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P2 — FLOWERING AND REPRODUCTION

P2.1

10:30 Monday 29th June 2009
95 years of photoperiodism: A long night's journey into day

Brian Thomas (Warwick)

The decisive role of the daily duration of light in promoting flowering of certain species was proposed independently by Klebs and Tournois at the beginning of the 20th century. This concept was taken forward in classic studies by Garner and Allard who introduced the terms photoperiod and photoperiodism. For the next seventy years, the physiologists held sway, defining the arguments about mechanisms through whole plant studies. In the last 20 years, the development of *Arabidopsis* as a model has completely redefined the research agenda and to a large extent the ways of thinking about photoperiodism. In this talk, the way in which recent molecular and genetic information relates to classic physiological concepts will be examined. In some cases there is a close alignment while in others, outstanding questions need to be resolved.

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P2.2

11:30 Monday 29th June 2009
Adaptive variation in photoperiod response in wheat and barley

David Laurie (John Innes Centre)

The timing of flowering during the year is an important adaptive trait and in cereals it has strong effects on grain yield and quality. Many plants use day length (photoperiod) and periods of low temperature (vernalization) to regulate flowering. The genetic pathways that control these responses are extensively studied in model species like *Arabidopsis* and this provides a platform for understanding other species. Responses to photoperiod and vernalization have been altered by selection during domestication and this is a major factor in the productivity of barley and wheat in the wide range of global environments they now occupy. Barley and wheat are closely related and their domestication provides a replicated experiment in evolution. An interesting finding is that mutations in orthologous photoperiod (Ppd) and vernalization (Vrn) genes have been selected to provide adaptation. The mutations underlying adaptive change are now well understood and the ways in which these mutations affect plant development are being uncovered. In the case of the Ppd genes, a loss of function mutation has been selected where there is a need to retard flowering and extend the growing season, while mutations altering expression have been selected where there is a need to compress the growing season or to flower in environments where the optimum growing season has short day conditions. The latter include the day neutral or "photoperiod insensitive" wheats of the green revolution. Knowledge of the underlying genes also allows us to understand how photoperiod and vernalization are integrated to regulate cereal growth.

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P2.3

12:00 Monday 29th June 2009
Control of perennial flowering and perenniality in *Arabis alpina*, a relative of *Arabidopsis thaliana*

Renhou Wang (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Sara Farrona (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Coral Vincent (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Fabio Fornara (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Anika Joecker (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Heiko Schoof (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Franziska Turck (Max-Planck Institute for Plant Breeding Research Cologne, Germany), Carlos Alonso-Blanco (Departamento de Genética Molecular de Plantas Centro Nacional de Biotecnología Cantoblanco 28049), Maria Albani (Max-Planck Institute for Plant Breeding Research Cologne, Germany), George Coupland (Max-Planck Institute for Plant Breeding Research Cologne, Germany)

Annual plants complete their life cycle in one year and initiate flowering only once, whereas perennials live for many years and flower

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repeatedly. Perenniality of higher perennial plants is closely related to their specific flowering behaviours. Although the molecular mechanism of flowering time control has been extensively studied in annual species such as *Arabidopsis thaliana*, little is known in perennials. We have developed a perennial model *Arabis alpina*, which is a relative of *A. thaliana*, to study perennial specific flowering time control and perenniality related issues including seasonal flowering, juvenility and polycarpy. We have generated *A. alpina* mutants showing altered flowering time and perenniality related behaviours. A spectrum of genes controlling flowering time have been cloned from *A. alpina* and their involvement in control of seasonal flowering, juvenility and polycarpy have been investigated. Our data show that some of these genes play critical roles in regulating perenniality related traits.

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P2.4

13:45 Monday 29th June 2009

FT control of floral transition and tuber formation in potato

Jose Antonio Abelenda (CNB, Madrid), Salomé Prat (CNB, Madrid), Cristina Navarro (CNB, Madrid), Javier Silva (CNB, Madrid)

Short-days promote tuber formation in all potato varieties and are a strict requirement for *Andigena* species to tuberize. Grafting experiments showed that inductive day length conditions are perceived by the leaves, a mobile *tuberigen* signal being produced in these organs and transported through the graft junction to the underground stems to induce tuber formation. Heterograft studies using flowering tobacco plants, in addition, showed that the flowering signal produced in the tobacco scions is able to induce tuber formation of the grafted potato stocks, hence suggesting that nature of both *florigen* and *tuberigen* signals might be related.

We have shown that the *florigen* FLOWERING LOCUS T (FT) protein functions in potato as a strong inducer of tuberization. Ectopic expression of a *rolC*:Hd3a-GFP construct, encoding the rice ortholog of *Arabidopsis FT*, induced tuberization transition of *Andigena* plants under non-inductive LDs. Moreover, we detected the Hd3a-GFP protein in the stolon tips of wild-type stocks grafted to these plants, consistent with a function of FT as the mobile *tuberigen* signal. Evidence will be provided showing that different type of meristem cells undergo floral or tuberization transitions and that interaction of FT with different partner proteins in these cells is likely to trigger these developmental processes. Isolation of potato FT orthologs, on the other hand, has shown that these transitions are signalled by different members of the FT gene family and that whereas an ortholog of the *SINGLE FLOWER TRUSS* (*SFT*) gene would mediate dayneutral floral transition, an additional FT paralog, regulated by CO, controls tuberization in SDs.

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P2.5

14:45 Monday 29th June 2009

The balance between CONSTANS and TEMPRANILLO controls floral induction

Soraya Pelaz (ICREA and CRAG (CSIC-IRTA-UAB) Barcelona)

Seasonal changes in day-length influence flowering time in many plant species. In *Arabidopsis* flowering is accelerated by exposure to long-day (LD). Those inductive photoperiods are perceived in leaves and initiate a long distance signaling mediated by CO and FT. *CO* is expressed in the phloem following a circadian rhythm. Only under LD does CO induce FT expression as high levels of CO in the evening coincide with the external light that stabilizes CO protein. Subsequently FT protein travels through the phloem to the shoot apex where, together with FD, initiates flowering. Despite the photoperiodic induction, a mechanism of floral repression is needed to avoid precocious flowering. TEMPRANILLO genes (TEM1 and TEM2) act as novel direct FT repressors. Molecular and genetic analyses suggest that a quantitative balance between the activator CO and the repressor TEM determines FT levels. Moreover, developmental TEM down-regulation marks the timing of flowering, as it shifts the CO/TEM balance in favour of CO activity, allowing FT transcript to reach the threshold level required to trigger flowering. We envision that this might be a general mechanism between long-day plants to ensure a tight regulation of flowering time.

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P2.6

15:45 Monday 29th June 2009

RNA processing mediated transcriptional silencing of *FLC* in flowering time regulation

Fuquan Liu (John Innes Centre), Sebastian Marquardt (John Innes Centre), Caroline Dean (John Innes Centre)

In *Arabidopsis thaliana*, autonomous pathway proteins accelerate flowering by repressing the floral repressor FLC. Genetic analysis further divided the autonomous pathway into different epistatic pathways, in one of them the RNA binding protein FCA physically interacts with a plant specific C-terminal extension of FY, the component of the RNA 3′ end formation complex CPSF, to repress *FLC*. RNA processing analysis of another FCA/FY pathway target, the *FCA* gene, showed that FCA/FY interaction enhances proximal, intronic polyadenylation. However, genetic analysis in order to identify more components required for FCA/FY to repress *FLC* revealed the requirement of the histone H3K4 me2 demethylase FLD. This suggests an involvement of chromatin silencing activities in FCA/FY mediated *FLC* repression. Recently, our biochemical work demonstrated that one step in this FCA mediated gene silencing pathway involves changing the composition of CPSF. Further forward genetic screening identified conserved 3′ end formation factors (CstF). Tilling array, nascent transcript RT-PCR, Pol II ChIP and histone modification analysis all support a model in which regulated RNA 3′ end processing is linked to downstream chromatin silencing activities to confer transcriptional repression of *FLC*.

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P2.7

16:15 Monday 29th June 2009

Juvenile phase change: Towards a physiological and genetic understanding

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Plants undergo a series of qualitative transitions during their life-cycle in response to both environmental and internal factors. One of the most distinguishable is the transition from a vegetative to reproductive phase of development. This stage is preceded by the juvenile to adult transition within the vegetative phase. During the juvenile phase (JP) plants are incompetent to initiate reproductive development and are effectively insensitive to photoperiod. With the change to adult phase, plants attain competence to respond to floral inducers, which is required for the transition to the reproductive phase.

Here we exploit *Antirrhinum*, a facultative long day plant that has a defined JP that is sensitive to light, to understand the genetic and environmental factors that regulate juvenility. A physiological assay has been developed in *Antirrhinum* that exploits photoperiod sensitivity to allow the length of the JP to be estimated. Environmental factors such as irradiance and CO_2 concentrations have been found as key modifiers of the length of the JP. A correlation between limiting photosynthetic assimilates and vegetative phase transition has been revealed by HPLC analysis of total soluble carbohydrates in plants at defined developmental stages. Studies are being carried out to determine whether plants are florally incompetent during the JP due to inactivity of the photoperiodic floral induction pathway.

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P2.8

16:35 Monday 29th June 2009

Flowering time diversity in *Miscanthus*: A tool for the optimisation of biomass

Elaine F. Jensen (IBERS)

The C4 tropical grass, *Miscanthus*, is a leading candidate for the provision of carbon neutral energy. Increasing pressures on land for food and fuel necessitate the optimisation of all crops for yield and quality. IBERS hosts one of the largest collections of *Miscanthus* germplasm and is the site of diverse and coordinated studies aimed at identifying and breeding top-performing *Miscanthus* varieties.

Plants grown for biomass require the longest possible season of vegetative growth as the switch to reproductive growth slows or stops biomass accumulation. Floral transition can also mark the initiation of senescence, when nutrients are remobilised to the underground rhizome for over-wintering. This remobilisation is critical for carbon neutrality, as well as improving combustion efficiency through the removal of harmful elements.

Phenological data accumulated over three years suggest a wide range of photoperiodic and thermal time requirements for flowering within the IBERS germplasm collection. This collection is the basis from which additional resources have been developed and are being used for association studies. A candidate gene approach has been adopted using sequences known to regulate floral transition in model species such as *Arabidopsis* and rice. A genetic map is under construction and quantitative trait loci will be identified using this and an F1 mapping family exhibiting diverse flowering times. In addition, transverse sections of plants grown in a controlled environment provide preliminary data concerning the photoperiodic and thermal time requirements of a number of genotypes, as well as days to heading following floral initiation.

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P2.9

Poster Session — Monday 29th June 2009

The EMS1 receptor kinase is required for non-meristematic proliferation of the *Arabidopsis* anther tapetum

Xiaoqi Feng (University of Oxford)

Animal cell fate is established following a fixed number and pattern of divisions of founder cells, whereas in plants cells are generated by meristems and acquire fates relying on positional signals. An exception may be in reproductive organs where, strict control appears to be exerted over the patterning and number of divisions of the parietal layers of the microsporangia.

We describe a signalling pathway required specifically for the patterned division of, and fate establishment in a small population of tapetal founder cells located at the periphery of the microsporogenous cells. *Arabidopsis* plants defective of the LRR receptor kinase EMS1/EXS, a member of this pathway, fail to form a tapetal cell layer. Instead, cells formed from the archesporial lineage that normally give rise to the tapetum remain undifferentiated, and the meiocytes are over-proliferated. Using the AtA9 tapetal-specific promoter (normally activated once the tapetum is formed) to drive the EMS1 kinase in ems1 plants, we have succeeded in reactivating these tapetal 'founder' cells inducing both division pattern and tapetal fate, and suppression of meiocyte over-proliferation.

Our data show conclusively the tapetal cell layer of the *Arabidopsis* microsporangium to be formed as a result of patterned anticlinal divisions by a small group of founder cells located at the periphery of the sporogenous cells, confirming that tapetal and sporogenous cells are derived from distinct cell lineages. We also demonstrate that a signalling pathway including both the EMS1 receptor kinase and its putative ligand TPD1, is necessary for this pattern of division.

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P2.10

Poster Session — Monday 29th June 2009

How to change your fate

Katja E. Jaeger (John Innes Centre), Sergey Lamsin (University of Tuebingen), Philip A. Wigge (John Innes Centre), Richard Morris (John Innes Centre)

The transition to flowering is a fundamental switch in the plant lifecycle, which is reflected in its complex regulation. Genes controlling the floral transition in the model plant *Arabidopsis thaliana* are grouped into 4 major pathways. A major integrator of these pathways is the gene *FLOWERING LOCUS T* (*FT*). Genetic approaches have revealed most of the components necessary for flowering and how these interact. The floral switch also has a number of dynamic properties, including commitment, tunability and the ability to integrate diverse environmental signals over time. To understand how the major regulators of the floral transition might confer these dynamic properties, we developed a mathematical model incorporating our current knowledge of the floral transition. We initially sought to recreate the qualitative behaviour of the floral transition to verify whether our gene network structure was capable of reproducing the expected switch-like behaviour. By including new experimental data we were able to generate a quantitative model. Simulations we ran on flowering time mutants or plants exposed to changing environmental conditions are in agreement with experimental data. This suggests our model

captures important aspects of the floral transition. Furthermore, our model makes a number of predictions about the behaviour of specific genetic backgrounds that we have verified.

We discuss how features of our network confer specific characteristics such as commitment, sensitivity and tunability to the floral transition. In particular we are interested in understanding how developmental networks are able to integrate noisy information over time to provide meaningful outcomes.

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P2.11

Poster Session — Monday 29th June 2009

Identification of alleles conferring delayed bolting in lettuce

Aaron R. Abbott (University of Warwick), Steve Jackson (University of Warwick)

The time of bolting is an important factor in lettuce production because it affects the yield and quality of the harvested crop. Bolting is promoted by higher temperatures and is an increasing problem for growers with the current trend for warmer summers. The development of late bolting varieties, which would have a greater 'holding ability' in the field, would result in reduced crop losses and an extension to the growing season.

In many plants, the timing of the transition from vegetative growth to flowering is controlled by environmental cues. Studies in *Arabidopsis* have led to the identification of several different pathways that come together to regulate flowering time, research has shown that components of these pathways are conserved in other crop species.

A lettuce BAC library has been screened and homologues of *Arabidopsis* flowering time genes, principally from the autonomous pathway, have been isolated. Lettuce lines which bolt significantly later than wild-type have been identified from EMS mutagenised populations of cultivated lettuce and a diversity set of wild lettuce. These lines will be analysed to identify new alleles of known flowering time genes carrying mutations causing late bolting.

Comparison of target gene sequences in wild-type and the late-bolting lines are being analysed, any polymorphisms identified will be analysed in segregating backcross populations to establish co-segregation with the phenotype. These new alleles can then be used in breeding programs aimed at delaying bolting and improving the 'holding ability' of commercial lettuce crops.

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P2.12

Poster Session — Monday 29th June 2009

The photo-thermal control of flowering in teff (*Eragrostis tef (Zuccagni) Trotter*)

Sander H. Van Delden (Wageningen University), Tjeerd-Jan Stomph (Wageningen University), Jan Vos (Wageningen University), Gerard Brouwer (Wageningen University)

Teff is a short day C4 cereal crop species, originating from Ethiopia. Because of several health benefits there has been an interest in growing the crop outside Ethiopia for specialty food markets. Teff can be grown in the temperate climates of NW Europe, such as in The Netherlands. However, photoperiod sensitivity causes late harvest associated with increased chances on seed losses by adverse weather conditions, diseases and lodging. Early flowering could advance the seed filling period and decrease lodging susceptibility by decreasing the number of internodes. This paper reports on the effects of photoperiod and temperature on time to flowering and internode number in teff. A preliminary model will be presented of temperature and day length effects on time to flowering.

Several phytotron, greenhouse and field experiments with various teff cultivars were conducted. Reciprocal transfer treatments (photoperiod, temperature) were used to determine the durations of the basic vegetative phase, the photoperiod sensitive phase and the post photoperiod sensitive phase.

Between genotypes, clear differences were observed in the duration of each distinguished phase. This indicated that there are options for breeding for a genotype of which the phenology is best adapted to European latitudes. Additionally, in contrast to other crop species, panicle initiation started during the beginning of the photoperiod sensitive phase and not near the end (rice) or even later (sorghum). Data from reciprocal transfer experiments were instrumental to develop a new method to identify the switch from the vegetative to generative phase of the apex.

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P2.13

Poster Session — Monday 29th June 2009

The effects of PRD on flowering and fruit set in tomato

Radmila Stikic (Faculty of Agriculture University of Belgrade, Serbia), Zorica Jovanovic (Faculty of Agriculture University of Belgrade, Serbia), Sladjana Savic (Faculty of Biofarming Megatrend University, Serbia)

Partial root drying (PRD) is a new irrigation strategy which applies alternating regimes of irrigation to half the root system while the other half dries out. In PRD treated tomato (*Lycopersicon esculentum* L., v. Astona) plants 60% of water of fully irrigated plants (FI) plants was applied to one half of the root system while the other half dried down. The irrigation was shifted when soil water content of the dry side decreased for 15%. Although flowering occurred earlier in PRD comparing to FI, PRD treatment did not stimulate the development of more flowers on each inflorescence. However, the numbers and diameter of fruits were similar in PRD and FI treatments pointed out a stimulative effect of PRD on fruit set and development.

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P2.14

Poster Session — Monday 29th June 2009

Functional analysis of an *FLC-LIKE* gene in root chicory

Claire Périlleux (Université de Liège), Alexandra Pieltain (Université de Liège), Maria D' Aloia (Université de Liège), Olivier Maudoux (Cosucra Groupe Warcoing), Stanley Lutts (Université Catholique de Louvain), Jean-Marie Kinet (Université Catholique de Louvain)

Vernalization is known to promote flowering in *Arabidopsis thaliana* by inhibiting the expression of a strong repressor: *FLOWERING LOCUS C* (*FLC*). The recent cloning of an *FLC-LIKE* gene in sugar beet (*Beta vulgaris*; *BvFL1*) and—here—in root chicory (*Cichorium*

intybus; *CiFL1*) suggests the conservation of *FLC* biological function during evolution of eudicots. Hence physiological questions that remain difficult to address in *Arabidopsis* can be studied in other species. We investigated the correlation between *CiFL1* expression and plant-age dependent responsiveness to vernalization. We also studied the effect of post-vernalization growing temperature, which can stabilize or erase the vernalized state.

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P2.15

Poster Session — Monday 29th June 2009

The impact of retardant Bonzi on growth and flowering of *Hibiscus rosa-sinensis* L.

Anna Gogoláková (Constantine the Philosopher University in Nitra, Slovakia), Peter Štrba (Constantine the Philosopher University in Nitra, Slovakia)

Growth retardants are the most commonly used and important chemical growth regulators in floriculture. Chemical substance Bonzi is very important retardant with impact on habit and plant growth parameters. We observed high-significantly retardant influence on *Hibiscus rosa-sinensis* L. high, statistically significant to high-significantly difference between fresh and also dry weight of sprayed and non-sprayed plant during vegetation pot experiment by method of growth analyse and statistical test. Substance Bonzi does not have an influence on number of flowers and buds (there is non-significant difference between number of flowers and buds). We observed early flowering of non-sprayed plant approximately one week and irregular growth of plant sprouts. Growth retardant Bonzi stalls of flowering date of sprayed plants, it slows vegetative growth by inhibiting gibberellin biosynthesis and forms their compact habit.

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P2.16

Poster Session — Monday 29th June 2009

Generative reproduction of critical endangered species *Arctous alpina* (L.) Nied. (alpine bearberry)

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The subject of study was the population of critical endangered species with arcto-alpine distribution—*Arctous alpina* (L.) Nied. (*Ericaceae*). The aim of this work was the acquirement of the information about generative reproduction of the species. During the research we used regular non-destructive methods of population biology. Inquiries of terrain data were realized by random choice in the population in Belianske Tatry Mts (Northern Slovakia). We made out a variable number of flowers on the ramet. Generative reproduction potential of population was very low. Average width of fruits was 6.98 mm and length 8.8 mm. Average fruits' mass was 0.268 g. Average mass of one fruit's seeds 0.029 g represents 10.82% of average fruits' mass. In every fruit was found 5 seeds. The presence of at least one aborted seed was registered in 55.2% of the whole number of fruits. We observed no seedlings at the locality. The population survives through vegetative reproduction. The most important reasons of abortive generative reproduction are climatic conditions at the time of flowering, too low number of safe sites, necessary of mycorhizas and endozoochory type of spreading, plants' species competition and influence of chamois. This work was supported by the Slovak Research and Development Agency under the contract No. LPP-0125-07.

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P2.17

Poster Session — Monday 29th June 2009

A comparison of tobacco and poplar diurnal gene expression with the model plant *Arabidopsis thaliana*

Kieron D. Edwards (Advanced Technologies Cambridge Ltd), A.J. Millar (Institute of Molecular Plant Sciences University of Edinburgh), F. Allen (Advanced Technologies Cambridge Ltd), M.E. Eriksson (Umea Plant Science Centre Department of Plant Physiology Umea University)

The majority of eukaryotes and some prokaryotes possess an endogenous 24 h time-keeping mechanism. This circadian clock allows organisms to temporally regulate their behaviour and biochemistry to match the predictable changes associated with the day/night cycle. Correct timing provided by the circadian clock has been shown to improve growth and fitness in *Arabidopsis* and Cycanobacteria (Dodd et al., 2005, Ouyang et al., 1998). Such benefits could potentially result in increased survival and improved yield in commercially cultivated plants. This study compares microarray gene expression data from tobacco and Poplar grown under long day diurnal cycles with existing data from the model plant *Arabidopsis thaliana* and asks whether the same core clock genes are operating, and whether the phase of homologous genes and/or biological process outputs are shared between the species.

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