



Genetic monitoring of inbred mice as supplied by the University of Adelaide's Laboratory Animal Services - June, 2008

Six inbred strains of laboratory mouse were provided for assessments of their genetic authenticity. A set of standard electrophoretic markers known to display genetically-determined variation amongst both inbred and outbred strains was screened for the 12 animals supplied. The results of the electrophoretic screen are shown in the table below.

Allelic profiles at fifteen genetic markers for the six strains provided. The marker NDPK has not yet been formally described; it does however exhibit genetically-determined variation, with two co-dominant allozymes, s ("slow") and f ("fast"). (N = 2 for each strain)

Strain	<i>Ahd-1</i>	<i>Akp-1</i>	<i>Es-1</i>	<i>Es-3</i>	<i>Got-2</i>	<i>Gpd-1</i>	<i>Gpi-1</i>	<i>Gr-1</i>	<i>Hbb</i>	<i>Idh-1</i>	<i>Itp-1</i>	<i>Mod-1</i>	<i>Pep-3</i>	<i>Pgm-1</i>	<i>NDPK</i>
Balb/c	b	b	b	a	b	b	a	a	d	a	a	a	a	a	s
SCID	b	b	b	a	b	b	a	a	d	a	a	a	a	a	s
CBA	b	b	b	c	b	b	b	a	d	b	b	b	b	b	f
C57/BL6	a	a	a	a	b	a	b	a	s	a	b	b	a	a	s
129/SV	a	b	b	c	b	a	a	a	d	a	b	a	b	a	s
SJL/J	b	b	b	c	b	b	a	b	s	b	b	a	b	b	s

Nomenclature for allelic profiles according to Mouse Newsletter and "Standardized Nomenclature for Inbred Strains of Mice" Staats, J. (1980) *Cancer Res.* **40**: 2083-2138.

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 identical to previous screens and consistent with the published literature.
3. As shown in the table, BALB/c and SCID 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 sublimes of the same original strain. 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.

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