PublisherInfo				
PublisherName	:	BioMed Central		
PublisherLocation		London		
PublisherImprintName	:	BioMed Central		

Mouse mutagenesis

ArticleInfo		
ArticleID	:	4410
ArticleDOI	:	10.1186/gb-spotlight-20020226-01
ArticleCitationID	:	spotlight-20020226-01
ArticleSequenceNumber	:	76
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate: 2002–2–26OnlineDate: 2002–2–26
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

Jonathan B Weitzman Email: jonathanweitzman@hotmail.com

Large-scale mutagenesis projects using the chemical mutagen ethylnitrosurea (ENU) are being developed to help with the functional annotation of the mouse genome. In an Advanced Online Publication in Nature Genetics, Coghill *et al.* describe a gene-driven approach to find mutant mice (19 February 2002, DOI:10.1038/ng847). They screened over 2,000 samples contained within an archive of DNA and sperm from the UK ENU mutagenesis program. They screened the archives for four genes using denaturing liquid chromatography and found mutations in three of them. They were able to isolate three mutations (one missense and one stop mutation) within the *Gjb2* gene that encodes connexin 26 (which is mutated in cases of human nonsyndromic deafness). They could also recover mutant mice from the frozen sperm archive using *in vitro* fertilization, and to confirm the ENU-induced mutation rate is around 1 nucleotide change per 2.38 Mb of coding sequence; parallel DNA and sperm archives will facilitate simple screening for point mutations in the mouse genome.

References

1. A systematic, genome-wide, phenotype-driven mutagenesis programme for gene function studies in the mouse.

2. Nature Genetics, [http://www.nature.com/ng]