

Supporting Information to

Red light controls adventitious root regeneration by modulating hormone homeostasis in *Picea abies* seedlings

Sanaria Alallaq^{1,2}, Alok Ranjan^{1,#}, Federica Brunoni^{1,§}, Ondřej Novák^{3,4}, Abdellah Lakehal^{1,*}, Catherine Bellini^{1,5,*}

¹ Umeå Plant Science Centre, Department of Plant Physiology, Umeå University, SE-90736 Umeå, Sweden

² Department of Biology, College of Science for Women, Baghdad University, 10071, Baghdad, Iraq

³ Umeå Plant Science Centre, Department of Forest Genetics and Physiology, Swedish Agriculture University, SE-90183 Umeå, Sweden

⁴ Laboratory of Growth Regulators, Faculty of Science, Palacký University and Institute of Experimental Botany, The Czech Academy of Sciences, 78371 Olomouc, Czech Republic

⁵ Institut Jean-Pierre Bourgin, INRAE, AgroParisTech, Université Paris-Saclay, FR-78000 Versailles, France

#Present address: Unité de recherche en Physiologie et Génétique moléculaire des Plantes. Faculté des Sciences Campus de la Plaine, 1050 Bruxelles, Belgium

§ Present address: Laboratory of Growth Regulators, Faculty of Science, Palacký University and Institute of Experimental Botany, The Czech Academy of Sciences, 78371 Olomouc, Czech Republic

***Corresponding authors:**

Pr Catherine Bellini email: catherine.bellini@umu.se

Dr Abdellah Lakehal email: abdellah.lakehal@umu.se

The following Supporting Information is available in this PDF:

Figure S1: Method for *de novo* root organogenesis under different light conditions

Figure S2: Spectral emission curves for the various light sources used in this study

Figure S3: Phylogenetic trees

Figure S4: Coding sequences used for the phylogenetic analysis

Table S1 Primers used for qPCR experiments in this study

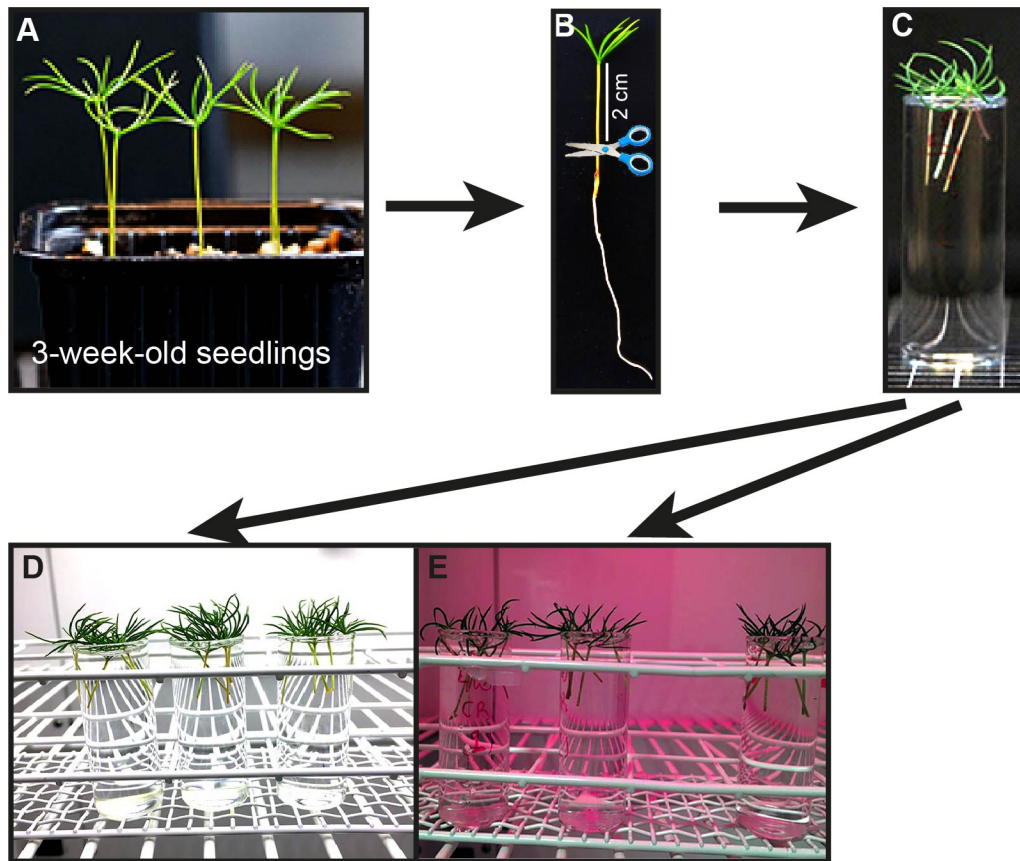


Figure. S1 Method for *de novo* root organogenesis under different light conditions

- (A) Three-week-old Norway spruce seedlings grown in vermiculite in a growth chamber under long day conditions
- (B) Three-week-old Norway spruce seedling before cutting.
- (C) Hypocotyl cuttings transferred to 24 ml vials filled with distilled water and placed in monochromatic cabinets equipped with white (D) or red (E) LEDs

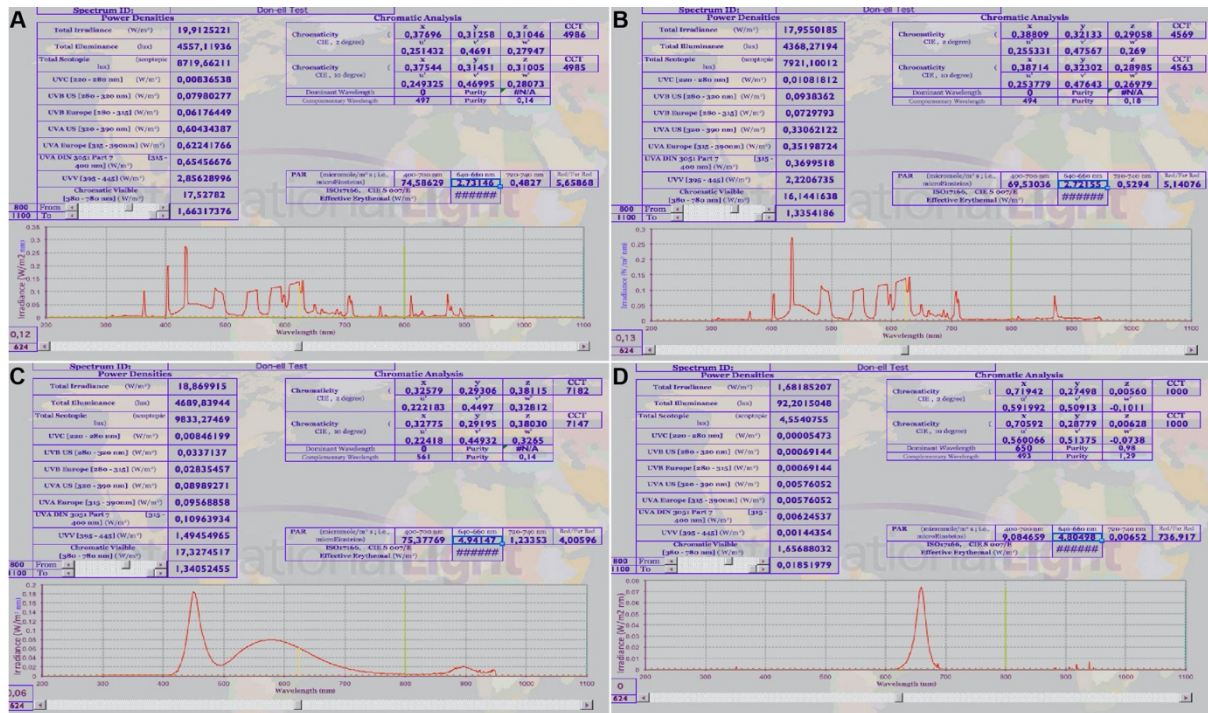


Figure S2: Spectral emission curves for the various light sources used in this study.

- (A) White light TL-D 36W/840 Philips master, long days
- (B) Cool white light F17T8/TL741, 17 W Philips, long days
- (C) Continuous white light LED (cWL)
- (D) Continuous red light LED (cRL).

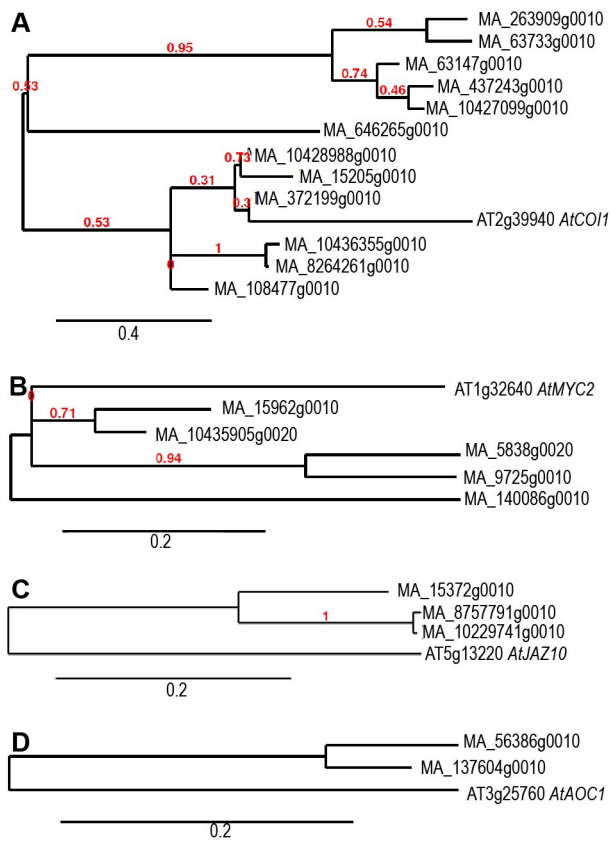


Figure S3 Phylogenetic trees

Neighbor-Joining phylogenetic trees (1000 bootstrap replicates), based on alignment of coding sequences of (A) *COII* (B) *MYC2* (C) *JAZ10* and (D) *ACO1* (E) from *Picea abies* (MA) and *A. thaliana* (AT). The gene orthologs were named according to the <http://congenie.org/> database. The sequences are provided in Figure S4.

Figure S4 Coding sequences used for the phylogenetic analysis

Arabidopsis thaliana and *Picea abies* coding sequences (CDS) were obtained from the TAIR (<https://www.arabidopsis.org>) and congenie (<http://congenie.org/>) databases respectively. To find putative *Arabidopsis* orthologs in *Picea abies*, a BLAST alignment of the coding sequences of selected genes was generated using "Genome Tools" at <http://congenie.org/> with default settings. Subsequently, <http://www.phylogeny.fr> was used to construct phylogenetic trees based on the neighbor-joining method (with 1000 bootstrap replicates). Gene orthologs were named according to the <http://congenie.org> database.

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Table S1 Primers used for qPCR experiments in this study

Gene ID	Given Name	Forward (5'-3')	Reverse (5'-3')	Efficiency
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MA_5838g0020	<i>PaMYC2</i>	AATACTTTGCCATATTCTGCTGTTTC	GGATAAGAATTACAAGTTTCGCTGA	2,353
MA_6326g0010	<i>PaJAZ3</i>	AAGGGAGAGCAAGCAGCAGGAACAAC	AGAGGCTCCGACAACAGGCAAGAAAG	2,32
MA_10229741g0010	<i>PaJAZ10</i>	TGGCTTCCATTTCTCCTGCTGCAA C	CCGGCCTGGAAATTGTCCATTGTC	2,942
MA_56386g0010	<i>PaAOC1</i>	CTCCTCTCTGGTGCAGTGA	GGGCTTCTCTGTCCAATC	2,466
MA_50378g0010	<i>PaEIF4A1</i>	TTGGTCGGAGTGGACGATTGG	GTCTGCAGCATTCTCTCGTCA	2,041
MA_13020g0010	<i>PaUBC28</i>	GGATCTCTGTAAACCGCGTCGTTG	AGGATCCGCTTAGACGCCATT	1,989