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Paper

Evo-Devo-EpiR: a genome-wide search platform for epistatic control on the evolution of development

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Abstract

Evo-devo is a theory proposed to study how phenotypes evolve by comparing the developmental processes of different organisms or the same organism experiencing changing environments. It has been recognized that nonallelic interactions at different genes or quantitative trait loci, known as epistasis, may play a pivotal role in the evolution of development, but it has proven difficult to quantify and elucidate this role into a coherent picture. We implement a high-dimensional genome-wide association study model into the evo-devo paradigm and pack it into the R-based Evo-Devo-EpiR, aimed at facilitating the genome-wide landscaping of epistasis for the diversification of phenotypic development. By analyzing a high-throughput assay of DNA markers and their pairs simultaneously, Evo-Devo-EpiR is equipped with a capacity to systematically characterize various epistatic interactions that impact on the pattern and timing of development and its evolution. Enabling a global search for all possible genetic interactions for developmental processes throughout the whole genome, Evo-Devo-EpiR provides a computational tool to illustrate a precise genotype-phenotype map at interface between epistasis, development and evolution.

Key words: developmental process; epistasis; evolution; functional mapping; QTL; variable selection

Introduction

As the raw material of evolution, genetic variation is first translated into phenotypic variation through development, followed by phenotypic diversification and speciation [1–3]. To cope with this developmental complexity of evolution, the modern synthetic theory of phenotypic evolution has incorporated the interplay between developmental components and gene actions, leading to the emergence of evolutionary developmental biology (evo-devo) as a distinct field [4, 5]. It has been widely recognized that, in each of the multiple stages of phenotypic development, many genes operate jointly, often forming a complex network of interactions between different genes and between genes and environments [6]. To better understand the genetic mechanisms of trait evolution, therefore, a detailed picture of how genes act and interact to control various stages of development must be illustrated in a quantitative way.

The advent of DNA-based genome-wide linkage maps and association studies has revolutionized quantitative genetic analysis approaches by mapping and estimating individual quantitative trait loci (QTLs) that contribute to the genetic architecture of complex traits [7–10]. These studies, implemented with variable selection, provide a fuel to systematically search for all possible genetic variants at a time from a large pool of DNA markers. Xu and group presented several first models that can estimate all genetic effects on static complex traits using markers from the whole genome [11, 12]. Beyond the analysis of static phenotypes measured at single time points, a statistical method—functional mapping—can reveal the developmental change of genetic effects over time [10, 13–16]. Functional mapping can estimate the dynamic changes of

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