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Application of mathematical modeling to analyze the flowering activation motif during vernalization in legumes

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Motivation and Aim: The mechanism of vernalization-induced flowering has been extensively studied in *Arabidopsis* but remains largely unknown in legumes. The orthologs of the *FLOWERING LOCUS C (FLC)* gene, a major regulator of vernalization response in *Arabidopsis*, are absent or non-functional in the vernalization-sensitive legume species. Nevertheless, the legume integrator genes *FLOWERING LOCUS T* (*FT*) and *SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1* (*SOC1*) have been shown to be involved in the vernalization-induced floral transition. However, their regulatory contribution remains unexplored. The *FT* and *SOC1* genes are usually present in several paralogous copies in the legume genomes. We performed the theoretical and data-driven analyses of a feed-forward regulatory motif that includes a vernalization-responsive *FT* gene and several *SOC1* genes, which independently activate the meristem identity gene *PROLIFERATING INFLORESCENCE MERISTEM* (*PIM*) and thereby mediate floral transition [1].

Methods and Algorithms: The model is formulated in terms of the ordinary differential equations. The dynamical models to fit the experimental data are based on the kinetic equations with the Michaelis–Menten kinetics.

Results: Our theoretical model showed that the multiple regulatory branches in the regulatory motif facilitated the elimination of meaningless signals and amplified useful signals from the upstream regulator. We further developed and analyzed four data-driven models of *PIM* activation in *Medicago trancatula* in vernalized and non-vernalized conditions in wild type and *fta1-1* mutants [2]. The model with *FTa1* providing both direct activation and indirect activation via three intermediate activators, *SOC1a*, *SOC1b*, and *SOC1c*, resulted in the most relevant *PIM* dynamics. In this model, the difference between regulatory inputs of *SOC1* genes was nonessential. As a result, in the *M. trancatula* model, the cumulative action of *SOC1a*, *SOC1b*, and *SOC1c* was favored [1]. This is in line with the suggested hypothesis of functional redundancy of *SOC1* genes.

Conclusion: Overall, we first performed the in silico analysis of vernalization-induced flowering in legumes. The considered vernalization network motif can be supplemented with additional regulatory branches as new experimental data become available.

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