

A New Mutation on Chromosome 18 named Black and White (*baw*)

Linda L. Washburn, Patricia F. Ward-Bailey, Richard M. Samples, Leona H. Gagnon, Roderick T. Bronson, Eva M. Eicher and Muriel T. Davisson.

Source of Support: The research was supported by NIH/NCRR grant RR01183 to the Mouse Mutant Resources (M. T. Davisson PI) and Cancer Center Core Grant CA34196.

Mutation (allele) symbol: *baw*

Mutation (allele) name: black and white

Gene symbol: *baw*

Strain of origin: C57BL/10SnJ

Current strain name: C57BL/10SnJ-*baw*/GrsrJ

Stock #006157 (jaxmice.jax.org)

Phenotype categories: coat color

Origin and Description

This new spontaneous recessive mutation causes a light coat color on the ventrum of affected mice. The pattern is like that seen on the mutation named black and tan (a^t), but the hair is white on *baw* (see photos) rather than tan. In addition, the remaining coat is flecked with white hairs, particularly obvious as the mice age. It was expected that this phenotype would be the result of a remutation to a^{twp} on Chr 2, however the chromosomal location on Chr 18 for this new mutation ruled out allelism.





ventral coat of a *baw* homozygote

Genetic Analysis

Using The Mouse Mutant Resource standard mapping procedures, a female C57BL/10SnJ-*baw* was mated to a male AKR/J. A female F1 from this cross was backcrossed to a male C57BL/10SnJ-*baw*. Forty-eight progeny from the backcross were used to map this mutation. A genome wide scan was started with markers on Chr 2 near nonagouti (*a*) because the phenotype was similar to black and tan (*a^t*); however *baw* did not map to that location. Linkage was first detected with *D18Mit122* at 31 cM. The recombination estimates with the standard errors and the best gene order are centromere - *D18Mit19* -10.00 +/- 6.71-*D18Mit20* -15 +/- 7.98 - *D18Mit111* - 5.0 +/- 4.87 - [*D18Mit17*, *baw*] - 8.33 +/- 3.99 - *D18Mit178* - 5.0 +/- 4.87 - *D18Mit24* - 5.0 +/- 4.87 - *D18Mit122*. We detect no recombination between *baw* and *D18Mit17* at the 20 cM position in 48 animals tested. Based on the Ensembl assembly NCBI 32 for Chr 18 our non-recombinant marker (*D18Mit17*) places the chromosomal position for *baw* around 39.7 Mb.

Pathology

Our standard pathological screen of a female homozygote and a heterozygote at 8 weeks of age showed no lesions.

Hearing assessed by ABR testing on 2 homozygous and two heterozygous mice at 4 weeks of age was normal.

Acknowledgements

The authors wish to thank Dan Foss for discovery of the mutant and Heping Yu for excellent technical skill.

References

Manley KF (1993) A MacIntosh program for storage and analysis of experimental mapping data. *Mamm Genome* 4, 303-313.

Mouse Genome Database (MGD) Mouse Genome Informatics Project, The Jackson Laboratory, Bar Harbor, Maine. World Wide Web (www.informatics.jax.org)