

Figure S1. Dot-plot analysis of genomic sequence surrounding the HA cluster. The genomic sequence from AO090011000406 to 418 in *A. oryzae* RIB40 was compared with the corresponding sequence in *A. sojae* NBRC 4239. Dots were plotted when 8 of 10 bases matched.

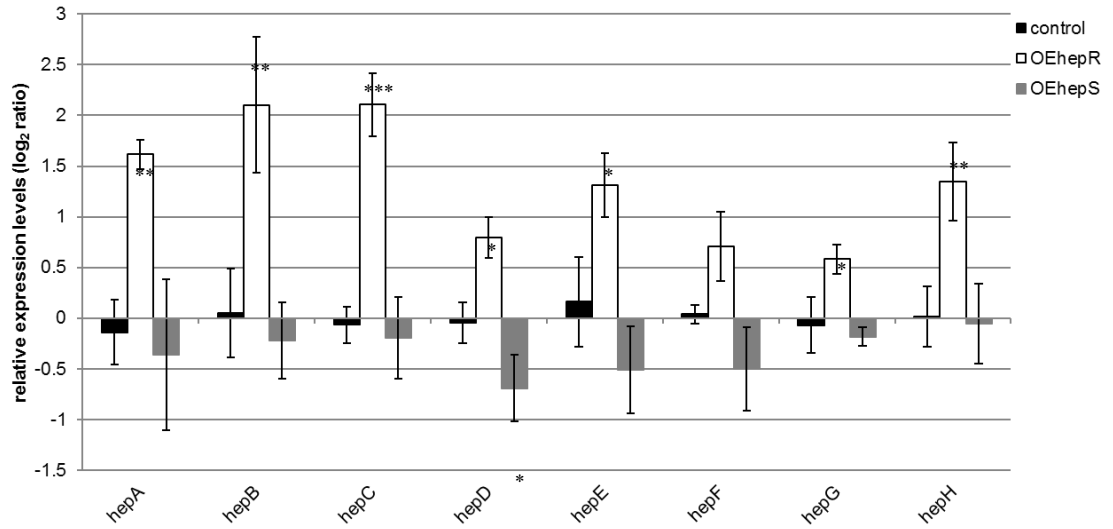


Figure S2. Gene expression levels of HA cluster genes in *hepR* and *hepS* overexpression strains. The relative expression levels of each gene were determined by qRT-PCR. Histone 2B was used as an endogenous reference gene. All data are presented as mean \pm SD (n = 3). Asterisks represent significant difference compared with the control strain by Dunnett's test (** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$). RKuAFN *niaD*⁺ was used as a control strain.

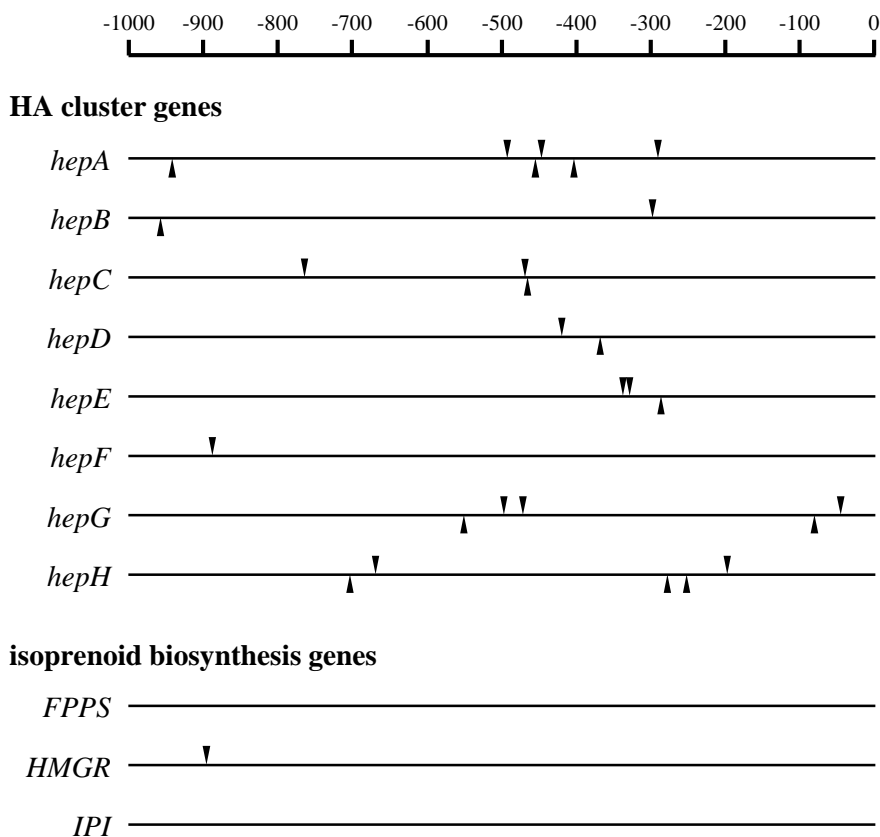


Figure S3. Positions of the Tri6 binding motif in the 5'-flanking region of HA cluster genes and isoprenoid biosynthesis genes in *A. oryzae*. The horizontal lines represent 1000 bp upstream of the translation initiation site of each gene. Each triangle represents the position of the sequence YNAGGCC in the forward or reverse strand.

Table S1. PCR primers used in this study

Primer name	Sequence (5' to 3')	Primer name	Sequence (5' to 3')
hepA-LU	TAGCTAGCATCTCTGGAGTGAG	hepD-LU	AGAGACCCGTAATGTGTGCCCAA
hepA-LL	AGGGTACGTCTGTTGTCTTCTTAGGGGGATAGAGA	hepD-LL	GTACGTCTGTTGTGCGACTGTTCCCCGAGCGAGTGA
hepA-RU	CTTCTGAGGTGCAGTTTCGTATCTAATGACCTCCTG	hepD-RU	CTGAGGTGCAGTTTCAGAATCGCCTCCAGCACGAGC
hepA-RL	ACTGTTTACTAGGGCCACCT	hepD-RL	ACCTTGTGCTTGGAGTCCAGACTGA
hepA-LU-2	GAACGCGCAAATGGCTCGACT	hepD-LU-2	CTGGGCGTATCGTGGGTCCATAG
hepA-RL-2	GCCATCAGTGCCCTCCGTACA	hepD-RL-2	TTCACAGGGTGCAAGTTCACCCAT
hepR-LU	TCTTCTGCCTAGTTACGGAGGACT	hepE-LU	GCTCGTCCTAAGAGTGGCCAG
hepR-LL	GTACGTCTGTTGTGCCATCGACAGAACATCACGCGA	hepE-LL	GTACGTCTGTTGTAGAGACCCGTAATGTGTGCCCAATG
hepR-RU	CTGAGGTGCAGTTCAGCCACTACGCGGGTCAAGA	hepE-RU	CTGAGGTGCAGTTCATGGACCATCTGAAGCTCTCGGA
hepR-RL	ATCCTCGACGCTGCAGGAGACT	hepE-RL	CAGTGTGACGCATCGCTCGGTT
hepR-LU-2	GGTACGGAGTACTGATCCGCCT	hepE-LU-2	TGGCCAGGATATCGAGCCAGAG
hepR-RL-2	ACTCCGCCTTAGAGCTGCGACT	hepE-RL-2	CCAGAGCATCGACTGCCCATGA
hepS-LU	AGGCGGATCAGTACTCCGTACC	hepF-LU	TGCTGCTCAGAACCTGATCCCGA
hepS-LL	GTACGTCTGTTGTCTTGTGTCAGTAGACTGAGGCAC	hepF-LL	GTACGTCTGTTGTTGGCGACCAATTCAATGGGTTCGTG
hepS-RU	CTGAGGTGCAGTTTATTTCCGGCGGAGATTAGTCCGCA	hepF-RU	CTGAGGTGCAGTTCAGAGCATCGACTGCCCATGATG
hepS-RL	ACTGCGCAAGTTCATCCTGGGT	hepF-RL	ATGGCGGATCTGGCTCGCAATC
hepS-LU-2	TTCAGTCCTCCGTAAGTAGGCAGA	hepF-LU-2	CAACCTCCAATGTGTCCGTGGTTGA
hepS-RL-2	GTCTTGCATCCAAAGATGAGCCA	hepF-RL-2	CCATGGACCATCTGAAGCTCTCGGA
pyrG-U	ACAACAGACGTACCCTGTGATGTTT	hepG-LU	ATTGCCGGTCATGATCCTCCGTGT
pyrG-L	AACTGCACCTCAGAAGAAAAGGATG	hepG-LL	GTACGTCTGTTGTTGCCGTTGACAACAATGGAGTCACC
pyrG-LU	ACAACAGACGTACCCTGTGATGTTT	hepG-RU	CTGAGGTGCAGTTCAACCTCCAATGTGTCCGTGGTTGA
pyrG-LL	AGTTTGGTACTGCTGGGTACGCCAAATCCAGCAGCTCT	hepG-RL	TGGCGACCAATTCAATGGGTTCGTG
pyrG-RU	CAGCAGTACCAAACTCCTGAGTCG	hepG-LU-2	GATCCGACGGAAGTTGGGCGTC
pyrG-RL	AACTGCACCTCAGAAGAAAAGGATG	hepG-RL-2	AGAGGCCGTAAATCACTGCGGTCT
pyrG-LU-2	GGTAATGTGCCCCAGGCTTGTC	hepH-LU	GAGTTGCGGAATACGATCCGACCGA
pyrG-RL-2	TTATGGCCGCTGTGCGATCAGGA	hepH-LL	GTACGTCTGTTGTTTCCGAGGGTCAGTCTGCCAT
hepB-LU	GTCGACAAGCTTGCGATGCCAT	hepH-RU	CTGAGGTGCAGTTCCTGTTAGCATGAGCCACGGAGAT
hepB-LL	GTACGTCTGTTGTAGCAACTACTCCAGAGATGCT	hepH-RL	TTGTAGGACCCGGTGCTGTGACA
hepB-RU	CTGAGGTGCAGTTTGCTGCGTATTGAGGAGGTCT	hepH-LU-2	GTAAGACGCCCCAATTCCGTCG
hepB-RL	GTATGCTCGGGGTACAGATCCTGC	hepH-RL-2	GACCCAAGGATTCAATGCCCTTGTC
hepB-LU-2	GCACAGCGAACTGGCCCTT	OEhepR-U	TTTGAATTCGAATCGATATGGCTGAAACATGGATGGCTCTTC
hepB-RL-2	AGATTTGGCCACCTTCATCGGTG	OEhepR-L	TACCCGGGTCACTAGTTTCACTTCTTGCCTCGATTTCATGATG
hepC-LU	AAGTCGAGCCATTTGCGCGTTC	OEhepS-U	TTTGAATTCGAATCGATATGATCTCAATGAGTGTACCTAG
hepC-LL	GTACGTCTGTTGTGCCAACTCCTGCAGAGTCGA	OEhepS-L	TACCCGGGTCACTAGTTTATGTAAGTAGTATTGGAGCT
hepC-RU	CTGAGGTGCAGTTCTGACAAGCGTTACCCGTTGCA	gpdA-U	TCGCCATATGGCTACCCCAAGGTTGGAATC
hepC-RL	ATCGGTGTTGGGATGCCCATGT	gpdA-L	ACTGCTGCAGCTACTGGCCATCGACCTTGAGATG
hepC-LU-2	GGTACTGCAACGCATTGGGTTCGT	gpdB-U	TCGCCATATGACCGCTAAAGTTGGTATC
hepC-RL2	TGGGTGAACTTGCACCTGTGA	gpdB-L	ACTGCTGCAGCTACTTCCCAACACTGGCAA

Table S2. qRT-PCR primers used in this study

Primer name	Sequence (5' to 3')	Target gene
hepA qRT-F	GACCGTCTTCAGACCTGCACA	AO090011000408 (hepA)
hepA qRT-R	CCGGAAATCGTTGGCTTTGTGG	
hepB qRT-F	ACGAACCCAATGCGTTGCAGT	AORIB40_NS.11930 (hepB)
hepB qRT-R	GACTCGCCGAAGCTCCGCTA	
hepC qRT-F	ATCGGACAGCACGTCCATTGC	AO090011000410 (hepC)
hepC qRT-R	ACGAAACCGGATCGCTCAGCT	
hepD qRT-F	ATCGGTGTTGGGATGCCCATGT	AO090011000411 (hepD)
hepD qRT-R	GAAAGGTTGCAGAGCGCCTTTCT	
hepE qRT-F	AGCGCCATCTGGGCTTTGGA	AO090011000412 (hepE)
hepE qRT-R	AACCGTTCCGGGGGCCAGTTCA	
hepF qRT-F	AGCCAGAGCATCGACTGCCCAT	AO090011000413 (hepF)
hepF qRT-R	CAGGCCGACAATCCCAGAGCCA	
hepG qRT-F	ACTTGACCTGTGCCTTGAGAA	AO090011000414 (hepG)
hepG qRT-R	CAC TTGAGACAACATCATCCTCG	
hepH qRT-F	ATCCTCGACGCTGCAGGAGACT	AO090011000415 (hepH)
hepH qRT-R	TAGTCGCAGCTCTAAGGCGGAGT	
hepR qRT-F	TGTAGGACCCGGTGCTGTGAC	AO090011000416 (hepR)
hepR qRT-R	ATAGTGCCGTCGAAGCTCG	
hepS qRT-F	CAGGAGAGTGTTTCTCGGACCATTG	AO090011000417 (hepS)
hepS qRT-R	CATGATCCGGTGCTGCCATGCA	
FPPS qRT-F	TGGGATGGCTCACCGAGCTT	AO090102000358 (FPP synthase)
FPPS qRT-R	TCCTGACGGTACCAGCATGGCTG	
HMGR qRT-F	GGACCAAGGCTACGTCTGCCGT	AO090120000217 (HMG-CoA reductase)
HMGR qRT-R	CACAGCATGCACCGTGAACCA	
IPI qRT-F	TTGCTGGCGAGACCGGTTCTGA	AO090023000500 (IPP isomerase)
IPI qRT-R	CCAGGGGTACTTGCTCCGGCTT	
H2B qRT-F	AAGAAGCGTGGAAGACCAGG	AO090020000006 (Histone 2B)
H2B qRT-R	GACATGGCACGAGTGGAGATT	