

AlloMap6: an R package for genetic linkage analysis in allohexaploids

Xuli Zhu,* Huan Li,* Meixia Ye, Libo Jiang, Mengmeng Sang and Rongling Wu

Corresponding author: Rongling Wu, Center for Computational Biology, College of Biological Sciences 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

*These authors contributed equally to this work.

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 polyploids, >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

Xuli Zhu is a Master's student in computational genetics in the Center for Computational Biology at Beijing Forestry University.

Huan Li is a doctoral student in plant genomics in the Center for Computational Biology, Beijing Forestry University.

Meixia Ye is a lecturer in computational biology and bioinformatics at the Center for Computational Biology at Beijing Forestry University, China.

Libo Jiang is a PhD candidate in computational genetics in the Center for Computational Biology at Beijing Forestry University, China.

Mengmeng Sang is a doctoral student in computational genetics in the Center for Computational Biology at Beijing Forestry University, China.

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, USA.

Submitted: 18 June 2016; Received (in revised form): 10 August 2016

© The Author 2016. Published by Oxford University Press. All rights reserved. For Permissions, please email: journals.permissions@oup.com