Project title: **Testing the benefits of the biological clock for plant growth in a changing environment.**

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Supervisor 2: Prof. Vincent Danos (School of Informatics)

Description of the PhD project:

This interdisciplinary project combines experimental and theoretical approaches to tackle a longstanding question, building on two recent advances in the Millar lab. The gene circuit of the biological clock drives 24-hour rhythms in many biological processes, in almost all eukaryotes. In general, the clocks are thought to allow organisms to anticipate and prepare for the predictable changes of the day-night cycle, and thus confer an evolutionary advantage. That hypothesis has rarely been tested (e.g. Dodd et al., Science 2005), so this project will test the biochemical mechanisms whereby biological rhythms in plants confer a physiological advantage.

Clocks control the human sleep-wake cycle and cell division, or in plants, elongation growth and ~30% of nuclear gene expression. Key molecular mechanisms are well understood, such as the day-length (photoperiod) sensor that allows the daily clock to control seasonal flowering. We recently developed mechanistic, mathematical models for this regulation, showing how the circadian clock allows day-length responses and successfully predicting regulatory interactions that were validated in experiments (Salazar et al. Cell 2009; Song et al. Science 2012).

Here we focus on plant biomass, as a predictor of yield, and a yield trait in bioenergy crops. Maximum biomass is controlled by the rate of vegetative growth and also by flowering time, which sets the duration of growth. We have recently developed the first Framework Model for the growth of whole Arabidopsis plants, including vegetative growth rate. This project will test the contribution of the clock in regulating two processes, starch breakdown and flowering in intermediate day lengths. qRT-PCR, tagged protein quantification, metabolite assays and physiological studies of Arabidopsis mutants in the clock and starch pathways will quantify how particular defects affect rhythms, starch and growth. Comparing the data to the model predictions will test how well these processes (in the model) account for the clock's contribution to growth, and how much other rhythmic processes contribute (in the plant). The project can be extended to test other candidate processes, or to compare with results in the field.

The project will provide broad training in interdisciplinary biology, with both mechanistic and conceptual challenges. Experimental training (here and with international collaborators) will include large-scale, quantitative assays using automated liquid handling (qRT-PCR, starch assays), protein quantification, live reporter gene imaging and plant physiology. The theoretical training aims to understand, evaluate, simulate and modify dynamic, multiscale models, using both public and our specialised Systems Biology infrastructure. These will give the student dual expertise in "wet" and "dry" Biology, with experience of teamwork in the outstanding, interdisciplinary environment of SynthSys, Edinburgh's centre for Synthetic and Systems Biology (www.synthsys.ed.ac.uk).