

Contribution of insertion-deletion polymorphism to vernalization-independent and photoperiod-insensitive flowering in legume plants

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Synchronization of flowering time with seasonal weather patterns is essential for the reproductive success of plants growing in climates experiencing significant annual cycles. Plants have evolved a complex molecular signaling network that promotes or inhibits flowering in response to environmental factors such as vernalization, photoperiod and high temperature. Photoperiod and vernalization responsiveness were the key adaptations that enabled plant reproduction in temperate climate. Their main function is to inhibit flowering in fall and winter, while promoting rapid transition to generative growth in the spring, when conditions for reproduction and seed maturation are optimal. These pathways differ by evolutionary timeline, as photoperiod detection appeared very early in plant history, whereas vernalization requirement had putatively evolved relatively recently, in response to major global cooling that occurred around 34 million years ago. It should be noted that major plant families, including legumes, were hypothetically already diversified at that time, therefore vernalization pathways may significantly differ between the model plant *Arabidopsis thaliana* and legumes.

Both pathways converge in the transcriptomic regulation of floral integratory genes, including the key component, *FLOWERING LOCUS T (FT)* gene. While *Arabidopsis* has only two *FT*-like genes (*FT* and a one close homolog, *TWIN SISTER OF FT*, that are partially sub-functionalized into photoperiod signaling and ambient temperature response), legume genomes usually encode higher number of *FT*-like genes, assigned into three subclades, *FTa*, *FTb* and *FTc*. The presence of multiple copies of floral integratory genes had relaxed selection pressure and driven rapid adaptation to local climatic conditions. It resulted in the loss of vernalization and/or photoperiod requirements, observed in selected breeding lines in response to spring sowing, as well as in some natural populations as a drought escape strategy. Knowledge about underlying mutations facilitates breeding of varieties better adapted to target agroecosystems.