

INFLUENCE OF SHORT-WAVELENGTH ULTRAVIOLET LIGHT ON GENES EXPRESSION IN *Arabidopsis thaliana* PLANTS

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Received 12.03.2019

Revised 21.05.2019

Accepted 05.07.2019

The aim of the work was to estimate the impact of the short wavelengths ultraviolet radiation (wavelength is 230 nm) on *Arabidopsis thaliana*. The stress response on some key flowering determination genes AP1, GI, LFY, FT, CO, and the repair gene RAD51 expression were investigated. The grown plants were applied by red (610–700 nm), violet (400–450 nm), neutral white (mixture wavelengths 380–750 nm), 20 W and high intensive white light (mixture wavelengths 380–750 nm) 40 W LED. The experimental group of plants was irradiated by short wavelengths ultraviolet on ontogenesis stage 5.1 by Boyes classification. The leaf length as growth parameter mark also was analyzed. The short wavelengths ultraviolet influence caused differences in photoperiodic pathway genes expression in plants grown under different illumination. Acceleration flowering phases under influence white intensive illumination and delay ones in case of violet and common white illumination were observed comparing with control groups. It was revealed that cryptochrome and phytochrome formation play an important role in plant development and stress resistance. It enables to understand the best way of plant cultivation in stressful condition.

Key words: illumination conditions, gene expression, short wavelengths ultraviolet, stress response.

The light illumination, nutrition and temperature strong are influence on plant development. Therefore the light illumination mode is one of the most important conditions for plants growth and development [1]. Light illumination conditions include light intensity, photoperiod and light spectrum. It is well known that the switch from vegetative growth to reproductive growth, i.e. flowering, is the critical event in a plant's life. Blooming is regulated either autonomously or by environmental factors which is regulated by the duration of the day and night periods, and spectra of the illumination of light, which is regulated by photosynthesis cell components, have been well studied. Additionally, it has become clear that stress also regulates flowering. The long wavelength ultraviolet B radiation can induce or accelerate blooming, or inhibit and delay it depend on plant species. This article focuses on the positive regulation of reproductive stage by stress. The induction or acceleration of blooming in response to

stress that is known as stress-induced flowering — a new category of flowering response [2]. This research aims to clarify the concept and to summarize the full range of its characteristics of stress-induced flowering from a predominately physiological perspective. There are relevant quantities to flowering time gene regulatory network of plants grow and develop [3].

Nowadays genetic mechanisms of flowering regulation of *Arabidopsis* are known [4]. Flowering time regulation has been widely studied on the plant model species *Arabidopsis thaliana*. There are three main pathways which include the photoperiodic, vernalisation and autonomous branches. The photoperiodic pathway is the most important for *Arabidopsis* because it is belongs on long day plant. Flowering time regulate by circadian clock and depend of day length [5]. The circadian clock genes are activated by the light spectrum. The light spectrum activates different photoreceptors in plant leaves. The impact of

light spectrum on plants development is studied during long time [6]. But today this environmental research problem has been relevant. The violet, blue, and red lights are important for plant growing and development [7] and they include the visible light spectrum within 380–730 nm. Different light spectrum excited signal transduction state and caused photomorphogenic changes. It also impacts on chlorophyll content in cells, dry mass accumulation and leaf surface square creating [8]. The visible light is absorbed mainly by chlorophyll a, b and carotenoids [1]. Blue (460 nm), orange (630 nm) and red light (660 nm) are playing a great role in photosynthesis [9], whereas violet (405 nm), and far-red influence to germination, vegetative growth, budding, and flowering processes [10, 1]. In experimental researches blue and red lights were necessary for investigation plant photosynthesis mechanisms, but violet and far-red usually were applied in secondary metabolite synthesis and photomorphogenesis studies [11].

Different spectrum is absorbed by several photoreceptors in leaves [7, 9]. Therefore several classes of photoreceptors have been described: phytochromes (PHYA-PHYE in *Arabidopsis*) generally absorb red and far-red light, but blue light is perceived by cryptochromes (CRY1 and CRY2), phototropins (Phot. 1 and Phot. 2), and Zeitlupes (ZKL, FKF1 and LKP2) [1].

In *Arabidopsis* the phytochromes involve in photoperiodic pathways [12, 13]. They interact on endogenous oscillators and activate expression of two floral genes *CONSTANTS* (*CO*) and *FLOWERING LOCUS T* (*FT*) in leaves [10]. The cryptochrome photoreceptors are present in organisms throughout the plant kingdom [7]. They enable absorbed the red light in plants. The red light in opposite of could down-regulate the gene *FT* expression and delay flowering [10].

A long wavelength ultraviolet (UV) radiation is a highly effective biological stress factor for plants. The UV-rays are similar to ionizing radiation regarding of biological action living cells [1]. Impact on plant UV-radiation is interesting to research for a time [14]. It is relevant to study during the last years too. The ozone layer gets thinner in combine with global warming. Therefore as a result it increases of atmospheric CO₂ and UV radiation [15, 16]. The investigation of the plant resistance to ambient factors now continues to be relevant.

UV light includes a long wavelength UV (wavelengths 320–400 nm), UVB (280–320 nm)

and short wavelength UV (wavelengths below 280 nm) (Sastry at al. 2000). A long wavelength UV comprises more than 95% of the solar UV radiation. Most of UVB and all of UVC are removed by the ozone layer. The shorter wavelengths are less present in incident sunlight [17]. But if the ozone layer will decrease the level of short wavelength UV irradiation opposite will increase. In the environmental the short wavelength UV will become the most active and drastic stress factor.

The recent researches have shown, short- and medium-wavelength of UV light cause photo lesions in DNA conformation. The high doses of UV increase DNA dissociation and structural disintegration [18].

A long wavelength produce the DNA thionucleotides indirectly. Also UV induces DNA photo damage by generating reactive oxygen species. Proteins targeted for oxidation damage include DNA repair factors [16]. UVB radiation affects leaf growth in a wide range of some species without causing any other visible stress symptoms [19].

Increasing environmental UV radiation can delay flowering and decrease harvest production in many plants species [20].

The arm of our study was to investigate the illumination impact combining with the UV-radiation on the expression of *APETALA 1* (*AP1*), *GIGANTIA* (*GI*), *FT*, *CO*, *RAD51* and *PCNA2*.

Materials and Methods

The plants of *Arabidopsis thaliana* (*ecotype Col*) were used in experiments. *A. thaliana* is a classical model object in molecular biology and genetics. This species is useful in lab and content a small genome [21]. Genetic mechanism of blooming term and growth phases' determination of *Arabidopsis* is widely studied [22]. We used light illumination with violet, red and white spectrum to growth plants. The plants grown were applied red (610–700 nm), violet (400–450 nm), neutral white (mixture wavelengths 380–750 nm), 20 W and high intensive white light (mixture wavelengths 380–750 nm) 40 W LED to grow plants. We irradiated plants by short wavelength UV. During vegetation growth and develop the irradiated plant with above-mentioned factors the length leaves was measured within twice per week.

The short wavelength UV irradiation

The short wavelength UV irradiation was done by 254 nm light generator with 30 W power. Each control and experimental group of plants

was implemented. Experimental groups were irradiated by short wavelength UV in shooting stage 5.9 [22]. We stressed plants with short wavelength UV irradiation in three different term modes 1, 2 and 5 minutes of UV exposure in the same distance from the generator.

Molecular studies

The RNA extraction isolated from leaves at 6.1 development stage at the starting of the flowering phase in according to Boyes (2001) classification. The RNA was isolated of each experimental and control groups after one week from UV irradiation. The total RNA was extracted by traditional phenol-chloroform method [23]. Quality of extraction RNA was checked with electrophoresis in 2% agarose gels. Concentration of extracted RNA was measured by spectrophotometer. The reverse transcription reaction was performed in order to obtain cDNA. In experiments, the RevertAid First Strand cDNA Synthesis Kit (Thermo Fisher Scientific Inc., Waltham, MA, USA) kit was used.

In order to evaluate the genetic alterations caused by UV exposure we determined changes in the photoperiod pathway gene expression levels. In our experiment, we measured the expression of researched genes *AP1*, *GI*, *FT*, *CO*, *RAD51* and *PCNA2*. The qPCR equipment LightCycler® Nano Instrument by Roshe Diagnostics, Switzerland was used. Different programs and protocols were tested to set up real time qPCR conditions. We used *Thermo scientific SYBR Green master mix*. The quantitative qPCR primers on genomic DNA of *Arabidopsis* resulting in selection the working primers were tested too. An *ACTIN PROTEIN 2 (ACT2)* and *PCNA2* on base preliminary experiments were chosen as a reference gene in our investigation. The standardization of real-time PCR primers was done in order to preliminary determines the efficiency of each primer.

Data analysis

Statistical analysis of vegetation data [24] was done by the help of StatPlus software. Relative expression of the genes statistically analyzed with double normalization on the base of reference gene and control group by the REST software [25].

Results and Discussion

Analysis of the plant's growth and vegetation development showed differences in grown with different light illumination [24].

Arabidopsis seedlings were started at 5.1 stage according to Boyes (2001) classification at 24 day-old age (Table 1) under the intensive white illumination at 24 °C temperature. The

plants transferred into 6.3 phase (flowering) on 27 day-olds. The seedlings transferred into 8th phase on 31 day-olds and 9 phase (harvesting) on 36 days. The seedlings started 5.1 stage on 27 day-olds, the 6.1 phase started on 31 days, the 8 phase started on 36 days under red light at 24 °C. The plant seedlings started 5.9 stage on 31 day-olds and the 6.3 phase at 36 days-old under common white and violet light at 24 °C.

















One-way Analysis of Variance (ANOVA) showed the significant differences between leaf length of different light spectrum growing plants (between groups $SS = 1.04$, within groups $SS = 458.11$, $F_{emp} > F_{crit}$, $P < 0.05$). See details in Fig. 1.

The leaf length of red light growing plants is different than common white light group ($t_{emp} > t_{crit}$, $P < 0.05$), as well as high intensive white light ($t_{emp} > t_{crit}$, $P < 0.05$) and violet light ($t_{emp} > t_{crit}$, $P < 0.05$) growing plants. The leaf length of the common white light growing plants is slightly different than white intensive light ($t_{emp} > t_{crit}$, $P < 0.05$) and violet light ($t_{emp} > t_{crit}$, $P < 0.05$) growing plants. The amount leaf length of the intensive white light growing plants is slightly higher than violet light growing plants ($t_{emp} > t_{crit}$, $P < 0.05$).

Comparative analysis of key photoperiodic pathway genes expression showed some differences between control and short wavelength UV irradiated groups ($P < 0,05$). The common white light illuminated plant group shown the changes in expression levels of key flowering determination genes after short wavelength UV treatment (Table 2). For example, **a) plants irradiated during 1 min by short wavelength UV:** The genes *RAD51* and *GI* are up-regulated in the experimental group in compare control plants by a mean factor of 2.936 and 1.494, comparatively. But the gene *CO* which take part in the circadian cycle is down-regulated for experimental plants with a mean factor of 0.648; **b) 3 min short wavelength UV:** The genes *RAD51* and *AP1* are up-regulated in an irradiated group of plants by a mean factor of 5.519 and of 31.685. The genes *CO* and *GI* are down-regulated in treatment group by a mean factor of 0.49 and 0.561; **c) 5 min UVC:** the genes *RAD51*, *AP1*, *CO* and *FT* are up-regulated in the experimental groups in compare of the control group by a mean factor of 46.869, 87.018, 137.253 and 6.15, comparatively.

We observed other features for activity some flowering, reparation, and proliferation genes of the violet illumination cultivated plants after that they were influenced UV-ray during several modes (Table 3). **a) 1 min UVC:**

Table 1. Evaluation and demonstration the phenology phases of cultivated plants in different light conditions in depend of aged

Light	Age, days	Phase		Age, days,	Phase		Age, days	Phase		Age, days	Phase	
Red	24	3.8		27	5.1		31	6.1		36	8	
White intensive		5.1			6.3			8			9	
Violet		3.6			3.8			5.9			6.3	
White common		3.6			3.8			5.9			6.3	

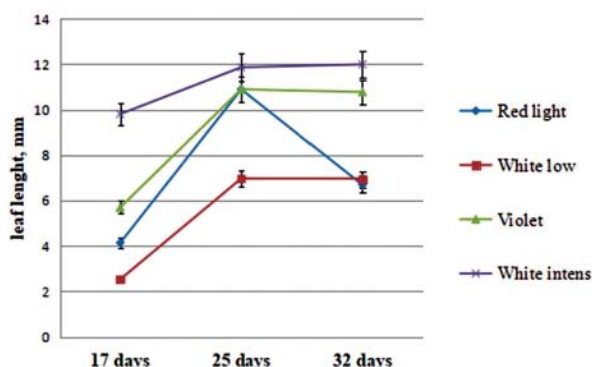


Fig. 1. Dynamic grown the leaves length (mm) plants in depend of vegetation terms (days)

AP1, *GI* and *FT* expression are down-regulated in experimental groups in compare of control group plants by a mean factor of 0.029, 0.444 and 0.074; **b) 3 min UVC:** *AP1* is up-regulated in experimental group plants by a mean factor of 4.966, **c) 5 min UVC:** *FT* is up-regulated in experimental group (in comparison to control group) by a mean factor of 1.748. But *CO* is down-regulated in the experimental group by a mean factor of 0.401.

The expression of key photoperiodic pathway genes after short wavelength UV in red light growing plants was described in Table 4. **a) 1 min UVC:** *AP1* is up-regulated in experimental group by a mean factor of 2.782 and genes *GI*, *CO*, *FT*, and *RAD51* are down-regulated in the experimental groups by mean factors of 0.171, 0.134, 0.025 and 0.450, comparatively; **b) 3 min UVC:** *AP1* and *FT* are down-regulated in

experimental groups by a mean factor of 0.586 and 0.445 in in comparison to the control group. The gene *CO* is up-regulated by a mean factor of 2.644; **c) 5 min UVC:** *FT* and *RAD51* are up-regulated in the experimental group by a mean factor of 5.214 and 1.914, comparatively. The similar effect we observed for violet illumination plus UV-radiation.

The phenology data revealed about necessary of the full spectrum of solar light to normal activation of circadian clock genes. It is known that *PHYA-PHYE* accepts the visible red light. We suggest that phytochromes involve in flowering time regulation in the non-full spectrum of light. *CRY1* i *CRY2* accept the blue light [26]. However, decreasing of red light in illumination caused blooming time delay to compare white light growing plants. It also was explained in recent studies [1].

Our results shown the trend of flowering genes expression depends on red, violet and white light spectrum. We observed that *AP1*, *GI*, *CO* and *RAD51* increase their activity after stress. The response of *CO* and *FT* genes to stress factor did not observed.

We believe that changes of genes activity depend on light illumination conditions. However increasing of *RAD51* gene expression has been shown the activity of reparation processes in plant cells [27]. The expression levels of *RAD51* have differences in samples group that were grown in white, violet and red illumination. The differences can cause by cryptochromes or phytochromes.

In addition, we did not show the significant changes of photoperiodic pathway genes

Table 2. Relative expression analyzes results of plants cultivated under common white light and treatment by 1, 3 and 5 min of UVC treatment

Gene	Expression	Std. Error	95% C.I.	P(H1)	Result ($P < 0.05$)
<i>1 min</i>					
<i>PCNA2</i> **	1				
<i>RAD51</i>	2.936	1.939–4.492	1.490–5.841	0	UP*
<i>API</i>	12.255	4.570–33.291	2.358–70.686	0.062	UP
<i>CO</i>	0.648	0.586–0.716	0.577–0.728	0	DOWN*
<i>GI</i>	1.494	1.273–1.757	1.161–1.925	0	UP*
<i>FT</i>	1.233	0.665–2.286	0.424–3.793	0.667	UP
<i>3 min</i>					
<i>PCNA2</i> **	1				
<i>RAD51</i>	5.519	3.430–8.431	3.118–9.986	0.049	UP
<i>API</i>	31.685	16.502–73.653	9.321–108.277	0	UP
<i>CO</i>	0.49	0.383–0.564	0.377–0.572	0.034	DOWN*
<i>Gi</i>	0.561	0.473–0.686	0.406–0.764	0.022	DOWN*
<i>FT</i>	0.998	0.625–1.933	0.426–2.255	0.918	DOWN
<i>5 min</i>					
<i>PCNA2</i> **	1				
<i>RAD51</i>	46.869	30.683–72.202	24.564–90.040	0	UP
<i>API</i>	87.018	39.391–192.333	37.248–203.375	0	UP
<i>CO</i>	137.253	110.717–179.260	109.005– 182.074	0	UP
<i>GI</i>	1.678	0.351–8.065	0.288–9.822	0.611	UP
<i>FT</i>	6.15	3.322–11.095	3.078–12.423	0.026	UP*

* Statistically significant

**Reference gene = 1

Hereinafter: the expression level values compare with reference gene expression = 1. The expression level values are calculated in base of row quantitative PCR data of control and experimental groups. The methodology shown the differences between control and treated groups as control — 1 min UV, control — 3 min UV, control — 5 min UV. It is not necessary to present the row control and experimental data. The hypothesis test P(H1) represents the probability of the difference between the sample and control groups.

expression after short wavelength UV in plants which cultivated in violet light, at 24 °C. We guess that the red and violet light growing plants have different expression because of the photoreceptors involved in short wavelength UV response. For example, the same short wavelength UV-doses cause different level of *API* expression in different groups (Fig. 2–4). This phenomenon could be explained by the involvement of cryptochromes in flowering regulation.

As known *RAD51* gene involved in repair processes after UV and ionizing radiation. Red light growing causes to increase *RAD51* activity (Table 4). At the same time increasing *RAD51* activity in violet and white light growing plants was observed only on 5 min short wavelength

UV. It can be related to the light wavelength of illumination. We believe that shorter wavelength can suppress repair processes in plant cells.

The previous data showed that short wavelength UV influences on plant biomass formation, photosynthesis and leaf size of agriculture plants [14]. Our results also demonstrated that short wavelength UV also drastic influences on repair and bloom processes. Other authors in the recent studies report similar data. They have shown that different light conditions effect on stress resistance in plants [28].

However, the question of relation photoreceptors of the plant due to photoperiodic pathway genes expression is

Table 3. Relative expression analyzes results of plants cultivated under violet light and treatment by 1, 3 and 5 min of UVC treatment

Gene	Expression	Std. Error	95% C.I.	P(H1)	Result ($P < 0.05$)
<i>1 min</i>					
ACT2**	2.286				
PCNA2**	0.438				
RAD51	4.57	1.080–19.487	0.872–24.120	0.174	UP*
CO	0.264	0.213–0.326	0.206–0.338	0.075	DOWN*
GI	0.444	0.343–0.577	0.299–0.663	0	DOWN
FT	0.074	0.047–0.117	0.044–0.125	0.041	DOWN
AP1	0.029	0.020–0.038	0.018–0.041	0	DOWN
<i>3 min</i>					
ACT2**	0.242				
PCNA2**	4.137				
RAD51	4.455	1.017–19.538	0.929–21.385	0.268	UP
CO	0.467	0.402–0.543	0.388–0.562	0.077	DOWN
GI	1.236	1.045–1.462	0.930–1.647	0.183	UP
FT	0.949	0.755–1.192	0.707–1.274	0.772	DOWN
AP1	4.966	3.155–7.823	2.939–8.397	0.037	UP*
<i>5 min</i>					
ACT2**	0.214				
PCNA2**	4.672				
RAD51	4.462	1.030–19.387	0.904–22.069	0.283	UP
CO	0.401	0.340–0.471	0.329–0.488	0.042	DOWN*
GI	0.792	0.700–0.896	0.640–0.982	0.135	DOWN
FT	1.748	1.579–1.936	1.480–2.065	0.022	UP*
AP1	4.18	3.893–4.489	3.687–4.743	0.057	UP

* Statistically significant; **Reference gene.

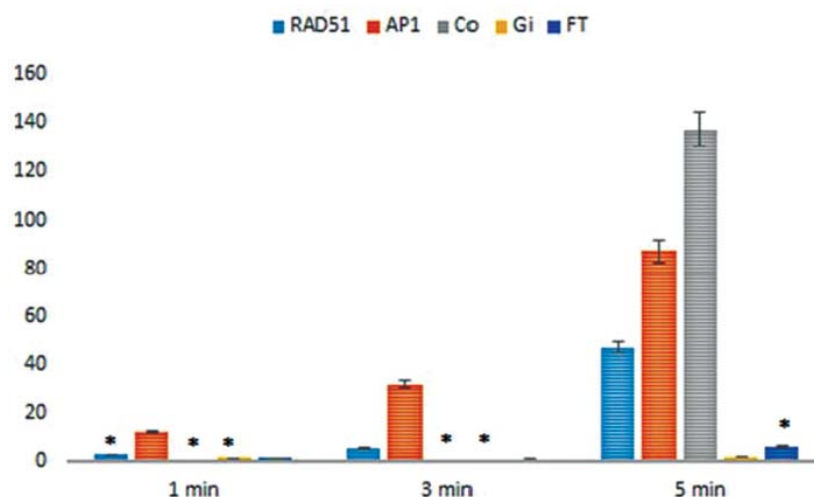


Fig. 2. Dynamic of flowering genes expression of plants grown under illumination common white light in depend of UV-treatment term:

Hereinafter: the expression level values compare with reference gene expression =1. The expression level values are calculated in base of row quantitative PCR data of control and experimental groups. The methodology shown the differences between control and treated groups as control — 1 min UV, control — 3 min UV, control — 5 min UV. It is not necessary to present the row control and experimental data. The data are comparing with control group. * Statistically significant

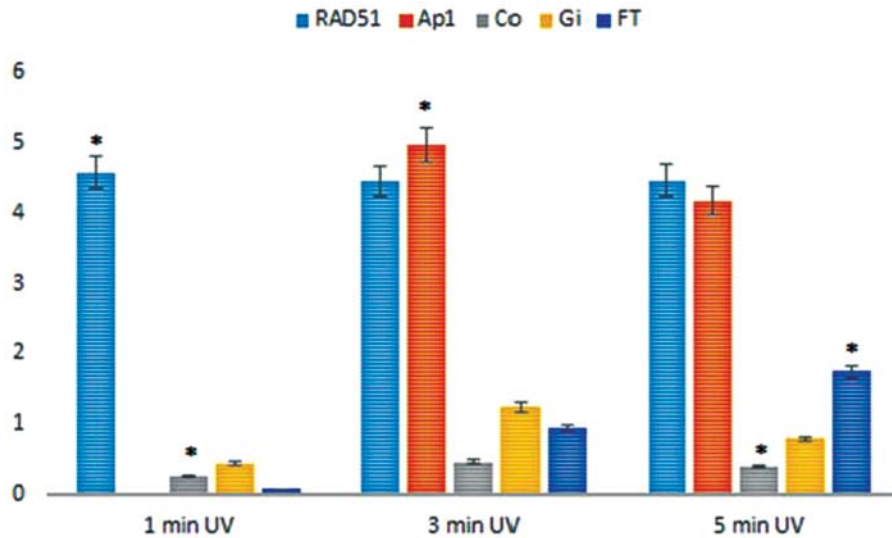


Fig. 3. Dynamic of flowering genes expression of plants grown under violet light in depend of UV-treatment term

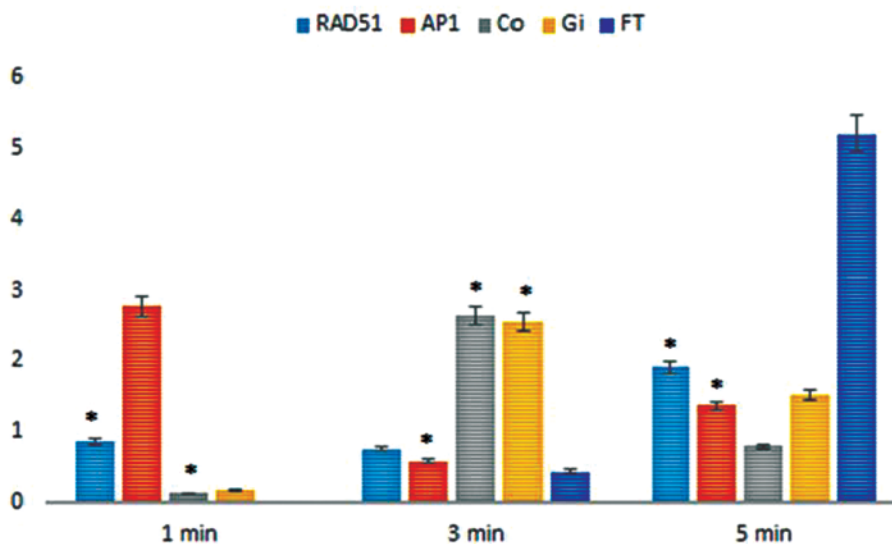


Fig. 4. Dynamic of flowering genes expression of plants grown under red light in depend of UV-treatment term

relevant. This phenomenon needs more dip studies of transcription factors, which are included in flowering regulation. The question of cultivation conditions impact on plant stress response is interesting for science and agriculture. The drought, salinity, oxidation stress are interested in scientists.

These researches will help to produce stress resistant sorts of agriculture plants, which can be planted in climate change conditions or unfavorable places of the planet [29].

Thus, our experimental data revealed that *Arabidopsis thaliana* plant cultivation under illumination of violet, red and

orange spectra of light could drastically influence on photoperiodic pathway genes expression.

Post-irradiated with short wavelength UV-irradiation of plants grown under red light illumination caused downregulation expression of genes related to circadian clock *CO* and *GI* and repair genes *RAD51*.

Our data demonstrate that the plant cryptochrome and phytochrome formation and development condition play an important role in UV-radiation resistant and on the response of main photoperiodic pathway and repair genes expression.

Table 4. Relative expression analyzes results of plants cultivated in red light and treatment by 1, 3 and 5 min of UVC treatment

Gene	Expression	Std. Error	95% C.I.	P(H1)	Result ($P < 0.05$)
<i>1 min</i>					
ACT2**	1.929				
PCNA2**	0.518				
RAD51	0.868	0.813–0.924	0.800–0.967	0.049	DOWN*
CO	2.782	2.419–3.309	2.329–3.436	0	UP*
GI	0.134	0.104–0.166	0.101–0.179	0.034	DOWN
FT	0.171	0.157–0.191	0.151–0.194	0	DOWN
AP1	0.025	0.024–0.026	0.023–0.027	0	DOWN
<i>3 min</i>					
ACT2**	0.76				
PCNA2**	1.316				
RAD51	0.759	0.629–0.876	0.591–0.993	0.153	DOWN
CO	0.586	0.484–0.686	0.452–0.797	0	DOWN*
GI	2.644	2.486–2.890	2.434–2.955	0	UP*
FT	2.552	2.386–2.780	2.236–2.897	0.097	DOWN
AP1	0.445	0.372–0.533	0.347–0.572	0	DOWN*
<i>5 min</i>					
ACT2**	0.76				
PCNA2**	1.316				
RAD51	1.914	1.755–2.041	1.713–2.183	0	UP*
CO	1.368	0.915–1.978	0.783–2.432	0.195	UP
GI	0.794	0.547–1.117	0.531–1.203	0.345	DOWN
FT	1.518	1.334–1.760	1.283–1.786	0.054	UP
AP1	5.214	3.962–6.861	3.824–7.108	0	UP*

* Statistically significant; **Reference gene.

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**ВПЛИВ КОРОТКОХВИЛЬОВОГО
УЛЬТРАФІОЛЕТОВОГО
ВИПРОМІНЮВАННЯ НА ЕКСПРЕСІЮ
ГЕНІВ У *Arabidopsis thaliana***

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Метою дослідження було вивчення впливу опромінення короткохвильовим ультрафіолетом (довжина хвилі 230 нм) рослин *Arabidopsis thaliana*. Досліджено стресову реакцію на деякі ключові гени фотоперіодичного механізму детермінації цвітіння: AP1, GI, FT, CO та репарації RAD51. Для вирощування рослин застосовували червоне (довжина хвилі 610–750 нм), фіолетове (довжина хвилі 400–450 нм), нейтральне видиме (змішані хвилі з довжиною 380–750 нм) освітлення з потужністю LED ламп 20 Вт та 40 Вт.

Після цього експериментальну групу рослин опромінювали короткохвильовим ультрафіолетом (довжина хвилі 230 нм) на стадії онтогенезу 5.1 за класифікацією Бойса (2001). Як маркер вегетаційного росту було проаналізовано довжину листа. Виявлено, що опромінення короткохвильовим ультрафіолетом спричинювало відмінності у профілях експресії генів фотоперіодичного механізму регуляції у рослин, вирощених за різного освітлення. Спостерігалось прискорення фази цвітіння за вирощування в інтенсивному білому освітленні та запізнення за фіолетового та помірного білого освітлення порівняно з контрольною групою. Таким чином було виявлено, що криптохроми і фітохроми відіграють важливу роль у формуванні стресостійкості рослин. Дані дослідження є важливими для біотехнології та сільського господарства і дадуть змогу визначити найбільш оптимальні способи вирощування рослин в умовах стресу.

Ключові слова: умови освітлення, експресія генів, ультрафіолет короткохвильового діапазону, відповідь на стрес.

**ВЛИЯНИЕ КОРОТКОВОЛНОВОГО
УЛЬТРАФИОЛЕТОВОГО ИЗЛУЧЕНИЯ
НА ЭКСПРЕССИЮ ГЕНОВ
У *Arabidopsis thaliana***

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Целью исследования было изучение влияния облучения коротковолновым ультрафиолетом (длина волны 230 нм) растений *Arabidopsis thaliana*. Исследована стрессовая реакция на некоторые ключевые гены фотопериодического механизма: AP1, GI, FT, CO и RAD51.

Для выращивания растений применяли красный (длина волны 610–750 нм), фиолетовый (длина волны 400–450 нм), нейтральный белый (смешанные волны с длиной 380–750 нм) с интенсивностью LED-ламп 20 Вт и 40 Вт. Экспериментальную группу растений облучали коротковолновым ультрафиолетом (длина волны 230 нм) на стадии онтогенеза 5.1 по классификации Бойса (2001). В качестве маркера вегетационного роста также была проанализирована длина листа. Облучение коротковолновым ультрафиолетом вызывало различия в профилях экспрессии генов фотопериодического механизма регуляции цветения у растений, выращенных при разном освещении. Наблюдалась раннее начало фазы цветения при выращивании в интенсивном белом освещении и позднее при фиолетовом и обычном белом освещении по сравнению с контрольной группой. Таким образом было выявлено, что криптохромы и фитохромы играют важную роль в формировании стрессоустойчивости растений. Данные исследования важны для биотехнологии и сельского хозяйства, что поможет определить наиболее оптимальные способы выращивания растений в условиях стресса.

Ключевые слова: условия освещения, экспрессия генов, коротковолновой ультрафиолет, ответ на стресс.