

# Identification, Phylogeny, and Comparative Expression of the Lipoxygenase Gene Family of the Aquatic Duckweed, *Spirodela polyrhiza*, during Growth and in Response to Methyl Jasmonate and Salt

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Supplementary Table 1: Gene sequences from plant species used to deduce evolutionary relatedness with the *Spirodela polyrhiza* LOX gene family.

Supplementary Table 2: List of genes and their primer sequences used for quantitative real– time PCR (qRT-PCR) analysis.

Supplementary Table 3: List of genes not considered as true LOXs\*.

Supplementary Table 4: *S. polyrhiza* LOXs within three released draft genome sequence.

Supplementary Figure 1: **Time dependent salt stress transcriptome analysis of LOX gene members in *Spirodela polyrhiza***

**Supplementary Table 1:** Gene sequences from plant species used to deduce evolutionary relatedness with the *Spirodela polyrhiza* LOX gene family

Plant Species	Name	Sequence ID	Protein Length (aa)
Tomato ( <i>S. lycopersicum</i> )	SILOX1	Solyc08g014000	860
	SILOX2	Solyc01g099190	858
	SILOX3	Solyc01g006540	896

	SILOX4	Solyc03g122340	908	
	SILOX5	Solyc01g099160	862	
	SILOX6	Solyc09g075860	877	
	SILOX7	Solyc01g099200	841	
	SILOX8	Solyc08g029000	861	
	SILOX9	Solyc01g099180	854	
	SILOX10	Solyc12g011040	892	
	SILOX11	Solyc05g014790	911	
	SILOX12	Solyc01g099210	902	
	SILOX13	Solyc01g006560	863	
	SILOX14	Solyc09g075870	854	
	Duckweed ( <i>S. polyrrhiza</i> )	SpLOX1	Spipo2G0068200	868
		SpLOX2	Spipo2G0068500	844
		SpLOX3	Spipo4G0070100	806
SpLOX4		Spipo7G0050500	916	
SpLOX5		Spipo15G0045200	792	
SpLOX6		Spipo28G0005500	904	
SpLOX7		Spipo28G0005600	904	
SpLOX8		Spipo28G0005700	637	
SpLOX9		Spipo0G0030100	920	
Arabidopsis ( <i>A. thaliana</i> )	AtLOX1	At1g55020	859	
	AtLOX2	At3g45140	896	
	AtLOX3	At1g17420	919	
	AtLOX4	At1g67560	917	
	AtLOX5	At3g22400	886	
	AtLOX6	At1g72520	926	
Rice ( <i>O. sativa</i> )	OsLOX1	Os02g10120	925	
	OsLOX2	Os02g19790	295	
	OsLOX3	Os03g08220	918	
	OsLOX4	Os03g49260	867	
	OsLOX5	Os03g52860	870	
	OsLOX6	Os03g52860	869	
	OsLOX7	Os04g37430	797	
	OsLOX8	Os05g23880	847	
	OsLOX9	Os06g04420	125	
	OsLOX10	Os08g39840	924	
	OsLOX11	Os08g39850	941	
	OsLOX12	Os11g36719	868	
	OsLOX13	Os12g37260	922	
	OsLOX14	Os12g37320	358	
Poplar ( <i>P. trichocarpa</i> )	PtLOX1	Potri.001G015300	898	
	PtLOX2	Potri.001G015400	902	
	PtLOX3	Potri.001G015500	898	
	PtLOX4	Potri.001G015600	898	
	PtLOX5	Potri.001G167700	923	
	PtLOX6	Potri.003G067600	925	
	PtLOX7	Potri.005G032400	866	
	PtLOX8	Potri.005G032600	796	
	PtLOX9	Potri.005G032700	866	
	PtLOX10	Potri.005G032800	863	
	PtLOX11	Potri.008G151500	880	
	PtLOX12	Potri.008G178000	827	
	PtLOX13	Potri.009G022400	901	
	PtLOX14	Potri.010G057100	926	
	PtLOX15	Potri.010G089500	881	
	PtLOX16	Potri.013G022000	871	
	PtLOX17	Potri.013G022100	862	
	PtLOX18	Potri.014G018200	860	
	PtLOX19	Potri.014G177200	860	
	PtLOX20	Potri.017G046200	898	

**Supplementary Table 2:** List of genes and their primer sequences used for quantitative real– time PCR (qRT-PCR) analysis.

Gene Name	Sequence ID	Forward Primer	Reverse Primer
<i>SpLOX1</i>	Spipo2G0068200	TCCAGGATGTGCTGAACCTCTA	AACTCTTCATCGGTCTCCAAG
<i>SpLOX2</i>	Spipo2G0068500	TCGAGGTCAATCCCGATAGAGT	CGTCGGAGGATTGCCTATAAAC
<i>SpLOX3</i>	Spipo4G0070100	CATGAACACCCTCTTCGACCT	GTAGCCGTA CTGGCCGAAGTT

<i>SpLOX4</i>	Spipo7G0050500	ATCCTCACCACCATCATCTGGA	TCCGGGATGAGCTTCTTCAT
<i>SpLOX5</i>	Spipo15G0045200	CACTATCAAGGACTATCCCTACGC	TAGTGAGCTTCCACGTATCTGC
<i>SpLOX6</i>	Spipo28G0005500	GTGGGCCATTACTATCCAGACC	GGCTCTTTCCTCTTGTTCAGCAT
<i>SpLOX7</i>	Spipo28G0005600	CTATAAAGGCGGCCTACGAGAG	CGGTTCTTCAGGTTCTGGTCTT
<i>SpLOX8</i>	Spipo28G0005700	CTCCGTGAAGACGGTGAAATC	TATAGCGGTAATGTGGGGGAAG
<i>SpLOX9</i>	Spipo0G0030100	TGGTCGAAGGGTTCTACAGGTT	TATGGAGATGCTGTTGGGGACT
<i>Actin</i>	Spipo17G0011400	GGCTACTCCTTACCACCAC	GCTCGTAGGTCTTCTCGACG
<i>18S rRNA</i>	Spipo23G0000600	CGGTCCTATTGTGTTGGCCT	TCCTTGGCAAATGCTTTCGC

**Supplementary Table 3: List of Genes not considered as true LOXs\***

<b>S.NO.</b>	<b>SGN IDs</b>	<b>Protein (aa)</b>	<b>Loss or incomplete protein domains</b>
1	Spipo0G0094800	209	No PLAT/LH2 domain; Truncated LOX domain
2	Spipo0G0169900	109	Neither PLAT/LH2 nor LOX domain
3	Spipo28G0005000	115	Neither PLAT/LH2 nor LOX domain
4	Spipo28G0005100	325	No PLAT/LH2 domain
5	Spipo28G0005200	181	No PLAT/LH2 domain; Truncated LOX domain

6	Spipo28G0005300	376	No PLAT/LH2 domain
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\*Genes excluded lack the complete PLAT/LH2 domain (Polycystin-1, lipoxygenase,  $\alpha$ -toxin domain or lipoxygenase homology), LOX domain (Lipoxygenase) or have an incomplete/truncated PLAT/LH2 or LOX domain.

**Supplementary Table 4: *S. polyrhiza* LOXs within three released draft genome sequence assemblies<sup>a b c</sup>**

Name	<i>S. polyrhiza</i> 7498v2 <sup>a</sup>	<i>S. polyrhiza</i> 9509 <sup>b</sup> Chromosome position	<i>S. polyrhiza</i> 7498v3 <sup>c</sup> sequence coordinates
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<i>SpLOX1</i>	Spipo2G0068200	Chr. 4 (CP019096.1: 3595583-3599560)	SWLF01000117.1: 5138474-5142450
<i>SpLOX2</i>	Spipo2G0068500	Chr. 4 (CP019096.1:3581789-3586763)	SWLF01000117.1: 5151172-5156496
<i>SpLOX3</i>	Spipo4G0070100	Chr. 1 (CP019093.1: 8606937-8610643)	SWLF01000080.1: 6149775-6153490
<i>SpLOX4</i>	Spipo7G0050500	Chr. 7 (CP019099.1:1639963-1645308)	SWLF01000027.1: 1630557-1635868
<i>SpLOX5</i>	Spipo15G0045200	Chr. 15 (CP019107.1:780100-782904)	SWLF01000108.1: 3932970-3935770
<i>SpLOX6</i>	Spipo28G0005500	Chr. 9 (CP019101.1:5602359- 5606311)	SWLF01000039.1: 7035417-7039363
<i>SpLOX7</i>	Spipo28G0005600	Chr. 9 (CP019101.1:5565220-5569201)	SWLF01000039.1: 7051551-7055538
<i>SpLOX8</i>	Spipo28G0005700	Chr. 9 (CP019101.1:5628591-5635242)	SWLF01000039.1:7061876-7067673
<i>SpLOX9</i>	Spipo0G0030100	Chr. 15 (CP019107.1:481984-485572)	SWLF01000108.1:4227121-4230719

- a) *S. polyrhiza*7498 v2 (Spirodela polyrhiza at Phytozome v13; GenBank assembly accession: GCA\_000504445.1) [13]
- b) *S. polyrhiza*9509 v3 (BioProject: PRJNA308109; GenBank assembly accession: GCA\_900492545.1) [50]
- c) *S. polyrhiza*7498 v3 (BioProject: PRJNA520740; GenBank assembly accession: GCA\_008360905.1) [17]

**Supplementary Figure 1: Time dependent salt stress transcriptome analysis of LOX gene members in *Spirodela polyrhiza*.** An earlier study [61] reported that salt stress (100mM) down regulates the expression of *SpLOX1*, *SpLOX5* and *SpLOX8* genes. The FPKM fold changes reported are presented below as heat map.

