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Title: Rediscovering flowering in the laboratory, with a little help from nature

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Abstract: The interaction between a plant's genes and the environment is reflected in its phenotype, a dramatic example is the seasonal control of flowering. Changing the environment from natural settings to artificial controlled conditions affects phenotypic and genetic responses relating to flowering time. Controlled growth parameters can be refined to stimulate more natural behaviour in Arabidopsis to improve our understanding of molecular mechanisms related to season responses in plants.

Plant development is controlled by seasonal factors that include light and temperature. In nature the model plant *Arabidopsis thaliana* has a cosmopolitan distribution. It is native to most of Euroasia and North Africa, and naturalised to North America, Australia and parts of South America and South Africa. In the array of potential biotic, altitudinal, climatic and seasonal distributions, these persistent little plants experience myriad of micro-niche environments. The cosiest, and perhaps bizarre, being the controlled conditions of growth cabinets in laboratories, where decades of *A. thaliana* research has occurred. The majority of our understanding of the behaviour and function of flowering-time mechanisms in *A. thaliana* comes from experiments in climate chambers, but like all plants, it evolved to grow outside. Here in this issue the Imaizumi group resolved a key question regarding the consistency of our understanding of genetic responses associated to phenology, fitness and adaptation derived from simplified conditions when applying that knowledge to plants grown in the far more dynamic field settings [1].

A. thaliana flowering mutants, isolated under controlled conditions, have been prominent to detangling the related genetic components and specific environment cues [2]. Many mutants used to generate current flowering-time models have been transgenic, thus legally constrained to controlled experiments. Non-transgenic equivalents are more difficult to generate in fewer ecotypic backgrounds. Pioneering field investigations that supported that *A. thaliana* flowering models do not capture natural phenology, have included quantitative-genetic studies and growing non transgenic mutants in different geographical (spatial) and seasonal (temporal) times. [3, 4]. New models were developed that relate to the transition of flowering in the field [4]. As there are revealed examples of genetic regions that correlated to strong effects in natural environments not originally seen in controlled conditions[5], perhaps indicating that the current *A. thaliana* flowering-time models cannot capture the full range of natural seasonal phenology.

In this issue the Imaizumi group explicitly examines the molecular-genetic responses of *A. thaliana* flowering time to explain the developmental difference of controlled compared to field growth [1]. They correlated flowering-time and gene-expression profiles in these contrasting conditions. The results of a "trial and error" approach improved settings in chambers to more accurately stimulate natural responses. They identified two conditions, light quality and thermal-oscillating, that achieved their goal. Using this simulated "natural" setting, numerous ecotypes from different latitudes recapitulated the models of flowering

time and response of the key photoperiod response genes *CONSTANS* (*CO*) and *FLOWERING LOCUS T* (*FT*).

To decipher the molecular pathways underlying the controlled and simulated-natural flowering responses, transgenic studies examined differences in the flowering network in the unmodified and "natural" growth chamber conditions. These responses were then compared to non-transgenic mutants in outside experiments that could be legally examined. A correlation was seen with a high morning peak of *FT* expression for plants growing under natural and synthetic-natural conditions, which was absent from studies in controlled conditions. Such responses were consistent in different ecotypes and could be defined by linear models. [1].

Since the detected morning *FT* peak associated with slower degradation of CO protein by cooler temperatures is "novel" in a growth chamber setting, Imaizumi's group investigated the molecular mechanisms responsible using mutants in the flowering response, ambient-temperature pathway, photoreceptor and circadian-clock genes[1]. They found that the photoreceptors CRYTOCHROME 1 and 2 (CRY1 and CRY2) played a positive regulatory role in the afternoon *FT* peak, but not the morning peak. These receptors also influence morning degradation of CO protein. A number of circadian-clock genes were essential for normal *FT* expression. Interesting here is that clock variation has also been associated to *A. thaliana* field responses [6]. Additionally ambient temperature response and morning circadian-clock genes had negative regulatory roles on *FT* to counteract CO, FHY1 and FHL induction in the morning and afternoon. Together a rational understanding of why flowering in outside grown plants is differing from climate-chamber plants was explored.

The work by Imaizumi *et al*. [1] revealed a strong association between solar radiation and temperature to a small number of sensitive genes in natural conditions on flowering time, which are conserved across populations of *A. thaliana*. The demonstration that low red/far red ratios and oscillating temperatures are the environmental traits necessary to induce the natural rapid flowering response supports modelling work [4], and similar work in rice [7], revealing an agricultural and well as ecological significance. Imaizumi *et al*. provided a starting point to explore the mechanisms behind the naturally induced flowering response of which has previously been uncharacterised in long-day control studies in climate chambers. Beyond transition to flowering, their work demonstrates multi-disciplinary approaches to address the dissonance between artificial and natural studies. In the end an annual plant's

destiny is to flower, as after all, its fate lies with its geography, and is subject to the choice to germinate and when to flower.

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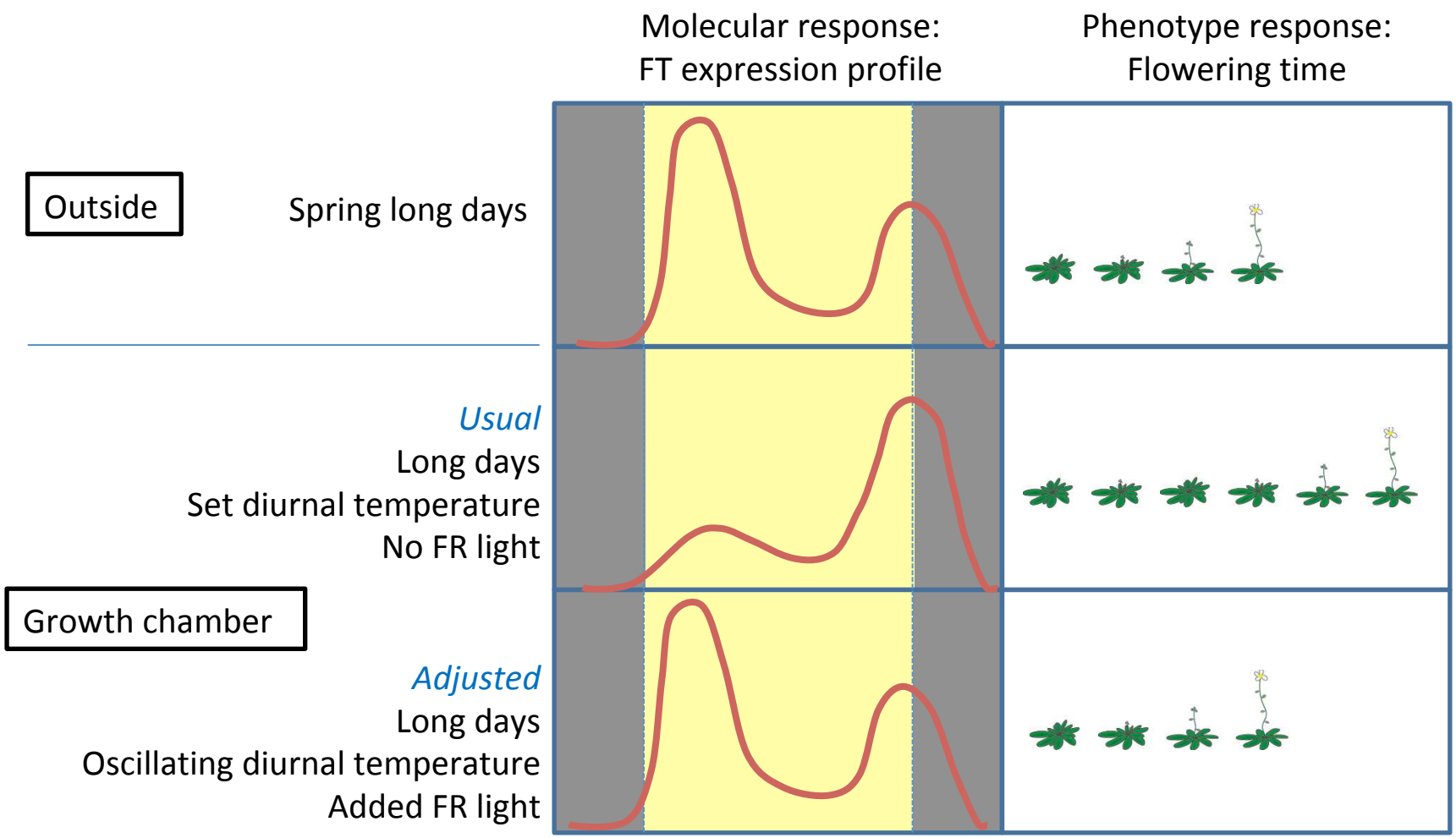

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