

Powdery mildew responsive genes of resistant grapevine cultivar 'Regent'

L. J. WELTER^{*1)}, C. TISCH²⁾, A. KORTEKAMP²⁾, R. TÖPFER¹⁾ and E. ZYPRIAN¹⁾

¹⁾JKI - Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany
²⁾ State Education and Research Center of Viticulture, Horticulture and Rural Development, Institute of Plant Protection, Neustadt, Germany

*Current Address: Federal University of Santa Catarina, Brazil

Supplementary Table

Primer sequences for RT-qPCR. Gene bank accession number, locus tag and annotation, predicted gene name, primer sequences and expected PCR-product length of the genes whose expression was evaluated by RT-qPCR during the interaction between grapevine and powdery mildew

Original Gene Bank Accession/ CRIBI annotation V2 locus tag	CRIBI annotation V2 Function	Primer sequence (forward)	Primer sequence (reverse)	Amplicon length (bp)	Genomic position
1. TC47186/ VIT_208s0058g00690	probable wrky transcription factor 33-like	ATCAAGCACTAGTATGAACAGAGCAG	CCTTGTGGCTTGGCATGA	74	Chr08
2. TC46952/ VIT_207s0031g00080	wrky transcription factor 7	CGTGGTCTCATCTAGAAATCTTC	GAGGTGCTATTCTACTCTCTGTGGCT	69	Chr07
3. TC41321/ VIT_201s0010g03930	wrky transcription factor 75	AGAGATGAGATCAITGCAGCTGAA	GTCACACCAAAATCTTTGGATCTCA	94	Chr01
4. TC50306/ VIT_210s0003g00580	ethylene responsive element binding factor 2	CACGTGGGGAATCAACAAGA	GCCCATGGATACTTACTTTGATCA	99	Chr10
5. TC54435/ VIT_216s0013g00980/950	ethylene-responsive transcription factor 5	CACCGTTAACGCCGTTATCAC	TGTCTTTGGTAAAGGTAACAACCTCTTTGAT	87	Chr16
6. TC42111/ VIT_205s0049g01020	myb-related transcription factor MYB15	CAGTCGCAGACGAATTACAGCTT	CTCCATGCCAATCAATCA	80	Chr05
7. TC54167/ VIT_213s00067g01070	CZF1, ankyrin repeat-containing domain; Zinc finger CCCH-type	GCAGTAGCAGCAGCAGTGATG	ATACCTCCCCTATCGATGAAGCT	80	Chr13
8. TC45048/ VIT_205s0077g01530	pathogenesis-related protein 10	GCACATCCCAGATGCCTATTAAAG	ACTTACTGAGACTGATAGATGCAATGAATA	101	Chr05
9. TC64228/ VIT_202s0025g04290	thaumatin-like protein	CCCTGATGAGCTCCGAGCT	GGACACCTATCCTTGAAAAACTTGG	129	Chr02
10. TC46460/ VIT_205s0077g01150	beta-1,3 -glucanase	TCGACTTAACACTTCTGGGCAACT	CAGAAAGCGGGACTTATTGTCTA	119	Chr05
11. TC38204/ VIT_219s0090g01340	hypothetical protein, glycine rich	AGACCAGCATGGCTGTGTGTA	GACGGCATTCATCATACTCCCAIT	77	Chr19
12. TC70328/ VIT_206s0004g04470	heat shock protein 70	CTTCTGCTGGAGGTCTGGT	AGACTCACTCCATATTTCCAAAACCTTGA	117	Chr06
13. TC50337/ VIT_205s0020g03030	probable LRR-receptor-like serine-threonine protein kinase	CACCACCTTCAGGAGCTTAAACA	GGTTGAACTACAAAGATTGAGCATAGA	89	Chr05
14. CB914701/ VIT_209s0002g03800/3820/3860/3870	Disease resistance protein NB-ARC-LRR	ATCCTGGAGAAAAGGCGATCA	TTGTAGCTGGACCGGCAGT	80	Chr09
15. TC39520/ VIT_206s0004g07830	CBL-interacting protein kinase 11 isoformX1 (<i>V.viniifera</i>)	TGAAACAGGAAGCAAGGACATG	GCTAACTCTTGCTTTGCTTCAGAA	99	Chr06

Supplementary Tab. 1, continued

Original Gene Bank Accession/ CRIBI annotation V2 locus tag	CRIBI annotation V2 Function	Primer sequence (forward)	Primer sequence (reverse)	Amplicon length (bp)	Genomic position
16. TC39349/ VIT_218s0001g06250	3-deoxy-d-arabino-heptulosonate 7-phosphate synthase	TCCACACCTAATTCGGGCAAT	TGCTCTTACTTCGGCCCTGTAT	139	Chr18
17. TC68756/ VIT_215s0048g00350	5-enolpyruvylshikimate-3-phosphate synthase	CATTACATGCTCGGAGCACTGA	ACTTCGCCACTGATCCATTCC	125	Chr15
18. TC66528/ VIT_216s0039g01100/1110/1120	phenylalanine ammonia-lyase PAL1	CTAAAAGTGGTGGATAGGGAACATG	TCCTTCAATTTTCGCCATTGCT	130	Chr06
19. TC70715/ VIT_206s0004g08150	cinnamate-4-hydroxylase C4H	GGCAAAGCACAAAAGAGCACAGA	AAGGACGTTGTCTCTCGTTGATC	100	Chr06
20. TC45576/ VIT_216s0098g00850	caffeic acid o-methyltransferase COMT	CTGCTTGAGCCTCTAGCTTGGT	CTTCAATACACAGTATAAAGCCACTTGTG	99	Chr16
21. TC52173/ VIT_219s0015g02590/2880	probable glutathione s-transferase GSTU25	GAAGGGGCACATGGGTCTTC	TAAAGCAAACACTCCTCTTACATTACCA	156	Chr19
22. TC57332/ VIT_201s0011g01110	molybdopterin cofactor	TCCCAAATTTGCTCCTGGATT	CATCCAAATGATCCCTGAGATATCA	80	Chr01
23. TC58552/ VIT_208s0040g00440	dihydrofolate reductase	CCTTTTGATGGTTTTGCTTGGGA	ACCTTCCCCTGTCCCTGGTA	80	Chr08
24. TC63583/ VIT_208s0007g01070/90	cysteine histidine-rich C1 domain-containing protein	TTATGGGAGCGAAGAGTTCCA	AATTGCATGTGTGGCATCGA	80	Chr08
25. TC64430/ VIT_218s0001g04640	hypothetical protein	GAGGAAGAAGGTCCATCCCAAT	TGCAAATGGGCTGCGCTTAGA	81	Chr18
26. TC63952/ VIT_200s0283g00030	calnexin homolog CNX1	TTCGACCTCAGGATGCTACATG	CTTCGGGTTCTTATGCTTTACGATA	131	ChrUn
27. AF196485/ VIT_208s0040g00980	tubulin beta chain (reference)	GGATGCCAAGAAACATGATGTGT	CACGGAAACATCGCTGAAGCT	74	Chr08
28. TC44917/ VIT_217s0000g10430	glyceraldehyde 3-phosphate dehydrogenase GAPC2 (reference)	ACAGCTCCCCTGTGATCGA	TAAAAGCTCTGCCCTTGGAAT	80	Chr17