

AlloMap6: an R package for genetic linkage analysis in allohexaploids

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Abstract

Allopolyploids are a group of polyploids with more than two sets of chromosomes derived from different species. Previous linkage analysis of allopolyploids is based on the assumption that different chromosomes pair randomly during meiosis. A more sophisticated model to relax this assumption has been developed for allotetraploids by incorporating the preferential pairing behavior of homologous over homoeologous chromosomes. Here, we show that the basic principle of this model can be extended to perform linkage analysis of higher-ploidy allohexaploids, where multiple preferential pairing factors are used to characterize chromosomal-pairing meiotic features between different constituent species. We implemented the extended model into an R package, called AlloMap6, allowing the recombination fractions and preferential pairing factors to be estimated simultaneously. AlloMap6 has two major functionalities, computer simulation and real-data analysis. By analyzing a real data from a full-sib family of allohexaploid persimmon, we tested and validated the usefulness and utility of this package. AlloMap6 lays a foundation for allohexaploid genetic mapping and provides a new horizon to explore the chromosomal kinship of allohexaploids.

Key words: allohexaploid; preferential pairing factor; recombination fraction; EM algorithm; persimmon

Introduction

Polyploidy is an important force for the evolution of plants [1, 2]. It was estimated that 70–80% of angiosperms are polyploids or have ever experienced phases of polyploids during their evolutionary process [3, 4]. Many crops, such as wheat, sugarcane, cotton and canola, are polyploids, which play a central role in agriculture [5]. Polyploids can be classified into two types, i.e. allopolyploids, whose chromosomes are composed of distinct genomes through interspecific hybridization, and autopolyploids, in which the chromosome doubling of genetically similar genomes is because of the fusion of unreduced gametes [2, 6, 7]. Of all ployploids, >75% are found to be allopolyploids [8].

A growing body of evidence indicates that allopolyploids have great advantages in response to selection and adaption [9, 10].

In addition, according to how chromosomes pair at meiosis, the nature of polyploids can be depicted by bivalent polyploids, multivalent polyploids and mixed polyploids [9]. In general, extreme allopolyploids present bivalent formation in which more similar chromosomes are expected to have higher pairing frequencies than less similar chromosomes, a phenomenon which can be described by the preferential pairing factor [11–13]. On the other hand, extreme autopolyploids are pervaded with multivalent formation in which more than two chromosomes pair at a time, resulting in the appearance of two sister chromatids into the same gamete, called double reduction [14]. Mixed polyploids

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