

GENETICS

Supporting Information

<http://www.genetics.org/cgi/content/full/genetics.110.117184/DC1>

**Interplay Between *NDT80* Homologs and the Protein Kinase IME-2
Regulates Sexual Development, but Not Meiosis,
in *Neurospora crassa***

Elizabeth A. Hutchison and N. Louise Glass

Copyright © 2010 by the Genetics Society of America
DOI: 10.1534/genetics.110.117184

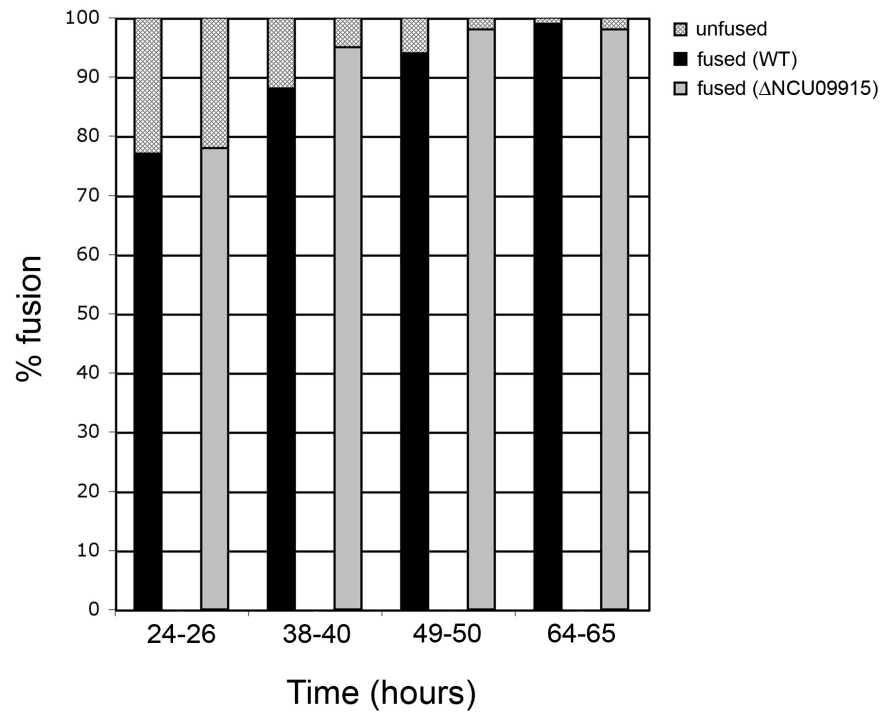


FIGURE S1.—Trichogyne assay for wild-type and $\Delta fcd-1$ crosses. Trichogyne assays over a time-course of 24-65 hours revealed that the $\Delta fcd-1$ deletion strain is not defective for trichogyne-microconidium fusion, as fusion levels for the mutant are not significantly different from wild-type throughout the time-course.

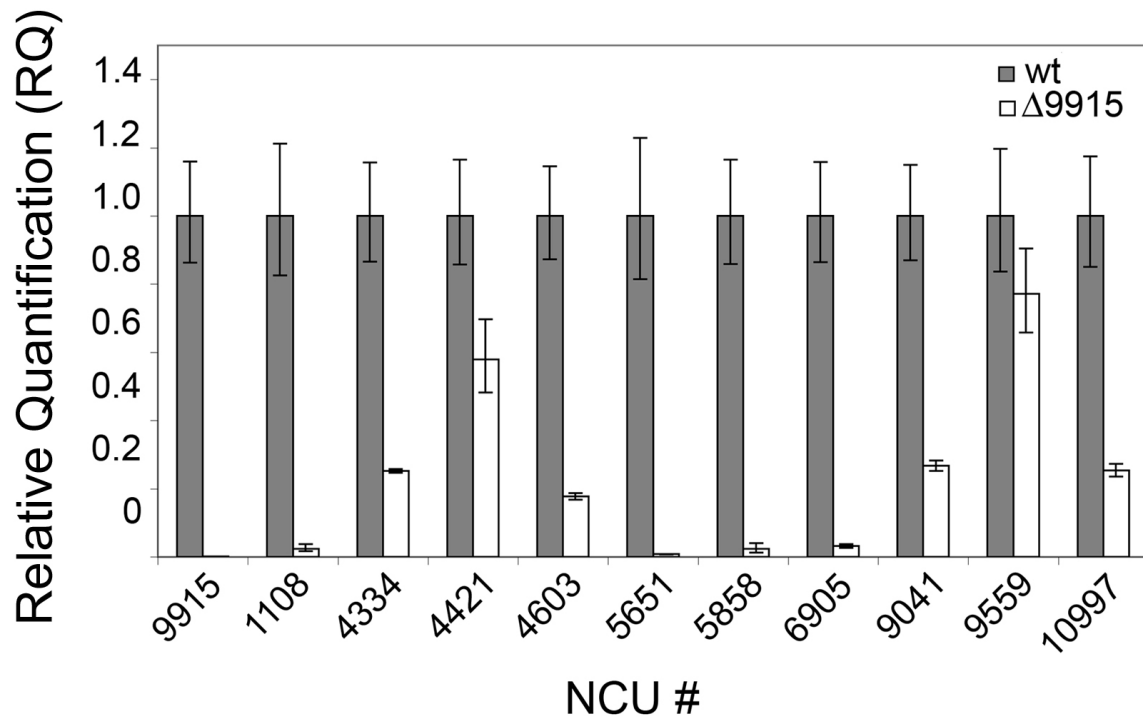


FIGURE S2.—Q-RT-PCR confirmation of microarray data. Ten genes were selected from the microarray dataset and confirmed independently via Q-RT-PCR; all ten of these genes were significantly up-regulated in a wild-type cross compared to a cross homozygous for an NCU09915 deletion, and the Q-RT-PCR data confirms this result. In addition, the Q-RT-PCR data confirms that although the female of the homozygous deletion cross was present as a heterokaryon with the helper strain, no NCU09915 (*fsd-1*) RNA is present in the perithecial tissue of this cross.

TABLE S1**List of fungal *NDT80* homologs**

Species	Number of <i>NDT80</i> homologs	Gene ID	Source for sequences used in FIGURE 2
<i>Neurospora crassa</i>	3	NCU03725, NCU04729, NCU09915	Broad Institute ^a
<i>Podospora anserina</i>	3	Pa_2_9470, Pa_4_8710, Pa_1_22920	http://podospora.igmors.u-psud.fr/
<i>Chaetomium globosum</i>	2	CHGG_02523, CHGG_03914	Broad Institute ^a
<i>Magnaporthe grisea</i>	3	MGG_00729, MGG_00622, MGG_01475	Broad Institute ^a
<i>Fusarium graminearum</i>	3	FGSC_7157, FGSC_8397, FGSG_09709	
<i>Nectria haematococca</i>	3	NHAE_EEU44303, NHAE_EEU46886, NHAE_EEU40284	
<i>Botryotinia fuckeliana</i>	3	BC1G_00547, BC1G_00333, BC1G_11604	
<i>Aspergillus oryzae</i>	2	AO090103000018, AO090011000646	
<i>Aspergillus clavatus</i>	2	ACLA_057380, ACLA_068960	
<i>Neosartorya fischeri</i>	2	NFIA_096760, NFIA_085330	
<i>Aspergillus flavus</i>	1	AFLA_012100	
<i>Aspergillus fumigatus</i>	2	AFUA_8G04050, AFUA_1G00580	
<i>Aspergillus nidulans</i>	2	ANID_01414, ANID_6015	Broad Institute ^a
<i>Aspergillus niger</i>	3	An16g09130, An16g05190, An12g01840	Accession Numbers: XM_001398173, XM_001397790, XM_001395233
<i>Aspergillus terreus</i>	2	ATEG_00017, ATEG_04426	
<i>Penicillium chrysogenum</i>	3	Pchr 8303965, Pchr 8307369, Pchr 8315995	
<i>Talaromyces stipitatus</i>	4	TSTA 108960, TSTA 122060, TSTA 053280, TSTA 122410	
<i>Microsporium canis</i>	2	EEQ31782, EEQ31742	
<i>Coccidioides posadasii</i>	2	EER29657, EER25737	
<i>Unicinocarpus reesii</i>	1	UREG 02151	
<i>Sclerotinium sclerotiorum</i>	3	SSIG_00692, SSIG_04059, SSIG_14485	
<i>Saccharomyces cerevisiae</i>	1	NDT80	SGD ^b
<i>Candida albicans</i>	3	CaNDT801, CaNDT802, CaO19.7521	
<i>Candida lusitanae</i>	3	CLUG 04000, CLUG 00404, CLUG 05634	
<i>Candida glabrata</i>	1	CAG62312.1	
<i>Ashbya gossypii</i>	1	AGR347W	
<i>Kluyveromyces lactis</i>	1	KLLA0F24420p	
<i>Yarrowia lipolytica</i>	2	YlipYALI0D24860p, YlipYALI0B14773p	

<i>Debaryomyces hansenii</i>	2	DEHA2E18304p, DEHA2A07282p
<i>Pichia guilliermondii</i>	3	PGUG 00339, PGUG 01255, PGUG 02096
<i>Pichia pastoris</i>	1	PAS 0362
<i>Schizosaccharomyces pombe</i>	0	-
<i>Coprinus cinereus</i>	0	-
<i>Phanerochaete chrysosporium</i>	0	-
<i>Ustilago maydis</i>	1	UM02775

^aBroad Institute Fungal Genome Initiative (<http://www.broadinstitute.org/science/projects/fungal-genome-initiative/fungal-genome-initiative>)

^bSaccharomyces Genome Database (<http://www.yeastgenome.org/>)