

Figure S1: Simplified pathway of wax biosynthesis in Arabidopsis (redrawn from Greer *et al.* [16] and Samuels *et al.* [61]). The enzyme mid-chain alkane hydroxylase (MAH1) which, according to Greer *et al.* [16], catalyzes the enzymatic conversions of alkanes to secondary alcohols and ketones is highlighted in red.

MLOC_15925.1 HO07G08 VIGS constr.	1	atggctgctgcatgcatgccaccgaggaaacttctcacatataaatggagccaagccatgtccatgcagcataaaacccaaagcaca	
MLOC_15925.1 HO07G08 VIGS constr.	91	gcatctccccatacactactcacaacaatgtctactatgtcattctcgaagagctgctcatctccaagctcgccatcattctgtttcc	
MLOC_15925.1 HO07G08 VIGS constr.	181	atgtacacggttgacctcaggtctagtagatcaaagggcccagcagctgtccccacaaaactggccaatagtggcgctgtccccccct	
MLOC_15925.1 HO07G08 VIGS constr.	271	gtgcaccaacctccacaacttgacgactacctcgcgctgctcctcgccggatcagggcacaacttcagggcaaccggccccgcccgggacc	
MLOC_15925.1 HO07G08 VIGS constr.	361	gggatgcggttcttctgctcacctgcgacccggccaacgtccggcacatcttcacgtccaaccacgcaaaacttccccaggcgcgaggttc	
MLOC_15925.1 HO07G08 VIGS constr.	451	gcccacatctttgacatcgcggtggcagcttcttcaccactgaaggagagccctggcgtcggcagcgacacagagcccagagagctttg	
MLOC_15925.1 HO07G08 VIGS constr.	541	agcaaccacggttggtgccaactatgaccgcttctgtcttgacaagggtggagaacggcctcctcccgggtctcatgcacatggcgacc	
MLOC_15925.1 HO07G08 VIGS constr.	631	accgcgaccccggtcgacctgcaagctttgacaacgaggttctgttgcacataaccgcccggcgcctcttcggcgctgacccgggcctc	
MLOC_15925.1 HO07G08 VIGS constr.	721 1	ctgtcctcggacatgcgccccatggatgcccgtgtcggcatggacacggtcatggagggtgaccttggcggcaatcgcgcccgcact ----- -----cggcac-----cggcac-----	
MLOC_15925.1 HO07G08 VIGS constr.	811 7	ggctggaaggtgatgaggcggctaaacatcgcccccggaaaggaagctcgcgcagcgacacccgtgctgcgcccgggttcggttgcagagatg ----- -----gaggcggctaaacatcgcccccggaaaggaagctcgcctcagcgacacccgtgctgcgcccgggttcggttgcagagatg	
MLOC_15925.1 HO07G08 VIGS constr.	901 83	atggagaggaggaagatgaaggaacatgctgctgctggtgacgaggaagccccttcgtccgtggacatctctgtcttccatcacatgacgat ----- -----atggagaggaggaagatgaaggaacatgctgctgctggtgacgaggaagccccttcgtccgtggacatctctgtcttccatcacatgacgat	
MLOC_15925.1 HO07G08 VIGS constr.	991 173	ccagactaccagcagaacgatggcttgcctcgcgacgctcatcaactacatgatcgcggggagggaacacgatcagcacagctttgaca ----- -----ccagactaccagcagaacgatggcttgcctcgcgacgctcatcaactacatgatcgcggggagggaacacgatcagcacagctttgaca	
MLOC_15925.1 HO07G08 VIGS constr.	1081 263 1	tgggtcttctacaacctcgcccagaacctcggtgatgtcgggtcaccgcaacgaactatcacccatcgcacacggaaagcagccagc ----- -----tgggtcttctacaacctcgcccagaacctcggtgatgtcgggtcaccgcaacgaactatcacccatcgcacacggaaagcagctagc ----- -----aacctatcacccatcgcacacggaaagcagctagc	
MLOC_15925.1 HO07G08 VIGS constr.	1171 353 36	gatagcagcagcaccatggtgatctttgaaccgaggagaccaaactctctgtctacatgagagctgcacctacaggagctctctcaggttg ----- -----gatagcagcagcaccatggtgatctttgaaccgaggagaccaaactctctgtctacatgagagctgcacctacaggagctctctcaggttg ----- -----gatagcagcagcaccatggtgatctttgaaccgaggagaccaaactctctgtctacatgagagctgcacctacaggagctctctcaggttg	
MLOC_15925.1 HO07G08 VIGS constr.	1261 443 126	caccgcccgggtccccatcgagcgttaagacagcggctgccagcagctgatgccagtgggccatgtggtgcatgccggtgacaccttattg ----- -----caccgcccgggtccccatcgagcgttaagacagcggctgccagcagctgatgccagtgggccatgtggtgcatgccggtgacaccttattg ----- -----caccgcccgggtccccatcgagcgttaagacagcggctgccagcagctgatgccagtgggccatgtggtgcatgccggtgacaccttattg	
MLOC_15925.1 HO07G08 VIGS constr.	1351 533 216	atctctctccactccatggggagaatggaagacgtgtggggaaagactgccgggagtataaccagatagatggctctcagaggatggc ----- -----atctctctccactccatggggagaatggaagacgtgtggggaaagactgccgggagtataaccagatagatggctctcagaggatggc ----- -----atctctctccactccatgg	
MLOC_15925.1 HO07G08 VIGS constr.	1441 623	aagaagctgcggtaactgcgctctcacaatttttggcattcagctccggcccagaggatttgcttggcaaggacatctcatttatgcag ----- -----aagaagctgcggtaactgcgctctcacaatttttggcattcagctccggcccagaggatttgcttggcaaggacatctcatttatgcag ----- -----aacctatcacccatcgcacacggaaagcagctagc	
MLOC_15925.1 HO07G08 VIGS constr.	1531 713	atgaataactattgtcgggcaatggtgtggaacttcgatgtggagctggttgacgggctcaaggtccagcccagagatgtctgtgtactg ----- -----atgaataactattgtcgggcaatggtgtggaacttcgatgtggagctggttgacgggctcaaggtccagcccagagatgtctgtgtactg ----- -----atgaataactattgtcggcggcaatggtgtggaacttcgatgtggagctggttgacgggctcaaggtccagcccagagatgtctgtgtactg	
MLOC_15925.1 HO07G08 VIGS constr.	1621 803	cgcatgaaaaatgggctcatggtgaagctgaagaagcagagaaaatg----- ----- -----cgcatgaaaaatgggctcatggtgaagctgaagaagcagagaaaatg----- ----- -----tagacctactt	
MLOC_15925.1 HO07G08 VIGS constr.	893	tcgggggtcgggacctcagggtatttgtatgtgtaactgctataagttttgtgtgcgaatgttttgctataataagttgataaatatagc	
MLOC_15925.1 HO07G08 VIGS constr.	983	tagacctactt	

Figure S2: Multiple Alignment of MLOC_15925.1, HO07G08 and re-sequenced *CYP96B22* construct used in VIGS experiments. The sequence of HO07G08 was taken from the IPK Crop EST database (<http://pgrc.ipk-gatersleben.de/cr-est/>) and used as BLASTN query against the transcript sequences published by the International Barley Sequencing Consortium [18]. The incomplete identity between MLOC_15925.1 and HO07G08 might be due to differences between barley cultivars or inaccuracies in the original sequencing of HO07G08 [27] or MLOC_15925.1. Identical parts of sequences are highlighted in yellow.

inoculation

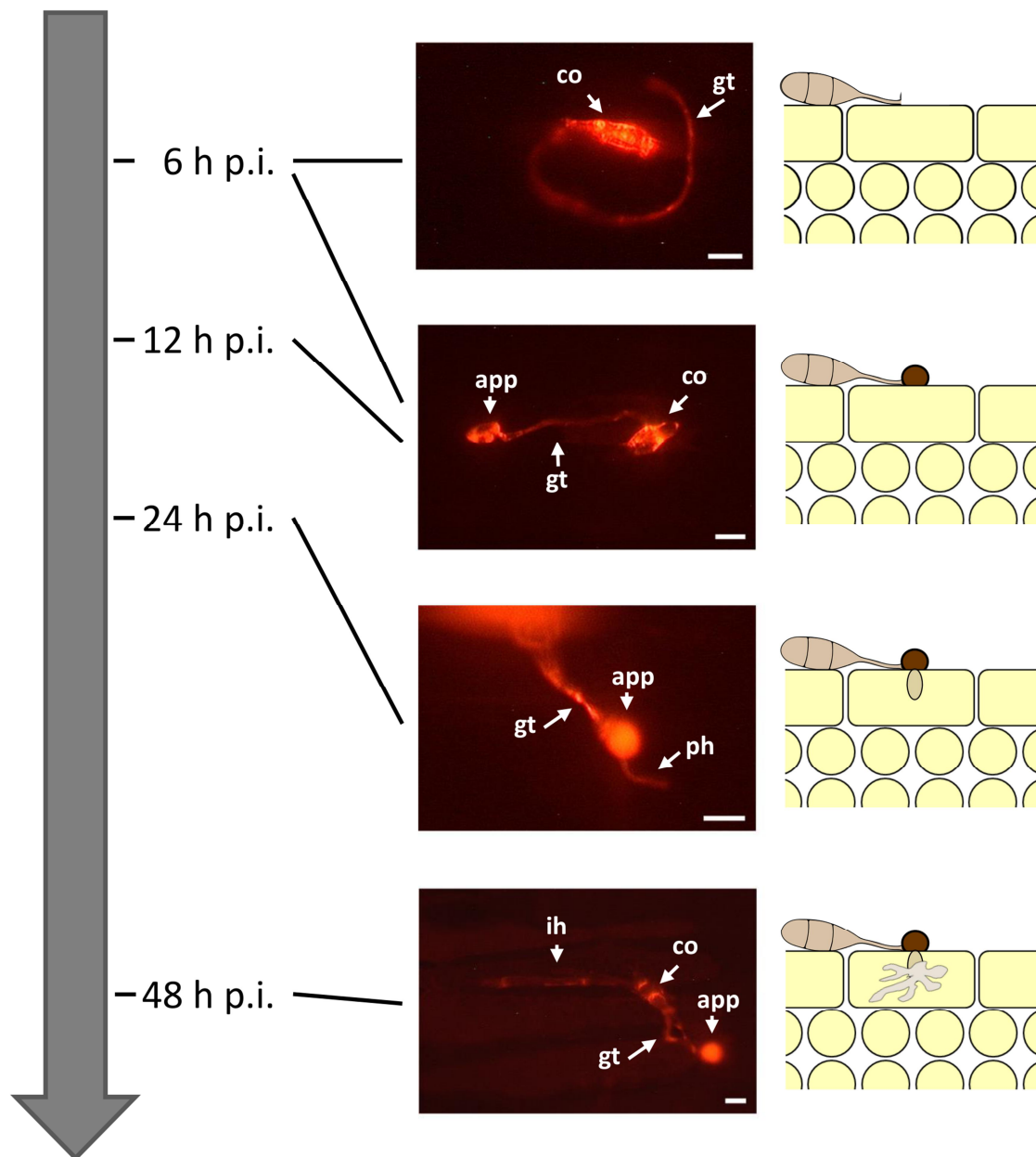


Figure S3: Time course study of the development of infection stages of *M. oryzae* on barley.

Transgenic fungi labeled with DsRed were generated for the *M. oryzae* host isolate TH6772 and inoculated onto barley primary leaves. At 6 h after inoculation (h p.i.) germinated spores were found on the leaf surface some of which had already developed appressoria. At 12 h p.i. almost all germinated conidia had formed appressoria and at 24 h p.i. penetration hyphae got visible beneath appressoria which further developed into larger invasive hyphae detected around 48 h p.i. A similar kinetic was observed for the development of infection structures of a transgenic, GFP-expressing, nonhost *Magnaporthe* isolate (CD180), however in this case invasive hyphae were only rarely detected (data not shown). scale bar: 10 μ m; co: conidium; gt: germ tube; app: appressorium; ph: penetration hypha; ih: bulbous invasive hypha

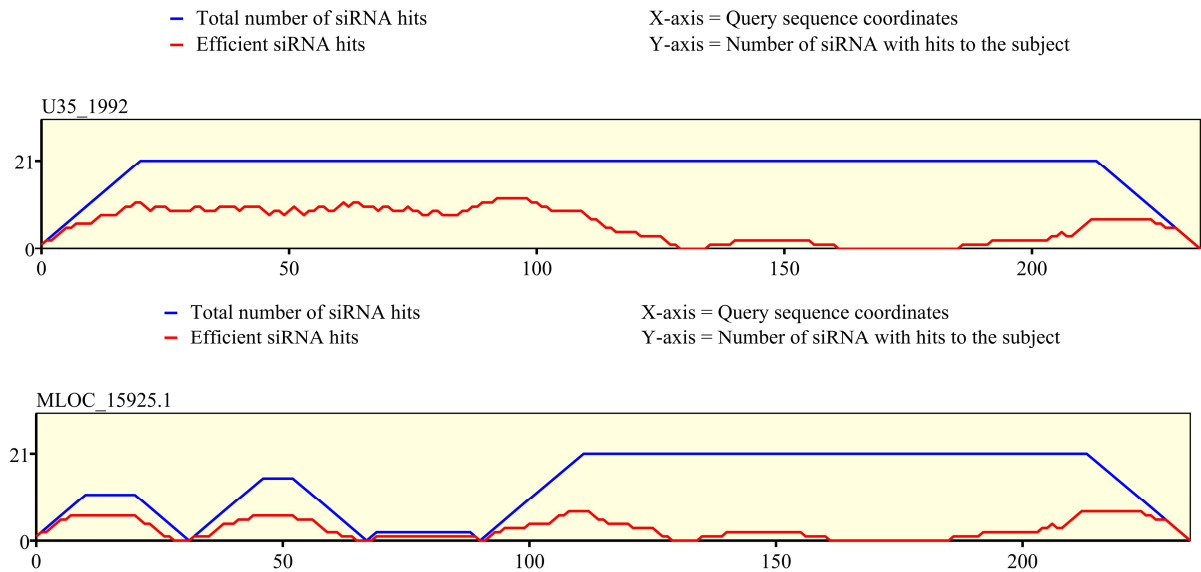


Figure S4: Prediction of targets in the transcriptome of barley by the siRNA used in this study. The target sequence for the *CYP96B22* silencing construct was predicted using the si-Fi software (<http://labtools.ipk-gatersleben.de/>). The 234 bp fragment of *CYP96B22* was used as a query to be scanned for potential generated siRNA and the predicted siRNA sequences were then checked for potential targets using the HarvEST database (assembly 35, <http://harvest.ucr.edu/>) or the high-confidence barley coding sequences [18]. In both databases a unique coding sequence was identified as potential target, both representing *CYP96B22* as deposited in HarvEST (U35_1992, <http://harvest.ucr.edu/>) or by Meyer *et al.* [18] (MLOC_15925.1).

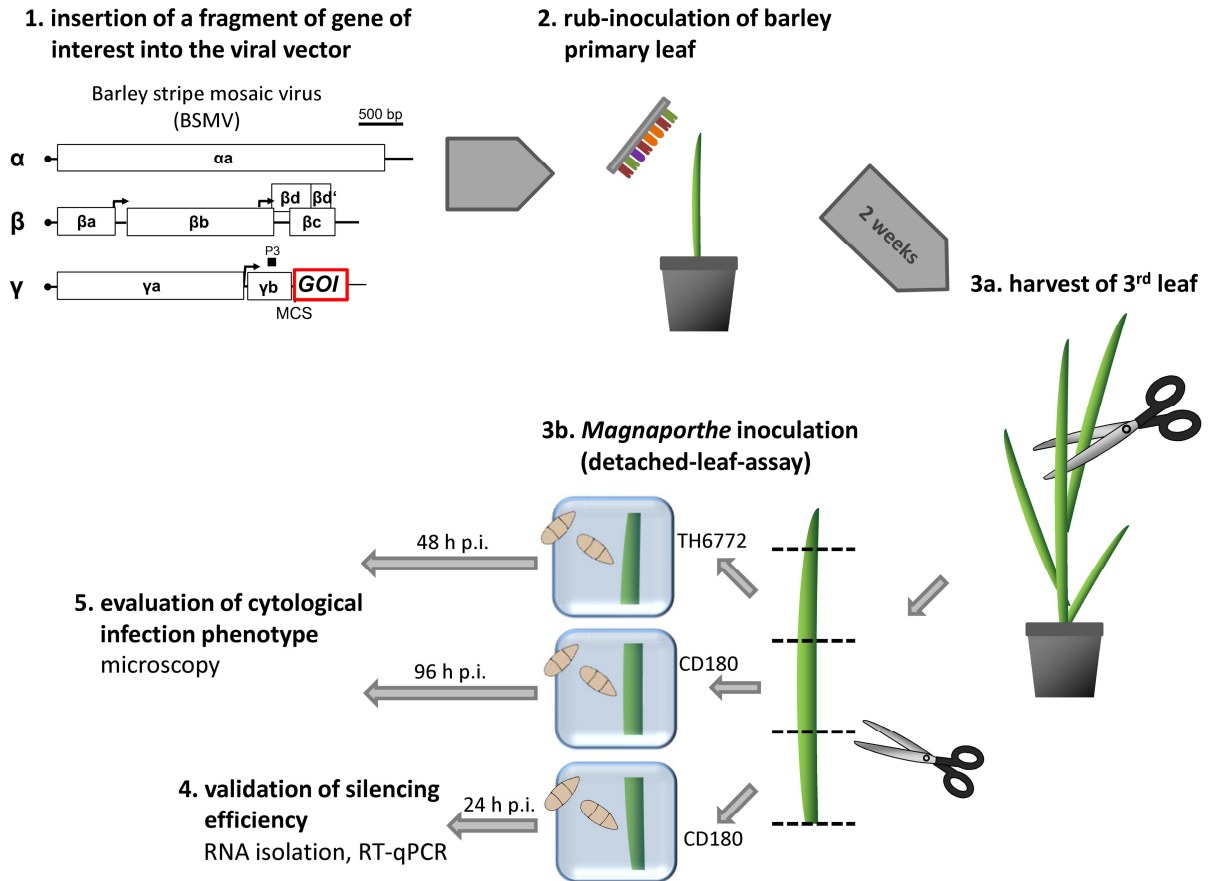


Figure S5: Experimental design of VIGS experiments.

A 234 bp fragment of *CYP96B22* was inserted into the γ -subunit of BSMV (1) (picture modified according to [59]). *In vitro* generated viral transcripts were rub-inoculated on barley primary leaves (2). Two weeks later the third leaf of plants showing viral disease symptoms was harvested and cut into three pieces, two of which were inoculated with the *Magnaporthe* nonhost isolate CD180 and one with the host isolate TH6772. Microscopic assessment of plant defense responses was done at time points indicated. Silencing efficiency was monitored by RT-qPCR using one leaf piece harvested at 24 h p.i. with CD180.