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A computational model of plant life cycle: genetic mechanism of local adaptation in flowering time

The timing of the transition from vegetative to reproductive development is a critical adaptive trait as it is essential for plants to complete seed production in favorable conditions. Proposed in A. thaliana, the gene regulatory model of floral transition describes the complex interactions between environmental signals (e.g., photoperiod and temperature) and endogenous cues (e.g., size, leaf number, or age). I modeled the interaction between photoperiod and vernalization (low-temperature) pathways, and combined this gene regulation dynamics and growth dynamics in a genetic-physiological model to explore local adaptation to two different environments (Hyogo; the western part of central Honshu, and Hakodate; the southern part of the north island in Japan). Temperature is warmer and seasonal variations in daylength are smaller in Hyogo than Hakodate. For simplicity, I assumed long-day plants that are self-compatible and evergreen. The analysis of the model demonstrated that there is a clear difference in sensitivity to daylength between the two plant populations. It was predicted that a Hakodate population responds to more extreme critical daylength than the one in Hyogo, which enables the plant flower in appropriate season in mid spring in Hakodate. I discuss the validity of the theoretical prediction using the data of Arabidopsis halleri.