

Supplementary Information

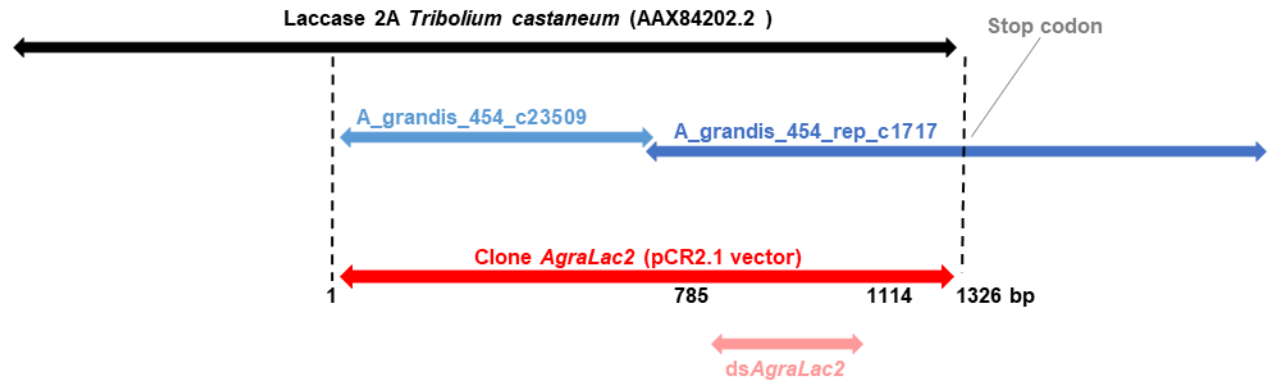


Figure S1. Schematic representation of the cloning strategy used to obtain a partial sequence of *Lac2* from *A. grandis* (*AgraLac2*).

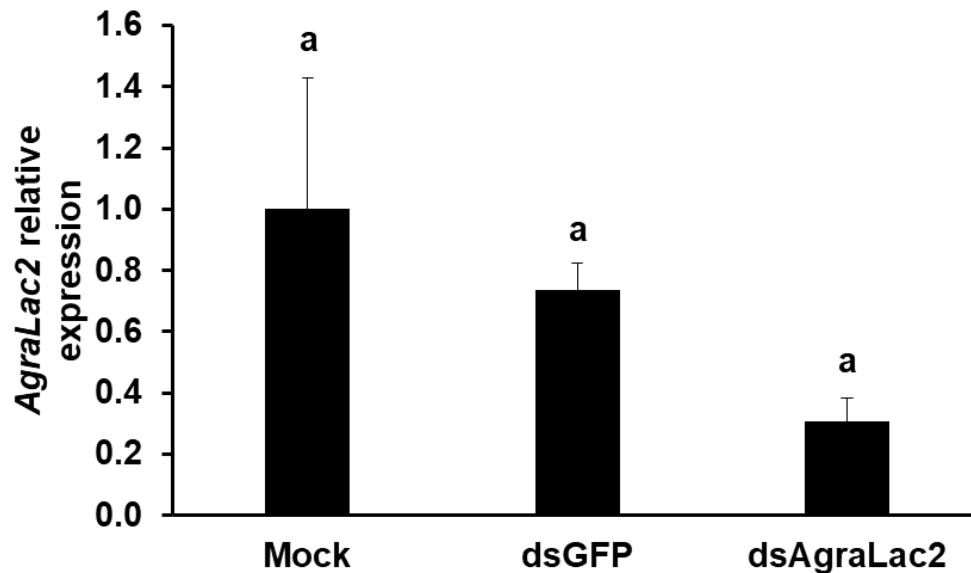


Figure S2. Relative transcript levels of *AgraLac2* after dsRNA exposure. Relative transcript levels of *AgraLac2* gene in *A. grandis* larvae at 2 days after water (mock), dsGFP or dsAgraLac2 injection evaluated by RT-qPCR. The expression data were normalized using *gapdh* and β -*tubulin* as reference genes. Values shown are the means and standard errors ($\pm$ SE) of two biological replicates each with three technical replicates. Data were analyzed by one-way ANOVA followed by a post hoc multiple comparisons test (Tukey's HSD test). Treatment groups with different letters are significantly different ($P < 0.05$).

Supplementary Data S2: Contig sequences of *Lac2* retrieved from *A. grandis* transcriptome

>A_grandis_454_c23509

AGATTTGACTACTCATGTTATTTTGGCTTTCTGATTGGATGCACGAAGATGCTGCCGAGAGATTCCCTGGT
AGATTGGCTGTTAACACCGGTCAAGATCCTGAAAAATTTACTCATCAACGGAAAAGGTCAATTCCGTGATC
CCAATACCGGTTTCATGACCAACACCCCTTGGAAATTTTCACGATGACTCCCGGAAAACGGTACAGATT
CCGTATGATCAACTCCTTGGCGTCAGTCTGTCTGCTCAWTTAACAGTCCAGGGACACACGTTGACTCTT
ATTGCCACCGATGGTGAACCTGTCCATCCAGTTAACGTGAACACCGTAATTTCTTTCTCAGGAGAAAGAT
ACGATTTTGTAAATCAACGCGGACCAATCAGTAGGAGCCTACTGGATCCAAGTGAGAGGCTTAGGAGAATG
TGGTATCAGAAGGGTACAGCAATTGGCTATTTTTGAGATACTACAAGGGACCATATACTCCATTCACCCA
AGCACCTACTTATGACTTCGGTATTCTTACAGGAGTGGTTCTGAATCCCCTAGACGCTATTTGTAATAAA
CCCAGGAAAGACGCAGTGTGCGTCNGTCAGCTAACGAATGCCAAAAAGTGGACGAAGCCATTTGCAAGAA
CGGCCTGATG

>A_grandis_454_rep_c1717

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CAATTGAAAAATGCCAGAGAAGTGGACAGGGCGCTGCTGATTGAAAAACCAAATGTGAAGATATTTTTGC
CATTGAGATTCCACGTTTATACACCGGAGGATCTTTTTTAATCCTAACAGTTACAACAGACATTTAGTTGC
GCCAAACGGAGACCACGTAATCAGTTTAATCGACGAAATCTCGTACATGGCTGCGCCAGCTCCGCTTCTA
TCTCAGTACGATGAAATTGACCCCGAGCAATTCTGTAATGGAGATAACAGACCACCCAATTGTGGACCTA
ACTGCATGTGTACCCACAAAATTGATATTCCATTAAATGCGATTGTGCAAGTTGTTCTGGTTGATGAAGT
TCAACAACCGAACTTATCCCATCCGTTCCATTTGCACGGTTATGCTTTTAATGTGGTCGGTATTGGTCGC
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AATTTGGTCCTGCAAGTGGGTACACATGCAGACATACCACCAGTGCCACCGAATTTCCCTACTTGCGGCG
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TAATATATTTTTGTGAAAAAATGTACAGGGTTATGCTACTCATGTATATTATTTTCAGGTAGGTATAATAAC
GCAATGTATATAATTTTTTACTAGCACAAATATTGTAAATATAACATATTTACACGATCTTATTTGTCACC
AACTGCTAGTATATTGTAGAGTTACCAAATTAATATTCTGAATATTTGGATTAAAGTCTTGCCATCCAAAA
ATGTCGAAAAATCAGTATTCTAAATTGAGTGTTCCTATATTATGTATTTTATTTATCTGATATTTATC
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TGTTTWTTTTTTGTTTTTTTTTAACATCACTATTGGTGTCTTTCTAAACTTATAAATCAATTATTTGAGT
TAAAATCTTTAAATATTTTTTTGATACTTTTCATAATAAGAAAAATGTTTTGGTTAATATTTTTTAATATGG
GAAATATTTAAAGATTTAAAGGTATGAACCCTTTCGTAAATAAATATTTCTTCCAGGAAGTAAGCTAAG
GTCTTTAATGTAAAAATTCTTATAGTTATAGTAGAAATTTTATGATTATGTCATTGGAAATGTTACCAAC
ATAACGAAGTAAATAAATATGAATTTTATCACATCTATACCACAAAAATAGGCACTTCATAGTACATTTT
TTGGTAAAAGAACCACCTAGTCTATTACAAAACCAAGACGAATATGAAAATAAGTCATCGTTGTAGATTT
GTATATAAATAAATAGTGTAAAGTACCAATGTATTTAAAGTAATAAAATTTGTGACTATATTTATGT

TGA - Stop codon

Supplementary Data S3: *AgraLac2* partial mRNA sequence obtained from the consensus of contig sequences (A_grandis_454_c23509 and A_grandis_454_rep_c1717) and the cloned *AgraLac2* sequence.

>*AgraLac2* partial, mRNA

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GATTTGACTACTCATGTTATTTTGGCTTTCTGATTGGATGCACGAAGATGCTGCCGAGAGATTCCCTGGTA
GATTGGCTGTTAACACCGGTCAAGATCCTGAAAATTTACTCATCAACGGAAAAGTCAATTCCGTGATCC
CAATACCGGTTTTCATGACCAACACCCCCTTGAAAATTTTACGATGACTCCCGGAAAACGGTACAGATTC
CGTATGATCAACTCCTTGGCGTCAGTCTGTCTGCTCAATTAACAGTCCAGGGACACACGTTGACTCTTA
TTGCCACCGATGGTGAACCTGTCCATCCAGTTAACGTGAACACCGTAATTTCTTTCTCAGGAGAAAAGATA
CGATTTTGTAAATCAACGCGGACCAATCAGTAGGAGCCTACTGGATCCAAGTGAGAGGCTTAGGAGAATGT
GGTATCAGAAGGGTACAGCAATTGGCTATTTTGAGATACTACAAGGGACCATATACTCCATTCACCCAAG
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CAAACAATGGATACGTAATCTTCAGATTCCGAGCAGACAATCCTGGTTTCTGGCTTTTCCACTGTCACCT
CTTGTTCCACATAGTTATAGGAATGAATTTGGTCCTGCAAGTGGGTACACATGCAGACATAACCACCAGTG
CCACCGAATTTCCCTACTTGCGGCGATCACACGCCACGAATCAATTTAGATCCAACGAAAATATGA
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Supplementary Data S4. Predicted protein *AgraLac2*

>Predicted protein *AgraLac2*, partial

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DLTTHVILLSDWMHEDAERFPGRLAVNTGQDPENLLINGKGQFRDPNTGFMTNTPLEIFTMTPGKRYRF
RMINSLASVCPAQLTVQGHTLTLLIATDGEVHPVNVNTVISFSGERYDFVINADQSVGAYWIQVRGLGEC
GIRRVQQLAILRYYKGPYPFTQAPTYDFGIPQGVVLNPLDAICNETRADAVCISQLKNAREVDRAILLIE
KPNVKIFLPFRFHVYTPEDLFNPNSYNRHLVAPNGDHVISLIDEISYMAAPAPLLSQYDEIDPEQFCNGD
NRPPNCGPNCMCTHKIDIPLNAIVEVVLVDEVQQPNLSHPFHLHGAFNVVGIGRSPDTSVKKINLKHALL
DLDRGLLHRHFDLPPGKDTIAVPNNGYVIFRFRADNPGFWLFHCHFLFHIVIGMNLVLQVGTHADIPPV
PPNFPTCGDHTPRINLDPTKI
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Table S1. Species distribution of BLASTx matches of *A. grandis* contigs.

<i>A. grandis</i> contig identification	BLASTx matches	Acession number	Identity (%)	E value	Query Cover (%)
A_grandis_454_c23509	laccase 2 [<i>Rhynchophorus ferrugineus</i>]	QGK89547.1	89.10	1.00E-98	96
	laccase2 [<i>Drosophila busckii</i>]	ALC45418.1	78.00	8.00E-93	77
	laccase 2 [<i>Phaedon cochleariae</i>]	AWK23446.1	85.90	4.00E-92	96
	multicopper oxidase 2 [<i>Nilaparvata lugens</i>]	AKN21380.1	82.69	5.00E-91	94
	laccase 2 isoform X2 [<i>Contarinia nasturtii</i>]	XP_031632951.1	83.33	6.00E-91	94
	laccase 2 precursor [<i>Tribolium castaneum</i>]	NP_001034487.2	83.23	6.00E-91	93
	laccase 2 [<i>Monochamus alternatus</i>]	ABU68466.1	83.23	7.00E-91	94
	laccase 2 isoform X3 [<i>Contarinia nasturtii</i>]	XP_031632952.1	83.33	7.00E-91	94
A_grandis_454_rep_c1717	laccase 2 [<i>Rhynchophorus ferrugineus</i>]	QGK89547.1	88.36	6.00E-171	48
	laccase 2 [<i>Phaedon cochleariae</i>]	AWK23446.1	84.38	6.00E-162	47
	laccase 2 [<i>Chrysomela populi</i>]	AWK23445.1	83.33	2.00E-160	47
	laccase 2 precursor [<i>Tribolium castaneum</i>]	NP_001034487.2	81.85	2.00E-156	48
	laccase 2 isoform A [<i>Anopheles gambiae</i>]	AAX49501.1	82.17	1.00E-152	47
	laccase 2 isoform A [<i>Anopheles sinensis</i>]	KFB50921.1	82.17	2.00E-152	47
	laccase 2 [<i>Anopheles sinensis</i>]	ARG47519.1	81.82	2.00E-151	47
	laccase 2 [<i>Drosophila mojavensis</i>]	XP_002005808.1	82.11	8.00E-151	47