Genomics to the Rescue

New types of models can help us better predict how well species will be able to adapt to climate change.

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Forests account for a significant portion of the Earth's biodiversity. They are one of the most important types of terrestrial ecosystems and have great potential in mitigating climate change. Given the fast pace of climate change, the future of the forests is a matter of grave concern. This makes it critical to develop new strategies to support the survival of forests at local, regional, and global scales.

Climate change is leading to a loss of biodiversity, thereby affecting the functioning and stability of forest ecosystems. This effect is expected to intensify in the near future, and we are already now increasingly seeing significant population declines in many tree species, especially in southern Europe. Therefore, much attention is being devoted to predicting the impact of climate change on the distribution and adaptation of forest tree species. Predicting species-level responses is thus one of the most pressing questions in evolutionary biology, and unraveling it is a prerequisite for developing effective conservation and management solutions of species that are oriented towards climate change adaptation.

Currently, this is possible thanks to the application of advanced computational methods and algorithms that can model species distribution under different future climate change scenarios. However, traditional forecasting methods do not account for the adaptive genetic variability of species and their populations

– nevertheless, it is clear that their capacity to adapt to changing environmental conditions is crucial for their evolutionary potential. Recent advances in the emerging field of *landscape genomics*, which for over a decade has been studying the genomic basis of local adaptation of populations across spatial and temporal scales, is opening up new possibilities, providing innovative solutions for sustainable and adaptive management and protection of forests in the future.

Three strategies

The capacity of tree species to cope with climate change is based on three complementary types of responses: *species migration*, *phenotypic plasticity*, and *hereditary adaptation*. Range shift is the most commonly considered response of tree species to these changes. In Europe, northward range shifts are predicted for most trees, while upward altitudinal migrations are expected for mountain species.

Our forests as we know them may therefore change significantly depending on how much the climate changes. Even under the most optimistic climate change scenario, which assumes a temperature increase of ~2.4°C, there is expected to be a significant loss of favorable habitat and a displacement of the climatic optimum for most forest trees beyond their current ranges, especially in southern Europe. However, this does not mean that we will have the Mediterranean forests growing in Central Europe in the future, just because suitable climatic conditions for them will be found in Central Europe. Among other things, this is due to the relatively slow pace of tree migration. For example, it is estimated that the average migration rate of late-successional tree species, such as the European beech, is only 15–25 meters per year.

Given this limitation, the current rate of climate change seems too fast for some species and their populations to adapt to keep up with the optimal conditions for them. This puts them at risk of maladaptation and eventually even extinction. Therefore, the ability of tree species to cope with environmental changes will mainly rely on the other two responses listed above: phenotypic plasticity and local hereditary adaptation. So, assuming a certain scenario of climate change, can we say what the future ranges of various species will be? To answer this question, reliable predictive models are needed, and developing them continues to be a challenge.

Genetic offset modelling

Traditional predictive models, mainly based on climatic aspects, have assumed full homogeneity in how populations of a given species respond across its whole range, thereby ignoring potential intra-species variability resulting from local adaptation. However, failure to account for adaptive variability can result in overestimated predictions, ultimately resulting in mistargeted species conservation and management efforts. A solution to this problem can be found in the recently developed concept of *genomic offset*, which has proven to be a promising tool integrating genomic and environmental data to assess the impact of climate change on patterns of adaptive genetic variability within a species' range.

This approach was developed by the US researchers Matthew C. Fitzpatrick and Stephen R. Keller to assess changes in the genetic composition of populations of the balsam poplar (*Populus balsamifera*). This new perspective on spatial modeling, resulting from advances in landscape genomics, represents a significant step toward making reliable predictions of species' responses to climate change. Simply put, genomic offset is a measure of the extent to which a given population will have to adapt to future environmental conditions within the species range, taking into account the adaptive variability of the population.

> The concept of *genomic offset* has recently gained attention in the context of developing strategies for managing and conserving forest tree resources.

This requires determining the genomic basis of local adaptation based on sequencing and environmental data, and applying advanced computational methods and multiple simulations. Essentially, the approach is a predictive measure of genome-wide changes in allele frequencies (gene versions) along environmental gradients, and is intended to determine the mismatch between a population's current genetic composition and one that would ensure its survival under changing environmental conditions. In other words, these predictions can help determine whether a population can be self-sustaining in the face of future environmental change, or whether it may require human intervention. Many scientific studies focusing primarily on forest tree species now emphasize the importance of incorporating the genomic basis of local adaptation into predicting population responses to climate change.

Modelling of future species distribution, taking into account changes in climatic conditions and

Diagram illustrating
the concept
of genomic offset
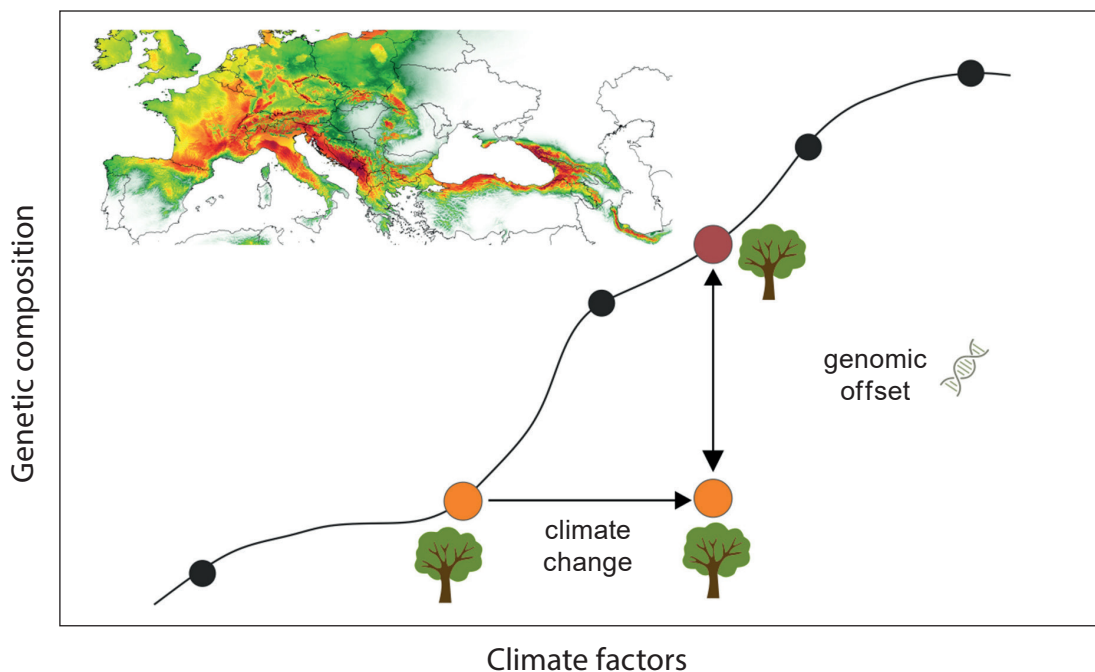
adaptation potential, has recently been performed for European beech in the western Alps, red spruce in the eastern part of North America, and Scottish populations of dwarf birch. These studies have assessed the risk of *in situ* population maladaptation, to map out future habitat suitability taking account of local adaptations, and to identify populations with the potential to provide seed material that maximizes genetic variation and minimizes population maladaptation in the face of climate change.

Accelerated resettlement

The distribution of the European beech is projected to change significantly in response to climate change. Traditional forecasting methods do not account for the adaptive variability of the species and their populations, and so we do not really know how well individual populations will be able to adapt to the new conditions

The capacity of tree species to adapt in the future primarily depends on their current genetic variability. Therefore, great attention is paid to preserving the widest level of variability, as well as to monitoring the demographic and genetic threats that stem from climate change. In practice, however – especially in the case of forest trees – very few conservation strategies take into account the resources of genetic diversity that determine a species' adaptive potential, which is of paramount importance for its sustainability. While genetic information is utilized in various conservation measures, the indicators often used (e.g. the Shapley index) are based solely on estimates of neutral genetic variability. Conservation efforts aimed solely at promoting or preserving neutral variability may be misguided; therefore, assessing adaptive variability should be an integral part of developing management and conservation strategies for forest tree species.

Climate change is likely to disrupt local adaptation and exceed the natural ability of species to respond by adaptation or migration, and population maladaptation poses the risk of local extinctions. To keep pace with climate change, scientists and foresters are seeking to develop tools to facilitate decisions about sustainable forest management in the face of climate change.

One of the new concepts, for example, involves moving beyond *in situ* conservation and the long-standing paradigm of "local is best" – which

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prioritizes the use of using local seed sources – and instead applying *assisted migration* to address the challenge. The term assisted migration encompasses a wide variety of conservation methods, including both *assisted gene flow* within the species' current range and *assisted colonization* beyond it. Essentially, this solution involves the human-assisted transfer of individuals/populations possessing alleles (gene versions) that are better adapted to the forecasted climatic conditions, as determined based on climate models. Assisted migration focuses on addressing the lagging adaptation of species or populations which do not adapt rapidly enough to ongoing climatic changes or have limited dispersal abilities to colonize climatically more suitable areas. Although this accelerated relocation is considered an effective forest management and conservation strategy to counter current climate change and associated threats, the application of such solutions still raises controversies due to the risk of failure. Firstly, climate change predictions are fraught with significant uncertainty. Secondly, factors other than climate may support local adaptation.

Another drawback in implementing this strategy is the potentially harmful genetic consequences, such as outbreeding depression, leading to the disruption of local adaptations. Therefore, to ensure that efforts in this regard do not fail, it is necessary to incorporate genomic data on local adaptation into climate models. Such models increasingly complement provenance experiments to identify populations containing desirable genotypes that, when translocated to target locations, would minimize disruptions to local climate adaptation, thus maximizing adaptation to changing environmental conditions. While not a perfect tool, such models offer some insight into what to expect in the future, taking the evolutionary potential of populations into account.

Preservation of resources

As mentioned above, the concept of genomic offsets has recently gained popularity in the development of forest management and conservation strategies focused on adaptation to climate change, such as assisted gene flow or assisted migration. For instance, by using an approach that integrates genotype–environment association analyses to detect local adaptations and to model adaptive alleles in the context of climate change, Swedish researchers Pär K. Ingvarsson and Carolina Bernhardsson have identified genetic shifts for European aspen (*Populus tremula*) populations in Sweden. Among the Swedish populations studied, they identified those that could respond well to climate change and serve as a source for introducing adaptive alleles into northern populations that

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Pine progeny testing plantation, Człuchów Forest District

are expected to experience significant maladaptation within a relatively short period (~50 years). The authors emphasize the usefulness of these results in developing assisted migration strategies.

Spatial modelling of environmental threats is becoming increasingly common, as practitioners seek information about the likely impact of environmental changes on ecosystems. This knowledge can be applied to forest conservation and management to meet the challenges of the coming years. Genomic offset-based predictions integrate intra-species genomic variation, filling the gap in our knowledge about adaptation to local environmental conditions. They provide the scientific basis for developing assisted gene flow or assisted migration strategies, which are currently the foundation of conservation programs focused on climate change adaptation. However, for such predictions to be fully utilized, we need a better understanding of how the uncertainty associated with these approaches might affect conservation planning. This can be achieved through provenance experiments, which are currently an essential part of climate adaptation research on trees. Although such experiments are often time-consuming and costly, they provide crucial comparative data, serving as a real-world verification of computer models.

Currently, the integration of traditional predictive models based on future climate change scenarios with population genomic variability is the latest research challenge being undertaken at the Institute of Dendrology PAS, as part of the project "Hybridization as an evolutionary process which reinforces the adaptive potential of tree species in the face of climate changes" (2020/39/D/NZ8/01522). ∎

Further reading:

Isabel N., Holliday J.A., Aitken S.N., Forest genomics: advancing climate adaptation, forest health, productivity, and conservation, *Evolutionary Applications* 2020.

Lewandowski A., Chmura D.J., Wójkiewicz B., Żukowska W.B., Silviculture in the Climate-Change Era, *Academia* 2019

Szmyt J., Silviculture and climate change – challenges, limitations and perspective. *Sylvan* 2020.