

Outwitting climate change with a plant 'dimmer'?

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For many plant species, such as the thale cress, which is often used in research, but also for food crops such as corn, rice and wheat, there are now initiatives currently mapping the genome of many subspecies and varieties. Credit: Regnault/ TUM

Plants possess molecular mechanisms that prevent them from blooming

in winter. Once the cold of winter has passed, they are deactivated. However, if it is still too cold in spring, plants adapt their blooming behavior accordingly. Scientists from the Technical University of Munich (TUM) have discovered genetic changes for this adaptive behavior. In light of the temperature changes resulting from climate change, this may come in useful for securing the production of food in the future.

Everyone knows that many plant species bloom at different times in spring. The time at which a plant blooms in spring does not follow the calendar, but is instead determined by environmental factors such as temperature and day length. Biologists have discovered that plants recognize these environmental factors via genetically determined programs and adapt their growth accordingly.

In order to adapt to new climate zones and to ensure the evolutionary success of the species, these genetic programs may be adapted over the course of evolution. These adaptive processes take place passively: Minor changes (mutations) take place in the genetic material (DNA sequence) of the [genes](#) involved. If an adaptation proves successful over the following years, a new population establishes itself as a genetically distinct subspecies.

Comparison of Biological Adaptations with Genetic Changes

In order to find out which mutations were used particularly frequently over the course of evolution, scientists compare biological adaptations such as shifts in the point in time at which blooming takes place with existing [genetic changes](#). For many plant species, such as the thale cress (*Arabidopsis thaliana*), which is often used in research, but also for food crops such as corn, rice, barley and wheat, there are now initiatives

currently mapping the genome (entire DNA sequence) of many subspecies and varieties. This makes comparisons at the DNA level particularly simple and efficient.

In the journal *eLife*, Ulrich Lutz from the Chair of Plant Systems Biology at the TUM and his colleagues from the Helmholtz Zentrum München jointly describe the results of a comparative sequence analysis of the FLM (FLOW-ERING LOCUS M) gene from over a thousand *Arabidopsis* genome sequences.

FLM binds directly to DNA, allowing it to influence the creation of other genes (transcription), which delays blooming. Via comparisons of the FLM DNA sequence from over a thousand subspecies, Lutz was able to determine which genetic changes occurred frequently as this plant evolved: Generally speaking, these are the changes that provide the plant with an adaptive advantage found in a large number of subspecies. Mutations that did not provide an advantage, on the other hand, were lost over time. The frequency of the changes is therefore an indication that these mutations were the most successful from an evolutionary point of view.

For the FLM gene he characterized, Lutz was able to demonstrate that the genetic changes that occur worldwide have an influence on how frequently and efficiently the FLM gene is read. As FLM is able to delay the point in time at which blooming occurs, a more intensive reading of the gene directly corresponds to later blooming. FLM behaves much like a light dimmer that the plant uses to regulate gene activity—and hence blooming—on a continuous scale.

FLM Gene Acts Like a Controller

The underlying gene changes influenced this reading of FLM. Modified DNA was found in the area of the gene 'switch' (promoter), which

regulates how much of the FLM gene is produced. In addition, the mechanism of [gene splicing](#) could also be observed: As part of this process, parts are cut out of the interim gene product. The quantity of active FLM can also be adapted via genetic changes that impact gene splicing. Hence, a direct dependency was found between the point in time of blooming and the quantity of the FLM gene, which in *Arabidopsis* can be finely adjusted via DNA sequence changes.

"The FLM variants we identified are ideal candidate genes that thale cress can use to adapt the point in time at which blooming takes place to the [temperature changes](#) caused by [climate change](#)," said Professor Claus Schwechheimer from the Chair of Plant Systems Biology at TUM.

Findings May Help Plants Adapt to Climate Change

Temperature changes of just a few degrees Celsius during the growth phase of crop plants such as canola or sugar beets have a negative impact on agricultural production. In the future, the findings obtained by the team including the TUM scientists may allow the FLM gene to be used as a regulator to help adapt the blooming period to different temperatures as a result of climate change. With this knowledge, the goal of efficient food production over the long term is now within reach.

More information: Ulrich Lutz et al, Natural haplotypes of non-coding sequences fine-tune flowering time in ambient spring temperatures in *Arabidopsis*, *eLife* (2017). [DOI: 10.7554/eLife.22114](https://doi.org/10.7554/eLife.22114)

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