A co-expression network for gene function characterization in barley

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Motivation

The recent advent of high-throughput technology and the exponential increase in computer power have moved biology into a revolutionary mode, shifting the focus of molecular biologists from single genes to whole genomes The possibility of exploring gene function is extremely attractive in such a context of high-throughput data generation and computational inference based on similarities in gene expression has been proved to be a valuable tool for functional characterization. The modern theory of networks offers a new conceptual framework for the analysis of gene expression both at the transcriptomic and proteomic levels: genome-scale data sets can infact be conveniently visualized as networks of gene/protein co-occurrences where genes/proteins are represented by nodes and the relationships between them are represented by connections. This paper reports just an "in silico" approach to gene expression analysis based on a gene co-expression network.

Methods

In the present study we developed and analysed a barley gene co-expression network resulting from "in silico" study of several cDNA libraries. The network was divided into communities and their functional characterization was analysed. Annotation confidence values were used as selection criteria for choosing those communities most likely to be biologically relevant. Moreover, experimental testing has been carried out to check the relationship between network and biological properties and to identify and suggest effective strategies of information extraction from the network-derived data.

Results

Our results illustrate the advantages of a dual approach, based either on "in silico" and "wet" biology, for functional genomics investigations and extraction of information from the huge amount of data publicly available nowdays. We believe that the network here reported could be a powerful tool in plant genomics representing an advanced starting point for opening global perspectives of genetic systems at the molecular level and a challenge for translating sequence into function.

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