

SUPPLEMENTARY MATERIAL:

(a)

Pestalotiopsis_microspora.txt	MVTHIHKQGDP...QSHQHNSPDTDGRPRHEIMVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	104
Alternaria_alternata.txt	LMNTIAVSNET....KSFPIRTRKGQCRINLQVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	97
Aschersonia_aleyrodis.txt	MASAVLLENA.SSWSQVPIRTRIKRSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	107
Cordyceps_bronnarii.txt	MFAAEKSSTMSRANQCRIRTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	107
Fusarium_langsethiae.txt	MATPSVITDS.KUTIAFIRTRTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	106
Fusarium_oxyphorum.txt	MATPSSIAEP.KDVINRIKTRTRRNNSLWYLVQPERARACGSFSSANDRREVDEFFFIRPTDGGSETDAEYDITMEVYSLFIFISLDRAPRLEGRV	106
Consensus	m r t y v qqperaracg g k drrpvdpvv l e t yn ffl sle ar a gr	
Pestalotiopsis_microspora.txt	TPPTISPFHILIGVPSACQILIRESEPGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	211
Alternaria_alternata.txt	SSAGFSSEPLIGVPSAGMAYLIRGADGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	202
Aschersonia_aleyrodis.txt	TATPTISPFHILIGVPSAGMAYLIRGADGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	210
Cordyceps_bronnarii.txt	TPCTVNPFLIGVPSAGMAYLIRGADGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	209
Fusarium_langsethiae.txt	NPNNANPFLIGVPSAGMAYLIRGADGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	209
Fusarium_oxyphorum.txt	TPRAGNPFLIGVPSAGMAYLIRGADGYF...FFDLSVRHEGRVFD...PFDLNRNKAQELNPIDOGDNWED...DGLFTTFIDYRSFPFVSAKKFPGFESTLISI	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 microspora* analyzed by protein basic local alignment search tool (BLASTP) of NCBI (<https://blast.ncbi.nlm.nih.gov>).

(a)

Pestalotiopsis_microspora.txt	..SDGTWTYD...ICDQF...RARMCGFGDKDRRPIITPPC...RLIVIDDCRKEUDUNQIEQCMILSVDWL...AGTSEDNIAKESFNSPSTTIGISTSYSYREEDKNAIVYGIAE	110
Colletotrichum_graminicola.txt	..DDMGRKRYD...VWQCF...RARMCGFGDKDRRPIITPPC...KUVVRDAPGSGPNENNDISAFVWICVDINSEGTS...ENIVRHSNTASIS...TICOFSYSAIREEGQAPQ.P	108
Fusarium_oxyphorum.txt	IEEGSGWVY...LIVQCFV...RARMCGFGDKDRRPIITPPC...RLIVVNTPEHGENDINSIDRAMEVSLWDLNH...HGTIDENVRSSTGTGAMA...SSTTYVNSLEGTISVQCS	111
Gaeumannomyces_tritici.txt	..ECQNTVYD...LIVQCF...RARMCGFGDKDRRPIITPPC...RLIVVNTPEHGENDINSIDRAMEVSLWDLNH...HGTIDENVRSSTGTGAMA...SSTTYVNSLEGTISVQCS	108
Rasamonia_emersonii.txt	..VHDGRWMS...HVQCF...RARMCGFGDKDRRPIITPPC...RLIVVNTPEHGENDINSIDRAMEVSLWDLNH...HGTIDENVRSSTGTGAMA...SSTTYVNSLEGTISVQCS	108
Verticillium_dahliae.txt	..DEGGRVYD...LIVQCF...RARMCGFGDKDRRPIITPPC...RLIVVNTPEHGENDINSIDRAMEVSLWDLNH...HGTIDENVRSSTGTGAMA...SSTTYVNSLEGTISVQCS	102
Consensus	1 qqp rarmcgfdkdrppc t e n vdw g e n l	108
Pestalotiopsis_microspora.txt	CEAHAYPS.....QQYGDPA...GYADLRS.HAMHT...IPEMVAA...HQFAAHAFV...SRPFCITQGLQQCD...MVA...GRNNNSVGGCGNGM...SRNLIGS	199
Colletotrichum_graminicola.txt	CGAYSCMPF...SYGAPMGYQ...QCFP...EQHHMPG.YGNTSG...SSWYFAYQ...SSNFCFAPPFY...YFPHRHN...AEVFCADMAYGHRCSLSMASFCGM...SRNLIGS	210
Fusarium_oxyphorum.txt	EFRESRGYG...QSQGINVQGD...IPEVQCS...QCAFPIY...PESSSYGF...QQYYP...RSGSYAET...SAFF...GFFFRN...YQCD...ONALTRM...AVVGCFCGM...SRNLIGS	210
Gaeumannomyces_tritici.txt	ESNRDIPQVGPAGPYF...PSTVTE...YAGGYQT...QAMFSVANF...YGMVNGFAGQTACYY...QGQATVHG...GMA...GANTFY...L...RMFNGTF...EMFNFQGHHRM...TASH...FCGM...SRNLIGS	218
Rasamonia_emersonii.txt	SETYPPYQG...NFGQO...EMGYGFVGEFY...GGNCF...M...Y...NFG...G...GNFQFVYPOY...G...G...SFLCH...ASMF...AEQOFMSAF...G...GM...SRNLIGS	185
Verticillium_dahliae.txt	ESSTSHTSHRE.....PFQFHSEN...G...ENASFY...PGAYGM...SN...Y...P...ESS...C...I...L...S...N...G...Y...G...P...A...P...F...G...M...T...R...N...L...I...G...S	208
Consensus	p gm rnligs	
Pestalotiopsis_microspora.txt	EVS...GNH...D...VDGKWC...W...V...QDLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...R...G	307
Colletotrichum_graminicola.txt	IN...S...A...P...P...R...V...P...D...V...G...W...V...I...Q...DLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...R...G	315
Fusarium_oxyphorum.txt	I...A...S...A...P...P...R...V...P...D...V...G...W...V...I...Q...DLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...R...G	311
Gaeumannomyces_tritici.txt	I...A...S...A...P...P...R...V...P...D...V...G...W...V...I...Q...DLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...R...G	325
Rasamonia_emersonii.txt	I...A...S...A...P...P...R...V...P...D...V...G...W...V...I...Q...DLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...R...G	289
Verticillium_dahliae.txt	I...A...S...A...P...P...R...V...P...D...V...G...W...V...I...Q...DLSVRT...G...FRL...R...F...S...G...W...V...G...N...T...G...N...Q...G...T...P...L...K...I...F...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.

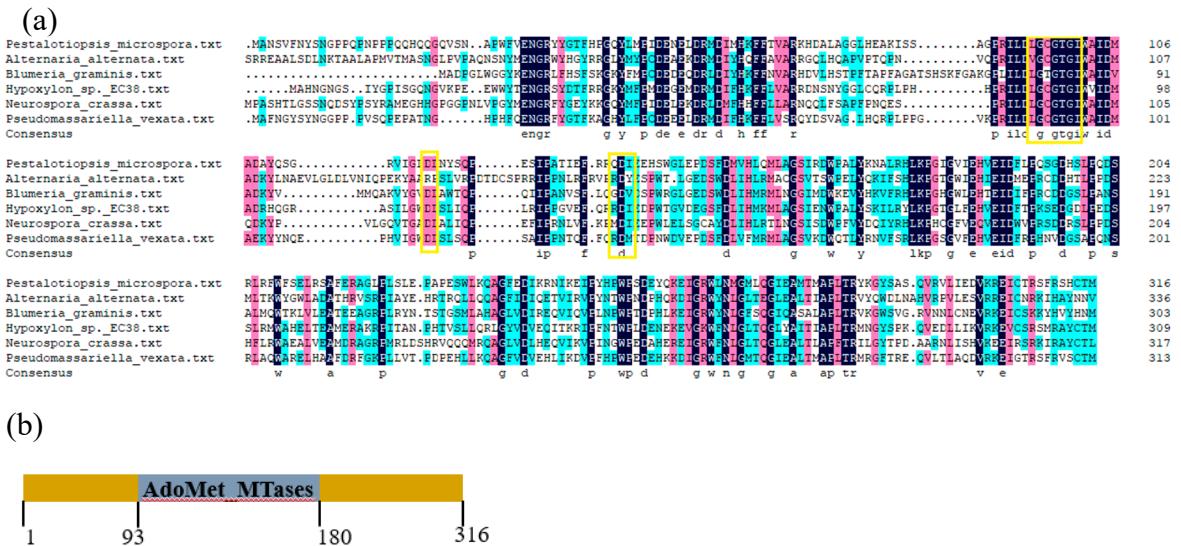


Figure S3 LeaA information. **(a)** Alignment of the deduced amino acid sequence of LaeA in *P. microspora* and the LaeA orthologs in other fungi. The amino acid sequences were aligned using DNAMAN (Version 8.0) software. **(b)** Schematic of the structure of *laeA* encoding protein from *P. microspore*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

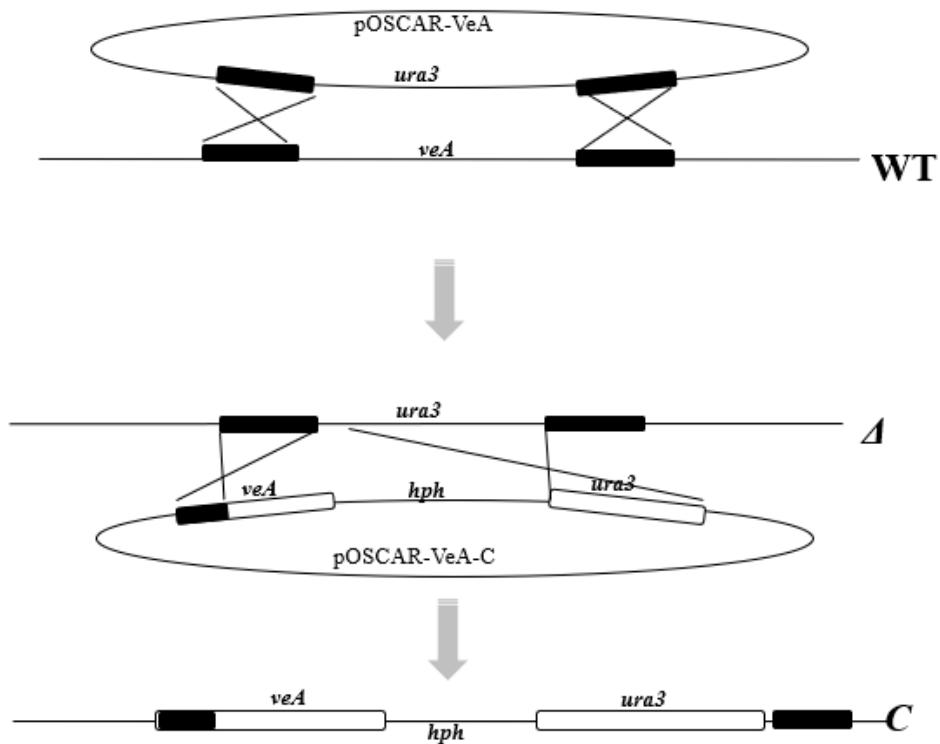


Figure S4. Construction of *veA* deletion and complement strains. Diagrams showing the strategy for generating *veA* deletion and complement strains by homologous recombination.

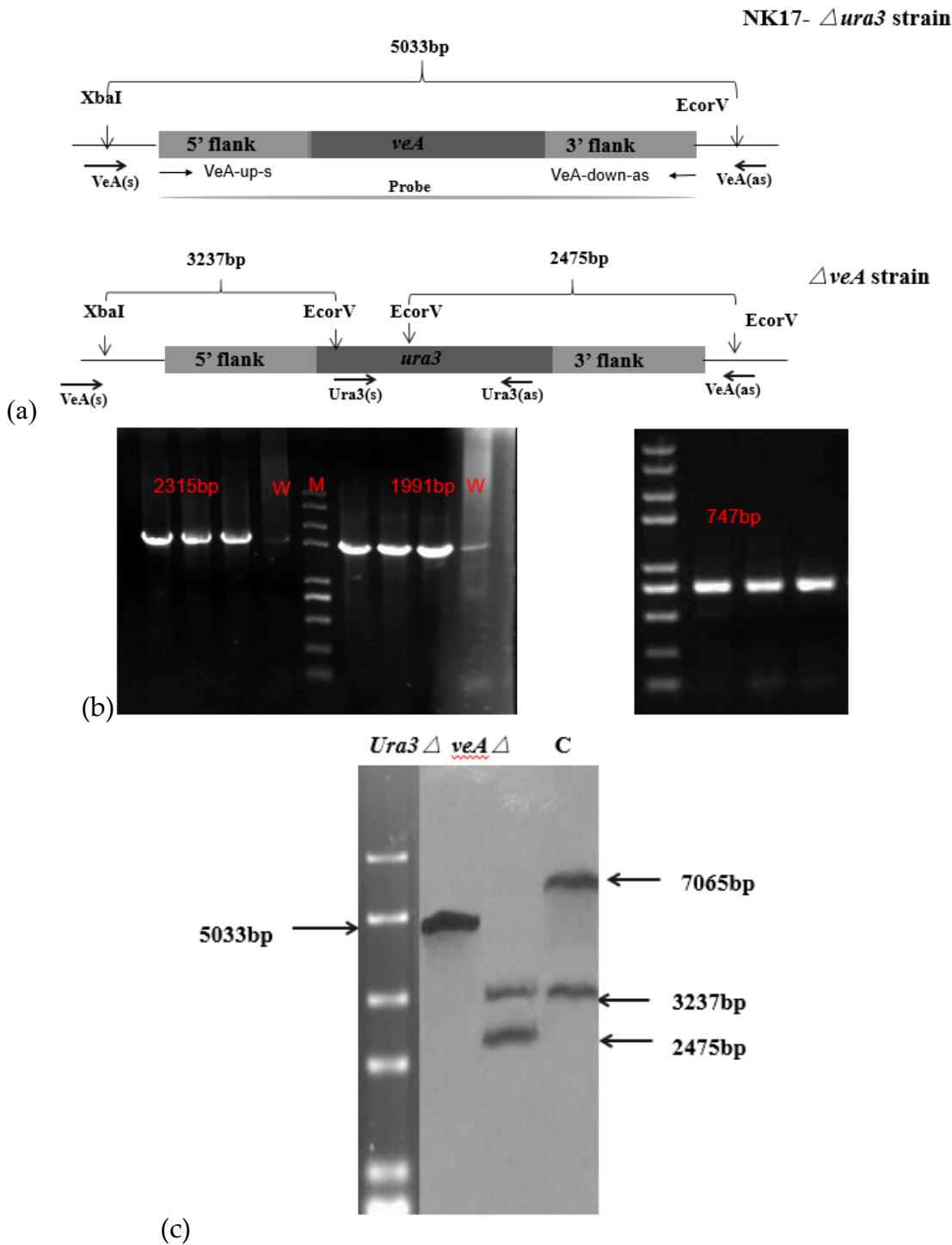


Figure S5. Deletion of *veA* in NK17. (a) Schematic of *veA* allele in NK17-*ura3* Δ and *ura3* in *veA* Δ . The primers used for PCR confirmation of *veA* Δ , the location of the recognition sites of Xba I, Ecor V, and the probes used for Southern blot were shown. (b) Screening of *veA* Δ (top) *veA* 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 Ecor 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).

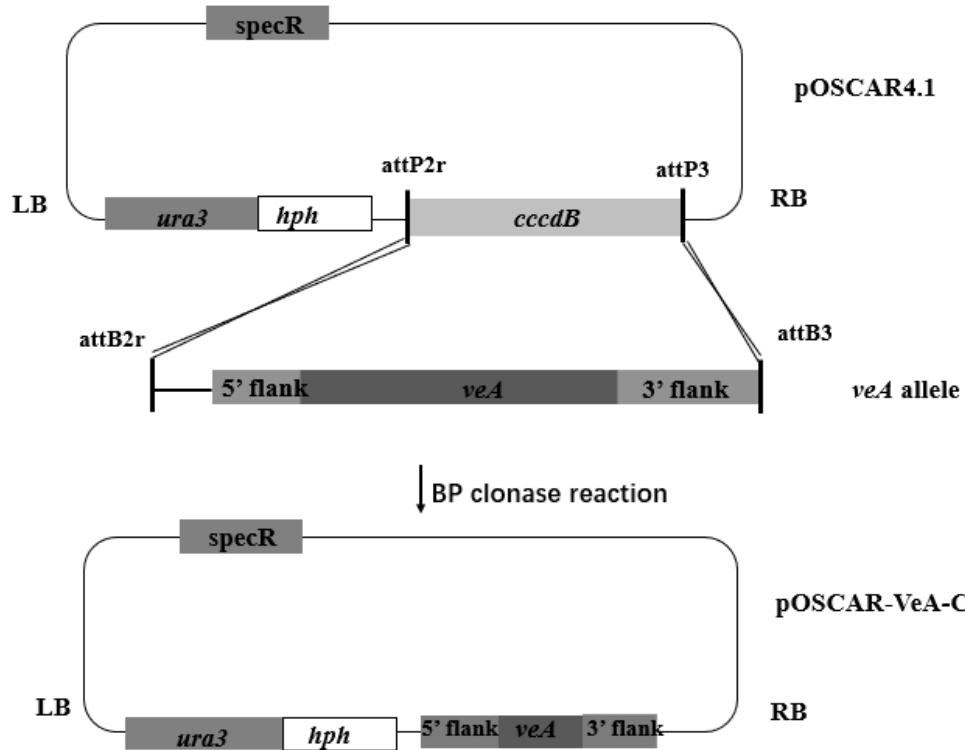


Figure S6. Schematic of pOSCAR4.1 and the vector pOSCAR-VeA-C for gene complementation was constructed by BP clonase. Location of primers used to amplify the *veA* allele were indicated.

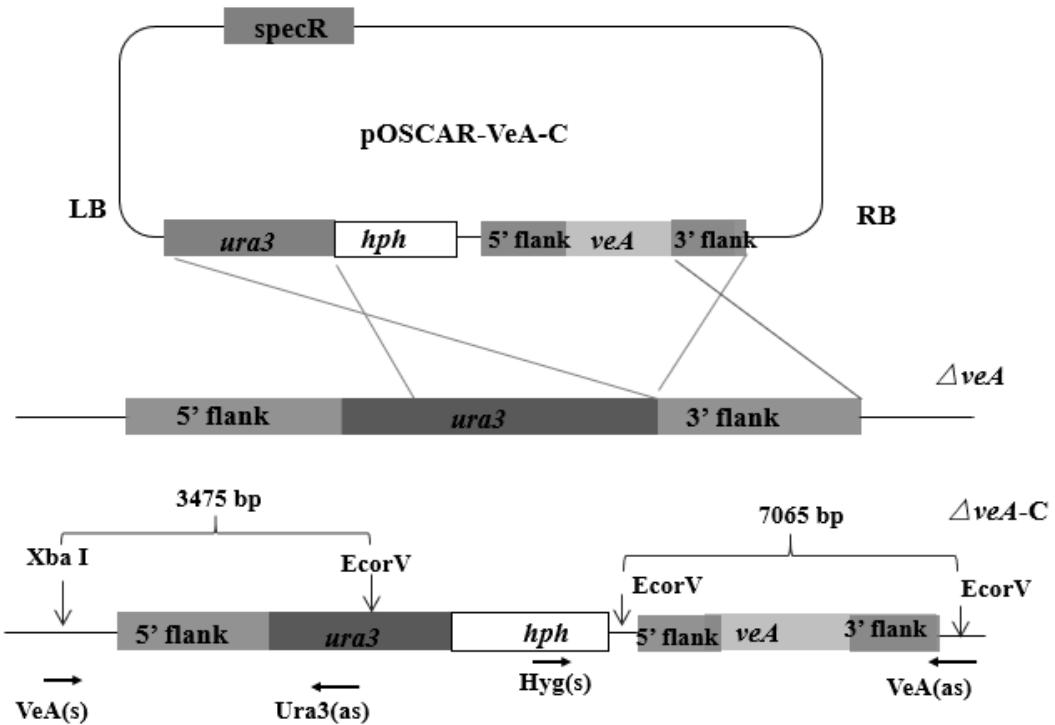


Figure S7. Schematic of the complement vector pOSCAR-VeA-C and construction of complemented strain ΔveA -C. The location of the recognition sites of XbaI and EcorV are indicated.

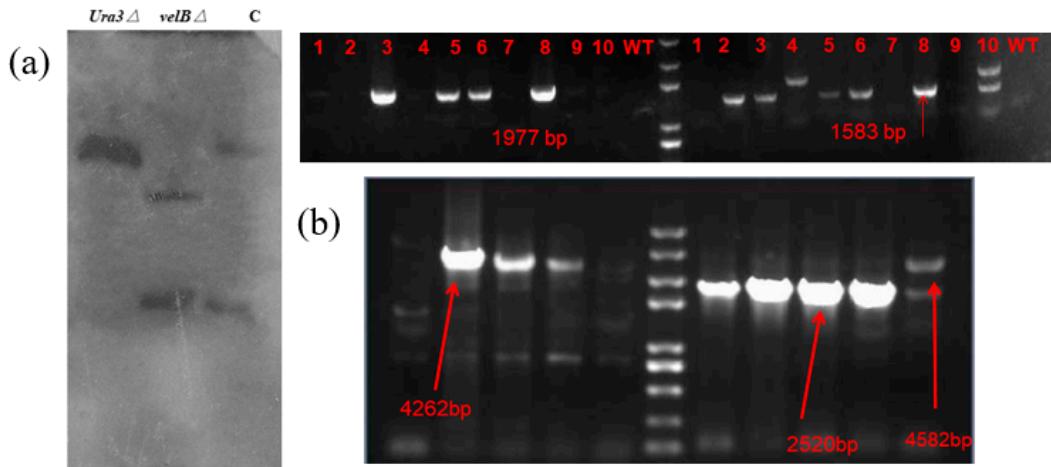


Figure S8. (a) Southern blot analysis of the $\Delta velB$ mutant. Genomic DNA from NK17- $\Delta ura3$, $\Delta velB$ or $\Delta velB-C$ was digested with Sac I probed with a 3.3-kb $velB$ fragment. Digestion of the NK17- $\Delta ura3$ genome yielded a 6.6 kb band, whereas the $\Delta velB$ had two 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 $\Delta laeA$.

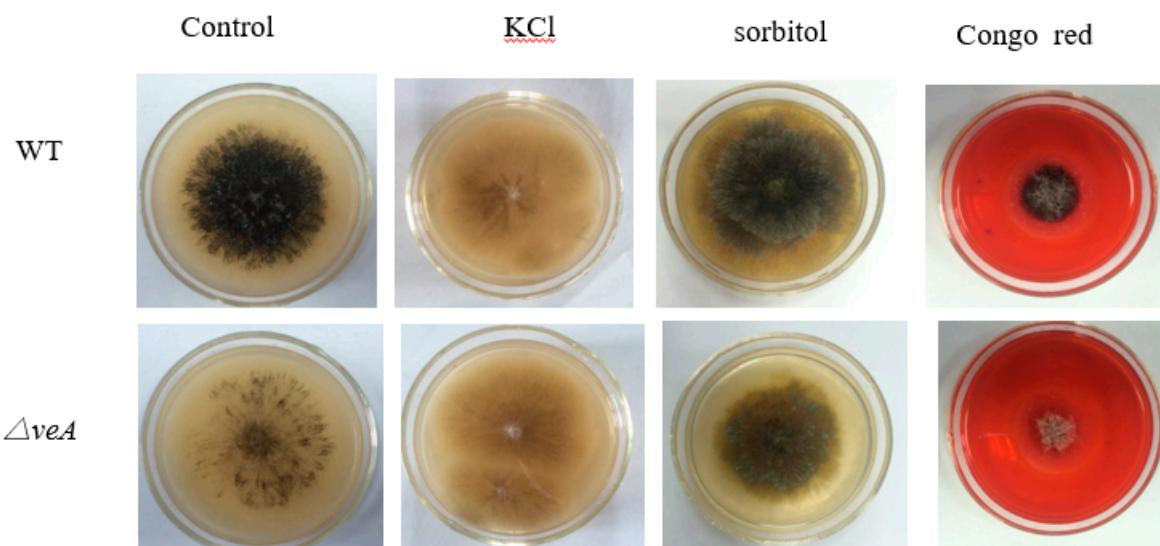


Figure S9. Sensitivity tests for NK17 and $\Delta velA$ strains. The strains incubated at 28 °C for five days on MM plates supplemented with 1M KCl, 2 M sorbitol, or 0.04% Congo red.