

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

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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

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