

## عنوان مقاله:

Analysis of floral development related gene co-expression networks in Arabidopsis thaliana

## محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

تعداد صفحات اصل مقاله: 1

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## خلاصه مقاله:

The study of flower development is of great scientific, practical and applicable importance; because in this way, flowering control can be provided in plants. For example, it can be used in the production of male sterile plants to produce hybrid seeds. It should be noted that many regulatory genes are involved in the flowering process that have been identified previously. The interactions of genes involved with the formation of flower components are complex. In general, identifying the function of individual genes involved in flower development has not led to a complete and accurate understanding of the developmental process. In order to overcome this challenge, nine co-expression genes network of Arabidopsis thaliana for two wild and three mutant ecotypes were reconstructed and analysed using WGCNA R package and cytoscape software platform. In the continuation of the research, the modules involved in trait control were identified and compared. After performing customized RandomWalk algorithm on the co-expression networks, 10 key genes in addition to the seed genes used in this study were determined that have an important role in phase transition. Topological and functional analysis of the networks indicated deeper changes during the phase transition phenomena in biochemical pathways (alternative pathways were activated). In conclusion, focusing on the hormone alternative pathways could provide novel approaches to control flowering by genetic engineering.

## کلمات کلیدی:

systems biology; Arabidopsis thaliana; floral development; network analysis; community detection; flower differentiation

## لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/1473740>

