

## PREDICTIVE GENOMICS

# Genomics helps to predict maladaptation to climate change

The combination of highly resolved climatic and genomic data allows assessment of putative maladaptation of populations to climate change and can identify high-risk populations. Now, a study that accounts for migration and dispersal shows high maladaptation of a North American tree species in the northern and eastern distribution range.

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Global climate change is altering habitat conditions at an unprecedented pace, and it is unclear if and how populations can keep pace with these changes to avoid local extinction. Fields like nature conservation, forestry and fishery have a keen interest in predicting how populations will respond to environmental change<sup>1</sup>. Species distribution models have often been used to project the fate of species under altered climates. However, these models often treat a species as a uniform entity and ignore demographic and evolutionary properties of the different locally adapted populations. Therefore, there is a need to include intraspecific genomic data into predictive models<sup>2</sup>. Writing in *Nature Climate Change*, Andrew V. Gougherty and colleagues<sup>3</sup> incorporate migration and dispersal into predictive genomic models to show the potential maladaptation of a North American forest tree species to the projected future climate across its distribution range.

Genetic maladaptation means that the genetic composition of an individual or a population does not match to the one required in its habitat. One recently developed and popular approach to predict such putative genetic maladaptation to future conditions is genetic offset<sup>4</sup>, also called genomic vulnerability<sup>5</sup> or risk of non-adaptedness<sup>6</sup>. Based on a statistical relationship between contemporary genomic and environmental data, it predicts the genetic distance of a specific population today to its theoretically required genetic composition under possible future conditions<sup>7</sup> (Fig. 1a). Importantly, only genomic regions that are most likely involved in climate adaptation are informative for such assessments. Genetic offset is often projected across the current range of the studied species, indicating regions that are at high risk of being maladapted to projected future climates<sup>4,5</sup>. However, the potential for migration or dispersal, including active movement,

to more suited habitats has largely been ignored.

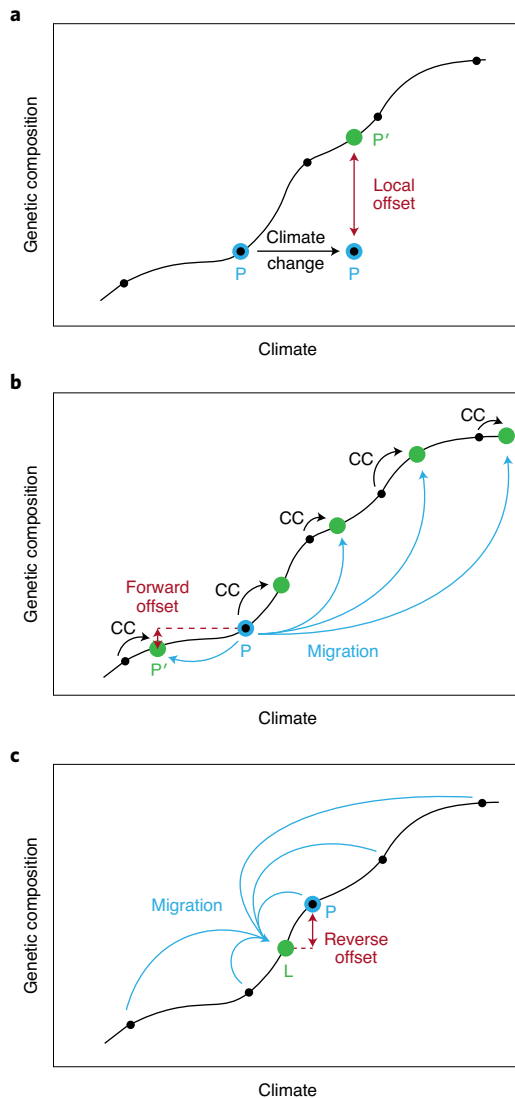
Gougherty and colleagues<sup>3</sup> extend the concept of genetic offset by including migration into their analyses. To do so, they look at genetic variation in flowering time genes of 81 Balsam poplar (*Populus balsamifera*) populations in North America. Flowering time genes are key in plants because they are involved in plant phenology by regulating the timing of growth, dormancy and reproduction. They have also been shown to play an important role in Balsam poplar's adaptation to climate<sup>8</sup>. Besides assessing the classic (local) genetic offset (Fig. 1a) associated with these genes that quantifies the risk of being maladapted to the future climate in situ (without migration), the authors developed two additional metrics. Forward genetic offset (Fig. 1b) indicates potential maladaptation assuming the populations have unlimited dispersal capacity to any location in North America. Since unlimited dispersal is unrealistic, the authors also assessed forward offset with different maximum dispersal distances. Reverse genetic offset shifts the focus from populations to locations, determining the degree of maladaptation of the contemporary population that genetically best matches the projected future climate of a specific location (Fig. 1c). Finally, the authors present a map that combines all three genetic offset measures to draw spatially explicit conclusions on the projected vulnerability towards changing climates.

Populations in the core of the distribution range exhibited the lowest risk of maladaptation to the projected future climate across the continent. This is in contrast to the general assumption that populations at the (warmer) southern range of the distribution are at lowest risk. The authors' explanation for this finding is that precipitation regimes, unlike temperature regimes, are expected to most prominently

shift along an east–west direction. In turn, northern and eastern populations exhibited the highest risk of genetic maladaptation. Given projected changes in climate, these high-risk populations would have to migrate across the whole continent within 50 years to reach a suitable climate, which is unrealistic given the dispersal capacity of the wind-dispersed Balsam poplar and the predominant wind directions (west to east).

The main novelty in the approach of Gougherty and colleagues<sup>3</sup> is the integration of migration (in a broad sense, ranging from active movement to exchange of genetic material) into the concept of genetic offset. But the actual strength of this study is that it touches on fundamental issues that help in the development of guidelines for conservation management and assisted migration (the intentional movement of individuals or seeds to a better suited habitat<sup>9</sup>). Besides assessing the potential in situ maladaptation of populations to the projected climatic changes, the approach can point to future habitats within dispersal distance that would match the current genetic characteristics of a population or identify provenances that one could choose for planting in a given site. Such assessments are especially important for long-lived species with long generation times, such as forest trees, which may have large problems keeping pace with climate change.

The concept of genetic offset has certain limitations. First of all, genetic offset does not predict if and how the populations will actually respond to climate change, but only assesses the risk of maladaptation from today's point of view. Second, the approach assumes that the relationship between climate and genetics that is observed today across space also holds true for the extrapolated future. Third, genetic offset does not include information on fitness-related phenotypic traits.



**Fig. 1 | Integrating migration to predict potential maladaptation to future climate change.** **a**, Local genetic offset. Based on a statistical relationship (black line) between the genetic composition of several populations (black dots) and their local, contemporary climate, the local offset (red) quantifies the genetic distance of a specific population today (P (blue)) to the one theoretically required under a future climate in situ (P' (green)); that is, without migration. **b**, Forward genetic offset. For this metric, a specific contemporary population (P (blue)) can migrate (blue arrows) to the habitat whose future climate (after climate change (CC)) best matches its genetic composition (P' (green)). Forward offset (red) then represents the genetic distance of P to P'. **c**, Reverse genetic offset. For a specific location and its future climate (L (green)), the reverse offset represents the minimum genetic distance of a contemporary population (P (blue)) to the theoretically required population for L. Fig. 1a is based on Fig. 3 in ref. <sup>7</sup>.

In other words, we cannot be sure whether the genetic polymorphisms included in assessing offset indeed influence fitness in

relation to climate. This shortcoming can only be solved with experiments that show which gene variants actually increase or

decrease fitness under certain climates<sup>10</sup>. Finally, this specific study includes only a handful of genes within the flowering time gene network, ignoring various gene networks that are of importance in climate adaptation<sup>11</sup>. The presented results should therefore be treated with caution. However, the study is important because it introduces an informative approach that should be extended to the genome-wide level.

In summary, genetic offset, originally promoted by Fitzpatrick and Keller<sup>3</sup> and developed further in the presented study, is a very promising approach to be used in conservation management and applied in assisted migration, especially with respect to future climate change. It incorporates the long-neglected intra-specific and adaptive characteristics of a species into spatiotemporal projections. In combination with other empirical, experimental and theoretical approaches, it can help to understand which populations are threatened in the future and identify human interventions that could mitigate the potential risks. The integration of migration and dispersal by Gougherty and colleagues<sup>3</sup> is an important step towards a comprehensive assessment of future maladaptation. □

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Published online: 18 January 2021

<https://doi.org/10.1038/s41558-020-00964-w>

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## Competing interests

The author declares no competing interests.