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The genetic architecture of heterochronsy as a quantitative trait: lessons from a computational model

Lidan Sun*, Mengmeng Sang*, Chenfei Zheng*, Dongyang Wang, Hexin Shi, Kaiyue Liu, Yanfang Guo, Tangren Cheng, Qixiang Zhang and Rongling Wu

Corresponding authors: Rongling Wu, Center for Computational Biology, College of Biological Science and Technology, Beijing Forestry University, Beijing 100083, China. Tel.: 01186 10 6233 6283; Fax: 01186 10 6233 6164; E-mail: rwu@bjfu.edu.cn or Center for Statistical Genetics, The Pennsylvania State University, Hershey, PA 17033, USA. Tel.: 001 717 531 2037; Fax: 001 717 531 0480; E-mail: rwu@phs.psu.edu; Qixiang Zhang, Beijing Key Laboratory of Ornamental Plants Germplasm Innovation & Molecular Breeding, National Engineering Research Center for Floriculture, Beijing Forestry University, Beijing 100083, China. Tel: 01186 10 6233 6321, Fax: 01186 10 6233 6321, Email: zqxbjfu@126.com
*These authors contributed to this work equally.

Abstract

Heterochrony is known as a developmental change in the timing or rate of ontogenetic events across phylogenetic lineages. It is a key concept synthesizing development into ecology and evolution to explore the mechanisms of how developmental processes impact on phenotypic novelties. A number of molecular experiments using contrasting organisms in developmental timing have identified specific genes involved in heterochronic variation. Beyond these classic approaches that can only identify single genes or pathways, quantitative models derived from current next-generation sequencing data serve as a more powerful tool to precisely capture heterochronic variation and systematically map a complete set of genes that contribute to heterochronic processes. In this opinion note, we discuss a computational framework of genetic mapping that can characterize heterochronic quantitative trait loci that determine the pattern and process of development. We propose a unifying model that charts the genetic architecture of heterochrony that perceives and responds to environmental perturbations and evolves over geologic time. The new model may potentially enhance our understanding of the adaptive value of heterochrony and its evolutionary origins, providing a useful context for designing new organisms that can best use future resources.

Key words: heterochrony; hQTL; genetic architecture; functional mapping; growth form; woody plant

Introduction

A fundamental question in biology is how plants adapt and evolve in a range of environmental changes. Plants adapt to the new environment through developing new physical structures and reproductive mechanisms [1–3]. Through Darwinian natural selection, some new structures and mechanisms become new species

Lidan Sun is a lecturer in Ornamental Genetics in Beijing Key Laboratory of Ornamental Plants Germplasm Innovation and Molecular Breeding, National Engineering Research Center for Floriculture at Beijing Forestry University.
Mengmeng Sang is a doctoral student in Computational Genetics in the Center for Computational Biology at Beijing Forestry University.
Chenfei Zheng is a doctoral student in Computational Genetics in the Center for Computational Biology at Beijing Forestry University.
Dongyang Wang is a Master's student in Computational Biology Center for Computational Biology at Beijing Forestry University.
Hexin Shi is a Master's student in Computational Biology in the Center for Computational Biology at Beijing Forestry University.
Kaiyue Liu is a Master's student in Computational Biology in the Center for Computational Biology at Beijing Forestry University.
Yanfang Guo is a Master's student in Computational biology in the Center for Computational Biology at Beijing Forestry University.
Tangren Cheng is an associate professor of Ornamental Genetics and the executive director of National Engineering Research Center for Floriculture at Beijing Forestry University.
Qixiang Zhang is a professor of Ornamental Genetics and the director of National Engineering Research Center for Floriculture at Beijing Forestry University.
Rongling Wu founded the Center for Computational Biology at Beijing Forestry University. He is distinguished professor of Statistics and director of the Center for Statistical Genetics at the Pennsylvania State University.
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