

**Table S1.**Strains used in this study.

Strain name	Brief description	Resistance	Reference
Ue_T14	Wild type strain of UeT14	/	Zhang,Yafen[24]
Ue_T55	Wild type strain of UeT55	/	Zhang,Yafen
Ue_MT46	Wild type strain of UeMT46	/	Zhang,Yafen
Ue_MT10	Wild type strain of UeMT10	/	Zhang,Yafen
Ue_T14 $\Delta$ <i>Ueg943</i>	<i>g943</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg943</i>	<i>g943</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg4344</i>	<i>g4344</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg4344</i>	<i>g4344</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg1072</i>	<i>g1072</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg1072</i>	<i>g1072</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg4195</i>	<i>g4195</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg4195</i>	<i>g4195</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg4740</i>	<i>g4740</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg4740</i>	<i>g4740</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg5676</i>	<i>g5676</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg5676</i>	<i>g5676</i> deletion in UeT55	Hygromycin B	This study
Ue_T14 $\Delta$ <i>Ueg6161</i>	<i>g6161</i> deletion in UeT14	Hygromycin B	This study
Ue_T55 $\Delta$ <i>Ueg6161</i>	<i>g6161</i> deletion in UeT55	Hygromycin B	This study
WT	UeT14 and UeT55 cross	/	Zhang,Yafen
$\Delta$ <i>g943</i>	UeT14 $\Delta$ <i>g943</i> and UeT55 $\Delta$ <i>g943</i> cross	Hygromycin B	This study
$\Delta$ <i>g4344</i>	UeT14 $\Delta$ <i>g4344</i> and UeT55 $\Delta$ <i>g4344</i> cross	Hygromycin B	This study
$\Delta$ <i>g1072</i>	UeT14 $\Delta$ <i>g1072</i> and UeT55 $\Delta$ <i>g1072</i> cross	Hygromycin B	This study
$\Delta$ <i>g4195</i>	UeT14 $\Delta$ <i>g4195</i> and UeT55 $\Delta$ <i>g4195</i> cross	Hygromycin B	This study
$\Delta$ <i>g4740</i>	UeT14 $\Delta$ <i>g4740</i> and UeT55 $\Delta$ <i>g4740</i> cross	Hygromycin B	This study
$\Delta$ <i>g5676</i>	UeT14 $\Delta$ <i>g5676</i> and UeT55 $\Delta$ <i>g5676</i> cross	Hygromycin B	This study
$\Delta$ <i>g6161</i>	UeT14 $\Delta$ <i>g6161</i> and UeT55 $\Delta$ <i>g6161</i> cross	Hygromycin B	This study

**Table S2.** The quality evaluation for transcriptome sequencing data.

Sample name	Raw reads	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
T_0h_1	63028620	61828626	9.27G	0.03	97.41	93.29	57.73
T_0h_2	58465256	56911444	8.54G	0.02	98.02	94.83	56.9
T_0h_3	61717374	60387654	9.06G	0.02	98.11	94.98	57.71
T_24h_1	51982916	50884824	7.63G	0.02	98.06	94.79	57.47
T_24h_2	63126784	62101672	9.32G	0.02	97.97	94.61	57.45
T_24h_3	58069690	56615754	8.49G	0.02	98.02	94.79	57.59
T_36h_1	65575728	64566864	9.69G	0.03	97.88	94.39	57.38
T_36h_2	58135734	57011646	8.55G	0.03	97.78	94.24	57.48
T_36h_3	57233694	56133656	8.42G	0.02	98.03	94.79	57.45
T_48h_1	57646070	56654842	8.5G	0.02	98.04	94.79	57.51
T_48h_2	63453004	62290970	9.34G	0.02	98.05	94.81	57.41
T_48h_3	59929234	58029586	8.7G	0.02	98.11	95	57.5
T_60h_1	57738162	56761712	8.51G	0.02	98.11	94.96	57.43
T_60h_2	58035490	56884260	8.53G	0.03	97.32	92.92	57.31
T_60h_3	49590524	48484326	7.27G	0.02	97.96	94.67	57.37
MT_0h_1	72564574	70807538	10.62G	0.02	97.98	94.67	57.63
MT_0h_2	60399364	59153946	8.87G	0.02	98.04	94.79	57.62
MT_0h_3	66734618	65241168	9.79G	0.02	98.19	95.13	57.71
MT_24h_1	59926520	58762080	8.81G	0.02	98.03	94.78	57.55
MT_24h_2	67568086	66342040	9.95G	0.02	97.96	94.61	57.51
MT_24h_3	66903844	65777874	9.87G	0.02	97.94	94.54	57.43
MT_36h_1	52764300	51781094	7.77G	0.02	98.27	95.36	57.45
MT_36h_2	59412234	58027264	8.7G	0.02	98.03	94.79	57.48
MT_36h_3	47897528	46808134	7.02G	0.02	98.15	95.08	57.45
MT_48h_1	67878802	66064674	9.91G	0.02	98.05	94.87	57.31
MT_48h_2	70880600	69455894	10.42G	0.03	97.78	94.18	57.33
MT_48h_3	55946556	54882000	8.23G	0.03	97.83	94.33	57.55
MT_60h_1	52010644	50872250	7.63G	0.02	98.12	95.01	57.36
MT_60h_2	62363934	60532096	9.08G	0.02	98.08	94.94	57.18
MT_60h_3	66081768	64332542	9.65G	0.02	97.93	94.53	57.51

**Table S3.**Primers used in this study.

Primer	Sequence (5'→ 3')	Purpose
g943-cF	GGCATCCTCCTTGGGGCAATGG	Clone
g943-cR	ATGAAGTTCGCCTTCGGTACCCTTGTCTG	
g4344-cF	ATGAAGATCCAGGCCTCTTTCGTGAC	
g4344-cR	GTAGGACACGCCCCCGCCGGAAGTCTC	
g1072-cF	ATGCAGAATTTCTCGTTCTCCTCCC	
g1072-cR	GGAGGTCAAAGGCTGG	
g4195-cF	ATGGTCAAGCTTCAGCAGTG	
g4195-cR	GTTCTGGACGGCGTCTTTCTTGTCG	
g4740-cF	ATGGCTTCGAAATCAGACCGAAGAGG	
g4740-cR	GAACTGGGCCGAGAGGAAAATTGG	
g5676-cF	ATGACCATCAAAGTCAGCCCTATTGCC	
g5676-cR	ATCGTGGTAGTGCTTCTCAGGGTCCTTGG	
g6161-cF	ATGGTCGGCGCTAAGCTGG	
g6161-cR	TTAGCGACGACGGCGAGAG	
g943-UF1	ACTTTACGGGAGCGGGGTACCCACTACTACGATCATTGCTTCAAGC	Delection mutant construction and Verifcation
g943-UR1	TCTAGAGGATCCCCGGGTACCCCGTCCCGTAAAGTCACAA	
g943-DF1	ACCTGCAGGCATGCAAGCTTCTTTCGGCGTTTTGGGACA	
g943-DR1	AGGGTGGAAGGGATTGAAGCTTGGCGTAATCATGGTCATA	
g4344-UF1	GAGAGCACACGCATCGGTACCTAGCTTCAGCGTTGAGCTCGA	
g4344-UR1	TCTAGAGGATCCCCGGGTACCGATGCGTGTGCTCTCTTTTCCG	
g4344-DF1	GACCTGCAGGCATGCAAGCTTGCAAGTCAAAGGTCACGTATTCTACA	
g4344-DR1	TGACCTTTGACTTGCAAGCTTTTACGGTTTCTCACAGCATCAAGT	
g1072-UF1	AGTGAATTCGAGCTCGGTACCGGGTGATGTTGGTATCTTGGAATT	
g1072-UR1	TCTAGAGGATCCCCGGGTACCCTGGACGGTGTGCTGGTTACG	
g1072-DF1	GACCTGCAGGCATGCAAGCTTCCTGTCCATCTTCCGCCC	

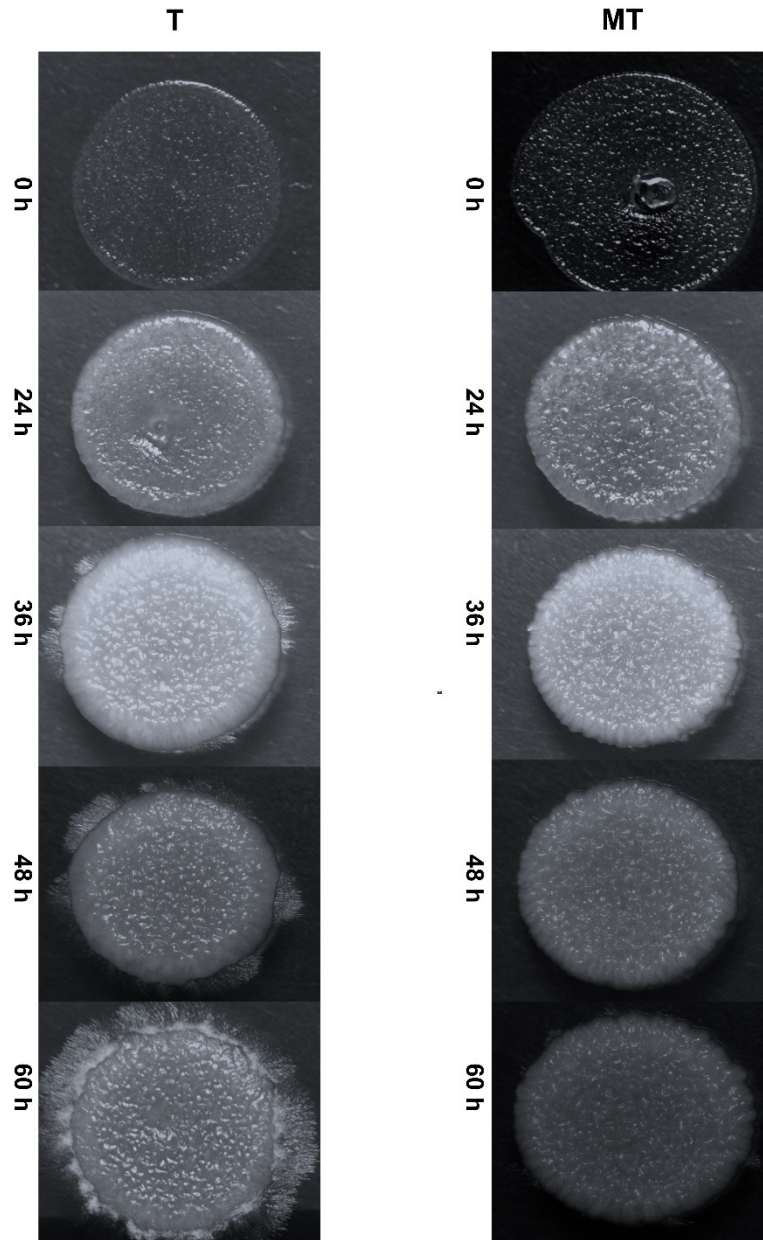
g1072-DR1	GACCATGATTACGCCAAGCTTCCGCAGGCTTTGCCCCAG
g4195-UF1	AGTGAATTCGAGCTCGGTACCGCACGTCCCCAACCACACA
g4195-UR1	TCTAGAGGATCCCCGGGTACCTGAAAGCCCTACCTTATCCACC
g4195-DF1	GACCTGCAGGCATGCAAGCTTCGAAGCGAGGTGAGGAGGG
g4195-DR1	GACCATGATTACGCCAAGCTTTCCACCAAGACATGTGCTTGC
g4740-UF1	AGTGAATTCGAGCTCGGTACCGCACGTCCCCAACCACACA
g4740-UR1	TCTAGAGGATCCCCGGGTACCTGAAAGCCCTACCTTATCCACC
g4740-DF1	GACCTGCAGGCATGCAAGCTTCGAAGCGAGGTGAGGAGGG
g4740-DR1	GACCATGATTACGCCAAGCTTTCCACCAAGACATGTGCTTGC
g5676-UF1	AGTGAATTCGAGCTCGGTACCCCTCGCCCCCTCGCTCCA
g5676-UR1	TCTAGAGGATCCCCGGGTACCGCTGAAGTCCGGGTGGTCA
g5676-DF1	GACCTGCAGGCATGCAAGCTTTATAATTAATTTCTATTAATTTTCAAGTCTTCTG
g5676-DR1	GACCATGATTACGCCAAGCTTTGTGATGAAGTAATTTGCATAGGCA
g6161-UF1	TTCGAGCTCGGTACCTTCAGAATCGGCTCTGGCTC
g6161-UR1	GAGGATCCCCGGGTACCGTACTCCCTCCCTAAACCAT
g6161-DF1	TCGACCTGCAGGCATGCAAGCTTTGGGCAGAGAGAAAAGGGGA
g6161-DR1	ATGACCATGATTACGCCAAGCTTACATATCAGCTCCCGCTCGA

g943-QF	TGCAAGTGGAGGAGCTACAAC
g943-QR	GCTTGGACCCAGTAGCTGTCGTGCTCATC
g4344-QF	CGCTCAAACCAACTCCGATG
g4344-QR	AGCCGTCGTCACTGTTCTGC
g1072-QF	CAGAATTTCTCTCGTTCTCCTCCCTCTTG
g1072-QR	TGAACCTCGCCGTCTTCCAGTCG
g4195-QF	ATGATGGTACTGACTCCGGTCGTGGCGACTCC
g4195-QR	AGTCTTCAGAGCAGAAGCCGGTGGTTCG
g4740-QF	ACGCCATGGTCATCATGGTCTCG
g4740-QR	GGTCAGGCAGTTGAGGAGCATCAGCATCATC
g5676-QF	CACGCACTTCGGATTTGAGTGTAGCATGG
g5676-QR	CCGCCTTCCCTGAACGAGAAGTTCTTCC

q-PCR

g6161-QF	CAATGGTTCGGGAATGTGC
g6161-QR	GGGATACTTGAGCGTGAGGA

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**Figure S1.** Mating and filamentous growth of the T- and MT-type *U. esculenta*. T-type mating strain was hybridized by the compatible T14 strain and T55 strain, and MT type mating strain was hybridized by the compatible MT10 strain and MT46 strain. They were grown on YEPS medium. Take photos at 0 h, 24 h, 36 h, 48 h and 60 h under stereo microscope.

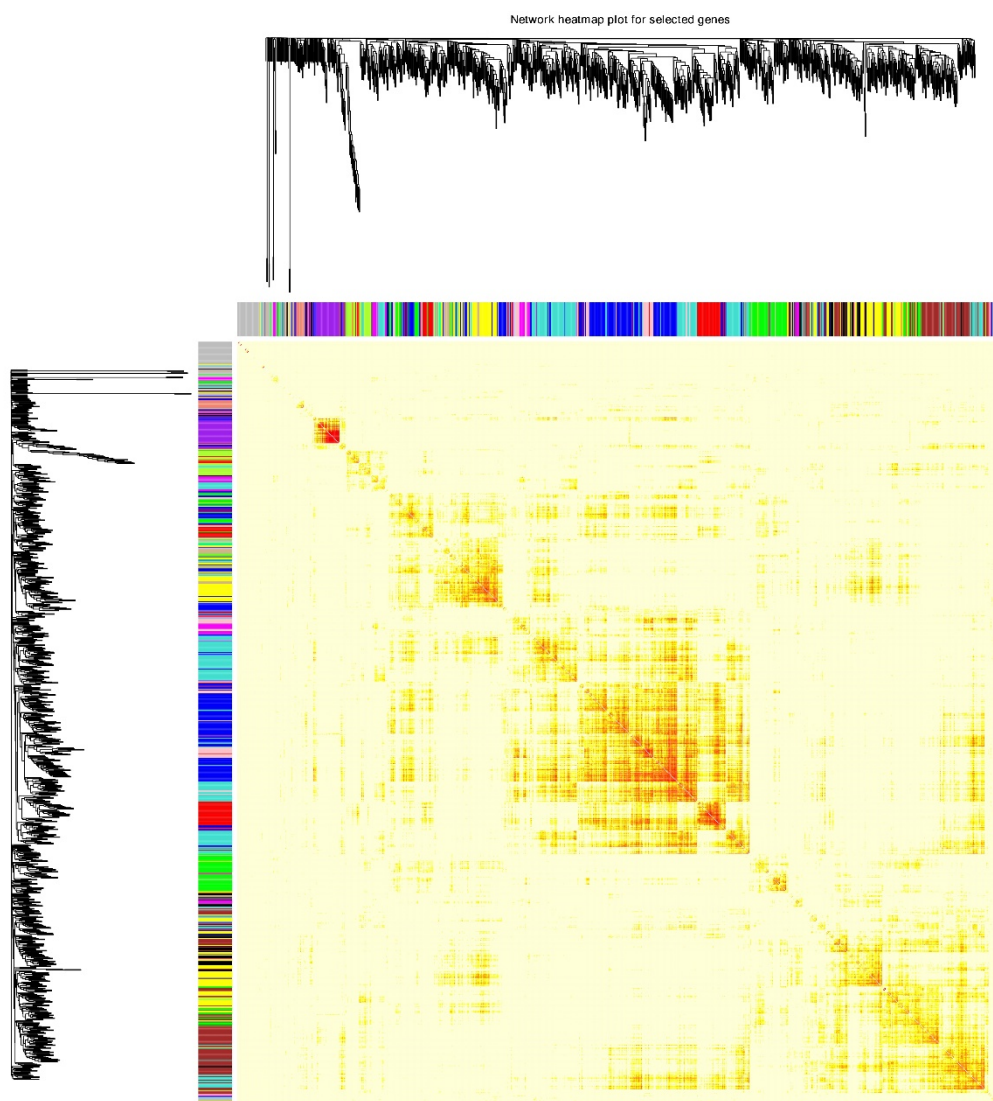
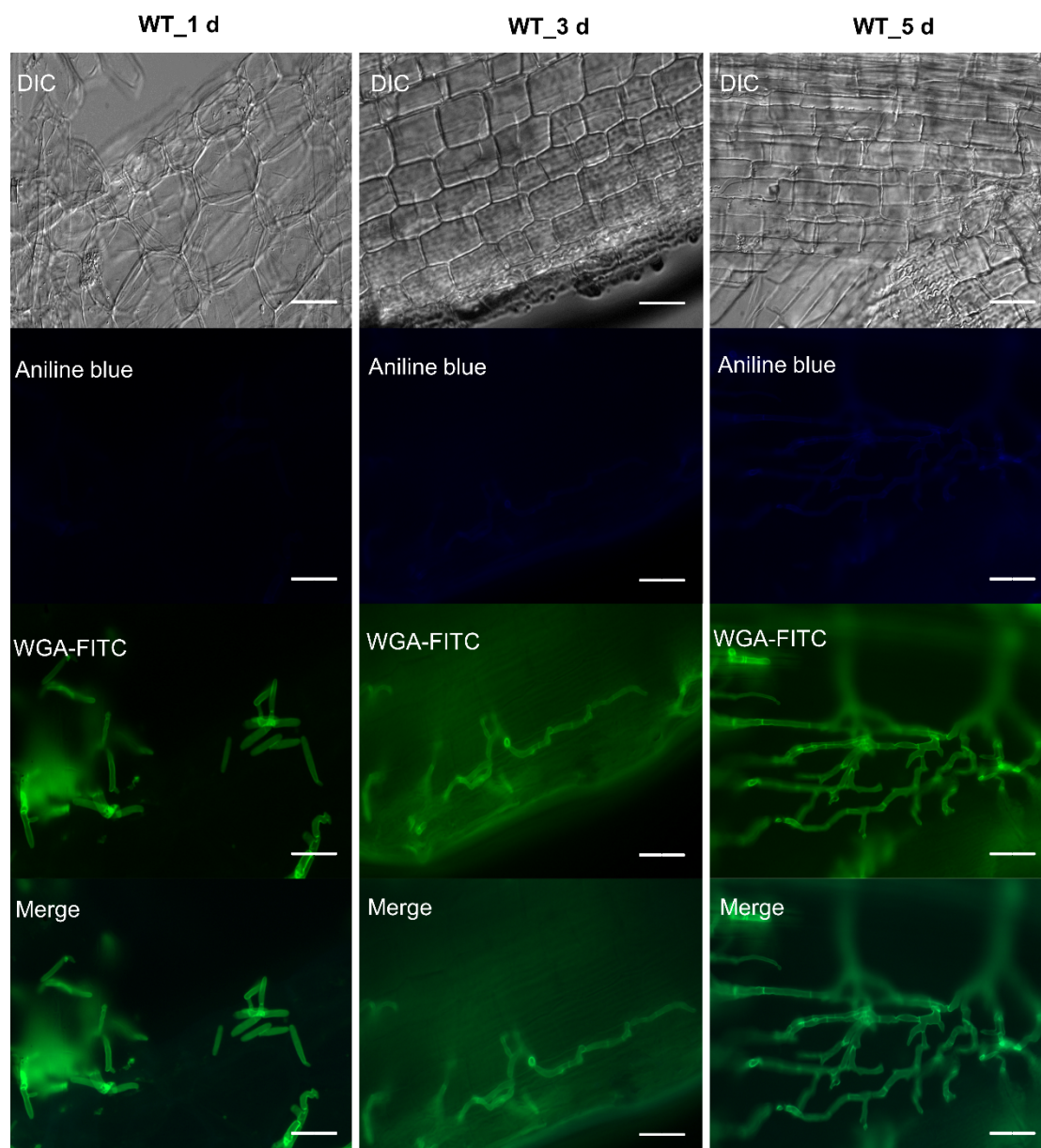
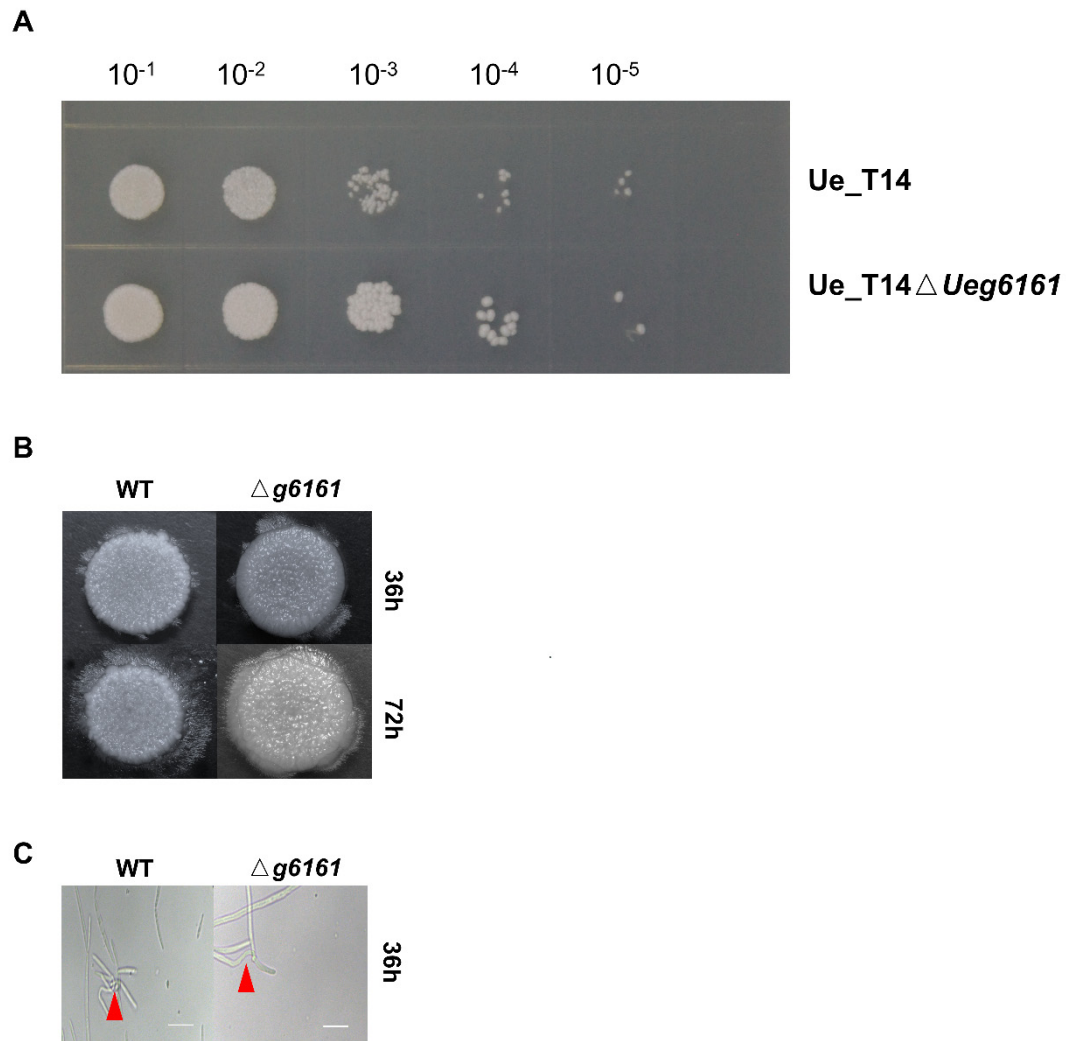


Figure S2: The overall relevance of different modules.

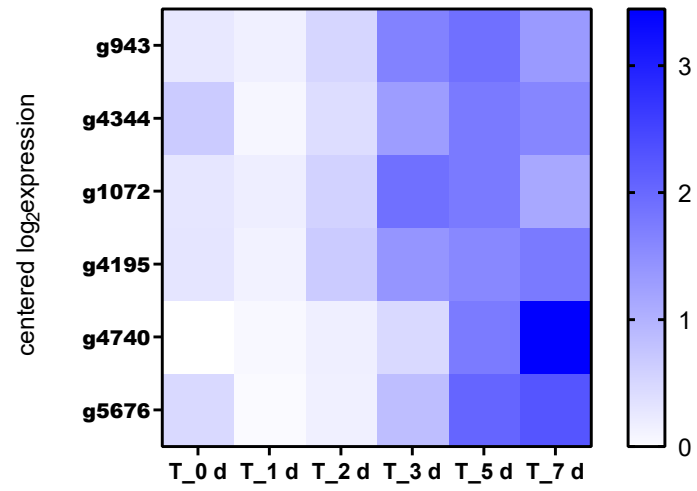


**Figure S3.** The infection of T-type *U. esculenta* did not induce callose deposition. Photomicrographs were taken 1, 3, and 5 dpi post infection (dpi). The WT strain does not induce callose deposition. The callose was stained by Aniline blue. It is excited at 405 nm, and the fluorescence was detected at 440 to 460 nm. The mycelium of *U. esculenta* is stained by WGA-FITC. It is excited at 488 nm, and the fluorescence was detected at 495 to 530 nm. Plant cell structure is detected by DIC. Merge image shows the superimposition of mycelium display image and aniline blue deposition image. The scale bar represents 62.5  $\mu$ m.

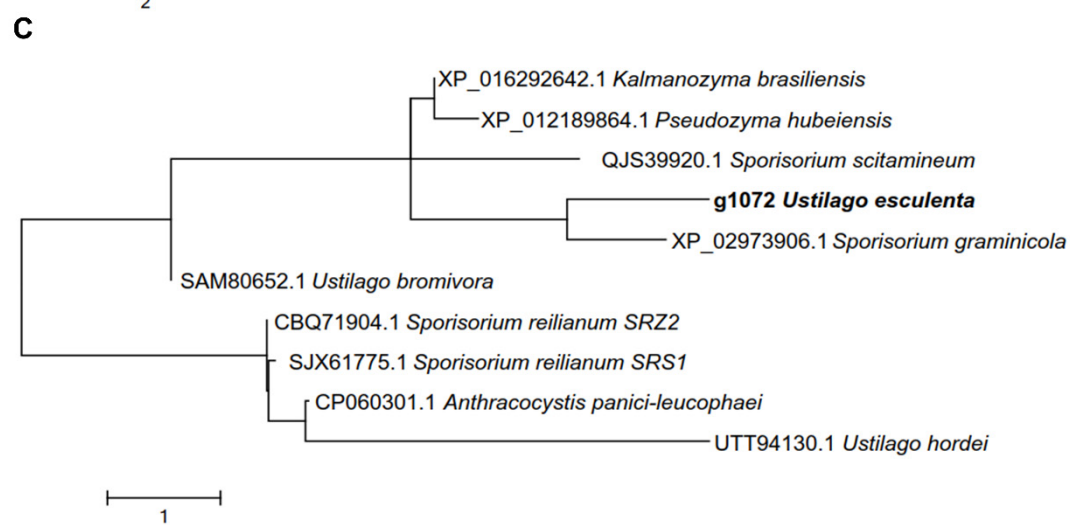
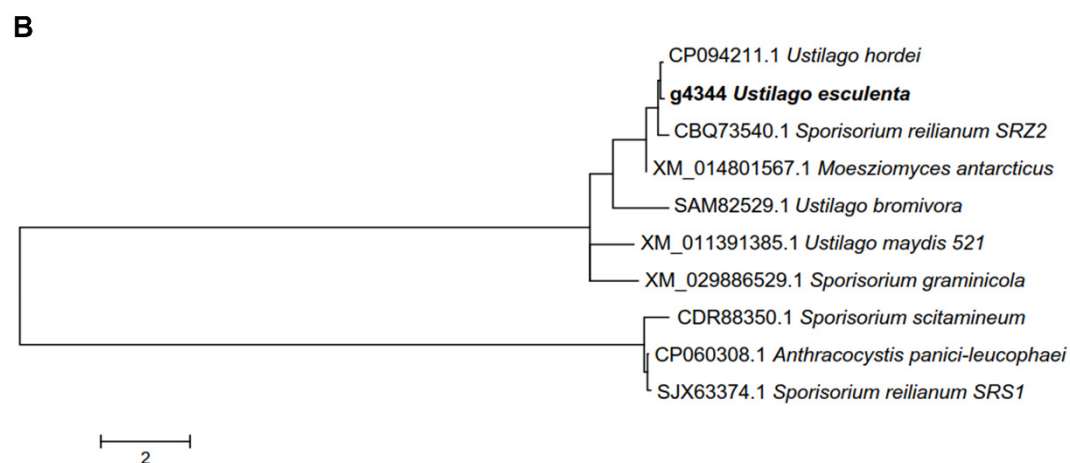
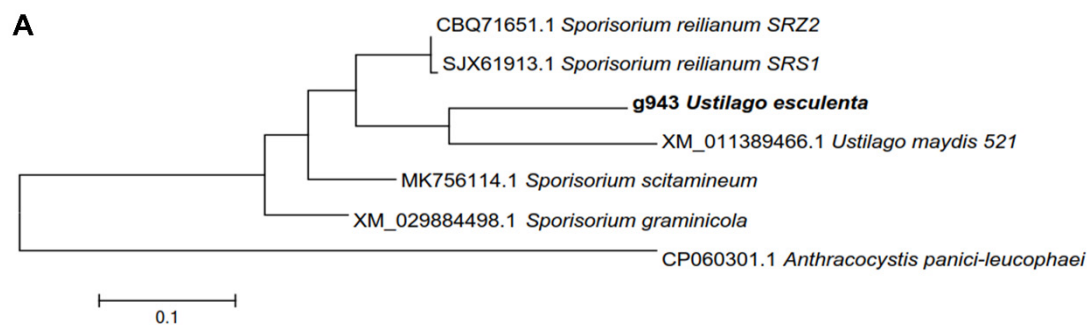


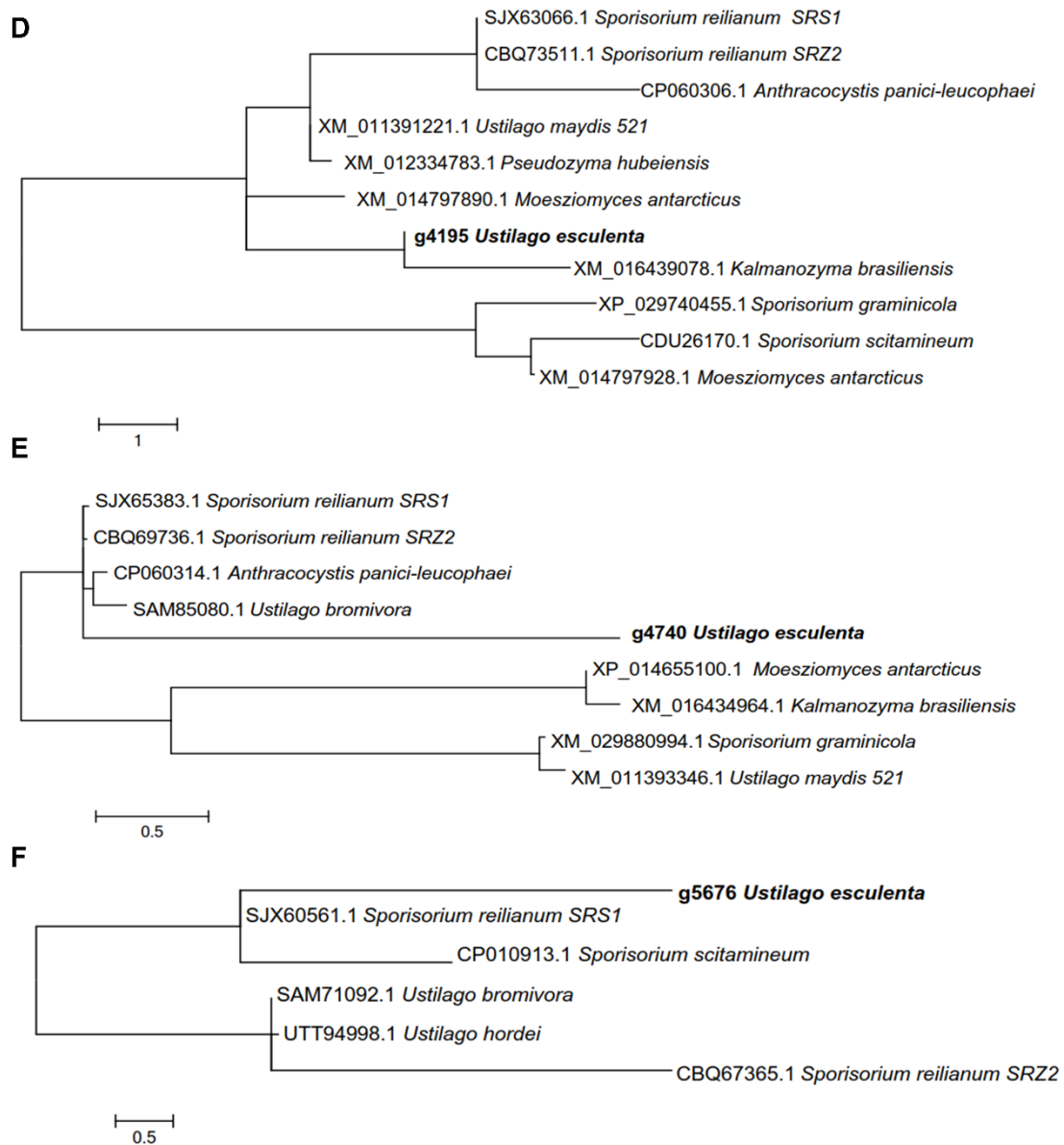


**Figure S4.** Effects of *g6161* deletion on haploid growth and mating. They were grown on YEPS medium. Photographs were taken at 72 h under at 36 h under a stereo microscope. UeT14 and UeT55 cross. UeT14Δ*g6161* and UeT55Δ*g6161*cross. (A) Deletion of *g6161* didn't impair haploid growth. Photograph the 72 h haploid growth state with camera. (B) Compared with WT, mating and filamentous growth of the gene deletion of *g6161*. Deletion of *g6161* didn't impair hypha mating. (C) Compared with the WT type, Forming state of the conjugation tube of the gene deletions of *g6161* at 36 h. Deletion of *g6161* didn't impair forming of the conjugation tube. (forming of conjugation tube pointed by red arrow). The scale bar represents 62.5  $\mu$ m in 36 h.

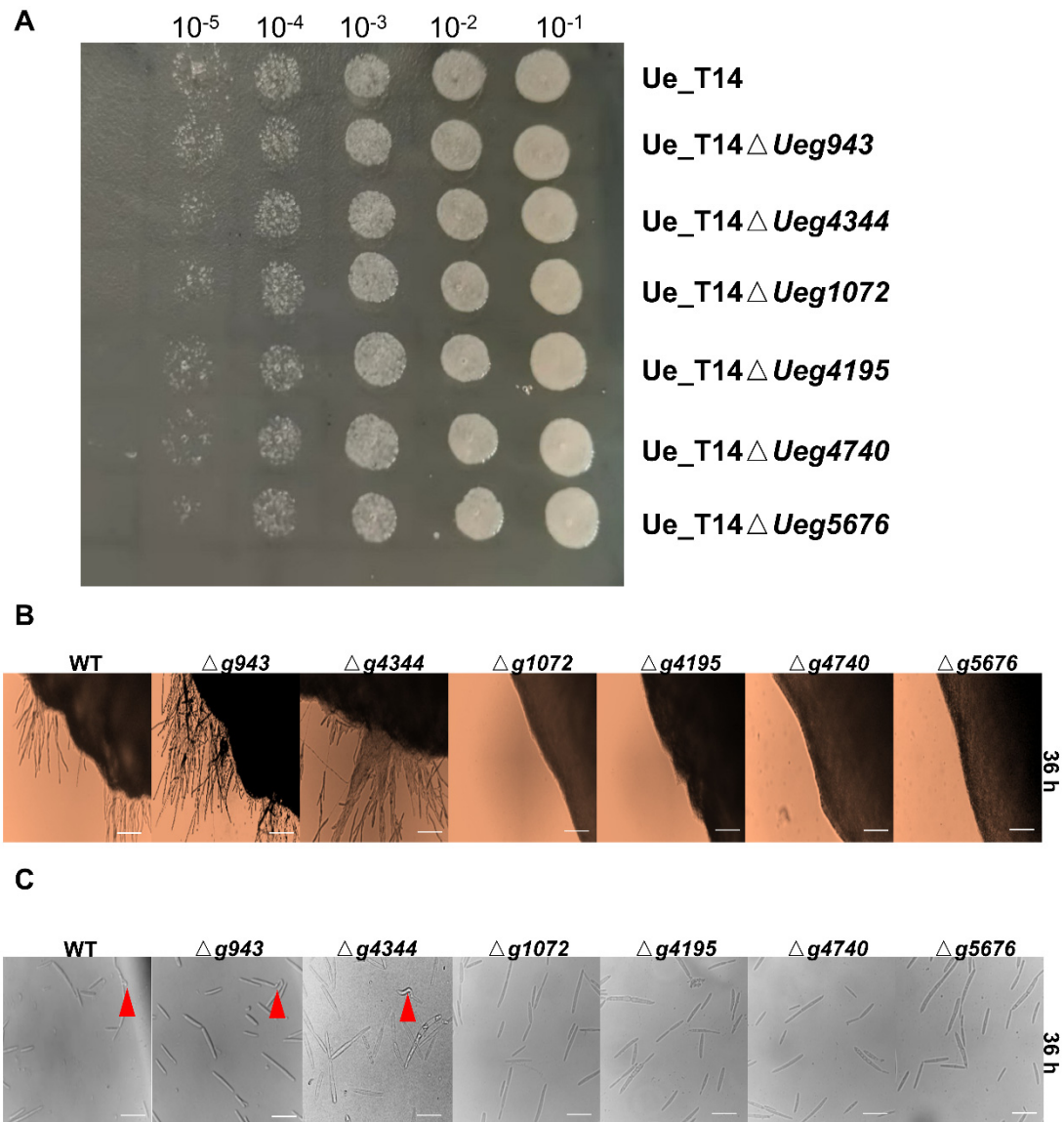


**Figure S5.** Gene expression pattern during the infection. The heat map shows the expression profiles of the expression of genes. Log<sub>2</sub> expression levels are visualized relative to the mean expression across 0 d, 1 d, 2 d, 3 d, 5 d, 7 d stages of T-type *U. esculenta*.



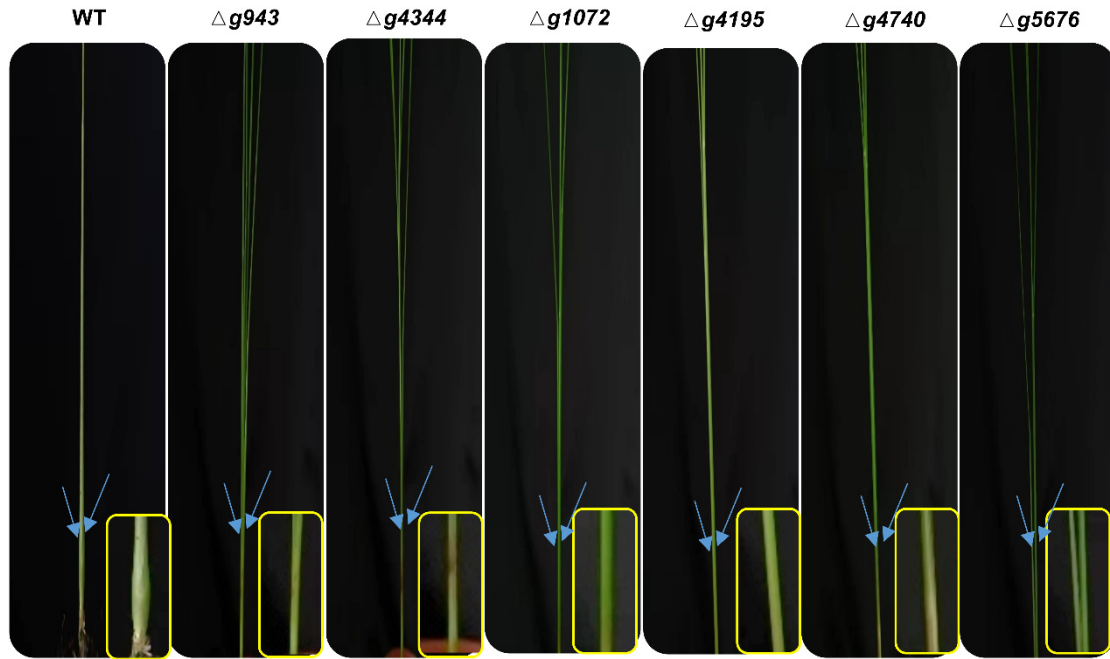


**Figure S6.** Phylogenetic analysis of putative secretory proteins. Homologs of secreted proteins were identified by searching against the NR database (NCBI). The phylogenetic trees were constructed in MEGA 7.0 by using the maximum-likelihood, in which bootstrap replications was 1000 times, and the model used was Jones-Taylor-Thornton (JTT) model.

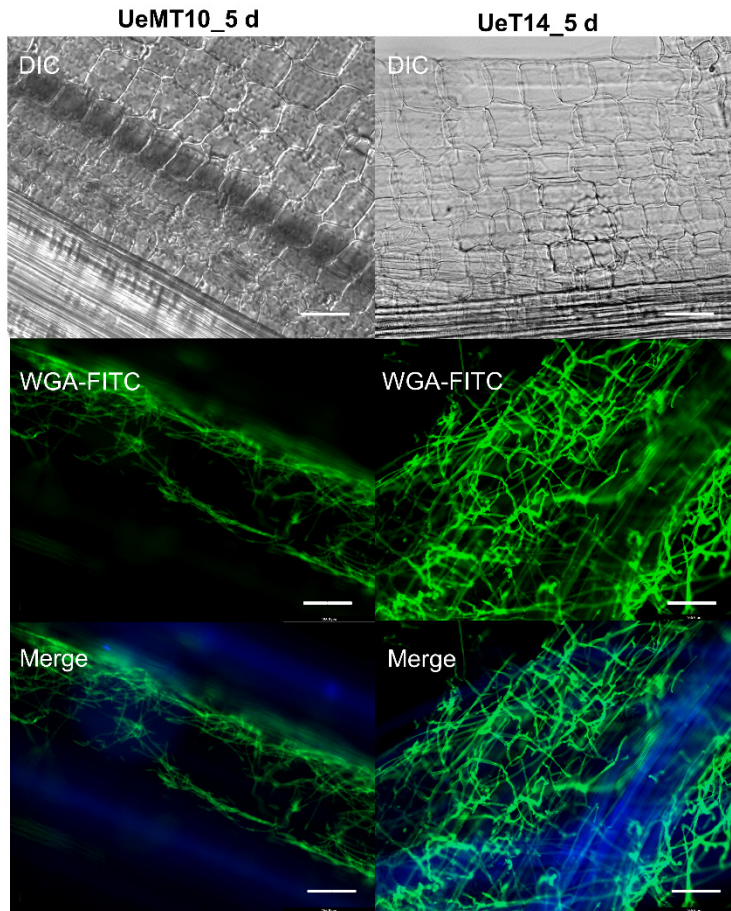


**Figure S7.** Effects of *g943*, *g4344*, *g1072*, *g4195*, *g4740*, *g5676* deletion on haploid growth, mating and filamentous growth. They were spotted onto YEPS medium. UeT14Δ*g943* and UeT55Δ*g943* cross, UeT14Δ*g4344* and UeT55Δ*g4344* cross, UeT14Δ*g1072* and UeT55Δ*g1072* cross, UeT14Δ*g4195* and UeT55Δ*g4195* cross, UeT14Δ*g4740* and UeT55Δ*g4740* cross, UeT14Δ*g5676* and UeT55Δ*g5676* cross (A) Deletion of *g943*, *g4344*, *g1072*, *g4195*, *g4740* and *g5676* didn't impair haploid growth. Photograph the 72 h haploid growth state with camera (B) Compared with WT, mating and filamentous growth of the gene deletion of *g943*, *g4344*, *g1072*, *g4195*, *g4740*, *g5676*. Deletion of *g943* and *g4344* didn't impair mating and filamentous growth. Deletion of *g1072*, *g4195*, *g4740* and *g5676* impair mating and filamentous growth. Photograph the 36 h filamentous growth state with light microscope. The scale bar represents 100 μm in 36 h. (C) Compared with the WT type, forming state of the conjugation tube of the gene deletions of *g943*, *g4344*, *g1072*, *g4195*, *g4740*, and *g5676* at 36 h. Deletion of *g943* and *g4344* didn't impair forming of the conjugation tube. Deletion of *g1072*, *g4195*, *g4740* and *g5676* impair forming of the conjugation tube. (forming of conjugation tube pointed by red arrow). Photograph the 36 h conjugation tube state with light microscope. The scale bar represents 62.5 μm

m in 36 h.



**Figure S8.** Phenotypes of the swollen stems. Samples infected with the wild-type strains UeT14 × UeT55 (left) and the corresponding  $\Delta g943$  (UeT14 $\Delta g943$  × UeT55 $\Delta g943$ ),  $\Delta g4344$  (UeT14 $\Delta g4344$  × UeT55 $\Delta g4344$ ),  $\Delta g1072$  (UeT14 $\Delta g1072$  × UeT55 $\Delta g1072$ ),  $g4195$  (UeT14 $\Delta g4195$  × UeT55 $\Delta g4195$ ),  $\Delta g4740$  (UeT14 $\Delta g4740$  × UeT55 $\Delta g4740$ ),  $\Delta g5675$  (UeT14 $\Delta g5676$  × UeT55 $\Delta g5676$ ) mating strains (right) were collected at 90 dpi. The yellow box at the lower right corner magnifies the stem swelling phenotype.



**Figure S9.** The phenotypes of haploids on plant surface. Photomicrographs were taken 5 dpi post infection (dpi). The UeT14 strain and UeMT10 strain do not induce callose deposition. The callose was stained by Aniline blue. It is excited at 405 nm, and the fluorescence was detected at 440 to 460 nm. The mycelium of *U. esculenta* is stained by WGA-FITC. It is excited at 488 nm, and the fluorescence was detected at 495 to 530 nm. Plant cell structure is detected by DIC. Merge images show the superimposition of mycelium display image and aniline blue deposition image. Scale bar represents 62.5  $\mu\text{m}$ .