

Chapter IV: Adaptive potential - a partial insurance against climate change risks

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To exploit natural adaptation to climate: a weapon to cope with climate change

Adaptation of forests to climate change can occur via inherent processes or may be triggered by measures instigated by humans. The rationale for considering inherent physiological processes comes from the evidence that tree populations have undergone profound genetic changes during the natural warming after the last glaciations facilitating their adaptation to changing climate (Petit et al., 2008). Provenance refers to the specific geographical location that marks the natural origin of a tree. Natural selection by evolution has adapted each provenance to its local environment, hence, there are genetic differences between different provenances of the same tree species. In provenance testing, seed is collected from several provenances and planted for comparison in random replicated experiments at various forest locations. (Figure 1). Since provenance tests were first installed by forest practitioners, results accumulated showing substantial population divergence for almost any adaptive trait that has been investigated so far. During the past decade, the evolutionary historical trajectories during the Holocene (our current interglacial climate period) have been reconstructed for most of the European tree species, providing some clues about the rates of evolutionary changes. A prevailing view resulting from combined genetic and historical investigations is that adaptation can occur at rapid time scales – even contemporary time scales- provided that there is enough genetic variation. The issue of future adaptation to on-going climate change can therefore also be thought of in evolutionary terms.

The fate of extant (or living) tree populations undergoing severe environmental changes is related to their adaptive potential. Practitioners are seeking studies which imitate climate change so they may evaluate adaptive potential that would guide their management options. Evolutionary scientists are attempting to identify ecological and genetic drivers or processes contributing to the adaptive potential.

Adaptive potential of a tree population can be defined as its capacity to respond to a given environmental change, by modifying its own genetic composition and/or by modifying its phenotypic expression. In more scientific terms, adaptive potential is the sum of the changes due to genetic adaptation¹ and changes due to phenotypic plasticity².

¹ Genetic adaptation is shaped by evolutionary forces as natural selection, genetic drift, migration, type of mating and recombination.

² Phenotypic plasticity is the capacity of an organism to change its phenotype in response to a change in environment.

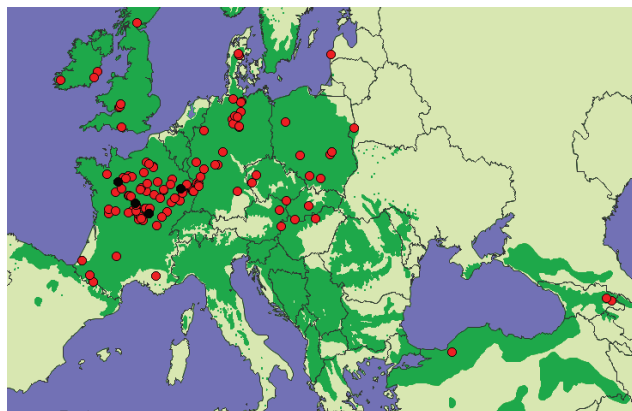
a**b**

Figure 1. Illustration of provenance tests concept (a). The green background represents the distribution area of *Quercus petraea*. Black dots represent the planting site, where the performance of each provenance, red dots, is tested in the same environment (provenance test). For example, if provenances have different heights in their native environment; such differences could be due to genetic or to environmental properties. If differences in height between provenances are conserved in the planting site (provenance test), it means differences in height are genetic. Illustration of genetic difference for a phenological trait (b). On the left side, defoliated trees (beginning of bud burst) are from a french provenance (bertanges) and, on the right, foliated trees (end of bud burst and leaf elongation) are from an austrian provenance (klostermarienberg).

Measuring adaptive potential: response and transfer functions

Adaptive potential in tree species is assessed by monitoring the same provenance in different ecological settings (see Figure 1), for instance by planting a “northern” provenance more in a “southern” provenance test location. This approach is relevant in the context of climate change especially if environmental changes over spatial gradient can mimic future climate changes.

Adaptive potential is, then, described by a response and/or transfer function. The response function describes the provenance’s performance along a climatic gradient, indeed data is needed from several provenances tests (>6) with the same populations in each. These experiments are laborious, costly, and only available for some valuable species as pine, Norway spruce or beech. For the majority of tree species, there are few provenance experiments with many provenances tested.

A valuable alternative strategy is to use a transfer function i.e. the provenance’s performance (or standardized proxy) is described along a transfer distance (see below). This method relies more on assessing contrasts between populations at the same site, rather than contrasts

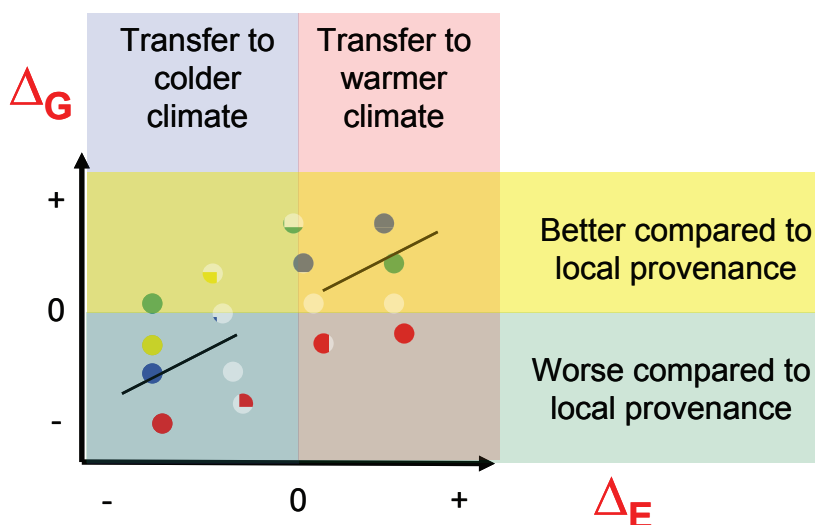


Figure 2. Illustration of the construction of species transfer function. The x axis (Δ_E , the unit is the same as the climatic variable) represents the difference between the mean of a given climatic variable at the test site (provenance test) and the mean of the same climatic variable at origin of the provenance. The y axis (Δ_G , the unit is the same as the measured trait) represents the difference between the performance of foreign provenance and the performance of local provenance. It is also possible to represent the performance of populations without any standardization.

between same populations at different sites. Here, we present a statistic free approach to illustrate this concept.

For each population the transfer distance (Δ_E , see Figure 2) was calculated as the difference between the mean of a given climatic variable (usually temperature) at the testing site (provenance test) and the mean of the same climatic variable at origin of the provenance. When temperature is used as the climatic variable, negative values on the x axis can therefore represent transfer to warmer climates ($\Delta_E < 0$), while positive values indicate transfer to cooler climates ($\Delta_E > 0$). Each population performance was also standardized by the local population performance (Δ_G , see Figure 2). A negative value of Δ_G means that populations performed less well compared to the local population and positive values mean that the foreign population outperformed the local population. A species response function with a positive slope, as it is illustrated in Figure 2, means a transferred provenance in a warmer climate could increase provenance performance when compared with local provenance.

Re-analysis of old *Quercus petraea* provenance tests

Almost all available provenances tests were not designed to mimic climate change. However, the comparison between the transfer distance realized in four French provenance tests (with

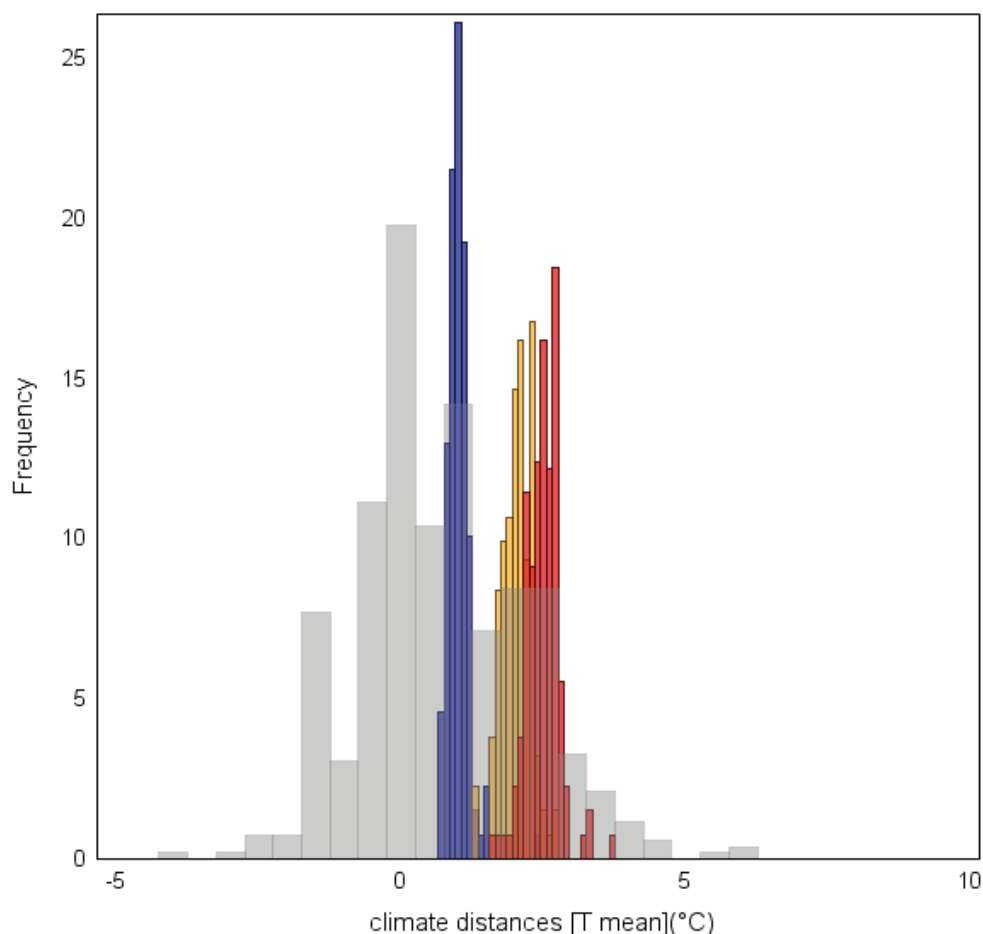
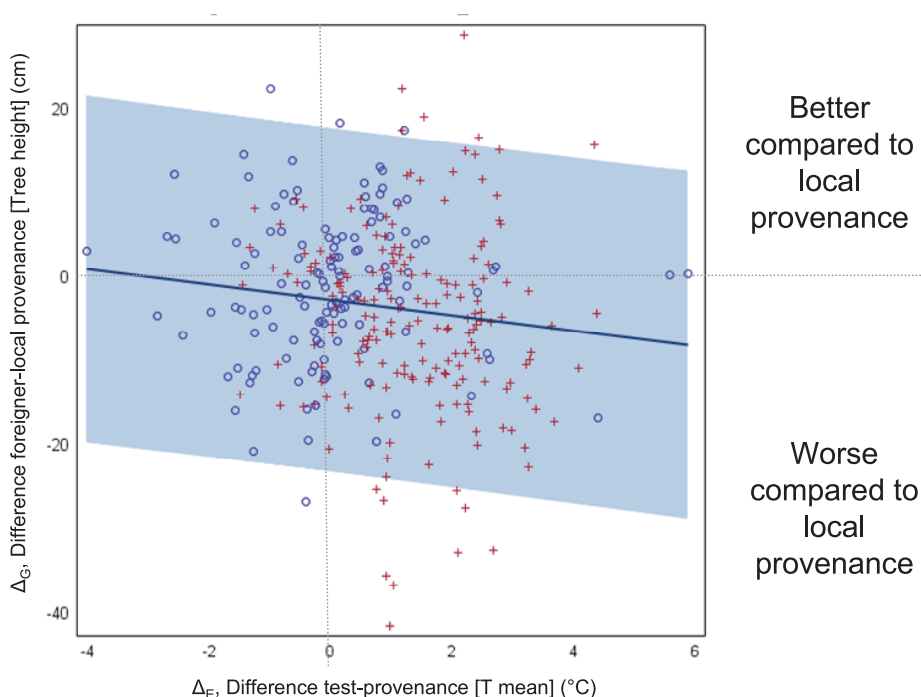


Figure 3. Comparison between transfer distances (light grey histogram) realized on four French provenance tests and the expected climate change at the provenance origins (blue histogram: expected warming over 2011–2040, yellow histogram: expected warming over 2011–2070, red histogram: expected warming over 2011–2100).

more than 100 provenances tested) on *Quercus petraea* and the expected climatic change at the provenance origin showed that provenance tests are valuable tools for prediction about provenance performance in the climate change context.

Figure 3 shows how the transfer distances realized in the French provenance tests overlap the expected climatic change at the provenance origins, however, only the transfer to warmer climates are useful (transfer distance > 0). For example, a Western German provenance planted in a Northern French test location simulates a rise in temperature of 1.5 °C. Such an increase in temperature is expected in Germany by 2040. Using the described strategy for old data from *Quercus petraea*, we adjusted a species transfer function (see Figure 4).



Transfer to colder climate

Transfer to warmer climate

Figure 4. *Quercus petraea* transfer function for tree height at 4 years old along, adjusted on 124 populations replicated in 4 provenance tests. The x axis is the transfer distance and the y axis is the standardized performance of provenances in each provenance test (for more explanations see text). The blue line (regression line) is the expected deviation of a provenance comparing to a local provenance after a given transfer distance, the associated blue area represents the confidence interval for the prediction. Thin grey lines symbolized the 0 values on x and y axis.

As seen in Figure 4, most populations show positive transfer distances, meaning that they were moved on average towards warmer climates. The y axis is the difference in height between the transferred population and the local population (at the site where the test is established). All populations above the 0 on the y axis are taller than local populations. The transfer function has a negative slope, suggesting that on average transfer to warmer climates is likely to reduce the tree height. An increase of 1°C in the mean annual temperature decreased tree height by 12.3 cm at 10 years old. However there was a very large population variation around the mean response. At least 8 populations (see populations above the confidence interval) actually will grow better than the local population when they are transferred to warmer climates.

Such approaches, in order to accelerate forest adaptation, are under evaluation in North-America, and future seed transfer guidelines will take in account such considerations. In

contrast European countries are just starting such work despite large numbers of provenance trials and an old tradition in forest science. These genetic approaches coupled with adaptive management strategies could buffer or maintain sustainable levels of forest productivity and ecosystem health.

References

- Aitken, S.N., Yeaman, S., Holliday, J.A., Wang, T. and Curtis-McLane, S. 2008. Adaptation, migration or extirpation: climate change outcomes for tree populations. *Evolutionary Applications* (1):95–111
- Kremer, A. and Le Corre, V. 2011. Decoupling of differentiation between traits and their underlying genes in response to divergent selection. *Heredity* 108(4):375–385.
- Petit, R.J., Hu, F.S. and Dick, C.W. 2008. A Window to future changes. *Science* (320):1450–1451