



## Genetic monitoring of inbred mice as supplied by the University of Adelaide's Laboratory Animal Services - June, 2015

Laboratory mice representing four 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 eight animals supplied. The results of these genetic analyses are shown in Table 1.

**Table 1. Allelic profiles at 15 genetic markers for the eight animals screened.** 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).

Animal/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>Hbb</i>	<i>Idh-1</i>	<i>Itp-1</i>	<i>Mod-1</i>	<i>Mpi-1</i>	<i>Pep-3</i>	<i>Pgm-1</i>	NDPK
<b><i>Balb/c reference</i></b>	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>d</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>s</i>
Balb/c (blue 181 ♂)	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
Balb/c (yellow 168 ♂)	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
Nude (60 ♀)	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
Nude (red 96 ♀)	b	b	b	a	b	b	a	d	a	a	a	b	a	a	s
<b><i>CBA reference</i></b>	<i>b</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>d</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>f</i>
CBA (red 88 ♀)	b	b	b	c	b	b	b	d	b	b	b	b	b	b	f
CBA (blue 87 ♂)	b	b	b	c	b	b	b	d	b	b	b	b	b	b	f
<b><i>C57/BL6 reference</i></b>	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>s</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>s</i>
C57 (silver 140 ♂)	a	a	a	a	b	a	b	s	a	b	b	b	a	a	s
C57 (yellow 76 ♂)	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 four inbred strains. All individuals tested were homozygous at those markers which display co-dominant alleles (all markers except *Es-3*, where *Es-3<sup>c</sup>* is dominant to *Es-3<sup>a</sup>*).
2. There is no evidence of genetic contamination in any strain. The allelic profiles obtained are consistent with previous screens (last screened June, 2014; report M459) and with the published literature.
3. As shown in the table, the two BALB/c substrains possess identical allelic profiles at all

genetic markers examined. Although multi-gene genetic monitoring readily distinguishes all major groups of inbred strain from one another and from all outbred strains (e.g. C57BL versus C3H versus CBA versus BALB/c versus Swiss etc.), the same does not usually apply to different substrains within a major group (e.g. C57BL/6 versus C57BL/10). This latter result is of course not surprising, given that substrains are usually either congenic or are sublimes 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 most substrains using routine genetic monitoring procedures (although there are known exceptions, e.g. CBA/N versus CBA/J). 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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