

SUPPLEMENTARY MATERIAL:

(a)

Pestalotiopsis_microspora.txt	MVTHIHKQGDP...QSHQHNSPDTDGRPRHEIMVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	104
Alternaria_alternata.txt	LMNTIAVSNET....KSQFIRITKGQICRHNLQVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	97
Aschersonnia_aleyrodis.txt	MASAVLLENA.SSWSQHPIRTRIKRSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	107
Cordyceps_bronnialrtii.txt	MFAAEKSTMSRANQYRIRTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	107
Fusarium_langsethiae.txt	MATPSVITDS.KUTIAFIRTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	106
Fusarium_oxyphorum.txt	MATPSSIAEFP.KDVINRIKTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDQSETMADKTDMEVYSLFIFISLDRAPRLEGRV	106
Consensus	m r t y v qqperaracg g k drrpvdpvv l e t yn ffl sle ar a gr	
Pestalotiopsis_microspora.txt	TPPTISPFHILIGVPSACQILIRESEPGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	211
Alternaria_alternata.txt	SSAGFSSEVLLIGVPSAGMAYLIRGEGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	202
Aschersonnia_aleyrodis.txt	TATATTCGILIGVPSAGMAYLIRGEGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	210
Cordyceps_bronnialrtii.txt	TPCTVNPILIGVPSAGMAYLIRGEGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	209
Fusarium_langsethiae.txt	NPNNNPHILIGVPSAGMAYLIRGEGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	209
Fusarium_oxyphorum.txt	TPAGNRPILIGVPSAGMAYLIRGEGYF...FFDLSVRHEGRVFDIPLRNKAQELNPIDQGWEDDEGLFTTFIDYRSFPINSAKKFPGFESTLSQT	209
Consensus	a p l tg p yl rp agyf fpdlsvrheg l f l e d e pf v sakkfpgl est ls	

(b)



Figure S1. VeA information. (a) Alignment of the deduced amino acid sequence of VeA in *P. microspora* and the VeA orthologs in other fungi. The amino acid sequences were aligned using DNAMAN (Version 8.0) software. (b) Schematic of the structure of *veA* encoding protein from *Pestalotiopsis microspore* analyzed by protein basic local alignment search tool (BLASTP) of NCBI (<https://blast.ncbi.nlm.nih.gov>).

(a)

Pestalotiopsis_microspora.txt	..SDGTWTYDYLICDQF...RARMCGFGDKDRRPIITPPC...RLIVIDDCRKEUDUNQIEQCMILSVDWWAGTSEDNIAKESFNSPSTTIGISTSYSYREEDKNAIVGYIAE	110
Colletotrichum_graminicola.txt	..DDMGRKRYD...VWQCF...RARMCGFGDKDRRPIITPPC...KUVVRDAPGSGPNENNDISAFVWICVDINSEGTSCEVNIVRHSNTASIS.TICOFSYSAIREEGQAP.Q	108
Fusarium_oxyphorum.txt	IEEGSGWVYSLVFOGVV...RARMCGFGDKDRRPIITPPC...RLIVIINTERPGEVDNDSIDRAFMVSLVLDWNGHGT...DVIWRSTSSTGJGMA..SSTTYVNSLEGTISVQCS	111
Gaeumannomyces_tritici.txt	..ECQNTVTPYLVQCF...RARMCGFGDKDRRPIITPPC...RLIVVTPHGEHEDVNEIDEMMVVLNVVLDKSEGLKE...NIVRHTSATPSIS.TTPAFAEANIDEATRAFSP.F	108
Rasamonia_emersonii.txt	..WDGRINM...HVQCF...RARMCGFGDKDRRPIITPPC...RLIVVRDACHEREWVNEIDETSEFWLIVLRACTISPE...NIVRHEATPSIS.TAISSSVP.....BFFCN.I	102
Verticillium_dahliae.txt	..DEGGRVYI...DVQCF...RARMCGFGDKDRRPIITPPC...RLIVIPF...S...E...D...S...M...W...V...L...D...E...C...G...D...N...W...T...S...A...I...S...T...T...C...Y...N...T...T...A...F...G...I	108
Consensus	1 qqp raimcgfdkdrpittppc t e n v d i w g e n l	
Pestalotiopsis_microspora.txt	QEHAHAYPS.....QQYGDPA...GYADLRS.HAMHHT...IPEMVAA...HQFAAHAFV...SRVFCITQGLQQCD...MVA...GRNNNSVGGCGNGM...SRNLIGS	199
Colletotrichum_graminicola.txt	CGAYSCMPF...SYGAPMGYQ...QCFP...EQHHMPG.YGNTSG...SSWYFAYQ...SSNFCFAPPFY...YFPHH...AEVFC...ADMAYG...GHRC...LSMAS...FCGM...TRNLIGS	210
Fusarium_oxyphorum.txt	...FRESREGYG...QSQGINVQGD...IPEVQCS...QCAF...Y...FESSSYGF...QQYF...RSGSYAET...SAFF...GFF...FRNF...YQCD...ONALTR...AVV...G...FCGM...TRNLIGS	210
Gaeumannomyces_tritici.txt	...SNRDI...PQYGA...P...SVT...YAGGY...T...QAMF...VAN...Y...G...V...N...F...G...A...G...T...A...C...Y...F...G...Q...A...V...H...G...M...A...M...T...Y...G...L...I...R...M...F...N...G...T...E...M...F...P...G...H...H...R...T...A...S...H...J...C...G...M...TRNLIGS	218
Rasamonia_emersonii.txt	SETYPPYQ...NFGQ...EMGYGFVGFY...EGNCF...M...Y...N...F...G...I...G...N...F...O...Y...G...G...S...F...L...C...H...A...S...M...F...A...G...E...G...M...I...R...N...L...I...G...S	185
Verticillium_dahliae.txt	ESSTSHRE.....PFQFHSENN...G...I...ENAS...I...PGAYGM...S...N...Y...P...E...S...C...I...E...L...S...N...G...Y...G...P...A...F...Y...G...I...N...G...S...I...E...Y...R...T...Y...G...Q...N...Q...F...O...R...N...I...G...G...A...F...G...M...I...R...N...L...I...G...S	208
Consensus	p gm rnligs	
Pestalotiopsis_microspora.txt	EVSGGNHID...VDGKWC...WV...QDLSVRTEG...FRL...RES...S...G...W...N...T...G...N...Q...Q...T...S...D...P...L...K...N...C...R...V...H...L...V...I...N...A...P...C...V...I...S...A...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	307
Colletotrichum_graminicola.txt	...T...E...S...A...P...P...R...P...V...E...D...V...G...W...I...C...Q...L...S...V...R...T...E...G...F...R...F...S...V...A...R...P...D...Q...I...S...A...D...S...L...V...N...G...T...P...D...A...S...I...F...I...V...F...V...S...A...R...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	315
Fusarium_oxyphorum.txt	I...A...S...A...P...R...I...T...E...G...Q...S...W...V...I...C...Q...L...S...V...R...T...E...G...F...R...F...S...V...A...R...P...D...Q...I...S...A...D...S...L...V...N...G...T...P...D...A...S...I...F...I...V...F...V...S...A...R...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	311
Gaeumannomyces_tritici.txt	I...S...A...S...A...P...R...I...T...E...G...Q...S...W...V...I...C...Q...L...S...V...R...T...E...G...F...R...F...S...V...A...R...P...D...Q...I...S...A...D...S...L...V...N...G...T...P...D...A...S...I...F...I...V...F...V...S...A...R...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	325
Rasamonia_emersonii.txt	I...S...A...S...A...P...R...I...T...E...G...Q...S...W...V...I...C...Q...L...S...V...R...T...E...G...F...R...F...S...V...A...R...P...D...Q...I...S...A...D...S...L...V...N...G...T...P...D...A...S...I...F...I...V...F...V...S...A...R...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	289
Verticillium_dahliae.txt	I...S...A...S...A...P...R...I...T...E...G...Q...S...W...V...I...C...Q...L...S...V...R...T...E...G...F...R...F...S...V...A...R...P...D...Q...I...S...A...D...S...L...V...N...G...T...P...D...A...S...I...F...I...V...F...V...S...A...R...K...K...F...G...V...C...E...S...I...L...S...K...C...F...A...I...G...K...I...P...I...R...G	317
Consensus	s l d g wf qdlsvrteg frl f v g p l s f v sakkfpgv est lsk fa gqkipirk	

(b)



Figure S2. VelB information. (a) Alignment of the deduced amino acid sequence of VelB in *P. microspora* and the VelB orthologs in other fungi. The amino acid sequences were aligned using DNAMAN (Version 8.0) software. (b) Schematic of the structure of *velB* encoding protein from *P. microspora* analyzed by BLASTP of NCBI.

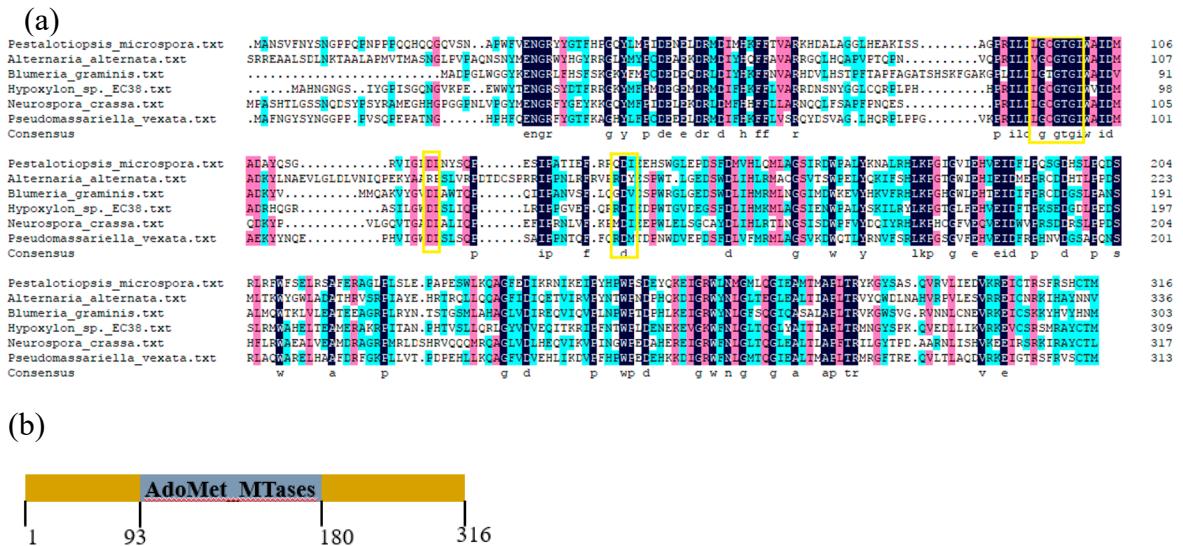


Figure S3 LeaA information. **(a)** Alignment of the deduced amino acid sequence of LaeA in *P. microspora* and the LaeA orthologs in other fungi. The amino acid sequences were aligned using DNAMAN (Version 8.0) software. **(b)** Schematic of the structure of *laeA* encoding protein from *P. microspore* analyzed by BlastP of NCBI. Conserved protein methyltransferase S-adenosylmethionine binding sites are boxed.

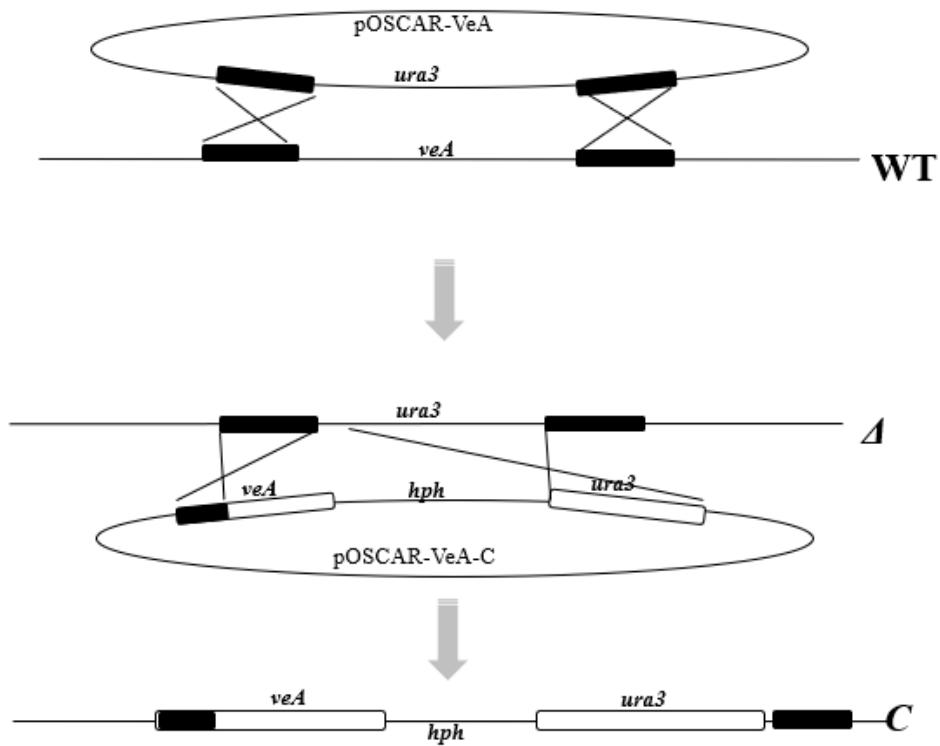


Figure S4. Construction of *veA* deletion and complement strains. Diagrams showing the strategy for generating *veA* deletion and complement strains by homologous recombination.

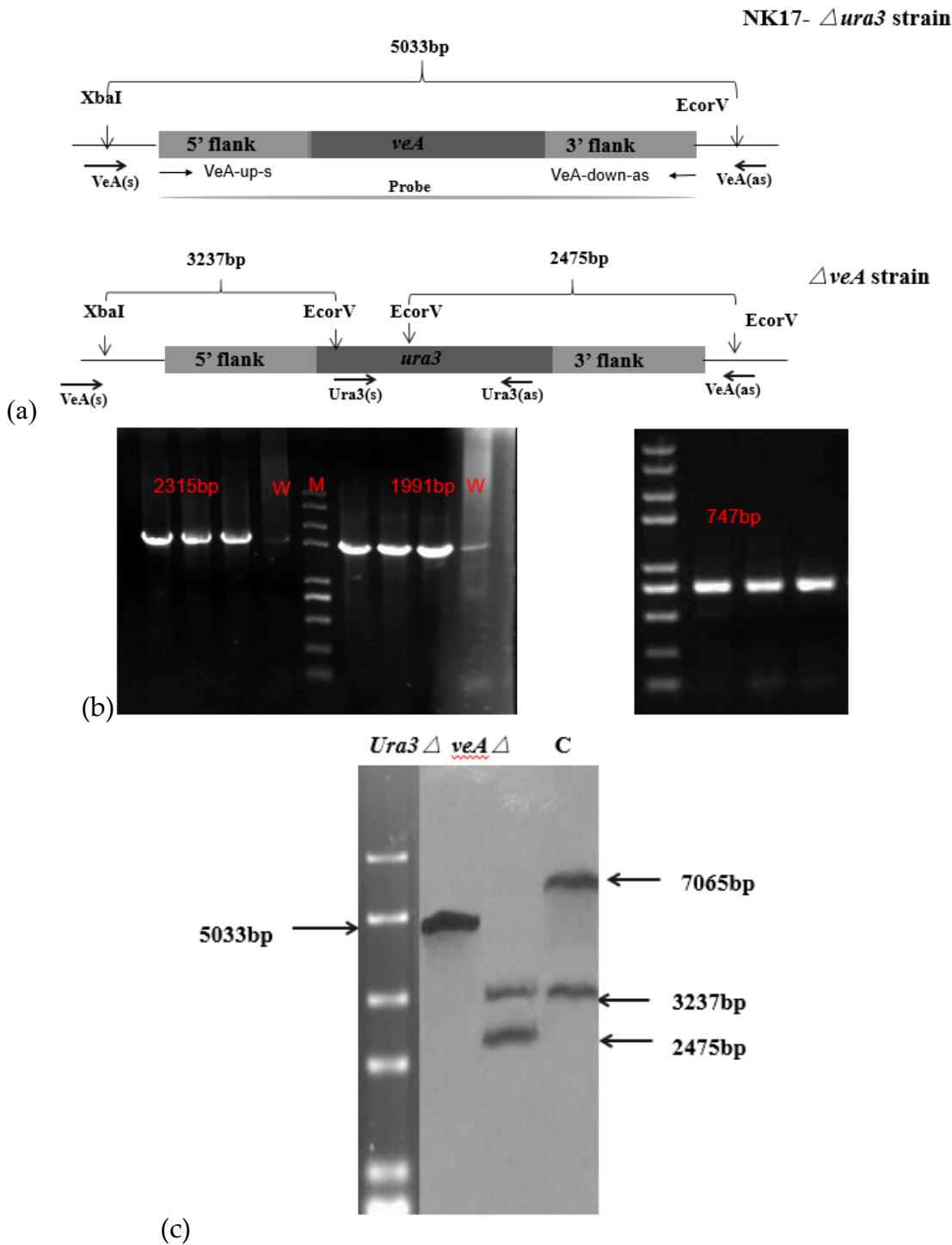


Figure S5. Deletion of *veA* in NK17. (a) Schematic of *veA* allele in NK17-*ura3* Δ and *ura3* in *veA* Δ . The primers used for PCR confirmation of *veA* Δ , the location of the recognition sites of Xba I, Eco V, and the probes used for Southern blot were shown. (b) Screening of *veA* Δ (top) *veA* Δ -C transformants by PCR. The expected size of PCR products with primer pairs VeA(s)/Ura3(as) and VeA(as)/Ura3(s) were 2315 bp (left) and 1991 bp (right) for *veA* Δ , respectively. A pair of primer Hyg(s) and Hyg(as) generated 747 bp sequence in *veA* Δ -C. M is molecular marker, W presents NK17 strain (Trans2K plusII, TransGen, China). (c) Southern blot analysis of the *veA* Δ mutant. Genomic DNA from NK17-*ura3* Δ , *veA* Δ or *veA* Δ -C was digested with Xba I and Eco V, and probed with a 1.7-kb *veA* fragment. Digestion of the NK17-*ura3* Δ genome yielded a 5.0 kb band, whereas the *veA* Δ had two bands, 3.2 and 2.5kb in length. Two bands, 3.2 and 7.0 kb were detected for complemented strain *veA* Δ -C (Schematic of construction of the complemented strain was represented in Figure S4).

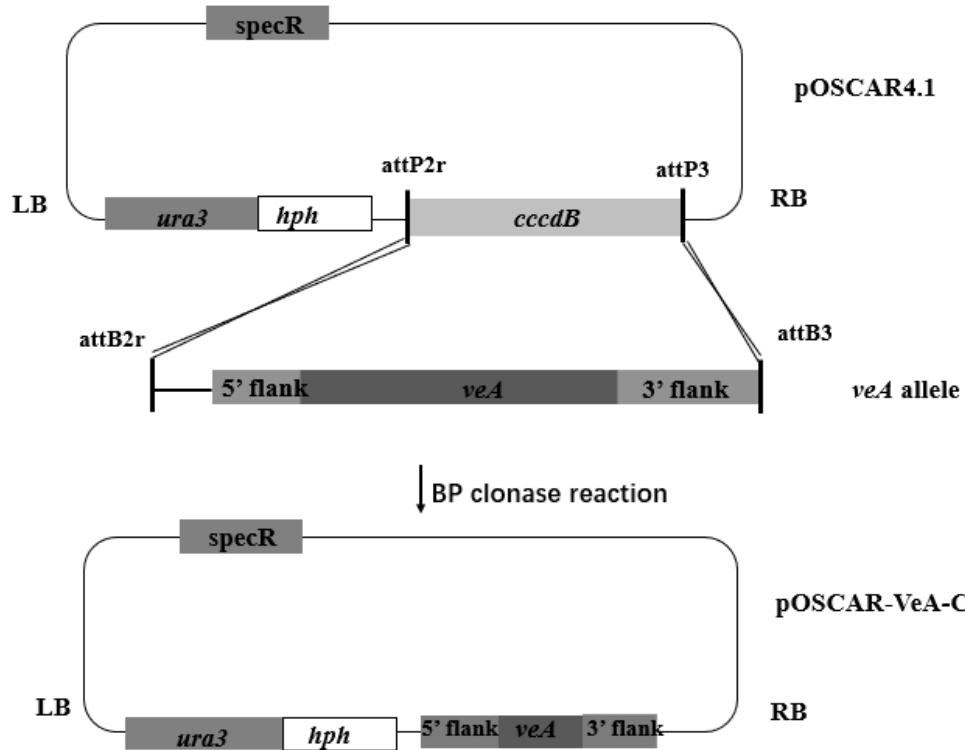


Figure S6. Schematic of pOSCAR4.1 and the vector pOSCAR-VeA-C for gene complementation was constructed by BP clonase. Location of primers used to amplify the *veA* allele were indicated.

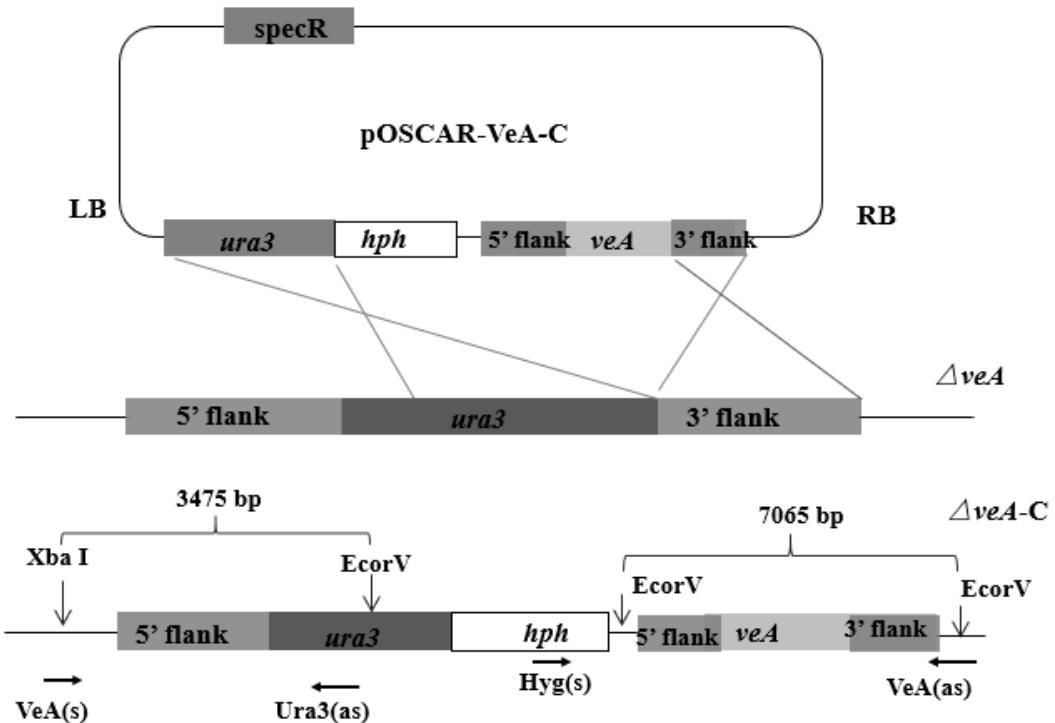


Figure S7. Schematic of the complement vector pOSCAR-VeA-C and construction of complemented strain ΔveA -C. The location of the recognition sites of XbaI and EcoRV are indicated.

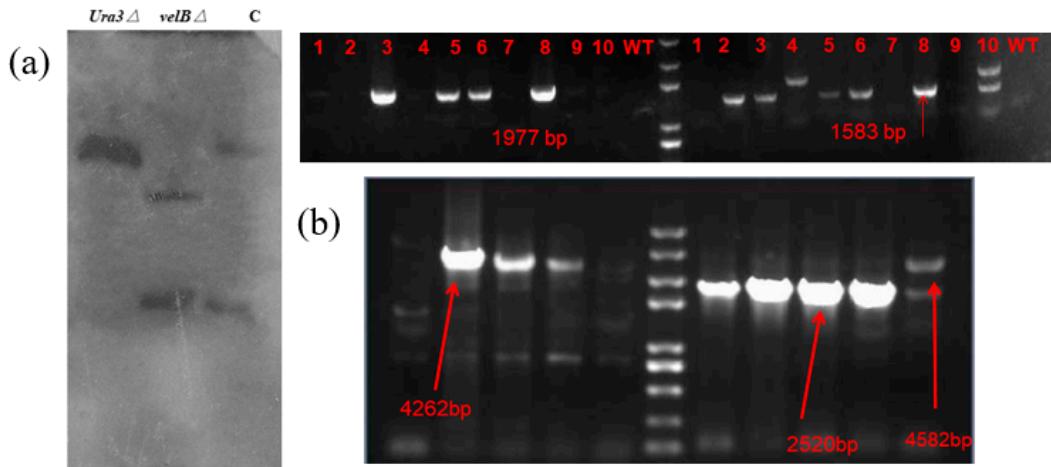


Figure S8. (a) Southern blot analysis of the $\Delta velB$ mutant. Genomic DNA from NK17- $\Delta ura3$, $\Delta velB$ or $\Delta velB-C$ was digested with Sac I probed with a 3.3-kb $velB$ fragment. Digestion of the NK17- $\Delta ura3$ genome yielded a 6.6 kb band, whereas the $\Delta velB$ had two bands, 4.5 and 2.3 kb in length. Two bands, 7.7 and 2.3 kb were detected for complemented strain $\Delta velB-C$. (b) PCR verification for $\Delta laeA$ mutants (top) and $\Delta laeA-C$ strains (bottom). The expected size of PCR products with primer pairs VelB(s)/Ura3(as) and VelB(as)/Ura3(s) were 2315 bp (left) and 1991 bp (right) for $\Delta velB$, respectively. The anticipated length of PCR product with primer pair LaeA-up-s/Hyg(R) was 4262 bp for the complemented strain $\Delta laeA-C$, while no band was seen for $\Delta laeA$; The predicted PCR product with primer pair LaeA-down-as/ura3(s) was 2520 bp in length for complemented strain, while 4582 bp for $\Delta laeA$.

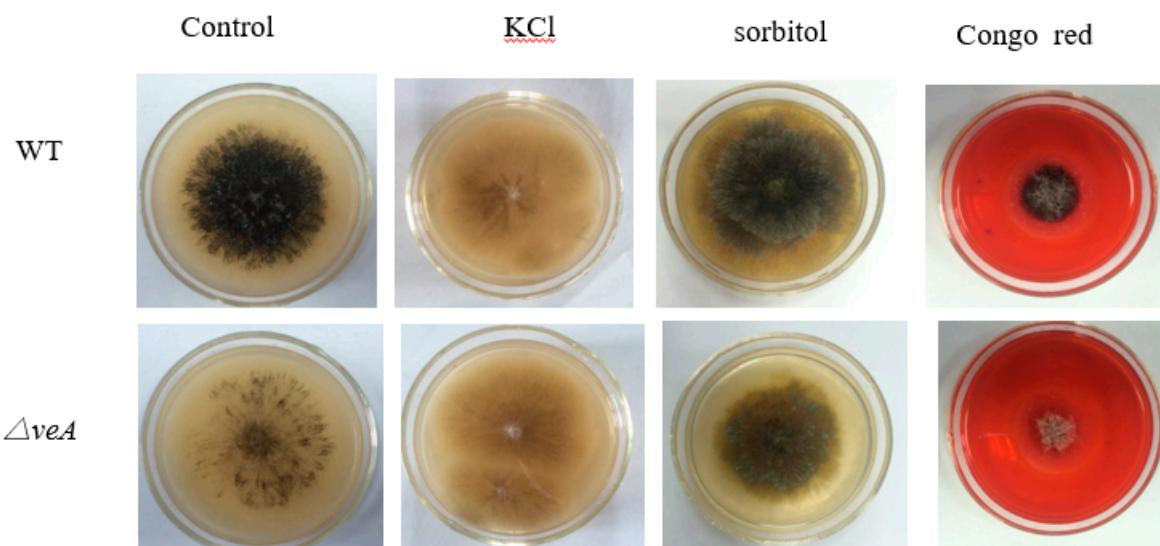


Figure S9. Sensitivity tests for NK17 and $\Delta velA$ strains. The strains incubated at 28 °C for five days on MM plates supplemented with 1M KCl, 2 M sorbitol, or 0.04% Congo red.