

Computational Prediction of Gene Regulatory Networks in Plant Growth and Development

Current Opinion in Plant Biology

February 1, 2019

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Plants integrate a wide range of cellular, developmental, and environmental signals to regulate complex patterns of gene expression. Recent advances in genomic technologies enable differential gene expression analysis at a systems level, allowing for improved inference of the network of regulatory interactions between genes. These gene regulatory networks, or GRNs, are used to visualize the causal regulatory relationships between regulators and their downstream target genes. Accordingly, these GRNs can represent spatial, temporal, and/or environmental regulations and can identify functional genes. This review summarizes recent computational approaches applied to different types of gene expression data to infer GRNs in the context of plant growth and development. Three stages of GRN inference are described: first, data collection and analysis based on the dataset type; second, network inference application based on data availability and proposed hypotheses; and third, validation based on in silico, in vivo, and in planta methods. In addition, this review relates data collection strategies to biological questions, organizes inference algorithms based on statistical methods and data types, discusses experimental design considerations, and provides guidelines for GRN inference with an emphasis on the benefits of integrative approaches, especially when a priori information is limited. Finally, this review concludes that computational frameworks integrating large-scale heterogeneous datasets are needed for a more accurate (e.g. fewer false interactions), detailed (e.g. discrimination between direct versus indirect interactions), and comprehensive (e.g. genetic regulation under various conditions and spatial locations) inference of GRNs.

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