

Supplementary Material

Table S1. Primer sequence and application

Name	Forward / Reverse primer sequence (5'-3')	Temperature/°C	Application
<i>IIWRKY22</i>	F:CTCCCAACAAACTCTCT CCCTAG	56°C	PCR amplification reaction
<i>IIWRKY22</i>	R:CAACAAAATAATCAGCT TGCCCC		
<i>AtActin</i>	F:CTCCTTTGTTGCTGTTGA CTAC	60°C	Fluorescence quantitative reference genes
<i>AtActin</i>	R:GCACAATGTTACCGTAC AGATC		
<i>IIWRKY22</i>	F:GATTGGAGTTGAGATGG GCTT	56°C	Fluorescence quantitative PCR reaction
<i>IIWRKY22</i>	R:ACTGTATAGTGGTGCTG AGGC		
<i>IIWRKY22</i> -BamHI	F:TTGATACATATGCCCCGT CGACTTCTCTCCATCCCCT CTTT	60°C	PCR amplification reaction
<i>IIWRKY22</i> -SalI	R:CCCTTGCTCACCATGGA TCCGCTCCCACCACCGGC AACGG		
<i>CO</i>	F:CACAGGTGAATACAGTC AACACC	60°C	Fluorescence quantification
<i>CO</i>	R:CCATGGATGAAATGTAT GCGTTATGG		
<i>GA20OX</i>	F:CGGTTTTGCGACGACAT GAG	60°C	Fluorescence quantification

<i>GA20OX</i>	R:TAGCCCCAGAAGCTCCA TGA		
<i>VRN1</i>	F:CTGAGGGTCCCAGATAA GTTTG	60°C	Fluorescence quantification
<i>VRN1</i>	R:GTCAGCTTTCCTTAGTCC TACAC		
<i>SPL3</i>	F:CTCATGTTCGGATCTCTG GTC	60°C	Fluorescence quantification
<i>SPL3</i>	R:TTTCCGCCTTCTCTCGTT GTG		
<i>FCA</i>	F:GCTCTTGTCGCAGCAAA CTC	60°C	Fluorescence quantification
<i>FCA</i>	R;GATCCAGCCCACTGTTG TTTAC		
<i>SVP</i>	F:GAAGAGAACGAGCGACT TGG	60°C	Fluorescence quantification
<i>SVP</i>	R:GAGCTCTCGGAGTCAAC AGG		
<i>SOC1</i>	F:GATCGAGTCAGCACCAA ACC	60°C	Fluorescence quantification
<i>SOC1</i>	R:TCCTATGCCTTCTCCCAA GA		
<i>TPS1</i>	F:ATTGGCATAGATTCTGA TCGGT	60°C	Fluorescence quantification
<i>TPS1</i>	R:TCAAGACGATCAACACC TAACA		
<i>FLC</i>	F:AGCCAAGAAGACCGAAC TCA	60°C	Fluorescence quantification

<i>FLC</i>	R:AGCTTCTGCTCCACAT GAT		
<i>NtHAK1</i>	F:ATCCACACCGAGCTTGT TTCAGGA	60°C	Fluorescence quantitative PCR reaction
<i>NtHAK1</i>	R:TGGGTCCAATTCTTCCC ACCAAGA		
<i>NtSOS1</i>	F:GCGTGCTTATTTCCACCT TTTG	60°C	Fluorescence quantitative PCR reaction
<i>NtSOS1</i>	R:TTTGATGACGGCTCCCC AGT		
<i>NtPMA4</i>	F:TTTCCCGAGCACAAGTA TGA	60°C	Fluorescence quantitative PCR reaction
<i>NtPMA4</i>	R:GGTAACCTCCAAGAACA ACAC		
<i>NtSOD</i>	F:CTCCTACCGTCGCCAAA T	60°C	Fluorescence quantitative PCR reaction
<i>NtSOD</i>	R:GCCCCAACCAAGAGAACC C		
<i>NtCAT</i>	F:AGGTACCGCTCATTAC ACC	60°C	Fluorescence quantitative PCR reaction
<i>NtCAT</i>	R:AAGCAAGCTTTTGACCC AGA		
<i>NtPOD</i>	F:CCTCAGCTTCAAGCATT ATGTCCA	60°C	Fluorescence quantitative PCR reaction
<i>NtPOD</i>	R:ACCTTTGTAGAAGCATC GGTCCAC		
<i>NtActin</i>	F:CGGAATCCACGAGACTA ACATACAAC	60°C	

*NtActin*R:GGTGCTGAGGGAAGCCA
AGATAFluorescence
quantitative PCR
reaction**Table S2.** Functional prediction of *WRKY* transcription factor family members in *I. laevigata*

Group	<i>A. thaliana</i>	<i>I. laevigata</i>	Function
I		isoform 3308	They are involved in disease resistance, abiotic stress (salt, cold, heat), senescence and some developmental processes (pollen development, seed coat development). A response to a light stimulus.
		isoform 275946	
		isoform 813581	
		isoform 336911	
	<i>AtWRKY1</i>	isoform 460429	
	<i>AtWRKY2</i>	isoform 71297	
	<i>AtWRKY3</i>	isoform 722579	
	<i>AtWRKY4</i>	isoform 629169	
	<i>AtWRKY25</i>	isoform 239732	
	<i>AtWRKY26</i>	isoform 238068	
	<i>AtWRKY32</i>	isoform 687755	
	<i>AtWRKY33</i>	isoform 416995	
	<i>AtWRKY34</i>	isoform 342824	
	<i>AtWRKY44</i>	isoform 439137	
	<i>AtWRKY58</i>	isoform 312565	
		isoform 658241	
		isoform 7202	
		isoform 6445	
		isoform 232908	
		isoform 564486	

Group	<i>A. thaliana</i>	<i>I. laevigata</i>	Function
IIa		isoform 298714	A defensive response to bacteria or fungi.
		isoform 319525	
		isoform 49561	
		isoform 305653	
	<i>AtWRKY40</i>	isoform 347489	
	<i>AtWRKY60</i>	isoform 63513	
		isoform 684413	
	<i>AtWRKY6</i>	isoform 358692	
	<i>AtWRKY9</i>	isoform 56218	
	<i>AtWRKY31</i>	isoform 320236	
IIb	<i>AtWRKY36</i>	isoform 40279	Defense responses to bacteria, fungi, oxidative stress; expression of genes involved in cold, leaf senescence. Root development.
	<i>AtWRKY42</i>	isoform 478449	
	<i>AtWRKY47</i>	isoform 303256	
	<i>AtWRKY72</i>	isoform 14002	
	<i>AtWRKY8</i>		
	<i>AtWRKY12</i>		
	<i>AtWRKY13</i>	isoform 735698	
IIc	<i>AtWRKY23</i>		They are involved in disease resistance (bacteria, fungi), abiotic stress (salt, cadmium, drought) , senescence and some developmental processes (lignin synthesis, pollen development, florescence regulation) Auxin transport.
	<i>AtWRKY24</i>		
	<i>AtWRKY28</i>		

Group	<i>A. thaliana</i>	<i>I. laevigata</i>	Function
IId	<i>AtWRKY43</i>		
	<i>AtWRKY48</i>		
	<i>AtWRKY49</i>		
	<i>AtWRKY50</i>		
	<i>AtWRKY51</i>		
	<i>AtWRKY56</i>		
	<i>AtWRKY57</i>		
	<i>AtWRKY59</i>		
	<i>AtWRKY71</i>		
	<i>AtWRKY75</i>		
		isoform 352866	
		isoform 287969	
		isoform 241617	
	<i>AtWRKY7</i>	isoform 279981	They are involved in plant disease resistance (bacteria, fungi), senescence (apoptosis) and some developmental processes (flower development, florescence regulation), regulation of jasmonic acid signaling pathway, response to light stimulation, calmodulin binding, reaction of salicylic acid.
	<i>AtWRKY11</i>	isoform 327411	
	<i>AtWRKY15</i>	isoform 297487	
	<i>AtWRKY21</i>	isoform 410198	
	<i>AtWRKY21</i>	isoform 41879	
	<i>AtWRKY39</i>	isoform 567039	
	<i>AtWRKY74</i>	isoform 513126	
		isoform 286734	
		isoform 305537	
		isoform 596689	

Group	<i>A. thaliana</i>	<i>I. laevigata</i>	Function
IIe		isoform 561421	They are involved in disease resistance (bacteria), senescence and some developmental processes (epidermis development, flower development, plant organ and root morphogenesis, florescence regulation), auxin transport.
		isoform 494831	
	<i>AtWRKY14</i>	isoform 588901	
	<i>AtWRKY16</i>	isoform 420051	
	<i>AtWRKY22</i>	isoform 234765	
	<i>AtWRKY27</i>	isoform 635473	
	<i>AtWRKY29</i>	isoform 51755	
	<i>AtWRKY35</i>	isoform 422731	
		isoform 304457	
III	<i>AtWRKY30</i>	isoform 507977	Involved in plant disease resistance (bacteria, fungi), abiotic stress (ozone, temperature, drought), senescence and some developmental processes (lateral root development, leaf development); response to salicylic acid, regulation of abscisic acid signaling pathway. Regulates brassinosteroid, ethylene and jasmonic acid-mediated signaling pathways.
	<i>AtWRKY38</i>	isoform 31149	
	<i>AtWRKY41</i>	isoform 614906	
	<i>AtWRKY46</i>	isoform 69705	
	<i>AtWRKY53</i>	isoform 38178	
	<i>AtWRKY54</i>	isoform 487979	
	<i>AtWRKY55</i>	isoform 645693	
	<i>AtWRKY63</i>	isoform 629546	
	<i>AtWRKY64</i>	isoform 44179	
	<i>AtWRKY66</i>	isoform 481801	
	<i>AtWRKY70</i>	isoform 20352	

Table S3. Abbreviations

Name	Online addresses
CO	constans
FLC	flowering locus C
CDF	cycling dof factors
FT	flowering locus T
SOC1	suppressor of overexpression of constans1
ABA	abscisic acid
GA20OX	GA-20 oxidase
SPL3	squamosa promoter binding protein like3
WT	wild type
NJ	neighbor-joining
VRN1	vernalization1
FCA	flowering control local A
TPS1	trehalose-6-phosphate synthase1
SVP	short vegetative phase
Pn	net photosynthetic rate
Gs	stomatal conductance
Ci	intercellular CO ₂ concentration
Tr	transpiration rate

Chl content	chlorophyll content
dpt	days post-treatment
ROS	reactive oxygen species
MDA	malondialdehyde
SOD	superoxide dismutase
CAT	catalase
POD	peroxidase
DAB	3,3 '-diaminobenzidine tetrahydrochloride
NCBI	National Center for Biotechnology Information
NBT	p-Nitro-Blue tetrazolium chloride
