

**Sherald, A.F.\* and R.A. Voelker.†** \* - George Mason University, Fairfax, Virginia. † - NIEHS, Research Triangle Park, North Carolina USNA. Cytogenetics of suppressor of black.

Five recessive, suppressor of black alleles (*su(b)*) have been mapped to the distal tip of the X and, on the basis of non-suppression in *Df(1)260-1/su(b)* females, the suppressor locus was placed proximal to 1B4-6 (Sherald 1981). However, since this deficiency is male lethal (Lindsley & Grell 1968) and FM4 contains *su(b)*<sup>+</sup>, some ambiguity was indicated by the sporadic appearance of non-black males and Bar, yellow, black females from the cross; *Df(1)260-1/FM4; b x su(b)/Y; b*. The *Df(1)260-1/FM4* stock was analyzed, and the exceptional progeny were determined to result from nondisjunction caused by the presence of a Y chromosome in some of the females: Single pair matings of *Df(1)260-1/FM4 x Df(1)y<sup>RT10</sup>/y<sup>2sc</sup>Y* were used to generate *Df(1)260-1/y<sup>2sc</sup>Y* males which were crossed individually to *C(1)DX/y<sup>2sc</sup>Y* females. In four out of 12 crosses, some *y<sup>1</sup>* female progeny (*C(1)DX/Y*) were found, indicating an unmarked Y derived from the grandparental females. While this analysis was performed for the stock obtained from Bowling Green, other crosses with the same stock from the Pasadena collection have also produced similar results suggestive of a free Y. The crossing scheme above was also used to isolate three stocks in which *Df(1)260-1* was carried in males with only the *y<sup>2sc</sup>* marked Y, and each stock was used to construct *Df(1)260-1/su(b); +/b* females for the test cross (Table 1, top). No black males were found in the progeny of these crosses, and the recovery of black females again confirms that *Df(1)260-1* contains *su(b)*<sup>+</sup>.

Table 1. Non-black and black progeny from the cross: *Df/su(b); b/+ x su(b)/Y; b* for ten terminal X deficiencies.

Deficiency	Breakpoint*	Males		
		Non-black	Non-black	Black
<i>Df(1)260-1</i>	1B4-6			
stock a		203	430	145
stock b		198	337	127
stock c		133	277	75
-----				
<i>Df(1)y<sup>RT8</sup></i>	-**	379	565	0
<i>Df(1)y<sup>RT10</sup></i>	1B7-10	223	447	0
<i>Df(1)y<sup>RT12</sup></i>	1B7-9	87	151	0
<i>Df(1)y<sup>RT18</sup></i>	1B7-10	430	712	0
<i>Df(1)y<sup>RT19</sup></i>	1B7-10	410	844	0
<i>Df(1)y<sup>RT20</sup></i>	-**	321	497	0
<i>Df(1)y<sup>RT21</sup></i>	1B10-12	258	498	0
<i>Df(1)y<sup>RT30</sup></i>	1B3-8	586	832	0
<i>Df(1)svr</i>	1B10-13	414	752	0

\* Breakpoints for *Df(1)svr* and *Df(1)260-1* are from Lindsley & Grell (1968); other breakpoint determinations were by Drs. G. Lefevre, J. Lim, E. Strobel and/or H. Gyurkovics. For explanation of the three *Df(1)260-1* stocks, see text.

\*\*Breakpoints for these deficiencies have not been cytologically determined; genetically they are *y<sup>1</sup> sc<sup>-</sup> 1(1)EC<sup>+</sup> su(s)<sup>+</sup>*.

To determine the cytogenetic position of the suppressor locus more precisely, nine terminal, male lethal deficiencies were tested by crossing *Df/su(b); +/b* females to *su(b)/Y; b* males (Table 1, bottom). The same suppressor allele, *su(b)*<sup>31</sup>, was used for all tests and, except for *Df(1)y<sup>RT12</sup>*, the progeny were obtained from duplicate crosses. While black homozygotes should constitute approximately half the progeny, none of the males displayed a black phenotype because all viable male zygotes were hemizygous for *su(b)*. The absence of black female progeny indicated that all nine of the deficiencies uncovered the *su(b)* locus which must, therefore, lie at least distal to 1B8. Taken together with the data from *Df(1)260-1*, these data indicate that *su(b)* lies between 1B4-6 and 1B8. This provides cytological confirmation for the previously reported nonallelism between *su(b)* and suppressor of sable, since *su(s)* is proximal to 1B10-13 (Lindsley & Grell 1968). Assuming that the *su(b)* alleles represent reisolations of the lost *su(b)* mutation reported by Plough (1927), this finding is at variance with the arbitrary cytogenetic map in Lindsley & Grell (1968); the black suppressor locus should be distal to *su(s)*.

The locus for the silver mutation may also fall within this region, either in 1B7-8 or slightly to either side (Lefevre 1981). However, no evidence has been obtained for allelism between *svr* and *su(b)*. None of the *su(b)* alleles have a visible phenotype, and *svr/su(b)*<sup>31</sup> heterozygotes were found to be wild type, not silver. Nor was black suppression observed for *svr*, either as a hemizygote or in combination with *su(b)*<sup>31</sup>.

**References:** Lindsley, D.L. & E.H. Grell 1968, *Carn. Inst. Wash. Publ.*; Lefevre, G. 1981, *Genetics* 99: 461-480; Plough, H.H. 1927, *Proc. 5th Inter. Cong. Genet.* 2: 1193-1200; Sherald, A.F. 1981, *Mol. Gen. Genet.* 183: 102-106.