

## Some observations concerning *sp* and *ure-2* in *Neurospora*

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# Some observations concerning *sp* and *ure-2* in *Neurospora*

## **Abstract**

We are currently seeking *rec-2* which is proximal to *am* on linkage group V and are gleaning incidental information on genes in this region and elsewhere. So far, the following is apparent: *sp* is recessive: each of 15 heterokaryons forced between *his-3* K874; *sp* B132 and *am1* 32213 strains by growth on Vogel's + glycine medium had wild-type morphology.

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# Some observations concerning *sp* and *ure-2* in *Neurospora*

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We are currently seeking *rec-2* which is proximal to *am* on linkage group V and are gleaning incidental information on genes in this region and elsewhere. So far, the following is apparent:

*sp* is recessive: each of 15 heterokaryons forced between *his-3* K874; *sp* B132 and *am1* 32213 strains by growth on Vogel's + glycine medium had wild-type morphology.

The gene order *sp*, *ure-2*, *am* inferred from two point crosses is confirmed by three point data: FGSC 3809 (*a*; *ure-2* D74) was crossed to F11089 (*A*; *sp* B132, *am* B501). 320 random spores were isolated, 79% germinated.

Zygote genotype									
and									
recombination percent		Parental combinations			Singles Region I		Singles		
Region II									
<i>sp</i>	+	<i>am</i>	<i>sp</i> + <i>am</i>	+ <i>ure-2</i> +	<i>sp</i> <i>ure-2</i> +	+ + <i>am</i>	<i>sp</i> + +	+	
<i>ure-2</i>	<i>am</i>								
+	<i>ure-2</i>	+	135	92	9	11	5		
0									
	7.9	2.0							

A gene in FGSC 4299 interferes with Kolmark's urease test: While seeking to order *sp*, *ure-2* and *am*, we set up a cross between FGSC 4299 (*a*; *ure-2* 47, *am* 32213) and T9043 (*A*; *his-3* K874; *sp* B132). Of 320 random spores, 92% germinated and were scored for urease activity by dabbing conidia onto paper soaked in urea and a pH indicator to detect ammonia production (Kolmark 1969, Mutation Res. 8:51-63). By this test, T9043 was urease positive and FGSC 4299 urease negative. However, only 23% of the progeny were urease positive, suggesting the segregation of a second mutation unlinked to *ure-2*. There is preliminary evidence that this additional locus could be linked to *his-3*.