

The Cardamine hirsuta genome offers insight into the evolution of morphological diversity

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Xiangchao Gan, Angela Hay, Michiel Kwantes, Georg Haberer, Asis Hallab, Raffaele Dello Iorio, Hugo Hofhuis, Bjorn Pieper, Maria Cartolano, Ulla Neumann, Lachezar A. Nikolov, Baoxing Song, Mohsen Hajheidari, Roman Briskine, Evangelia Kougioumoutzi, Daniela Vlad, Suvi Broholm, Jotun Hein, Khalid Meksem, David Lightfoot, Kentaro K. Shimizu, Rie Shimizu-Inatsugi, Martha Imprialou, David Kudrna, Rod Wing, Shusei Sato, Peter Huijser, Dmitry Filatov, Klaus F. X. Mayer, Richard Mott & Miltos Tsiantis

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Abstract

Finding causal relationships between genotypic and phenotypic variation is a key focus of evolutionary biology, human genetics and plant breeding. To identify genome-wide patterns underlying trait diversity, we assembled a high-quality reference genome of *Cardamine hirsuta*, a close relative of the model plant *Arabidopsis thaliana*. We combined comparative genome and transcriptome analyses with the experimental tools available in *C. hirsuta* to investigate gene function and phenotypic diversification. Our findings highlight the prevalent role of transcription factors and tandem gene duplications in morphological evolution. We identified a specific role for the transcriptional regulators PLETHORA5/7 in shaping leaf diversity and link tandem gene duplication with differential gene expression in the explosive seed pod of *C. hirsuta*. Our work highlights the value of comparative approaches in genetically tractable species to understand the genetic basis for evolutionary change.

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