South Australian **Museum**

EVOLUTIONARY BIOLOGY UNIT
Genetic Monitoring Service

Genetic monitoring of inbred mice as supplied by the University of Adelaide's Laboratory Animal Services - June, 2014

Laboratory mice representing five inbred strains or colonies were provided for assessments of their genetic authenticity using the molecular genetic technique of allozyme electrophoresis (see Adams *et al*. (1990) for a detailed description of the technique). A set of standard genetic markers known to display allelic variation amongst inbred and outbred strains was screened for the 10 animals supplied. The results of these genetic analyses are shown in Table 1.

Table 1. Allelic profiles at 15 genetic markers for the strains or colonies provided. Although not formally described, the marker NDPK exhibits genetically-determined variation, involving two co-dominant allozymes, s ("slow") and f ("fast"). Substrains or congenic strains with the same profile are grouped together in the table. Nomenclature for allelic profiles according to Mouse Newsletter and Staats (1980). (n = 2 for each strain or colony)

Strain	***Ahd-1***	***Akp-1***	***Es-1***	***Es-3***	***Got-2***	***Gpd-1***	***Gpi-1***	***Hbb***	***Idh-1***	***Itp-1***	***Mod-1***	***Mpi-1***	***Pep-3***	***Pgm-1***	**NDPK**
Balb/c	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
SCID	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
Nude	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
CBA	b	b	b	c	b	b	b	d	b	b	b	b	b	b	f
C57/BL6	a	a	a	a	b	a	b	s	a	b	b	b	a	a	s

Comments and conclusions

1. There is no evidence of genetic variability within any of these inbred strains. All individuals tested were homozygous at those markers which display co-dominant alleles (all markers except *Es-3*, where *Es-3*^{c} is dominant to *Es-3*^{a}).

2. There is no evidence of genetic contamination in any strain. The allelic profiles obtained are consistent with previous screens (last screened June, 2013; report M451) and with the published literature.

3. As shown in the table, the BALB/c group of substrains possess identical allelic profiles at all genetic markers examined. Such a result is of course expected, given that substrains are usually either congenic or are sublines of the same original strain. However, as a result of their near genetic identity, it is usually not possible to detect a cross-contamination event between these substrains using routine genetic monitoring procedures. This highlights the need for (a)

the physical separation of substrains so that cross-contamination is not possible, and (b) researchers to institute (where necessary) a reliable monitoring program to confirm the identity of the substrain being used.

Contact details

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References

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