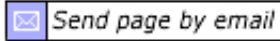
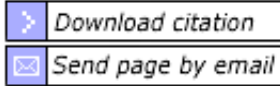


Exceptional

F1000 Factor **9.0**

EndNote



Extension of a genetic network model by iterative experimentation and mathematical analysis.

Locke JCW, Southern MM, ... , Turner MS, Millar AJ

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Faculty Comments

Faculty Member

Charles Auffray

 Centre National de la
 Recherche Scientifique
 (CNRS), France
 PHYSIOLOGY

 Hypothesis

 Tech Advance

Comments

This is, in my view, a milestone paper for the emerging field of systems biology, demonstrating the power of an iterative process combining modeling and simulation of experimental data to generate and test hypotheses on the functioning of biological systems. The authors went two cycles of model building and refinement based on existing and newly designed experiments on circadian clocks in *Arabidopsis*. As an initial feedback loop failed to account for some of the known features of the circadian rhythms, including control of time delays, they first introduced an additional unknown component X in their model, which had a better but incomplete fit with observations. In the second iteration, they introduced a second unknown component Y and an interlocked feedback loop, resulting in a much better fit of the model, which also accounts for the robustness of the circadian clock. They further identified GIGANTEA as a likely candidate for the Y component, and proposed novel experiments for further refinement of their model. This is an example which should inspire systems biologists in other research areas. See also comments by Lee Sweetlove [[nonpub113939](#)]. For the abstract of this paper, please see

<http://www.nature.com/msb/journal/v1/n1/full/msb4100018.html>

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