

Genetic mapping of the *N. crassa pho-5* gene

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We have recently cloned and disrupted (by RIP) the *N. crassa pho-5* gene which encodes a phosphate-repressible, high-affinity phosphate permease (Versaw 1995 Gene 153:135-139). RFLP analysis indicates that *pho-5* maps to Linkage group IV, near *pyr-1*. We wished to determine the map position of *pho-5* more accurately. *pho-5* null mutants have no obvious phenotype. Therefore, we constructed parental mapping strains which also contained a null allele of *pho-4*, a previously isolated high-affinity phosphate permease encoding gene (Mann et al. 1988 Mol. Cell. Biol. 8:1376-1379). *pho-5* mutants in a *pho-4* background are easily scored by their failure to grow on high pH, low phosphate medium like that used to score *nuc-1* and *nuc-2* mutants (Metzenberg and Chia 1979 Genetics 93:625-643). Results of the genetic mapping are shown in Table 1. The gene order on Linkage group IV is *pyr-1*, *pho-5*, *cot-1*.

Table 1. Genetic mapping of *pho-5*

	Genotype			No. of progeny
Parentals	<i>pyr-1</i>	+	<i>cot-1</i>	52
	+	<i>pho-5</i>	+	63
Region I crossovers	+	+	<i>cot-1</i>	5
	<i>pyr-1</i>	<i>pho-5</i>	+	2
Region II crossovers	+	<i>pho-5</i>	<i>cot-1</i>	11
	<i>pyr-1</i>	+	+	11
Double crossovers	+	+	+	0
	<i>pyr-1</i>	<i>pho-5</i>	<i>cot-1</i>	0

Region I map distance: 4.9 cM

Region II map distance: 15.3 cM