Mouseac

Gene expression data from the Mouse Dementia Network, University College London Mouse DemNet UCL

The aim of Mouseac is to provide to the scientific community an easy to use tool to investigate gene expression changes in a number of mouse models of dementia across their lifespan relating to neurodegenerative disorders such as Alzheimer's disease.

Overview

Mouseac is an interface that provides access to the dataset presented in Matarin et al [INSERT PUBMED LINKWHEN PUBLISHED]. The aim of Mouseac is to provide a tool with which to explore the dataset resulting from a genome-wide microarray of genes expressed in 3 brain regions across 4 ages in 5 transgenic mouse models of dementia and their wild-type counterparts.

Detailed methodology can be found in the main manuscript [LINK].

All procedures were performed in agreement with the UK Animals (Scientific Procedures) Act, 1988, under HO PPL licence 70/7279 with local ethical agreement and following the GlaxoSmithKline statement on the use of animals.

Mouse models studied

The transgenic mouse models of dementia included in the study were developed by GlaxoSmithKline and incorporate mutant human genes responsible for familial forms of dementia.

TAS10 mice carry a human gene for amyloid precursor protein (*APP*) harbouring the Swedish mutation (K670N/M671L) that causes early-onset familial Alzheimer's disease.

TPM mice carry a human gene for presenilin 1 (*PSEN1*) harbouring the M146V mutation that causes early-onset familial Alzheimer's disease.

Heterozygous (HET) TASTPM mice are transgenic for both genes in the TAS10 and TPM mice.

Homozygous (HO) TASTPM mice carry twice the number of copies of both genes in the HET TASTPM.

TAU mice carry a human microtubule-associated protein tau (*MAPT*) gene harbouring the P301L mutation, which causes Frontotemporal dementia with Parkinsonism linked to chromosome 17.

WILD TYPE mice were C57BL/6 mice, which are the back-ground strain for each of the transgenic mice including WT littermates from the TAS10, TPM and TAU mice.

Ages and brain regions studied

Gene expression has been determined within the hippocampus, cerebral cortex and cerebellum from mice aged 2, 4, 8 and 18 months of age.

Correlation to pathology

The presence of pathology (amyloid plaques for TAS, TPM, HET-TASTPM and HO-TASTPM; presence

of neurofibrillary tangles for TAU mice) was assessed using fluorescent immunohistochemistry in brain sections from the contralateral brain hemispheres of the same mice used for the microarrays. The semi-quantitative assessment of pathology within the hippocampus and cortex are presented alongside the microarray data. No plaques or tangles were identified in the cerebellum of transgenic mice at any age.

Correlations of the pathology to genetic expression data are presented in Matarin et al [link]

Genes included in the data set

Genome-wide microarrays were performed on tissue from each brain region obtained from at least 3 male mice of each genotype at each age point using the MouseRef8 v2 (Illumina) microarray platform. Raw expression data were $\log_2$ transformed and all samples were quantile normalized together. After quality control steps, described in detail in Matarin et al., data were available for at least 3 samples per group, representing 12,588 genes. The normalised data set is available in Mouseac.

Using the interface

Use of the interface is simple. Type the official mouse gene name (MGI; link to http://www.informatics.jax.org) into the search box, select which mice you are interested in (by default, all are selected) and press SUBMIT. It may take several seconds for changes to be applied. The resulting plots can be downloaded as a Portable Document Format (*.pdf) file or the raw data from each mouse (including information on brain region, age and mouse model) can be downloaded as a comma delimited (*.cvs) file that can be opened in most spreadsheet applications.

Statistics

Statistics have not been included in this online-database. Any statistics carried out from downloaded data should be corrected appropriately for multiple comparisons.