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Preface

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Plant flowering behaviors vary widely among taxa. Some plants are annuals that flower only once in their life cycle and then die. By contrast, perennials live for many years and flower repeatedly. Among perennials, many woody plants exhibit a large year-to-year variation in flowering or fruiting. Understanding why and how such diversity in flowering behavior emerges is a central aim in ecology and evolutionary biology.

Recent advances in genomics and molecular biology using a model plant species *Arabidopsis thaliana*, an annual herb, can benefit ecology by facilitating the study of genetic basis that contributes to evolution of diverse flowering behavior in nature. The gene regulatory model of floral transition describes the complex interactions between environmental signals (photoperiod and temperature) and endogenous cues (e.g., size, leaf number, or age) (Bäurle and Dean 2006; Andrés and Coupland 2012). Analysis of a large number of accessions across multiple environments showed that two genes in the cold-sensing pathway (called vernalization), *FRIGIDA* (*FRI*) and *FLOWERING LOCUS C* (*FLC*), are major factors generating variations in cold requirement (Stinchcombe et al. 2004; Lempe et al. 2005; Shindo et al. 2005), and have allowed evolution of summer annuals (that complete flowering and seed production before winter comes) from winter annuals (in which flowering is strongly delayed unless plants experience winter; Koornneef et al. 2004; Sung and Amasino 2004; Scarcelli et al. 2007; Michaels et al. 2003; Werner et al. 2005).

Applications of these findings from *A. thaliana* to crops, such as rice, barley, maize, tomatoes, sunflowers, and sugar beet, have suggested the rapid evolution in the regulatory pathways controlling flowering responses to

environmental cues even among closely related species, while functions of some genes controlling the time to flower are highly conserved (Andrés and Coupland 2012). One of the universal factors for floral induction is *FLOWERING LOCUS T* (*FT*), which is made in the companion cells of the leaves and is transported from the leaves to the meristem through phloem (Kardailsky et al. 1999; Kobayashi et al. 1999). *FT* is called the floral pathway integrator that unifies multiple signals including two major environmental signals, photoperiod and temperature.

These findings from model plant species and crops provide new insight into the mechanism and evolution of mast flowering or masting. Masting is characterized by a large year-to-year variation in flowers/fruits and synchrony in reproduction among different individuals (Kelly 1994). Various hypotheses have been proposed to explain the evolutionary and physiological mechanisms of masting (Kelly 1994; Kelly and Sork 2002). In recent years, the role of internal resource dynamics as one of the proximate factors for masting has attracted much attention (Crone et al. 2009; Smail et al. 2011) with strong theoretical support from the resource budget model (Isagi et al. 1997; Satake and Iwasa 2000, 2002a, 2002b). The resource budget model assumes that plants accumulate resources every year, set flowers when the stored resources exceed some threshold level, and set seeds and fruits at a rate limited by pollen or pollinator availability. The model demonstrates that fluctuation of reproductive efforts can be induced by resource depletion after heavy flowering, and synchrony emerges in a self-organized fashion by coupling through pollen or pollinators (Tachiki et al. 2010).

In addition to temperature and photoperiod, the importance of carbohydrate and nitrogen availability in determining the incidence of flowering has been reported in many plant species (Bernier et al. 1993; Corbesier et al. 2002; Miyazaki et al. 2002; Corbesier and Coupland 2006; Yasumura et al. 2006; Han et al. 2008; Smail et al. 2011). Thus, it is likely that these resources play essential roles in the initiation of flowering in masting

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species. If this is the case, the expression of key flowering genes, such as FT, would be influenced by resource levels, and might show annual fluctuation when the levels of resource vary between years. Thus, expression analysis of key flowering genes in masting species would be useful to explore the role of resource availability as well as other environmental factors in flower initiation and development. Besides, uncovering gene regulatory pathways in masting species and comparing regulatory pathways between different species may give an in-depth understanding on the evolution of masting. Moreover, it will enable us to test the fundamental assumption of the resource budget model, the enhancement of flower initiation by increased resource availability.

This special feature challenges to link the physiological and molecular studies about masting. We hope that this Special Feature will provide readers with a useful overview of this field, and inspire new directions for future investigation regarding studies of plant reproductive ecology. Genetic understanding of flowering phenology is especially important in facing climate warming. Thus, advances in genomics and molecular biology in flowering timing can benefit applied ecology as well as basic ecology by enabling genetic-informed prediction on the phenological changes in response to future climatic change.

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