

# A novel explanation for a floral genetic mystery

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Scientists at the University of Jena, Germany have put forth a novel explanation of the evolutionary driving force behind a genetic switching circuit that regulates flower development and survival. The hypothesis, based around the obligatory pairing of certain molecules, is published January 16 in the open-access journal *PLoS Computational Biology*.

The authors believe that their findings "strongly support the view that the unexpected complexity of the floral homeotic gene switch considered here was not simply produced by random genetic drift but evolved because it provided the plant with a clear selective advantage"

In the *Arabidopsis thaliana* flower, a particular class of genes - DEF-like and GLO-like floral homeotic genes - regulates the development of petals and stamens over long periods of time, using "genetic switches". These genes are self-activating via a heterodimer (a complex of two different molecules) of their protein products, therefore binding the activity of each gene to that of the other one. The reason for their total functional interdependence has long remained unclear.

The authors used computational modeling to investigate potential explanations for why these two interdependent genes exist, since one gene alone could in principle provide the switching functionality in these plants' organs. The group shows that the obligate heterodimerization mechanism found in DEF- and GLO-like genes reduces the susceptibility of the genetic switch to failure caused by stochastic noise or interference.

The study was targeted at a specific mechanism of genetic regulation and cannot directly be transferred to other mechanisms, caution the authors. However, the underlying methodology may be applicable to a whole range of genetic regulatory motifs.

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