

## Production of mutations in the white-spore strain

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# Production of mutations in the white-spore strain

## **Abstract**

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Previous studies of the white-spore mutant of *N. crassa* (Phillips and Srb 1967 *Can. J. Genet. Cytol.* 9:766) indicated that ascospores carrying the ws-1 marker germinate with a very low frequency.

Therefore, the introduction of additional genetic markers into the ws-1 strain is difficult but may be accomplished by isolating spores from the rare asci that contain more than four black spores. The exceptional black spores will be genotypically ws-1, barring mutation or gene conversion, and may carry the additional genetic markers. Another means of introducing new genetic markers into the ws-1 strain is through mutagenic treatment. The purpose of this investigation was to induce by UV-irradiation adenine and methionine mutations in the ws-1 strain. An auxotrophic ws-1 strain was needed for studies involving ws-1 in balanced heterocaryons.

The procedure was to subject approximately  $10^7$  conidia of the ws-1 strain (in 20 ml of minimal medium) to UV-irradiation for 90 seconds and then follow the filtration procedure of Woodward et al. (1954 *Proc. Natl. Acad. Sci. U.S.A.* 40:192). Aliquots (0.1 ml) of the filtered conidial suspension were spread over 20 plates each with 20 ml of solid minimal medium supplemented with adenine, methionine and sorbose. Approximately 500 slow-growing colonies were selected for further testing. From the 500 colonies, one albino, three adenine and 11 methionine mutants were obtained.

**Albino mutant:** The albino mutant (isol. #RP100) was found to be independent of T(I;II) 4637 al-1; T(IV;VI) 45502, pyr-3 (IVR); T(I;VII) 17084, thi-1; vel (IIIR); tryp-1 (IIIR); arg-1 (VIL). Linkage was detected in crosses with at (V cent), arg-4 (VR), arg-7 (VR), arg-8 (VR), T(V;VI) 46802 inos, and inos (VR). The recombination data indicate that the albino locus is in the right arm of LG V, less than one map unit from arg-8 and inos (Table 1). Complementation data from R. E. Subden (personal communication) also indicate that the new albino locus is discrete from al-1 and al-2; we are suggesting the designation al-3.

The al-3 mutant is an excellent visible marker; although obviously albino, it does have a very light pink color. The strain shows a high degree of crossability to all *Neurospora* strains tested, when used either as the protoperithecial or conidial parent. The al-3 ascospores germinate readily and grow well on minimal media.

**Adenine mutants.** The three adenine mutants (isol. #'s RPI01ad, RPI02 and RPI03) have been mapped and the linkage results are presented in Table 2. Linkage was not detected between RPI01ad (a purple adenine mutant) and fl (IIR) but was evident with m. f. (IL), ad-5 (IL) and ad-3B (IR). No recombinants were recovered from crosses of RPI01ad to ad-5 or ad-3B. Since RPI01ad complements with ad-5 but not ad-3B and is phenotypically similar to ad-3B, the adenine mutation in RPI01ad appears to be allelic to ad-3B. The lack of recombination between RPI01ad and ad-5 is probably the result of scoring an insufficient number of progeny.

The second adenine mutant (RPI02) showed independence with T(I;II) 4637 al-1; T(III;VI) 1, ylo-1; al-3 (RP101) (VR); and pl (VR). Linkage was observed in the crosses of RPI02 to pyr-1 (IVR); ad-6 (IVR); and T(IV;V) R2355 and cot-1 (IVR). No recombinants were recovered in the cross RPI02 x ad-6 nor was any complementation detected between these two mutants. RPI02 is presumably allelic to ad-6.

The third adenine mutant (RP103) is independent of T(I;II) 4637 al-1; T(IV;V) R2355; cot-1 (IVR) and ylo-1 (VII). Linkage was detected between RP103 and T(III;VI) 1, ylo-1; ad-2 (IIIR); tryp-1 (IIIR); and vel (IIIR). Crosses with ad-2 have not been successful. No complementation was observed, however, between ad-2 and RP103. ad-4 is also located on IIIR.

The above adenine mutants respond well to adenine. The fertility with other strains and spore germination rates also are quite satisfactory.

Table 1. Tests between al-3 (RP100) and linked genetic markers.

Tester strain	FGSC#	Linkage group(s)	Parental spores	Recombinant spores	% Germination	% Recombination
<u>at</u> (M111)	1884	V cent.	72	35	70	32.7
<u>arg-4</u> *		VR	110	7	71	4.3
<u>arg-7</u> **		VR	72	3	50	4.0
<u>arg-8</u> (44207)	1311	VR	137	1	81	0.7
T(V;VI) 46802 <u>inos</u>	1199	VR, VII	74	0	50	0
<u>inos</u> (37401)	406	VR	45	0	35	0

\* \* Strains kindly provided by Val Woodward

Table 2. Tests between the adenine mutants (RP101 ad, RP102 and RP103) and linked genetic markers.

Tester strain	FGSC#	Linkage group(s)	Parental spores	Recombinant spores	% Germ-ination	% Recombination
RP101ad						
<u>m. t.</u> (Em.)		IL	256	14	90	5.2
<u>ad-5</u> (Y175M253)	678	IL	69	0	23	0
<u>ad-3B</u> (35203)	360	IR	2236	0	75	0
RP102						
<u>pyr-1</u> (H263)	72	IVR	104	7	74	6.3
"alcoy" $\otimes$ •	998	IVR, VR	108	4	77	3.5
<u>ad-6</u> (Y175M221)	663	IVR	375	0	83	0
RP103						
"alcoy" A •	997	IIIR, VII	29	5	50	14.7**
<u>tryp-1</u> • $\otimes$		IIIR	143	15	53	9.5
<u>vel</u> ****		IIIR	145	13	53	8.2

• "alcoy" linkage tester = T(I;II)4637, al-1; T(IV;V)R2355, cot; T(III;VI)1, ylo-1.

\*\* Albino progeny were excluded from this calculation.

•• Strain was vel, tryp-1, ylo-1 synthesized by crossing vel, tryp-1 (B18, 10575) x tryp-1, ylo-1 (10575; Y30539) (FGSC#173 x FGSC#1207).

Table 3. Tests between os (RP101os) and linked genetic markers.

Tester strain	FGSC#	Linkage group(s)	Parental spores	Recombinant spores	% Germ-ination	% Recombination
<u>m. t.</u> (STA4)	262	IL	141	75	72	35.5
<u>m. t.</u> fl (P605)	297	IL	49	21	78	30.1
<u>ad</u> (RP101 ad)		IR	58	33	60	36.3
<u>al-2</u> (15300)	99	IR	83	11	63	11.7
<u>os-1</u> (8135)	951	IR	154	27	81	17.5

RP101 also carried a separate, visible marker morphologically similar to os-1 and unable to grow in complete medium supplemented with KCl (4%). Linkage and complementation tests indicate that RP101os is not allelic with or-1 (IR), although they are linked (Table 3). Linkage was also detected between RP101os and m. t. (IL), RP101ad (IR) and al-2 (IR). os-4 is also located in IL (Mays 1969 Genetics 63: 781). or-3 and os-5 are also in I but in the right arm.

Methionine mutants. None of the 11 methionine mutants have been mapped. Preliminary complementation tests revealed that eight of the mutants are in distinct complementation groups, while three overlap the others to varying extents.

In summary, the ws-1 mutant is now available with ad-38 (RP101 ad), ad-6 (RP102), ad (RP103), al-3 (RP100), the unidentified os (RP101 os), and the unidentified me mutants. These strains may be obtained from R.L. Phillips.

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