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Unravelling molecular basis of masting from transcriptome analysis and mathematical modelling

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The intermittent and synchronized production of a large amount of flowers and seeds is called masting or mast seeding. A family of resource budget models have been effective to evaluate proximate causes of masting. Applying recent advances in molecular and genetic studies about flowering time control to masting species is increasingly useful to unravel the underlying mechanism of masting. To uncover the molecular basis of masting, we performed global gene expression analyses in a typical masting species, *Fagus crenata* Blume. Using nonlinear time-series analyses, we examined causal relationships between gene expression, physiological status, and external environmental conditions. Our analyses unraveled the non-intuitive relationship between seasonal environment and expression profiles of genes involved in photoperiod and circadian clock pathways. The most striking result was the causal interaction between nitrogen transporter activity and expression of floral pathway integrator, *FLOWERING LOCUS T*. This result supports our previous finding that nitrogen is the key regulator of flowering in *F. crenata*. Our results highlight the importance of linking plant reproductive dynamics and nutrient cycling at ecosystem levels.

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