



Genetic monitoring of laboratory mice as supplied by The Chinese University of Hong Kong's Laboratory Animal Services Centre – June, 2015

Twelve laboratory mice, representing six inbred strains, 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). These mice were genotyped for a set of standard genetic markers known to display allelic variation amongst inbred and outbred strains. The results of these genetic analyses are shown in Table 1.

Table 1. Allelic profiles at 15 genetic markers for the 12 mice provided. Although not formally described, the marker NDPK exhibits genetically-determined variation, involving two co-dominant allozymes, s (“slow” mobility) and f (“fast” mobility). 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>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>	NDPK
<i>BALB/c</i> reference	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>d</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>s</i>
BALB/c animal #M1	b	b	b	a	b	b	a	a	d	a	a	a	a	a	s
BALB/c animal #M2	b	b	b	a	b	b	a	a	d	a	a	a	a	a	s
<i>C57BL/6</i> reference	<i>a</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>s</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>s</i>
C57 animal #M3	a	a	a	a	b	a	b	a	s	a	b	b	a	a	s
C57 animal #M4	a	a	a	a	b	a	b	a	s	a	b	b	a	a	s
<i>C57BLKS/J <db+/-db></i> reference	<i>b</i>	<i>a</i>	<i>a</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>s</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>s</i>
db+/-db animal #M5	b	a	a	a	b	a	b	a	s	b	b	b	a	a	s
db+/-db animal #M6	b	a	a	a	b	a	b	a	s	b	b	b	a	a	s
<i>SAMP8</i> reference	<i>b</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>d</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>s</i>
SAMP8 animal #M7	b	b	b	c	a	b	a	a	d	a	b	b	b	a	s
SAMP8 animal #M8	b	b	b	c	a	b	a	a	d	a	b	b	b	a	s
<i>SAMR1</i> reference	<i>b</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>d</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>a</i>	<i>s</i>
SAMR1 animal #M9	b	b	b	c	b	b	a	a	d	a	b	a	b	a	s
SAMR1 animal #M10	b	b	b	c	b	b	a	a	d	a	b	a	b	a	s
<i>SCID (NOD)</i> reference	<i>a</i>	<i>b</i>	<i>b</i>	<i>c</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>a</i>	<i>s</i>	<i>a</i>	<i>b</i>	<i>b</i>	<i>b</i>	<i>a</i>	<i>s</i>
SCID (NOD) animal #M11	a	b	b	c	b	b	a	a	s	a	b	b	b	a	s
SCID (NOD) animal #M12	a	b	b	c	b	b	a	a	s	a	b	b	b	a	s

Comments and conclusions

1. There is no evidence of genetic variability within any of these six strains. All animals 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 of all strains are identical to those found in previous screens (last screened in December 2013, report M455-M) and/or consistent with the published literature,

Contact details

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References

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