Short term perm (*stpm*): a new recessive curly coat mutation

Richard M. Samples, Patricia F. Ward-Bailey, Leah Rae Donahue, Roderick T. Bronson, and Muriel T. Davisson

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Mutation (allele) symbol: *stpm*

Mutation (allele) name: short term perm

Strain of origin: RHJ/LeJ/J

Current strain name: RHJ/LeJ-*stpm*/GrsrJ

Stock #005416 (jaxmice.jax.org)

Phenotype categories: Hair

Abstract
We have identified a new recessive mutation that causes a curly coat and have named it short term perm (*stpm*). Mutant mice can be identified at 8 days of age, with the first coat of fur. The mutation was mapped using an intercross to CAST/Ei and was found to be on Chromosome 11 near a previously described dominant curly coat mutation named Rex (*Re*) (MGD 2005). A direct test for allelism between mice carrying the *Rex* mutation and mice carrying this new mutation was negative. Another mutation causing an eye phenotype has been identified in this strain and will be described in a future publication.

Figure 1: A litter showing 4 homozygous stpm mutants (3 on the left and 1 on the lower right) and 1 control littermate on upper right. All at 16 days of age.

Origin and Description

This new recessive mutation arose spontaneously in a breeding colony of RHJ/LeJ mice at The Jackson Laboratory and was discovered by Suzanne Sullivan. The phenotype of this mutation can be identified by a curly coat, which is different from the smooth coat of control littermates. At 3 weeks of age, mice homozygous for this new mutation have very curly coats and slightly curved vibrissae. In several weeks time the curly coat disappears but the hair retains a rough texture, and the vibrissae then appear normal. Heterozygous mice have normal smooth coats and straight whiskers. The RHJ/LeJ strain carries *Rhino* (Hr^{rh}), an allele of the hairless mutation. This mutation has been bred out of the RHJ/LeJ-*stpm*/J strain. Both male and female mutant mice breed and live a normal lifespan.

Figure 2: An adult RHJ/LeJ-*stmp*/J homozygous mutant who has outgrown his curly coat on the right and a heterozygote control on the left. Both at 3 months of age.

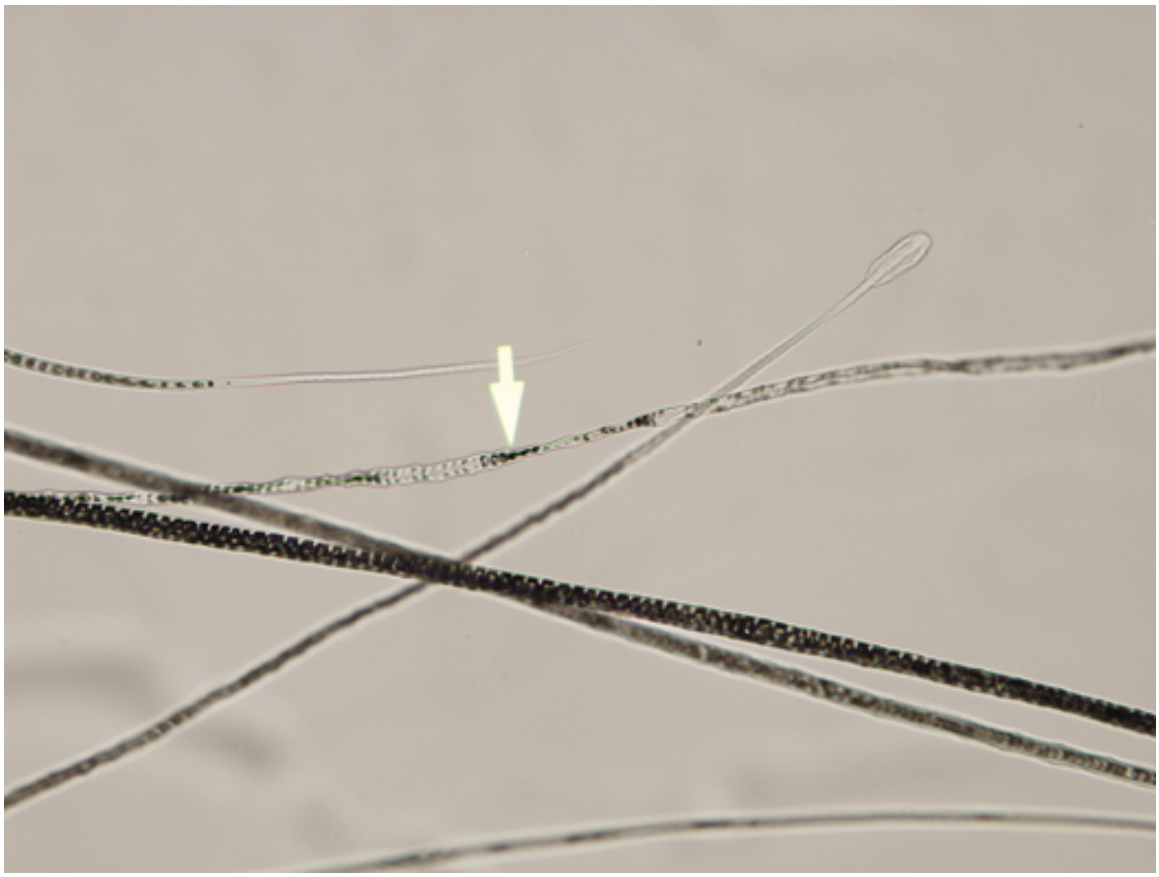
Genetic Analysis

This mutation was first identified as a recessive mutation by crossing an RHJ/LeJ-*stpm*/J mutant to an inbred C57BL/6Ei/J. In this cross no mutants were produced in the F1 generation, but mutants were produced in the F2 intercross generation. Using the standard mapping procedures of The Mouse Mutant Resource, an intercross with CAST/Ei was set up and generated 36 affected progeny that were used for linkage analysis. The mutation maps on mouse Chromosome 11 between *D11Mit285* (NCBIm33 position 89.7 Mb) and *D11Mit224* (NCBIm33 position 108.3 Mb) and is non-recombinant with *D11Mit59* (NCBIm33 position 99.9 Mb).

Based on the phenotype and map position similarity of this new mutation to the previously described Rex (*Re)* mutation, a direct test for allelism was set up by mating a mouse homozygous for the *stpm* mutation to a mouse homozygous for the *Re* mutation. When homozygous, the dominant *Rex* gene causes a curlier coat than when it is heterozygous. This curlier coat was not seen in the offspring produced in the test for allelism, indicating that the new mutation is not likely a remutation of *Re*.

Pathology

A routine pathological screen done on two mutants and two control littermates at 7 weeks of age showed no lesions in somatic organs. Hair samples and pelt pads taken at 4 and 5 weeks of age showed that the skin is histologically normal. There is a normal distribution of hair types present in affected animals, but the zigzag hairs have abnormal bends and kinks. A few of the zigzag hairs have variable thickness and guard hairs are rare.



Hearing as accessed by auditory brainstem response (ABR) on three mutant mice and two controls was normal.

Discussion

A previously unknown curly coat mutation has been identified and mapped to Chromosome 11 at the 58.5 cM position. The cause of this new mutation has not been determined. Besides *Re,* 5 other skin and hair mutations, bareskin (*Bsk*), reduced coat 2 (*Rco2*), defolliculated (*Dfl*), finnegan (*Fgn*), and Rex denuded *Re-den* (all mutations in the gasdermin 3 gene) map in this region of Chr 11. These mutations are phenotypically

different when compared to *stpm* mutants. *Bsk* is a dominant ENU induced mutation that causes alopecia beginning at 3 weeks and then thick, wrinkled skin. *Rco2* is a dominant ENU induced mutation that causes mutants to have a normal coat for 3 weeks, followed by a sparse second coat, and are hairless (except on the face) by 6 months of age. *Dfl* is a spontaneous dominant mutation that causes alopecia between 3 and 4 weeks of age and mutants develop thick, folded skin. *Fgn* is a dominant ENU induced mutation that causes alopecia at 6 weeks of age. $Gsdm3^{Re\text{-}den}$ is a spontaneous, semidominant mutation that causes affected animals to begin having alopecia at 3 weeks and develop thick, wrinkled skin. Another candidate gene in this region is keratin gene complex 1, acidic (*Krt1*) which is involved in hair follicle development. Tests for allelism were not performed with the *Gsdm3* mutations, because the mutations are available as cryopreserved only. Sequencing of the *Gsdm3* gene in search of the *stpm* mutation was not done. A test for allelism was not done for *Krt1* because the mice are not available.

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References
Mouse Genome Database (MGD) Mouse Genome Informatics Project, The Jackson Laboratory, Bar, Harbor, Maine. 2005 (www.informatics.jax.org)