



Supplementary Materials: Supplementary materials can be found at www.mdpi.com/xxx/s1.

phyB and HY5 are Involved in the Blue Light-Mediated Alleviation of Dormancy of *Arabidopsis* Seeds Possibly via the Modulation of Expression of Genes Related to Light, GA, and ABA

Marlena Stawska and Krystyna Oracz *

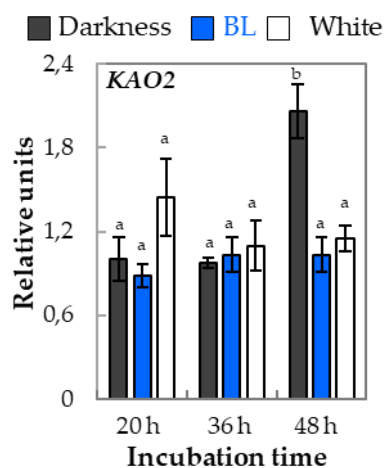
¹ Department of Plant Physiology, Institute of Biology, Warsaw University of Life Sciences – SGGW, Nowoursynowska str. 159, 02-776, Warsaw, Poland; krystyna_oracz@sggw.pl

* Correspondence: krystyna_oracz@sggw.pl; Tel.: (+48 22 59 325 35) (K.O.)

Supplementary Table S1. Effect of different combinations of pre- or post-incubations in darkness on BL light effect on germination rates of WT dormant *Arabidopsis* Col-0 seeds. Results are expressed as % of germinated seeds after 48 and 72 h of incubation in specific light conditions \pm SD. Experiments were conducted in three biological and two technical replicates (100 seeds per each replicate).

Light conditions of incubation	Germination (%) of WT dormant seeds after time of incubation:	
	48 h	72 h
3 h BL > Darkness (const.)	3.0 \pm 1.0 **	9.0 \pm 1.0 **
6 h BL > Darkness (const.)	5.6 \pm 0.5 **	12.0 \pm 1.5 **
24 h BL > Darkness (const.)	26.5 \pm 0.5 **	54.0 \pm 2.0
48 h BL > Darkness (const.)	19.5 \pm 2.5 *	50.6 \pm 2.5
6 h Darkness > 3 h BL > Darkness (const.)	25.5 \pm 1.0 *	46.6 \pm 0.5
24 h Darkness > 3 h BL > Darkness (const.)	11.0 \pm 0.5	27.0 \pm 0.5 **
BL (const.)	14.3 \pm 0.5	44.4 \pm 2.5
Darkness (const.)	0.70 \pm 0.5 **	0.7 \pm 0.5 **

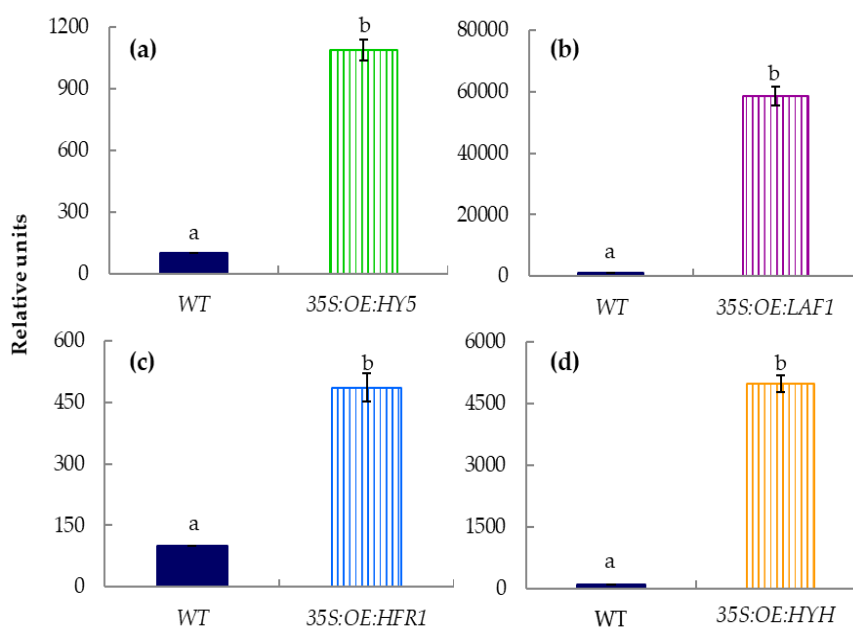
Supplementary Figure S1.



Supplementary Figure S1. The relative expression of *KAO2* gene in samples isolated from WT dormant *Arabidopsis* (Col-0) seeds incubated on water for 20, 36 and 48 h, in different light conditions: darkness, BL and white light, at temp. 25 °C. The transcripts level was normalized to reference genes (*ACT7*, *APC2*, *HBT*) and to the internal control which was the expression value of *KAO2* gene obtained in darkness, after 20 h of incubation. Three biological and two technical replicates were performed. The bars show the relative units \pm SD.

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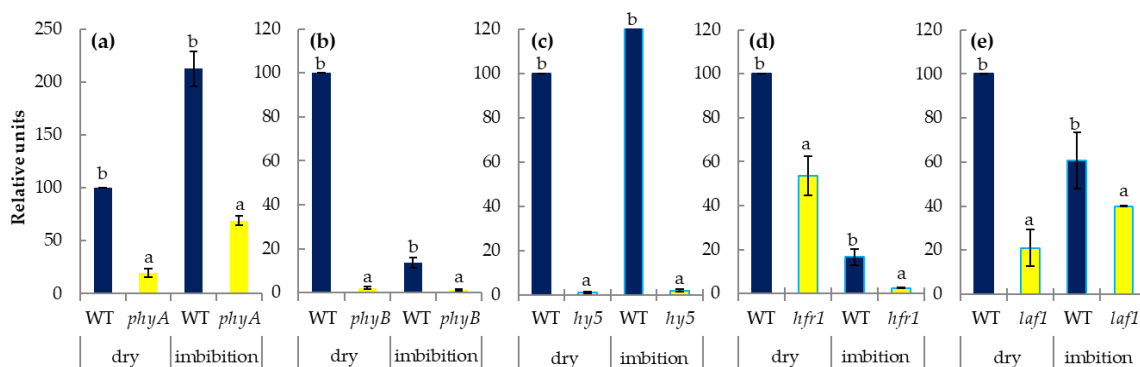
81 **Supplementary Figure S2.**



Supplementary Figure 2. The qRT-PCR analysis of relative expression of defined genes in 3 weeks old seedlings of overexpression lines of *Arabidopsis* transformants.

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Supplementary Figure S3.



Supplementary Figure 3. The qRT-PCR analysis of relative expression of defined genes in dormant seeds (dry and imbibed for 6 h on light) of *Arabidopsis* T-DNA insertion mutants.

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Supplementary Table S2. Characteristic of primers used in qRT-PCR analysis of genes relative expression

Gene	Full gene name	Gene accession no.	NCBI number	L/R	Sequence 5' --> 3'	Tm °C	Product size [bp]
Reference genes							
<i>ACT7</i>	<i>Actin 7</i>	At5g09810	NM_121018.3	L	GGAGCTGAGAGATTCCGTTG	58.1	197
				R	TCTTTGCTCATACGGTCAGC	57.9	
<i>APC2</i>	<i>Anaphase-Promoting Complex/Cyclosome 2</i>	At2g04660	NM_126495.2	L	GGAGGAGTTAAGCGCAATCA	57.9	154
				R	CACCAACTTGTCATGTCCCA	58.0	
<i>HBT</i>	<i>Hobbit</i>	At2g20000	NM_179663.2	L	ATCGATGAGAGCCCCTGAAA	59.2	181
				R	GGCTCTTGTGGCTGTGTTAC	58.1	
Light signaling related genes							
<i>PHYA</i>	<i>Phytochrome A</i>	At1g09570	NM_100828.3	L	CAAGGTCCGGATGATAGTTG	51.8	175
				R	AACTACAACCGCCATAACCA	49.7	
<i>PHYB</i>	<i>Phytochrome B</i>	At2g18790	NM_127435.3	L	AAAGAATCTGAGGCGGCTAT	49.7	199
				R	CTGCAATCTTAGCGTTCCAT	49.7	
<i>CRY1</i>	<i>Cryptochrome 1</i>	At4g08920	NM_116961.4	L	CAGCAGCGGAAGGAGAGAAA	60.0	232
				R	TTTCACCCGGAGTTACAGCCC	59.9	
<i>CRY2</i>	<i>Cryptochrome 2</i>	At1g04400	NM_100320.3	L	TTCGGGAAATAAGCGTCAG	57.9	221
				R	TCAACATCAGCATCCCAAGG	57.9	
<i>CRY3</i>	<i>Cryptochrome 3</i>	At5g24850	NM_122394.3	L	GGAGAGATGCCAAGACAGGG	59.8	269
				R	TTGTGCTTGCTTGGGAATGC	59.9	
<i>HY5</i>	<i>Elongated Hypocotyl 5</i>	At5g11260	NM_121164.4	L	CGGAGAAAGAGAACAAGCGG	58.9	226
				R	CCACCACCTCCTCTCTTGTT	58.9	
<i>HFR1</i>	<i>Long Hypocotyl in Far-Red</i>	At1g02340	NM_100115.3	L	CTAAATCCGGCGAATCACAT	49.7	164
				R	GGAACCAAACCGTGAAGAGA	51.8	

HYH	<i>HY5-Homolog</i>	At3g17609	NM_180274.2	L	CACAAGAAGCACAAAAGTGGG	53.0	233
				R	TGCGCTGATACTCTGTTCT	51.8	
LAF1	<i>Long After Far-Red Light 1</i>	At4g25560	NM_118688.3	L	CCCCTCCTTCGTCTTCATCA	58.8	181
				R	AGCCTTGGAAATCTCAGGAGC	59.4	
CIB1	<i>Cryptochrome Interacting Basic Helix-Loop-Helix 1</i>	At4g34530	NM_119618.3	L	CACAGCATAGCAGAACGAGT	58.0	191
				R	GGCCTTGGATTACAATTGC	57.9	
CIB5	<i>Cryptochrome Interacting Basic Helix-Loop-Helix 5</i>	At1g26260	NM_202184.2	L	TCGATGAAACTTTCGGCTGT	57.8	171
				R	TGAGGAAATGTTTCGGTTGCA	58.0	
SUB1	<i>Calcium Ion Binding Protein SUB1</i>	At4g08810	NM_116951.1	L	GAAGGGCAAGCATCGAAGTA	57.9	230
				R	CTCCACACCTGAACCAATCC	58.1	
PP7	<i>Serine/Threonine Phosphatase 7</i>	At5g63870	NM_125782.3	L	CTGGTCTTGGTGGAAATGGAC	58.1	171
				R	GAGGATCCGAGAAATCAGGC	57.8	
PHR2	<i>Photolyase/Blue Light Receptor 2</i>	At2g47590	NM_130327.3	L	ATCGCAGCGCTTGATCAATT	58.9	226
				R	CTGGTTCCCTTGCTCAACC	59.0	
COP1	<i>Constitutive Photomorphogenic 1</i>	At2g32950	NM_128855.3	L	TCTCACAGTGAACAGCGAGT	58.9	199
				R	ATTCGCAGTCAACATCGTGG	58.9	
Genes involved in ABA metabolism and signalling							
ABA1	<i>ABA Deficient 1</i>	At5g67030	NM_126103.2	L	TGGCTGCAATTATGGCTTCC	51.8	217
				R	TCGGCTTTGTGAGTGTCT	51.8	
NCED6	<i>Nine-Cis-Epoxy-carotenoid Dioxygenase 6</i>	At3g24220	NM_113327.2	L	AATGCGTGGGAAGAGAGAAC	57.9	205
				R	GGTTTATGTGACCCGCTTCT	57.9	
NCED9	<i>Nine-Cis-Epoxy-carotenoid Dioxygenase 9</i>	At1g78390	NM_106486.2	L	CAATGATAGCCCACCCGAAA	57.9	239
				R	ACCTCTTATCATCTCCGGCA	57.9	
CYP707A2	<i>Cytochrome P450, Family 707, Subfamily A, Polypeptide 2</i>	At2g29090	NM_001202700	L	GCAGCAAGTGTACTGTCCTT	58.1	232
				R	GCTCACTTCTGGACATGAG	57.9	
ABI3	<i>ABA Insensitive 3</i>	At3G24650	NM_113376.3	L	CATCTCCAGTCTCTGTCAAC	57.9	168

				R	CACCAGAAGAGTCGTCACAG	57.9	
ABI4	<i>ABA Insensitive 4</i>	At2G40220	NM_129580.1	L	GTTAGGGCAGGAACAAGGAG	57.8	155
				R	TATAACCCGGATCCAGACCC	57.9	
ABI5	<i>ABA Insensitive 5</i>	At2G36270	NM_129185.3	L	ATGATCAAGAACCGCGAGTC	58.1	221
				R	ATCAATGTCCGCAATCTCCC	58.0	
HAI1	<i>Highly ABA Induced PP2C Gene 1</i>	At5g59220	NM_125312.3	L	GTCACGAGCCATTGGAGATA	57.1	164
				R	AACACATTCGAACGACGCTA	57.9	
HAI2	<i>Highly ABA Induced PP2C Gene 2</i>	At1g07430	NM_100617.2	L	ATGTCACGAGCCATAGGAGA	57.9	236
				R	TCTTCTTCACTCCTCCTCCC	57.7	
HAI3	<i>Highly ABA Induced PP2C Gene 3</i>	At2g29380	NM_128492.2	L	CCGAGATTCCAAACGGTGAT	51.8	181
				R	CTCTTCTTCTACCGCACACC	53.8	
Genes involved in GA metabolism and signaling							
GA3ox1	<i>Gibberellin 3-Oxidase 1</i>	At1g15550	NM_101424.2	L	CTTGGGGTGCCTTCCAAATC	59.1	195
				R	AACCTTCGGACCACATTTGC	59.0	
GA3ox2	<i>Gibberellin 3-Oxidase 2</i>	At1g80340	NM_106683.1	L	CCAAGTTGATGTGGTTCGCA	59.0	176
				R	GAGGGTCGAGTCTGTATGGG	58.9	
GA2ox6	<i>Gibberellin 2-Oxidase 6</i>	At1g02400	NM_100121.4	L	AGCGAAGTGAGTGAGCTGAT	59.1	215
				R	GGGTCAGATGGGATTGGGAT	58.8	
GA2ox2	<i>Gibberellin 2-Oxidase 2</i>	At1g30040	NM_001036035.1	L	ATCCCCACATACAAACCGGT	59.0	193
				R	GCAAGCCGAAGAAGCCAATA	58.9	
GID1a	<i>GA Insensitive Dwarf1A</i>	At3g05120	NM_111384.3	L	TACTCTTTGTCGCAGGCTTG	51.8	239
				R	CCGATTCACCCGCTCTTAAA	51.8	
GID1b	<i>GA Insensitive Dwarf1B</i>	At3g63010	NM_116166.4	L	CCTCGAGCTAACCAAACCTC	53.8	151
				R	GACAACAACAACCCGCAAA	49.7	
GID1c	<i>GA Insensitive Dwarf1C</i>	At5g27320	NM_122614.3	L	TGTGCATAATGTGCGGTAA	49.7	193
				R	ATGCTCTGTCTTCACCCT	51.8	

RGL1	<i>RGA-Like 1</i>	At1g66350	NM_105306.3	L	AAGCATGCTCTCGGATCTTG	51.8	163
				R	AGAGCGCGTAGAGGATAACT	51.8	
RGL2	<i>RGA-Like 2</i>	At3g03450	NM_111216.2	L	ACCGGAGTTAGACTTGTCCA	51.8	176
				R	CGGTAAATACGACGAGCCAA	51.8	
RGL3	<i>RGA-Like 3</i>	At5g17490	NM_121755.2	L	ACTTACACTCTCCAGGTCCC	53.8	239
				R	GTTATCGTCTCCACCACCAC	53.8	
XERICO	<i>RING/U-box superfamily protein</i>	At2g04240	NM_201687.1	L	GCAAGAACAGGCAGACAA	48.9	172
				R	GGCACAACAACAAGAGGAG	51.1	
KAO2	<i>Arabidopsis thaliana Ent-kaurenoic acid oxidase 2</i>	At2g32440	NM_001202728	L	CAGGGAAGCAAAGAGTGATG	58.4	181
				R	CAAACCAAAAAGGAAGGAATG	57.1	

