A non-linear model to explain how plants integrate light and temperature to decide how much to grow

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Plants need to assess the environmental cues to decide how much to grow after germination. Buried in the ground, the plant's hypocotyl (its young stem) must grow until it reaches the surface. Once this happens, the hypocotyl stops growing and the plant develops leaves to absorb sunlight. Many signals and mechanisms take part in this process. It is of particular interest to understand how the plants integrates light and temperature signals in this decision-making process.

Recent work with *Arabidopsis thaliana* plants [1] shows that the protein phytochrome B (PHYB) integrates temperature and light signals, and therefore PHYB has been proposed as the main regulator of hypocotyl growth after germination.

Based on new experimental data growing *Arabidopsis* plants under different light and temperature conditions, we propose a non-linear, mechanistic model of hypocotyl growth which includes the effect of proteins early-flowering 3 (ELF3) and constitutively photomorphogenic 1 (COP1) as well as that of PHYB. ELF3 is a transcriptional regulator that is related to *Arabidopsis*'s circadian clock, while COP1 marks other proteins for degradation. Our simulations agree very well with the data (Fig. 1).

Our model suggests that COP1 plays a much more relevant role than that of PHYB in integrating both temperature and light signals for hypocotyl growth in *Arabidopsis* after germination.

[1] J.-H. Jung, M. Domijan, C. Klose, S. Biswas, D. Ezer, M. Gao, A. K. Khattak, M. S. Box, V. Charoensawan, S. Cortijo, M. Kumar, A. Grant, J. C. W. Locke, E. Schäfer, K. E. Jaeger, and P. A. Wigge, Phytochromes function as thermosensors in Arabidopsis, Science **354**, 886-889 (2016).

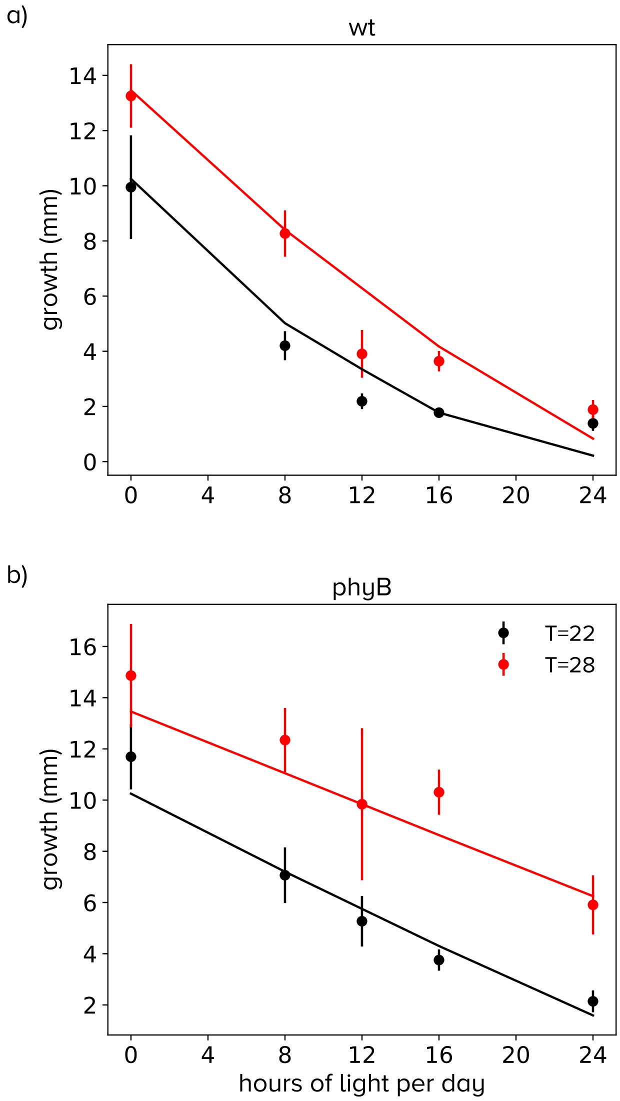

Fig. 1. Hypocotyl growth after 5 days. Plants were grown with red light for 5 days (120 horus), under two temperatures (22°C, black, and 28°C, red) and five daylength conditions (0, 8, 12, 16 and 24 hours of light per 24 hours of experiment). Points show average size of the plant (bars represent one standard deviation), while lines are the prediction of our dynamical model, for the wild type (a) and a mutant that lacks the protein PHYB (b).