings (Table 1, $N = 551$).
354 After removing *cw* hybrids ($N = 68$), seedlings sampled from misidentified mother trees ($N = 21$), the
355 *M. domestica* reference samples ($N = 40$) and individuals with a membership coefficient < 0.5 to any
356 cluster, seven wild apple populations (*i.e.*, groups of seedlings with a membership coefficient > 0.5 to
357 a wild apple cluster) were defined: French Western (“*FR-W*”, $N = 77$), French Eastern (“*FR-E*”, $N =$
358 50), French Lorraine (“*FR-Lor*”, $N = 28$), Danish (*DA*, $N = 78$), Italian (“*IT*”, $N = 27$), Austrian (“*AUT*”,
359 $N = 81$) and Romanian (“*RO*”, $N = 108$) (Figure S6). Each *M. sylvestris* population showed a high level
360 of genetic variation (Table S2). The Romanian population was the most genetically differentiated
361 population and was close to the Austrian population; the Danish and French Western populations were
362 genetically similar (Figure S7).

363

364 **No effect of seedling status on phenotypic variation**

365 Variation and correlations among traits are presented in Figures S8 to S11. Heritability estimates were
366 moderate to high for all traits except growth rate based on leaf number (Table S3). However, these
367 estimates need to be taken with caution given the limited sample size, as reflected by the large standard
368 deviations.

369 We did not find any significant effect of seedling status (*i.e.*, *pure*, *ww*, *cw*, *dom*) (Figure 5,
370 Table S4, Figure S12) or P_{dom} (Table S5, Figure S13) on phenotypic traits (*i.e.*, leaf and height AGR,
371 leaf and height RGR, whole leaf and height AGR). We therefore removed the seedling status and P_{dom}
372 effects from the model 4, as well as *dom* and *cw* individuals. We therefore only considered wild apple
373 seedlings (*i.e.*, *pure* and *ww*, $N = 449$), and focused on the ‘wild population of origin’ effect (Table S6).
374

375 **Significant variation in growth rates and chlorophyll content among populations**

376 Mean height variation along the course of the experiment among seedlings from different populations
377 is shown in Figure 2. There was significant variation among seedlings from different populations in
378 certain growth-related traits (Table 2). On average, seedlings belonging to the Austrian population were
379 taller (+11 cm, $P = 0.047$) whereas Romanian (-14.9 cm, $P = 0.008$) and Italian (-18.7 cm, $P = 0.044$)
380 seedlings were shorter (Figure 2) than seedlings from other populations. Seedlings from other
381 populations did not show a significant difference in height. In addition, the number of leaves and height
382 traits were negatively correlated, $r = -0.3$, $P < 0.001$). The Austrian population presented the lowest
383 number of leaves (average = 5, $sd = 4$) whereas seedlings belonging to the Romanian population had
384 the highest number of leaves (average = 8, $sd = 7$, Figure S15). The Romanian population also had the
385 largest *internode* (+ 0.02 leaf/cm, $P = 0.024$).

386 Chlorophyll content differed among populations with seedlings from the Italian population
387 producing on average more chlorophyll (+4.14 $\mu\text{g}/\text{cm}^2$, $P = 0.039$, Figure S16) than seedlings from
388 other populations. Flavonol content and NBI did not differ significantly among populations.

389

390 **Significant IBD and IBC**

391 Correlation plots between bioclimatic variables are provided in Figures S17 and S18; however, all
392 variables were included in the analysis as db-RDA can cope with correlated variables. The optimal
393 model was chosen according to its best AIC value. The optimal model explained up to 25.9% of the
394 genetic structure ($Adj-R^2 = 69.9\%$, $P = 0.001$) and contained seven variables (four geographic and three
395 bioclimatic variables) (Table 3): the geographical distance is represented by the 1st, 2nd, 3rd and 6th
396 axis of the PCNM analysis and three past climatic variables (Bio3: isothermality; Bio6: minimum
397 temperature of coldest month; Bio 9: mean temperature of driest quarter). In total, IBD explained 47%
398 of the variance of the wild apple tree population genetic structure, whereas IBC explained 22% (Figure
399 3). Taking geographical distance into account, we did not find a pattern of IBA i.e., covariation between
400 phenotype and genetic divergences.

401

402 **Discussion**

403 This study is the first to take into account the population genetic structure as well as the phenotypic
404 variation of a contributor to the cultivated apple genome (Cornille *et al.*, 2012), to investigate ecological
405 divergence. Bayesian clustering revealed seven *M. sylvestris* populations across Europe with a
406 substantial number of seedlings (11.6%, mainly from Western Europe) introgressed by *M. domestica*,
407 although this figure is less substantial than previously reported (Cornille *et al.*, 2013b, 2015; Feurtey *et*
408 *al.*, 2017). Although the crop-wild hybrid status of seedlings did not impact phenotypic variation, we
409 observed phenotypic variation among crabapple populations when grown in controlled conditions.
410 Phenotypic variation was found for growth and chlorophyll content among populations of the European
411 crabapple from different climates in Europe. Based on the IBA pattern, this phenotypic variation was
412 not adaptive. However, the IBC pattern revealed that climate was a driver of genetic differentiation
413 between populations. Given that the IBC pattern was still found after accounting for IBD, this implies
414 that there are sufficient levels of local adaptation to LGM climate to reduce gene flow among
415 populations. The European crabapple may therefore be locally adapted to the past climate conditions of
416 the LGM. The lack of signal of adaptive phenotypic divergence suggests that traits other than the ones
417 we investigated in this study may be under divergent selection. The results of this study pinpoints
418 adaptive divergence related to climate in a wild contributor to a fruit tree crop genome, which is a
419 starting point for future breeding programs and mitigating the impact of climate change of CWR of an
420 emblematic temperate fruit tree.

421

422 **Ongoing crop-to-wild gene flow in the European crabapple**

423 We revealed substantial gene flow from *M. domestica* to the European crabapple, with 11.8% of
424 seedlings, mostly from Western Europe, introgressed by *M. domestica*. Introgression rates were lower
425 compared to previous studies (*i.e.*, 37% in Cornille *et al.* (2013b) and 23.1% in Cornille *et al.* (2015)).
426 However, these studies genotyped more mother trees (*i.e.*, $N = 756$ and $N = 1,889$, respectively), which
427 could explain the difference in estimates of crop-to-wild gene flow. The results described here highlight
428 the fact that crop-to-wild gene flow is still ongoing in the European crabapple. The Spanish seedlings
429 sampled here were the progeny of trees growing in a location that is known to have high levels of *M.*
430 *domestica* introgression (pers. comment. G. Alins). It is even possible that the mother trees of these
431 seedlings were *M. domestica* and not *M. sylvestris*. The inclusion of reference cultivated apple samples
432 mainly from Western Europe may decrease the probability of detecting crop-to-wild introgression
433 events in wild populations from Eastern and Northern Europe. The lower crop-to-wild introgression
434 rates in wild seedlings from Eastern Europe can also be explained by their physical distance from
435 cultivated apple orchards. Indeed, distance can be a natural barrier to hybridization between *M.*
436 *domestica* and its wild relative (Larsen *et al.*, 2016), which we confirmed in this study. The position of
437 a *M. sylvestris* individual in a forest may also impact its level of introgression. Indeed, *M. sylvestris*
438 trees are often found in forest gaps and at the forest edge, corresponding to their ecophysiological
439 preferences (*i.e.*, preference for light and low competition). The effect of the location of the trees in the
440 forest on the level of crop-to-wild introgression needs to be studied further.

441 The consequences of crop-wild introgression on phenotypic variation between crop and wild
442 individuals have been studied more in annual crops (*e.g.*, maize, wheat, lettuce, rice) (Ellstrand *et al.*,
443 2013) than in perennial fruit trees. One study has shown that crop-wild hybrid seedlings of the European
444 crabapple have higher growth rates and showed earlier germination than wild apple seedlings (Feurtey
445 *et al.*, 2017). We did not detect any effect of the status of a seedling (pure, wild, crop-wild, dom) or the
446 level of introgression (*Pdom*) on growth and carbon uptake related fitness proxies. This could be due to
447 the low number of samples from the *cw* and *dom* categories. Note that we did not test the variation in
448 germination rate among seedlings as germination can be strongly impacted by stratification conditions.

449 450 **No adaptive phenotypic variation among populations, but signs of local adaptation to past climate** 451 **in the European crabapple**

452 Under controlled conditions, seedlings from the different populations were found to have significantly
453 different growth and morphology, but IBA analyses indicated that this variation was likely not adaptive.
454 Seedlings belonging to the Austrian population were the tallest, had the highest absolute growth rate
455 and the lowest number of leaves; by contrast, Romanian seedlings were the shortest, had the lowest
456 absolute growth rate and the highest number of leaves. Italian seedlings had the highest chlorophyll
457 content. The seedlings belonging to the Austrian population may be fitter in the climate conditions
458 simulated in this experiment. We tested whether this phenotypic variation was adaptive. However,
459 taking geographic distance into account, we did not find any significant covariation between genetic

460 and phenotypic variation. This suggests a lack of divergent selection on traits related to carbon uptake
461 or growth that are often associated with plant responses to climate (Bussotti *et al.*, 2015). Therefore,
462 the phenotypic variation we observed among populations under controlled conditions may be the result
463 of genetic drift alone; alternatively, the traits we selected (thought to be related to responses to climate)
464 are not good candidates for investigating divergent selection. Leaf mass per area (LMA) and foliar
465 nitrogen content demonstrated can be future targeted parameter to assess the responses of apple seedling
466 to environmental stress (Bussotti *et al.*, 2015). Another explanation could be that we did not phenotype
467 enough seedlings from each genetic group. Indeed, we observed a high variation in each phenotypic
468 trait and in their heritability estimates, suggesting that the traits we studied may be relevant but that a
469 larger number of seedlings should be phenotyped and analyzed (*e.g.*, (Klein *et al.*, 1973)). However,
470 some studies have found that even with large sample sizes, the standard error of heritability estimates
471 can still be large and vary greatly between experimental designs (Visscher & Goddard, 2015). The fairly
472 high heritability estimates for most of the traits considered here could be seen as consistent with rather
473 weak within population selection, enabling the maintenance of ample additive genetic variation
474 (Wheelwright *et al.*, 2014). Furthermore, high variation in seedling traits combined with high
475 heritability estimates could suggest that there is large room of genetic material for adaptation to work
476 on. In addition, the population of origin of the seedlings did not explain all phenotypic variation. Even
477 though we found an effect of the population of origin on phenotypic traits, its contribution was relatively
478 low (*e.g.*, model 4, R^2 for height = 0.119, and R^2 for height AGR= 0.047). Environment (*e.g.*, climate)
479 and interaction between genotype and environment could also impact fitness.

480 As *M. sylvestris* is distributed across gradient, we further investigated the role of climate in
481 shaping the genetic variation among populations of the European crabapple, without considering
482 phenotypic trait variation. We tested for an IBE pattern, where the pattern of neutral genetic variation
483 covaries with ecological variables (here climate). There was no combined effect of geographic and
484 climatic distance (IBD \cap IBC), which allowed us to assess the contribution of these processes separately
485 (Wang & Bradburd, 2014). We showed that IBD and IBC played a significant role ($R^2_{\text{adj}} = 47\%$ and
486 $R^2_{\text{adj}} = 22\%$, respectively) on the genetic differentiation of European crabapple populations. Weak but
487 significant IBD has been previously identified in wild apple relatives of the cultivated apple (*i.e.*, *M.*
488 *sylvestris*, *M. orientalis* and *M. sieversii*) suggesting they have high dispersal capacities (Cornille *et al.*,
489 2013b,a, 2015). Weak IBD is explained by self-incompatibility systems that prevent self-fertilization
490 (Brown, 1992), pollen dispersal by bees and flies (*Syrphidae*) and endozoochorous seed dispersal by
491 large mammals such as ungulates, wild pigs, brown bears or humans (Larsen *et al.*, 2006). We show
492 that in addition to IBD, IBC persisted after taking geographic distance into account. Climate can impose
493 divergent selection pressures on different locations and thus reduce gene flow between populations, so
494 that IBC contributes to genetic differentiation. The main variables explaining genetic differentiation in
495 the European crabapple were related to temperature during the LGM. This suggests that the European
496 crabapple may be locally adapted to its past temperature but not to its current climate. Local adaptation

497 to current climate is well studied in wind-dispersed trees (Savolainen *et al.*, 2013; Kremer & Hipp,
498 2019; Pyhäjärvi *et al.* 2020). However, to our knowledge no study has shown local adaptation to past
499 climate conditions in a tree species.

500 Additional factors other than climate can also shape adaptive divergence between populations.
501 *Malus sylvestris* is a pioneer species that needs high levels of light and is not very competitive. Local
502 adaptation to biotic factors such as the presence of other species is possible. Competition for light with
503 other species such as the European beech (*Fagus sylvatica*) could be a source of divergence between
504 populations. Local adaptation of fruit trees to biotic factors, including parasites (Olvera-Vazquez *et al.*,
505 2021), deserves further investigations. Besides selection, the potential role of phenotypic plasticity in
506 enabling growth and optimal fitness in changing environments also needs to be carefully evaluated
507 (Benito Garzón *et al.*, 2011).

508

509 **Further investigations needed on local adaptation and plasticity in response to climate in the** 510 **European crabapple**

511 Our study raises concerns regarding the future of wild apple populations and their current vulnerability
512 to current climate change. However, the adaptation of tree species to climate remains complex (Bussotti
513 *et al.*, 2015). For instance, in *Eucalyptus camaldulensis*, variation in leaf traits and performance proxies
514 was unrelated to the climate of genotype provenance (Asao *et al.*, 2020), whereas variation in several
515 photosynthetic traits was clearly related to the climate of genotype provenance across Australia (Dillon
516 *et al.*, 2018). In contrast, collective differences in leaf morphology and photosynthetic physiology, in
517 several *Populus* species may be adaptive for differences in growth season length, temperature and
518 insolation (Keller *et al.*, 2011; Kaluthota *et al.*, 2015). Further investigations on local adaptation and
519 plasticity to climate or biotic factors in the European crabapple are therefore needed. Genomic data will
520 be particularly useful for determining the relative influence of adaptive and neutral processes on
521 climate- or biotic- driven divergence by screening genomes from different populations in Europe.
522 Comparing the fitness of seedlings from different populations in reciprocal transplants will also be
523 important to further test for local adaptation. Our study therefore raises questions regarding the
524 processes of local adaptation of fruit trees, and is a starting point for apple breeding programs.

525

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540

541 **Authors contributions**

542 AC, GV, AR, SB, TU conceived and designed the experiments; AC, GV, AT, TU, TK obtained the
543 funding; AC, GV, AT, TU, KAO, SV, RR, XC, TK, CR sampled the material; XC, CR, AV, AR, GL,
544 KAO, RR, MLG, HB, VC, HC, SV, MF performed the molecular biology analyses; AC, AF, KomAvi
545 and XC analyzed the data. The manuscript was written by AC, KomAvi and AF, with essential input
546 from other co-authors.

547

548

Figures and Tables

Figure 1. Bayesian clustering of the *Malus sylvestris* seedlings sampled in this study ($N = 584$) and the reference samples of *Malus domestica* ($N = 40$) inferred with STRUCTURE for $K = 8$, and its associated map of mean membership per sampled site. Each individual is represented by a vertical bar partitioned into clusters. Visualization was improved by sorting genotypes by country; countries are separated by a white line. The reference *M. domestica* reference samples are shown on the far left of the map in the Atlantic. Circle size is proportional to the number of individuals within the cluster (scale shown on the top right-hand corner).

Figure 2. Mean height of apple seedlings measured over the time of the experiment in controlled conditions (including pure and wild-wild hybrid seedlings, $N = 449$, and seedlings assigned to the *M. domestica* gene pool, $N = 21$, as detected with STRUCTURE for $K=8$). The 40 reference *M. domestica* individuals were not measured under controlled conditions thus are not shown here. Vertical lines represent the standard deviation. Populations: AUT ($N = 81$), DA ($N = 78$), DOM ($N = 21$, includes 13 Spanish genotypes and seedlings from other countries), FR-E ($N = 50$), FR-Lor ($N = 28$), FR-W ($N = 77$), IT ($N = 27$), RO ($N = 108$).

Figure 3. Variance partitioning analysis of the db-RDA results obtained for *Malus sylvestris* ($N_{sites} = 21$, 13 microsatellite markers). Variation of the site pairwise genetic differentiation (F_{ST}) is explained by the variables generating isolation-by-distance (geographical distance) and isolation-by-climate (with three bioclimatic variables during the last glacial maximum: Bio3, isothermality; Bio6, minimum temperature of coldest month; Bio 9: mean temperature of driest quarter).

Table 1. Number of *M. sylvestris* seedlings used in this study for population genetic analyses inferred with STRUCTURE for $K = 8$ with 13 microsatellite markers and phenotyping (growth and carbon-uptake related traits).

Clusters	N_{pure}	N_{ww}	N_{cw}	N_{dom}	$N_{no\ cluster}$	Total measured for phenotypic traits	Wild population name
Q1 (light green)	32	46	7	0	10	92	FR-W
Q2 (yellow)	0	52	5	0	4	57	FR-E
Q3 (lor)	28	1	0	0		28	FR-Lor
Q4 (blue)	61	21	1	0	6	85	DA
Q5 (purple)	23	4	3	0	4	34	IT
Q6 (dark green)	66	17	1	0	1	83	AUT
Q7 (red)	77	34	5	0	0	113	RO
Q8 (black – <i>M. domestica</i>)	40	0	46	21	8	73	-
Total	287	175	68	21	33	551 (584)	
Total measured for height and number of leaves	282	167	63	21	32	533 (565)	

Total measured for leaf chlorophyll, flavonol and NBI contents	129	82	22	6	18	239 (257)
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N_{pure} : number of seedlings assigned to a wild gene pool with a membership coefficient > 0.9 ; N_{ww} , number of wild-wild hybrids (*i.e.*, seedlings with a membership coefficient > 0.1 to a wild gene pool other than its own wild gene pool and a membership coefficient < 0.1 to the *M. domestica* gene pool); N_{cw} : number of crop-wild hybrids (*i.e.*, seedling assigned to the *M. domestica* gene pool with a membership coefficient > 0.1). $N_{no\ cluster}$: seedlings that could not be assigned to any defined gene pool; Total measured for phenotypic traits : number of individuals measured for each phenotypic trait and included in the statistical analyses, the number in brackets represents the initial sample size before data were filtered for statistical analyses. Wild population name: populations defined with STRUCTURE at $K=8$ excluding crop-wild hybrids and seedlings from misidentified mother trees (*i.e.*, including only wild pure and wild-wild hybrids).

Table 2. Final model depicting effects of the *Malus sylvestris* population to which each seedling belonged (*i.e.*, cluster inferred with STRUCTURE at $K=8$) on phenotypic traits (*i.e.*, height, number of leaves, internode, chlorophyll and flavonol content, NBI) measured in 533 individuals. Variables in green are significant ($P < 0.05$).

Explanatory variable	Cluster			Mother		Model			Mother
	χ^2	<i>P-value</i>	df	REML	Standard Deviation	AIC	R ²	Corrected R ²	R ²
Height_AGR	17.863	0.007***	6	1,229	0.204	1248	0.047	0.091	0.044
Height_RGR	12.846	0.045*	6	-2,264	0.006	-2245	0,041	0.147	0.106
Leaf_AGR	-	-	-	-	-	-	-	-	-
Leaf_RGR	-	-	-	-	-	-	-	-	-
Height whole AGR	22.243	1.00e-03***	6	630	0.175	650	0.074	0.192	0.118
Leaf whole AGR	36.326	2.38e-06***	6	-1,277	0.009	-1,258	0.09	0.118	0.028

Height	31.623	1.93e-05***	6	4,113	11.69	4,131	0.119	0.301	0.182
Number of leaves	22.285	0.001***	6	-	0.084	2,659	0.052	0.064	0.012
Chlorophyll	14.418	0.025*	6	1,181	1.352	1,199	0.074	0.171	0.097
Flavonol	-	-	6	-	-	-	-	-	-
NBI	-	-	6	-	-	-	-	-	-
Internode (nleaf/height)	17.768	0.007***	6	-1,328	0.009	-1,309	0.044	0.073	0.029

***: P-value <0.001; **: 0.01 < P-value <0.001; *: 0.05 < P-value <0.01; AIC: Akaike Indice Criterion.

Table 3. Contribution of geography and climate to the genetic variation observed among *M. sylvestris* seedlings. Distance-based redundancy analyses tested the effects of geography, climate and phenotype on genetic differentiation among 21 sites from 13 microsatellites in the European crabapple. Only significant variables are presented.

	db-RDA			
	% of variance explained	d.f.	p-value	Adj-R ²
Global analysis	25.9	7	0.001	69.9
Residuals	11.3	13	-	
Marginal test				
<i>Geography (IBD)</i>	14.9	4	<0.015	
PCNM 1-2-3-6				
<i>Environment (IBC_LGM)</i>	11.04	3	<0.015	
BIO3_LGM				
BIO6_LGM				
BIO9_LGM				
Interaction			-	

Residuals	11.3%	-	-	
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BIO3_LGM: isothermality (BIO2/BIO7) ($\times 100$); BIO6_LGM: minimum temperature of coldest month; BIO9_LGM: mean temperature of driest quarter, IBD: isolation-by-distance; IBC_LGM: isolation-by-climate during the last glacial maximum.

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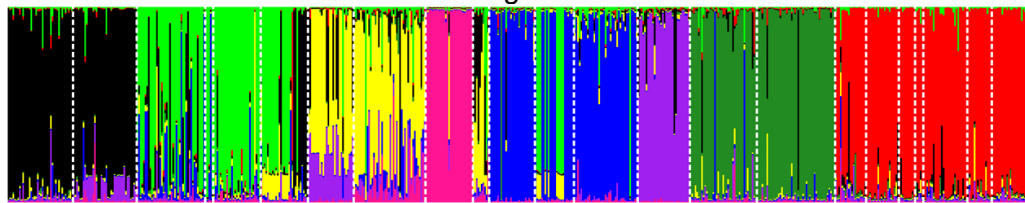
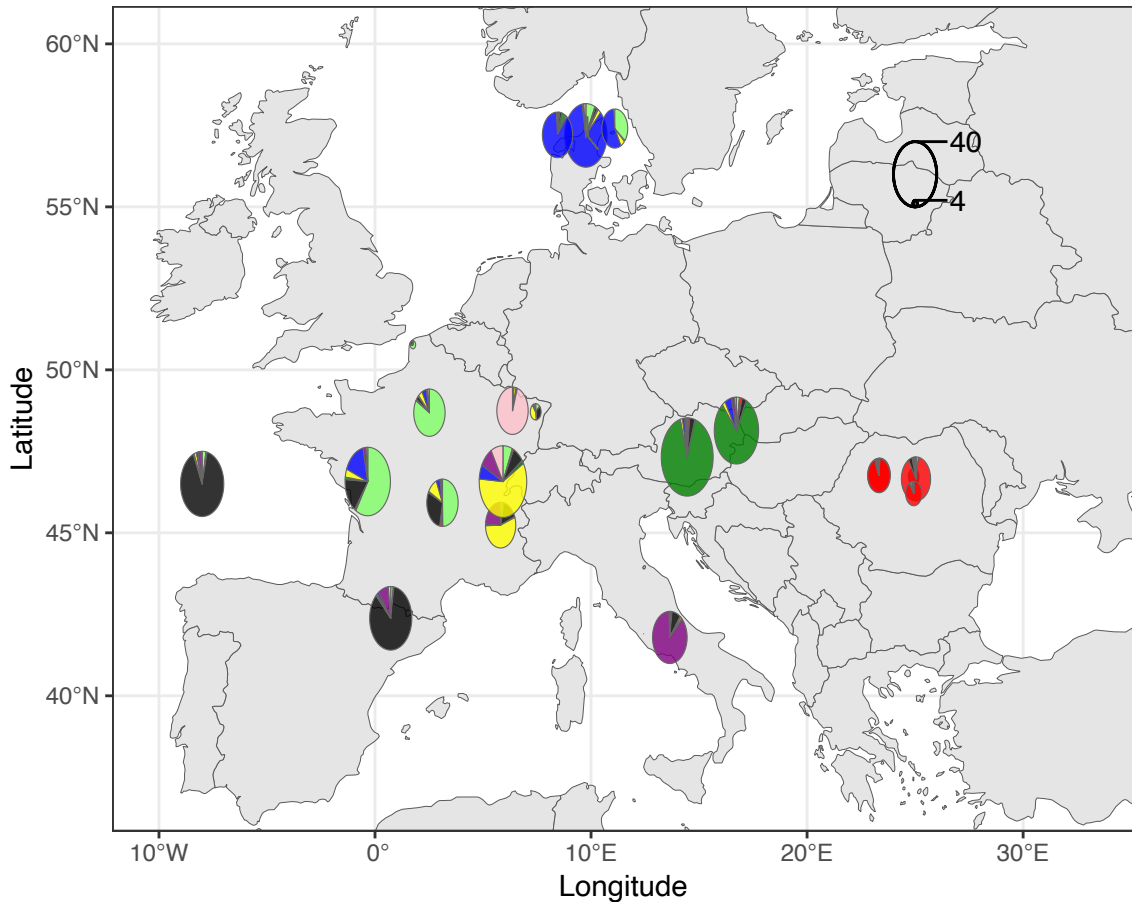
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Malus domestica

Spain

Western France

Eastern France

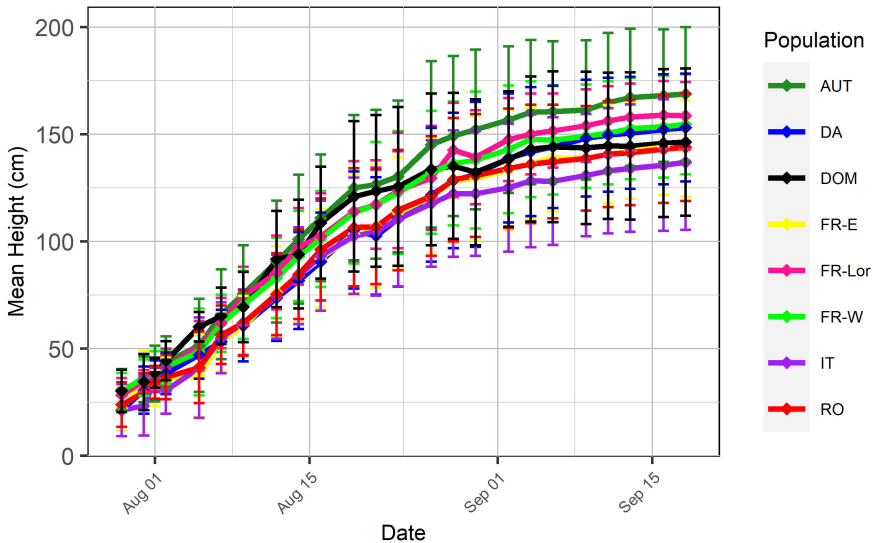
Denmark

Italy

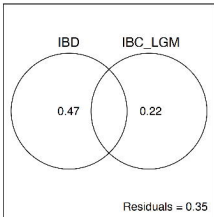
Austria

Romania

Evolution of height over time



Variance partitioning of the db-RDA results



Values <0 not shown