Cost Action UV4growth
mini-conference

Glasgow, Scotland 1/2 May 2012

Acclimation to UV-B

Programme and abstracts

University of Glasgow | Institute of Molecular, Cell & Systems Biology

Dear colleagues,

As organizers, we have the pleasure of welcoming you to the Institute of Molecular, Cell and Systems Biology of the University of Glasgow, Scotland to attend the mini-conference "Acclimation to UV-B". This meeting is organized by the workgroup 1 (WG1) action of UV4Growth. UV4Growth is a COST-funded network of researchers with interests in the effects of UV-B radiation on plants (http://www.ucc.ie/en/uv4growth/).

WG1 of the UV4Growth network explores UV-B responses at the molecular level. WG1 aims to produce a coherent vision of the molecular mechanisms underlying UV-B-mediated control of growth. Since UV-B responses are controlled at various molecular levels WG1 aims to reveal components of the UV-B signalling pathway and its mode of action, which includes analyses of gene expression, cell cycle adjustments, DNA and histone modification.

This mini-conference focuses in particular on the molecular basis of **acclimation to UV-B** and brings together both established and young scientists to present their most recent findings on the molecular and cellular mechanisms of UV-B perception, signalling and gene regulation, and the various downstream responses that underpin **acclimation to UV-B**. It includes presentations on the structure and regulation of the UV-B photoreceptor, functional characterizations of various UV-B controlled genes and proteins, UV-B induced damage to the photosynthetic apparatus and the DNA, the natural variation of growth upon exposure to chronic and mutagenic doses of UV-B, the gene expression and metabolite accumulation behavior of UV-B photoreceptor mutants in natural environments, the interaction between UV-B and other abiotic factors and the epigenetic regulation of the crosstalk between bacterial infection and UV-B responses.

Furthermore we are particularly happy that Gad Galili, Head of the Department of Plant Sciences at the Weizmann Institute of Science in Rehovot, Israel and member of the COST action FA0605 "Signalling control of stress tolerance and production of stress protective compounds in plants" will join this mini-conference corroborating the link between primary metabolism and stress.

We hope you have an enjoyable time in sunny Glasgow!

Best wishes,
Marie-Theres Hauser
Gareth Jenkins

About COST

COST- the acronym for European Cooperation in Science and Technology- is the oldest and widest European intergovernmental network for cooperation in research. Established by the Ministerial Conference in November 1971, COST is presently used by the scientific communities
of 35 European countries to cooperate in common research projects supported by national funds.

The funds provided by COST - less than 1% of the total value of the projects – support the COST cooperation networks (COST Actions) through which, with EUR 30 million per year, more than 30 000 European scientists are involved in research having a total value which exceeds EUR 2 billion per year. This is the financial worth of the European added value which COST achieves.

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ESF provides the COST Office

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PROGRAMME

1 MAY

09.30 Welcome

Chair: Marie-Theres Hauser

09.40-10.40 **Gareth Jenkins** (*Glasgow*) Structural basis of photoreception and signalling by the UV-B photoreceptor UVR8

Break

Chair: Jason Wargent

11.20-11.45 **Ferenc Nagy** (*Szeged*) Functional characterisation of components and molecular mechanisms mediating UVR8 controlled signalling

11.45-12.10 **Lisi Xie** (*Vienna*) Which photoreceptors are involved in the transcriptional regulation of *ARIADNE12* upon broad band UV-B radiation?

12.10-12.35 **Catherine Cloix/Kirsty McInnes** (*Glasgow*) UV-B perception and gene regulation in *Brassica*

Lunch

Chair: John Christie

14.00-15.00 **Roman Ulm** (*Genève*) Negative feedback regulation of the UV-B photoreceptor UVR8

15.00-15.25 **Luis Morales** (*Helsinki*) UVR8 is a key regulator of gene expression and metabolite accumulation in Arabidopsis leaves under solar UV radiation

Break

Chair: Roman Ulm

16.00-16.25 **Marie-Theres Hauser** (*Vienna*) Natural variation of growth upon exposure to chronic broad range UV-B radiation

16.25-16.50 **Ales Pecinka** (*MPI, Cologne*) **Setting up a genome-wide analysis of UV-B mutagenic effects for *Arabidopsis thaliana***

Later: dinner

2 MAY

Chair: Roman Ulm

09.30-10.30 **Lei Jiang** (*Guangzhou*) *Arabidopsis* STO/BBX24 negatively regulates UV-B signaling by interacting with COP1 and repressing HY5 transcriptional activity

Break

Chair: Marie-Theres Hauser

11.10-11.35 **Jason Wargent** (*Massey*) UV-B radiation regulates plant photoprotection for greater photosynthetic competence and enhanced abiotic stress tolerance

11.35-12.00 **István-Zoltán Vass** (*Szeged*) Relative contribution of damage to the photosynthetic apparatus and to the DNA under the exposure to UV-B radiation

12.00-12.25 **Fidel Rubio** (*Valencia*) Photosynthetic and respiratory responses of five submerged macrophyte species to different levels of UVB radiation

Lunch

Chair: Gareth Jenkins

1400-1500 **Gad Galili** (*Weizmann Institute*) The adjustment of plant metabolism and cell biology to stress

1500-1525 **Dirk Schenke** (*Halle*) Epigenetic Regulation of crosstalk between flg22 and UV-B stress responses in Arabidopsis

Break

1600-1625 **Challabathula Dinakar** (*Bonn*) Response to long light period and oxidative stress management in desiccation tolerant *L. brevidens* plants

End of meeting

Structural basis of photoreception and signaling by the UV-B photoreceptor UVR8

Gareth I. Jenkins[1] (e-mail: Gareth.Jenkins@Glasgow.ac.uk), Katherine J. Baxter[1], Bobby A. Brown[1], John M. Christie[1], Catherine Cloix[1], Monika Heilmann[1], Eirini Kaiserli[3], Sharon M. Kelly[1], Andrew O'Hara[1], Brian O. Smith[1], Andrew S. Arvai[2], Ashley J. Pratt[2], Michael Hothorn[3], Kenichi Hitomi[2], Elizabeth D. Getzoff[2]

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The UV-B photoreceptor UV RESISTANCE LOCUS 8 (UVR8) mediates photomorphogenic responses that underpin acclimation of plants to UV-B. In particular, UV-B perception by UVR8 regulates the expression of genes that are responsible for UV-protection. UVR8 is a 7-bladed b-propeller protein which, in the absence of UV-B, exists as a homodimer. Following UV-B absorption UVR8 rapidly forms monomers, interacts with the CONSTITUTIVELY PHOTOMORPHOGENIC 1 (COP1) protein and accumulates in the nucleus.

This presentation will show how structural and biophysical studies of UVR8, combined with mutagenesis, have provided insights into the mechanisms of photoreception and signal transduction.

Functional characterisation of components and molecular mechanisms mediating UVR8 controlled signaling

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The photoreceptor UVR8 orchestrates expression of about 150-200 genes in response to UVB irradiation and plays a critical role in optimising plant adaptation to the varying UVB content of sunlight. Key components of UVR8-controlled signaling, including RUP1/RUP2, COP1 and HY5/HYH have been identified. It is known that UVR8 associates with the HY5 chromatin and UVB induces nuclear accumulation of the photoreceptor, yet the precise mechanism by which UVR8 promotes expression of this bZIP transcription factor is not yet understood. To gain insight into the molecular mechanism mediating UVB-induced transcription of HY5/HYH we performed two sets of experiments. First we determined the critical cis-regulatory elements of the HY5 promoter involved in UVB-induced transcription of the HY5/luc reporter in transgenic plants, then performed a Y1H screen to identify the transcription factors that are potentially required to mediate this response. Parallel with these experiments we showed that UVR8 is exclusively expressed in the epidermal cell layer of young seedlings. To determine to what extent cell to cell signaling contributes to UVR8 mediated physiological responses, we created a set of transgenic plants expressing the biologically functional UVR8/YFP fusion protein only in the epidermal or vascular or mesophyll cells in uvr8 background, and analysed UVB-induced expression of HY5/HYH. The results of these experiments will be presented and discussed.

Which photoreceptors are involved in the transcriptional regulation of *ARIADNE12* upon broad band UV-B radiation?

Lisi Xie[1] (e-mail: sherris666@hotmail.com), Christina Lang-Mladek[1], Susanne Neubert[1], Marie-Theres Hauser[1]

[1]Department of Applied Genetics & Cell Biology, BOKU-University of Natural Resources and Life Sciences, Muthgasse 18, A-1190 Vienna, AUSTRIA

ARIADNE12 (ARI12) belongs to a family of 'RING between RING fingers' (RBR) domain proteins with E3 ligase activity. We have previously shown that under standard growth conditions *ARI12* is predominantly and only weakly expressed in roots and hypocotyls. However *ARI12* is strongly induced in leaves and this expression peaks 2–4 h after exposure to white light supplemented with either narrow band or broad band UV-B radiations. To test whether *ARI12's* transcriptional activation depends on key players of the UVB signaling pathway and different photoreceptors, *ARI12* expression was quantified in single and double mutants of the UV-B receptor, *RESISTANCE LOCUS8 (UVR8)*, the downstream signaling component *CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1*), *ELONGATED HYPOCOTYL5* (*HY5*) and HY5 HOMOLOG (*HYH*), the UVA and blue light receptors *CRYPTOCHROME 1* and 2 (*CRY1* and *2*) and *PHOTOTROPINS* (*PHOT1* and *2*) and the red light receptors *PHYTOCHROME A* and *B* (*PHYA* and *B*). We will present the results of the quantitative real-time PCR analyses of *ARI12* and known downstream components of the diverse light receptors upon white light supplemented with high fluence rate broad band UV-B radiation.

UV-B perception and gene regulation in *Brassica*

Catherine Cloix (e-mail: Catherine.Cloix@Glasgow.ac.uk), Kirsty J. McInnes (e-mail: k.mcinnes.1@research.gla.ac.uk), Pawel Herzyk, Gareth I. Jenkins

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UV-B wavelengths play an important role in promoting resistance of plants to attack by herbivores. UV-B stimulates the expression of various genes that change the biochemical composition of leaf tissue, making it less palatable to insects and other herbivorous pests. Oilseed rape (*Brassica napus*) suffers significant loss to the crop as a result of herbivory and we are therefore investigating how UV-B regulates gene expression in *Brassica* to promote resistance to herbivore attack.

We will report the identification of putative UVR8 orthologues in *Brassica* and the initial results of transcriptome analysis.

Negative feedback regulation of the UV-B photoreceptor UVR8

Marc Heijde, Roman Ulm (Roman.Ulm@unige.ch)

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Survival of plants in sunlight requires UV-protective responses. Plants respond to UV-B radiation with a coordinated photomorphogenic response that allows acclimation to this environmental stress factor. The UV-B photoreceptor UVR8 is highly specific and sensitive in perceiving UV-B radiation. However, an elevated UV-B response is associated with dwarf growth, indicating the importance of balancing UV-B–specific signaling. We will present data on how REPRESSOR OF UV-B PHOTOMORPHOGENESIS 1 (RUP1) and RUP2 function as crucial negative regulators of UVR8 action, providing new insight into the mechanism of UV-B photoreceptor regulation.

UVR8 is a key regulator of gene expression and metabolite accumulation in Arabidopsis leaves under solar UV radiation

Presenting author: Luis Orlando Morales, e-mail: luis.morales@helsinki.fi

Luis Orlando Morales[1], Mikael Brosché[1,2], Julia Vainonen[1], Gareth Jenkins[3], Nina Sipari[4], Jason Wargent[5], Riitta Tegelberg[6], Åke Strid[7], Anders Lindfors[8], Pedro José Aphalo[1]*

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Ultraviolet (UV) radiation is an important component of the solar spectrum which regulates several physiological processes in plants. The recent discoveries of the Arabidopsis UV RESISTANT LOCUS (UVR8) as UV-B (280-315 nm) photoreceptor and its mechanisms of UV-B absorption have advanced our understanding of UV-B perception in plants. However, how the UVR8 pathway operates in natural conditions remains unknown. Here, we used wild-type Arabidopsis and the *uvr8-2* mutant in an experimental design in field conditions where UV-A (315-400 nm) and UV-B irradiances were manipulated using plastic films. Gene expression, protein accumulation and metabolite signatures were analyzed in leaves exposed for 12 and 36 hours outdoors. We show that in natural environments UVR8 is a key regulator of plant responses to solar UV. At the transcript levels UVR8 regulates the expression of genes involved in UV protection, defense against herbivores and other abiotic stresses, biosynthesis and signaling of jasmonic acid and salicylic acid. High UV-A irradiance in the environment had large effects on gene expression, accumulation of metabolites and PDX1 in Arabidopsis leaves. Moreover, our findings indicate that UVR8 may interact with UV-A/blue light signaling pathways via COP1 to modulate UV-A responses. UVR8 is required for the

UV-B induction of quercetin and kaempferol derivatives, and also flavonoids and hydroxycinnamic acids in the leaf epidermis. In addition, UV-B acclimation dependent on UVR8, especially at early stages of plant development may be important for the plant to grow normally and could enhance fitness in natural conditions.

Natural variation of growth upon exposure to chronic broad range UV-B radiation

Marie-Theres Hauser (e-mail: marie-theres.hauser@boku.ac.at), Lisi Xie, Susanne Neubert, Julia Hilscher

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Molecular analyses of the natural variation of growth have been a powerful approach to identify genes that are important for adaptation to different environments. In previous studies it has been shown that *Arabidopsis thaliana* accessions exhibit a high variability of immediate responses upon short term exposures of UV-B radiation. Furthermore it has been proposed that trichomes on leaves protect plants from damaging UV-B radiation. We have shown that trichome density on rosette leaves varies by a factor greater than ten. Even glabrous *Arabidopsis thaliana* accessions have been identified in natural populations. Based on the hypothesis that trichome density is positively correlated with the resistance to UV-B a set of *Arabidopsis thaliana* accession for which trichome density data are available has been evaluated for their growth responses upon chronic broad range UV-B radiation. To determine the molecular basis for the UV-B sensitivity of some accession we initiated a speed mapping approach with several F2 populations for different combinations of sensitive and resistant accessions. We will present the current status on mapping and trichome density correlation analyses and discuss the advantages and shortcomings of our analyses to identify the genes that are responsible for the diverse growth responses of *Arabidopsis thaliana* accessions.

Setting up a genome-wide analysis of UV-B mutagenic effects for *Arabidopsis thaliana*

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Plants protect themselves from UV-B light because of its deteriorating effects. The best understood type of UV-B induced damage is at the level of DNA molecule where it causes mainly specific types of non-native bonds between two pyrimidine bases (C and T) – pyrimidine dimers (PDs). The PDs may block transcription, replication and result in mutations. The deteriorating power of UV-B and number of potential PDs is greatly reduced by a shield consisting of protective pigments. Induced PDs are repaired via direct reversal by photolyases and supposedly only a small amount results in mutations that are fixed and transmitted to the next generations. However, until recently, the measurements of UV-B mutagenic effects were only indirect, possible for a very small part of a genome or by using artificial constructs designed to detect other types of DNA damage. We will summarize existing data on the UV-B mutagenic effects in plants and present our project that aims at genome-wide analysis of UV-B induced mutations using the combined power of sun simulators, genetics and next generation sequencing.

Arabidopsis STO/BBX24 negatively regulates UV-B signaling by interacting with COP1 and repressing HY5 transcriptional activity

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UV-B (280–315 nm) is an integral part of solar radiation and can act either as a stress inducer or as a developmental signal. In recent years, increasing attention has been paid to the low fluence UV-B-induced photomorphogenic response and several key players in this response have been identified, which include UVR8 (a UV-B specific photoreceptor), COP1 (a WD40-repeat containing RING finger protein), HY5 (a bZIP transcription factor), and RUP1/2 (two UVR8-interacting proteins). Here we report that *Arabidopsis* SALT TOLERANCE (STO/BBX24), a known regulator for light signaling in plants, defines a new signaling component in UV-B-mediated photomorphogenesis. The *bbx24* mutant is hypersensitive to UV-B radiation and becomes extremely dwarfed under UV-B treatment. By contrast, BBX24 overexpression transgenic lines respond much weaker to UV-B than the *bbx24* and wild type plants. BBX24 expression is UV-B-inducible and its accumulation under UV-B requires COP1. Co-immunoprecipitation experiments indicate that BBX24 interacts with COP1 *in planta* upon UV-B illumination. Moreover, BBX24 interacts with HY5 and acts antagonistically with HY5 in UV-B-induced inhibition of hypocotyl elongation. Furthermore, BBX24 attenuates UV-B-induced HY5 accumulation and suppresses its transcription-activation activity. Taken together, our results reveal a previously uncharacterized function of the light-regulated BBX24 in UV-B responses and demonstrate that BBX24 functions as a negative regulator of photomorphogenic UV-B responses by interacting both with COP1 and HY5. The UV-B-inducible expression pattern and its suppression to HY5 activity suggest that BBX24 could be a new component of the feedback regulatory module of UV-B signaling in plants.

UV-B radiation regulates plant photoprotection for greater photosynthetic competence and enhanced abiotic stress tolerance

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Ultraviolet (UV) radiation is a significant environmental factor, and the range of responses regulated by UV, specifically UV-B radiation (290-320nm), is vast. Despite the fact that UV-B responses have typically been considered to be damaging in nature, there are now good indications that UV-B may act as a valuable regulatory cue, enabling plants to adapt to a changing environment. We have evaluated such consequential changes in several plant model systems, with beneficial outcomes for plant competence following early-stage exposure to UV-B observed, including higher photosynthetic rates in plants grown in the presence of UV-B radiation, and higher relative growth of plants pre-acclimatized to UV-B, in addition to higher maximum photochemical efficiency of photosystem II (PSII) F_v/F_m following subsequent exposure to high photosynthetically active radiation (PAR) and temperature stress. The UV-B photoreceptor UVR8 regulates expression of genes in response to UV-B that are concerned with acclimation to UV-B, and we have also examined whether UVR8 is important in maintaining photosynthetic competence by measuring F_v/F_m, and the operating efficiency of PSII (Φ_{PSII}) in wild-type and *uvr8* mutant *Arabidopsis*. Increasing our understanding of those inherent trade-offs between negative and positive outcomes of exposure to sunlight can only strengthen our ability to understand and predict UV-B response in plants and related interactions in order to further consider the now growing role of UV radiation as a key regulator of plant productivity.

Relative contribution of damage to the photosynthetic apparatus and to the DNA under the exposure to UV-B radiation

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Two of the most significant primary effects of UV-B irradiation are the damage to DNA and the impairment of active protein complexes, of which the most pronounced is the inactivation of PSII mainly by damaging the D1 protein. We investigated the correlation of the latter with the concomitant DNA damage and its repair. *Synechocystis* PCC6803 wild type (WT), its photolyase lacking mutant (ΔphrA) and photolyase homologue gene lacking mutant (Δsll 1629) cells were used for this purpose. We found that during UV-B treatments the ΔphrA cells exhibited a radical decrease in photosynthetic activity, accumulated a significant number of DNA damages, their D1 protein levels decreased, and after terminating the UV-B illumination, all these negative effects also proved to be permanent. The WT cells however didn't suffer significant damages to their DNA and their D1 protein pool maintained an effective turnover. The Δsll 1629 cells' photosynthetic activity significantly differed from that of the WT cells with distinct decrease, and their D1 protein turnover was also affected, next to moderate DNA damage. The stress related psbA3 gene's transcript levels were only affected significantly in ΔphrA cells, coinciding with the dramatic loss of D1 protein turnover ability.

Photosynthetic and respiratory responses of five submerged macrophyte species to different levels of UVB radiation

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Five species of submerged macrophytes from shallow littoral waterbodies (four charophytes: *Chara polyacantha, Chara baltica, Chara vulgaris* and *Nitella hyaline*, and one angiosperm: *Myriophyllum spicatum*) have been subjected to three UVB radiation (UVBR) treatments in a laboratory experiment: Reduced, Ambient and Enhanced. After 15 days of UVB irradiation doses photosynthetic and respiratory rates were determined in five individuals of each species for each treatment by means of the Winkler method and using an O_2 optical sensor with high accuracy. The photosynthetic response to UVBR was species-specific and with lack of an evident pattern: *C. polyacantha* and *C. vulgaris* showed increased rates under reduced UVBR; however, *C. baltica* rate increased when UVR was enhanced; *M. spicatum* rate was the lowest under the Reduced treatment and *N. hyalina* rates were not statistically different among treatments. The highest photosynthetic rates were reached by *C. vulgaris* (28 $mgO_2/h \cdot gDW$) and by *M. spicatum* (45 $mgO_2/h \cdot gDW$). Respiratory response was also species-specific: *C. polyacantha* and *M. spicatum* rates significantly decreased when UVB dose was reduced and there was not statistical difference in respiratory rates among treatments for the other species. Minimum respiratory rates reached by *M. spicatum* and *C. polyacantha* were 5 and 6 $mgO_2/h \cdot gDW$ respectively. The variability among replicates was large, the response to UVBR seems to be species-specific and photosynthetic and respiratory rates follow different trends. Therefore, more research on this topic should be done because these responses to UVBR might cause changes in the submerged plant community structure under a scenario of enhanced UVB radiation.

THE ADJUSTMENT OF PLANT METABOLISM AND CELL BIOLOGY TO STRESS

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Being sessile organisms, plants respond to stressful environments by consecutive and coordinated adjustments of their transcriptome, metabolome and cellular constituents. These further lead to specific phenotypic outputs that help plants survive or even tolerate these harmful conditions. Elucidating of the components of such harmonized adaptations and the interplay between them is not simple because the pattern of adaptation should be extensively adjusted to different stresses as well as along the progression of a given stress. To address this issue, we developed a dedicated computational approach aimed to elucidate the network expression regulation of multiple plant genes in response to various environmental perturbations. In my presentation, I will introduce an example illustrating how this approach enabled us to elucidate the common features and complexity of the response of plant metabolism to various environmental cues, particularly abiotic and biotic stresses. In the second part of my presentation, I will present our cell biology research focusing on autophagy, a cellular stress-associated degradation mechanism. In the study, we have recently identified two novel closely related plant proteins that bind the autophagy-associated Atg8f protein, illustrating the aid of selective autophagy in seed germination under sub-optimal conditions.

Epigenetic Regulation of crosstalk between flg22 and UV-B stress responses in Arabidopsis

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Sessile plants respond to both abiotic and biotic stresses with alterations in the expression of genes required to produce protective metabolites. When plants are challenged with different stresses simultaneously, they have to set priorities to deal with the most urgent threat. In case of the abiotic stress, UV-B light, plants produce UV-protective flavonols in Arabidopsis Col-0 cell suspension cultures and this accumulation is attenuated by concurrent application of the bacterial elicitor flg22 (simulating biotic stress). This inhibition correlates with strong suppression of the flavonol biosynthesis genes. In parallel, flg22 induces the production of defense related compounds, such as the phytoalexins camalexin and scopoletin, as well as lignin, a structural barrier thought to restrict pathogen spread. This correlated positively with flg22-mediated expression of enzymes for lignin, scopoletin and camalexin production. Since flavonols, lignin and scopoletin are all derived from phenylalanine, it appears that plants focus their secondary metabolism on production of scopoletin and lignin at the expense of flavonol production. Antagonistic regulation of two opposing MYB transcription factors, the positive regulator of the flavonol pathway, MYB12 (UV-B-induced and flg22-suppressed) and the negative regulator, MYB4 (UV-B- and flg22-induced), can explain this phenomenon, but the exact molecular mechanism is still obscure. However, preliminary ChIP experiments showed a further correlation between flavonol gene expression and changes in histone acetylation pattern, indicating this mechanism involves chromatin remodeling. *In silico* promoter and mutant analysis allows to present a working model, which is the basis for future research.

Response to long light period and oxidative stress management in desiccation tolerant *L. brevidens* plants

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Existence of both desiccation tolerant and sensitive plants in Linderniaceae family provides an advantage for comparing the responses of these plants to light and dehydration which aids in better understanding the physiology of the plant. In the present study, *Craterostigma plantagineum* (desiccation tolerant)*, Lindernia brevidens* (desiccation tolerant) *and Lindernia subracemosa* (desiccation sensitive) plants grown under short-day (8h photoperiod) were transferred to long-day conditions (16h photoperiod) to compare their phenotypic responses to varied light conditions. The responses of these plants to continuous light were not similar. Anthocyanin accumulation, though is quite uncommon in leaves of resurrection plants under normal growth conditions is observed in *Lindernia brevidens* plants under normal growth conditions with an extended light period. No major phenotypic differences were observed in *Craterostigma plantagineum* and *L. subracemosa* between short-day and long-day grown plants. The pigmentation in leaves of *L. brevidens* did not affect the desiccation tolerance behaviour but seems to be related to oxidative stress protection as indicated by the differential expression of transcripts encoding antioxidant enzymes. No significant differences were seen in the expression of desiccation-induced proteins and proteins involved in carbohydrate metabolism in short-day and long-day grown plants, whereas differences were observed in the expression of transcripts encoding chloroplast localized stress proteins and transcripts encoding antioxidant enzymes.

Delegates UV4Growth Mini-conference Glasgow May 2012

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