Curly tail-like (*ctl*): a new mutation on Mouse Chromosome 4

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Mutation (allele) symbol: *ctl*

Mutation (allele) name: curly tail-like

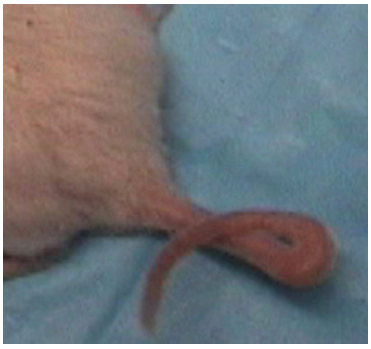
Gene symbol: *ctl*

Strain of origin: A/WySnJ

Current strain name: A/WySnJ-*ctl*/GrsrJ

Stock #005136 (jaxmice.jax.org)

Phenotype categories: skeletal



Abstract

A new recessive mouse mutation named curly tail-like causes a curly tail or a bend in the tail in affected animals and has been mapped to Chromosome 4 in a location near the curly tail mutation (*ct*). A test for allelism between *ctl/ctl* and *ct/ct* mice did not produce curly tail progeny; however, this result may be due to the low penetrance of the *ct* phenotype.

Origin and Description

The curly tail-like (*ctl*) mutation was discovered by Tracy Wark in a production colony at the Jackson Laboratory. This recessive mutation arose on the inbred strain A/WySnJ. Mice carrying the *ctl* mutation are easily recognizable at birth by their curly or bent tails.

Genetic Analysis

A test for allelism was done by mating homozygous curly tail mice to homozygous curly tail-like mice. No curly tail phenotypes were observed among the 56 progeny born from 4 matings. This result is not surprising as the original curly tail mutation produces variable percentages of curly tail mice even when homozygotes are mated together (usually less than 30 % affected mice are seen). The incidence of affected mice born when *ctl* homozygotes are mated to *ctl* heterozygous mice is 26%, far below the expected 50%. Using the standard mapping procedures of The Mouse Mutant Resource an inbred C57BL/6J was mated to a *ctl/ctl* to produce F1s. The normal appearing F1 animals were then intercrossed to produce F2 mice for linkage analysis. The curly tail-like mutation maps to Chromosome 4 between *D4Mit16* (59.1 cM) and *D4Mit54* (66 cM) and is non-recombinant with *D4Mit203* (60cM) and *D4Mit204* (61.9 cM). Recombination estimates with standard errors and the best gene order are centromere-[*D4Mit11*]- 1.9 +/- 1.9 - [*D4Mit16*] - 5.8 +/- 3.4 - [*D4Mit203*, *D4Mit 204*, ***ctl***]-5.8 +/- 3.4 - [*D4Mit54*] for the 100 meioses tested. Gene order and recombination frequencies were calculated with the Map Manager computer program (Manley). The chromosomal location of the original

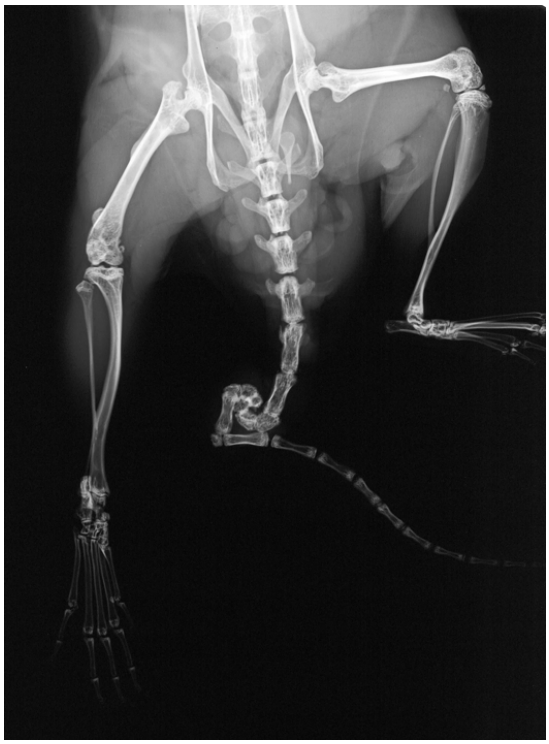
curly tail mutation is positioned at 69 cM.

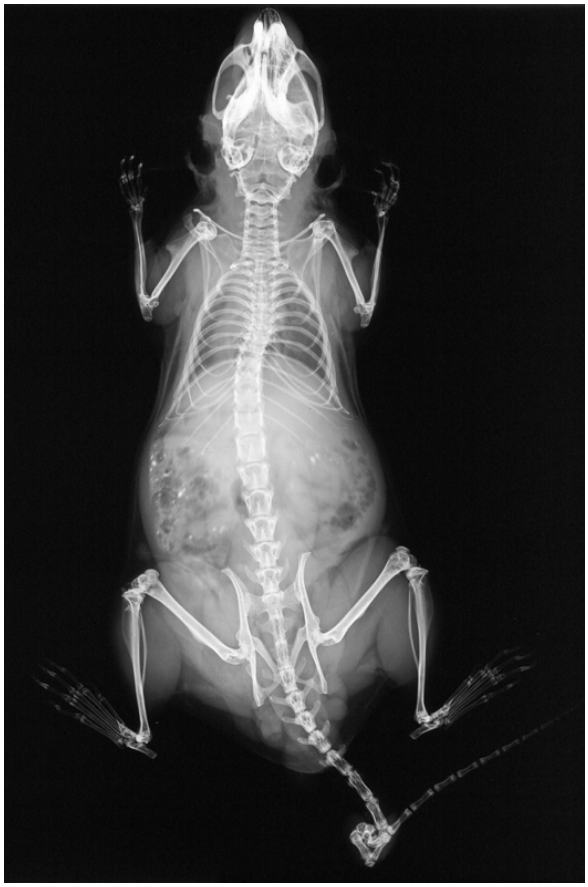
Pathology
Hearing as assessed by auditory-evoked brainstem response testing (ABR) on two homozygous and two heterozygous *ctl* mice at 6 weeks of age was normal.

The eyes of 6 week old and 3 month old mutants and controls were examined with an ophthalmoscope and were determined to be normal.

Our routine pathological screen showed no cerebellar lesions, mild hydrocephalus, and mild spinal arthritis in 3 month old animals.

X-rays of mutants revealed no skeletal dysmorphologies except for abnormally shaped tail vertebrae resulting in kinked tails.





Discussion
Phenotypically, curly tail and curly tail-like affected mice show similar bent or curly tail abnormalities with occasional spina bifida at a very low incidence. No other skeletal abnormalities have been observed. Both mutants are fertile. *In utero* studies of *ctl* mice have not been done, so a comparison with *ct in utero* studies which showed exencephaly was not possible. The name curly tail-like was chosen for this new mutation because of the phenotypic and chromosomal position similarities with the curly tail gene.

Acknowledgement
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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)