Sequence of the pink-eyed dilution 18 Jackson mutation

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Mutation (allele) symbol: *Oca2*$^{p\text{-}18J}$

Mutation (allele) name: pink-eyed dilution 18 Jackson

Gene symbol: *Oca2*

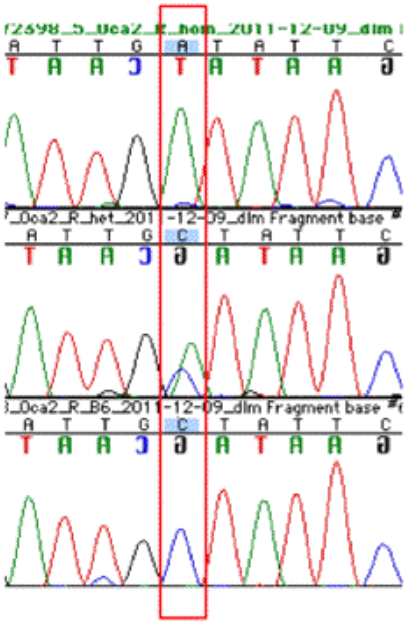
Strain of origin: B10.RIII-*H2-T18*^{b}/(7INS)SnJ

Current strain name: B10.Cg-*H2-T18*^{b} *Oca2*$^{p\text{-}18J}$/GrsrJ

Stock #: 14100

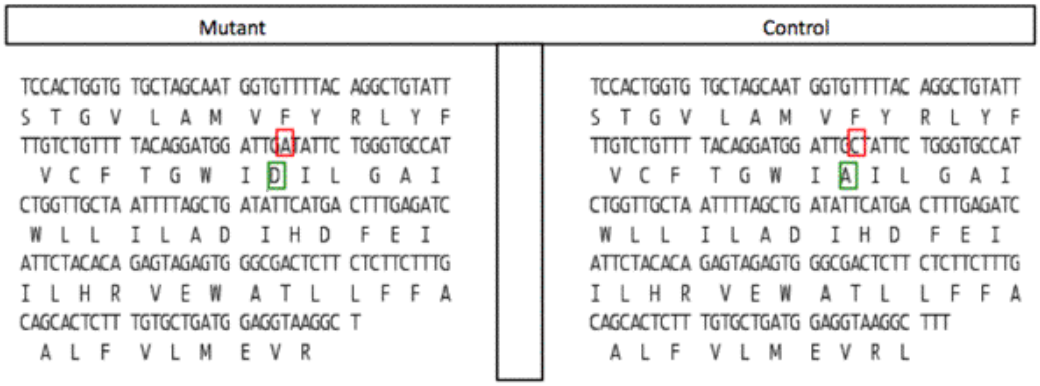
Phenotype categories: Pigmentation

The pink-eyed dilution 18 Jackson mutation (*Oca2*$^{p\text{-}18J}$) causes affected mice to have a diluted coat color and reduced eye pigmentation. This mutation was mapped and linkage to Chromosome 7 was previously demonstrated. Whole exome sequencing was used to identify candidate coding mutations in the mapped region. Briefly, genomic DNA was enriched for coding sequence by hybridization-based capture with probes representing 54 Mb of annotated coding sequence. The enriched DNA was then sequenced using the Illumina HiSeq high-throughput sequencing platform[1].



Comparison of sequence chromatograms of the *Oca2*$^{p\text{-}18J}$ homozygote, heterozygote and C57BL/6J control sequence. The red boxed region corresponds to the red boxed nucleotides in the accompanying sequence figure.

A single nucleotide polymorphism was found on Chromosome 7 in oculocutaneous albinism II (Oca2). Primers were generated that produce a 252 base pair product spanning the predicted mutation; Oca2 forward (GATAAATCATCCACTGGTGTGC) and Oca2 reverse (GCTTCACTCTGCAAACAAAATG). Sequence analysis of DNA samples from two additional mutants and three unaffected controls was used to confirm the presence of a single nucleotide transversion from C to A in at position 63612482. This is a missense mutation, changing alanine to aspartic acid at amino acid 649 (NP_068679.1, NCBI build 37.3).



A portion of the protein coding region of *Oca2*$^{p\text{-}18J}$. The control DNA sequence and its amino acid translation are shown on the right, and the *Oca2*$^{p\text{-}18J}$ mutant DNA and its translation on the left. A single nucleotide transition is enclosed by a red box in the mutant sequence and the control sequence. The mutation is predicted to change amino acid 649 from Alanine to Aspartic acid.

1 Exome Sequencing Protocol

The exome sequencing data referred to in this website were analyzed using tools and workflows provided by Genome Quest including processes for mapping (HS3), SNP calling and annotation of variants. Our analysis focused on novel variants, which were not positioned in repetitive sequence, had expected allele ratios (>0.95 for homozygous variants and >0.2 for heterozygous variants), and displayed sufficient locus coverage (at least 5X for homozygous variants and 10X for heterozygous variants) for effective mutation discovery. High priority was given to protein coding or splice variants within mapped regions, as well as unique variants that were not found in other exome data sets or in the Sanger Mouse Genomes Database. Following these analyses, re-sequencing of additional mutant and unaffected samples was performed to validate and determine the most likely causative mutation.