

Supplementary

Strain name	Genotype	Reference
RIB40	Wild-type	Machida et al., 2005
NSRku70-1-1	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB</i>	Escaño et al., 2009
NSRku70-1-1A	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB adeA</i>	Escaño et al., 2009
PA8GA _{Atg8}	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg8}::adeA PA_{oatg8}-egfp-A_{oatg8}::niaD</i>	Tadokoro et al., 2015
NSRku70-1-1A AnH2B-EGFP	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB adeA Ph2b-h2b-egfp::niaD</i>	This study
ΔA _{oatg1}	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg1}::adeA</i>	Yanagisawa et al., 2013
ΔA1EA8	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg1}::adeA PA_{oatg8}-egfp-A_{oatg8}::niaD</i>	Yanagisawa et al., 2013
DA _{oatg1} AnH2B	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg1}::adeA Ph2b-h2b-egfp::niaD</i>	This study
ΔA _{oatg8} -1-1	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg8}::adeA</i>	Kikuma et al., 2006
DA _{oatg8} AnH2B	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg8}::adeA Ph2b-h2b-egfp::niaD</i>	This study
ΔA _{oatg15}	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg15}::adeA</i>	Kikuma et al., 2011
DA _{oatg15} AoAtg8	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg15}::adeA PA_{oatg8}-egfp-A_{oatg8}::niaD</i>	This study
DA _{oatg15} AnH2B	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oatg15}::adeA Ph2b-h2b-egfp::niaD</i>	This study
DA _{oypt7}	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oypt7}::adeA</i>	This study
DA _{oypt7} AoAtg8	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oypt7}::adeA PA_{oatg8}-egfp-A_{oatg8}::niaD</i>	This study
DA _{oypt7} AnH2B	<i>niaD⁻ sC⁻ adeA⁻ ΔargB Δku70::argB ΔA_{oypt7}::adeA Ph2b-h2b-egfp::niaD</i>	This study

Table S1 Strain list

Primer name	Sequence
pUC19_Aoypt7_up_Fw	CTCGGTACCCGGGGATCGCTGCGGCGTGAGTCCTGTGA
pUC19_Aoypt7_up_Rv	GTCTAGCACCCATGCGGCCGGCTGTGGCTATGTAAAGA
pUC19_Aoypt7_down_Fw	AGCTCGGTACCCGGGGATCGCTAGCTACCCTAGTGATGGACATG
pUC19_Aoypt7_down_Rv	AGGTCGACTCTAGAGGATCATCGTCTGGGACGTAGGTC
pUC19_adeA_up	GCTCGGTACCCGGGGATCGCGGCCGCATGGGTGCTAGACTCACAT
pUC19_adeA_down	CCATCACTAGGGTAGCTAGCTAGACCGCAGGAACCTTA
Aoypt7 check 500-F	TCCTCTGTCCTCTCCTGAGA
Aoypt7 check 500-R	TACGGTCGTGTATTGCAGGC

Table S2 Primer list

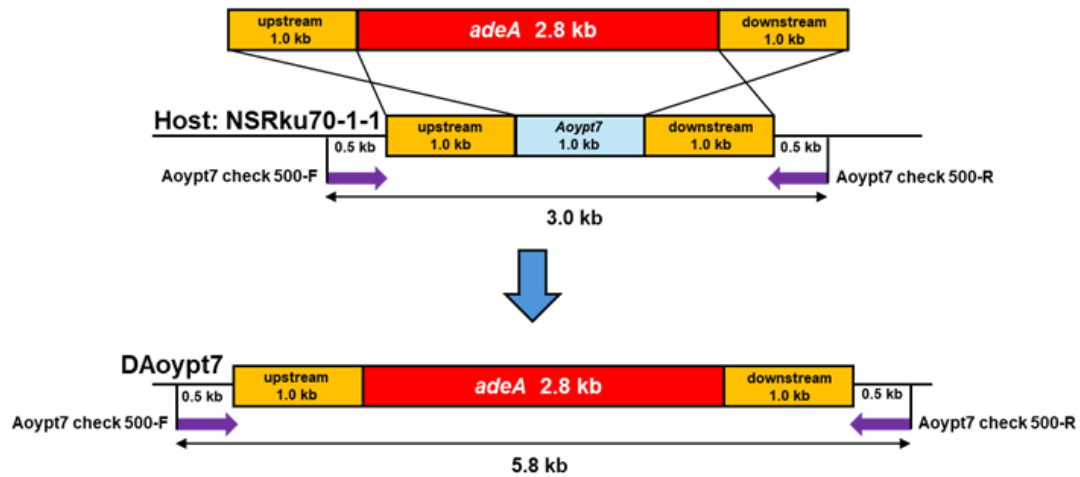
Score	Expect	Method	Identities	Positives	Gaps
293 bits(750)	8e-107	Compositional matrix adjust.	141/208(68%)	167/208(80%)	3/208(1%)
Ypt7	1	MSSRKKNILKVIILGDSGVGKTS_MHRYVNDKYSQQYKATIGADFLTKEVTVGDKVATM	60		
AoYpt7	1	MSSRKK +LKVIILGDSGVGKTS_M++YVN K+S YKATIGADFLTKEV VD D++ TM	59		
Ypt7	61	QVWDTAGQERFQSLGVAFYRGADCCVLVYDVTNASSFENIKSWRDEFLVHANVNSPETFP	120		
AoYpt7	60	QIWDTAGQERFQSLGVAFYRGADCCVLVYDVNNSKSFEALDSWRDEFLIQASPRDPENFP	119		
Ypt7	121	FVILGNKIDAEESKKIVSEKSAQELAKSLGDIPLFLTSAKNAINVDTAFEIARSALQQN	180		
AoYpt7	120	FV++GNKID EESK+++S K A +S G+IP F TSAK A+NV+ AFE IARSAL Q	179		
Ypt7	181	QADTEAFEDDYNDAINIRLDGENNSQSC	208		
AoYpt7	180	EA--EEFSGEFSDPINIHLDSERDGOAC	205		

Fig. S1 Amino acid sequence alignment of Ypt7 and AoYpt7

Amino acid sequence alignment of Ypt7 (P32939) from *S. cerevisiae* and AoYpt7

(XP_001824054) from *A. oryzae* showing 68% identity. Red, blue, and green boxes indicate the binding region to the HOPS complex, the GTP binding regions, and the cysteine residues to be geranylgeranylated, respectively.

(A)



(B)

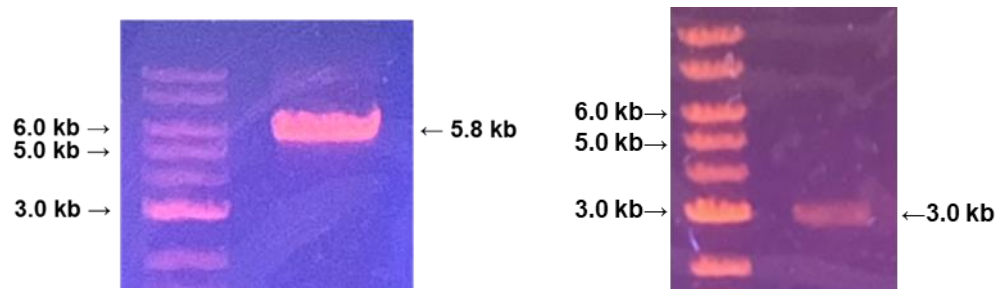


Fig. S2 Construction of *Aoypt7* disruptant

(A) *Aoypt7* gene of the host strain NSRku70-1-1 was disrupted by homologous recombination using the *adeA* selection marker. DNA fragment amplified with pUC19_ *Aoypt7*_up_Fw and pUC19_ *Aoypt7*_down_Rv primers using the plasmid pUC19_ *Aoypt7*_deletion as a template was used for transformation.

(B) PCR amplification was performed using Aoypt7 check 500-F and Aoypt7 check 500-R as primers and the **genomes recovered from the transformant (left) and NSRku70-1-1 (right), respectively, as templates**. 5.8 kb band was correctly obtained in the gene disruptant.

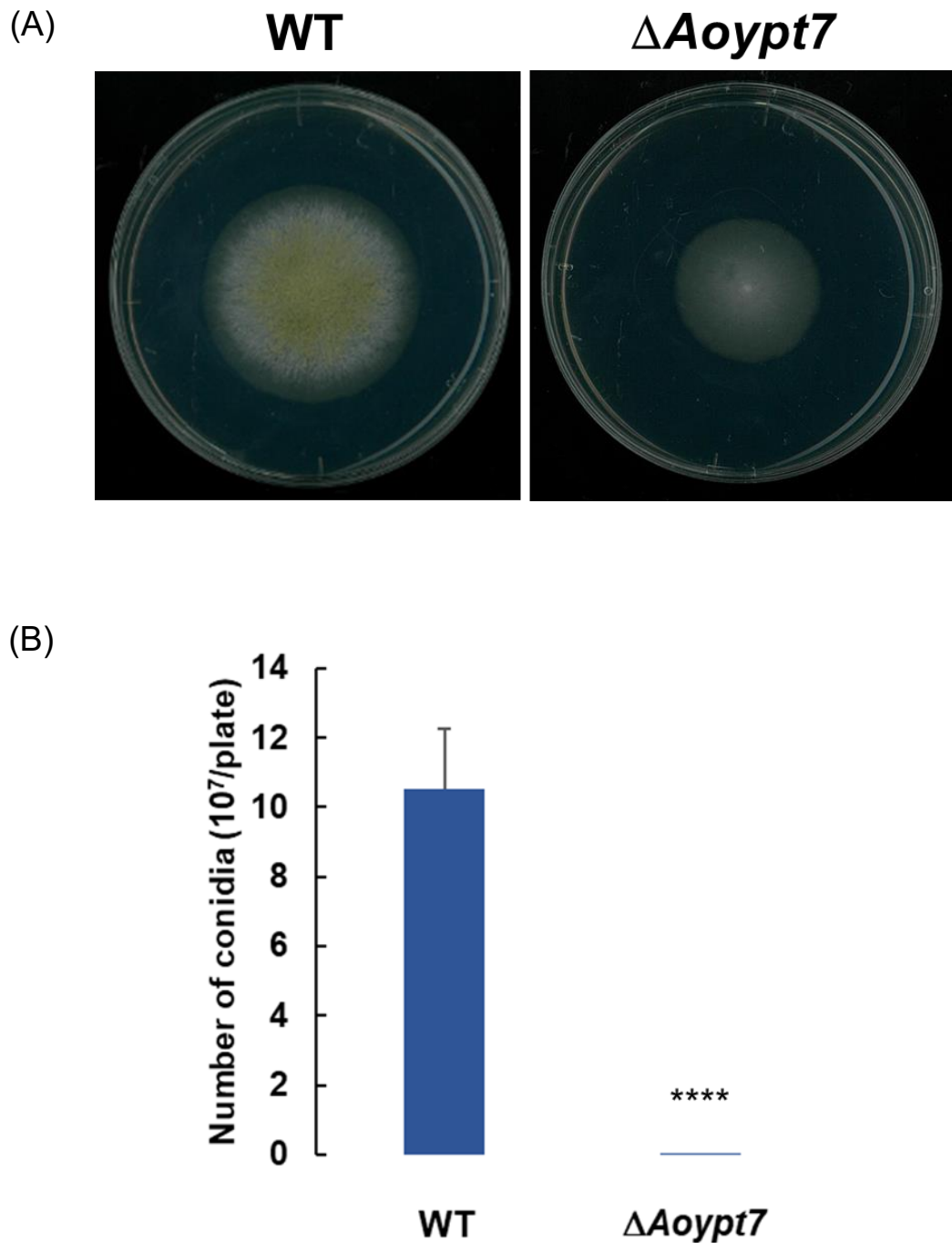


Fig. S3 Growth phenotypes of $\Delta Aoypt7$ strain

(A) Wild-type (NSRku70-1-1A) and $\Delta Aoypt7$ (DAoypt7) strains were inoculated onto PD plates and incubated for 4 d at 30°C. (B) Conidia were collected from the plates and the numbers were counted using a hemocytometer. Error bars, standard deviation (n=3). ****, $p < 0.0001$ by t -test.