South Australian **Museum**

EVOLUTIONARY BIOLOGY UNIT
Genetic Monitoring Service

Genetic monitoring of inbred rats as supplied by the University of Adelaide's Laboratory Animal Services - June, 2011

Two inbred strains of the laboratory rat were provided for assessments of their genetic authenticity using the molecular genetic technique of allozyme electrophoresis [see Richardson *et al.* (1986) or Adams *et al.* (1990a) 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 four animals supplied. The results of these genetic analyses are shown in Table 1.

Table 1. Allelic profiles at 15 genetic markers for the two strains provided. The marker AHD-K has not yet been formally described; it does nevertheless exhibit genetically-determined variation, expressing two co-dominant allozymes, s ("slow" mobility) and f ("fast" mobility). Nomenclature for allelic profiles according to Adams *et al.* (1990b). The strain profile expected for the DA strain is also shown italicized for reference. (N = 2 for each strain)

Strain	*Acon-1*	*Ahd-2*	*Ahd-C*	*Akp-1*	*Alp-1*	*Br-1*	*Es-4*	*Es-10*	*Fh*	*Hao-1*	*Hbb*	*Pep-3*	*Pgd*	*Pk*	*AHD-K*
DA - reference	*b*	*b*	*b*	*b*	*a*	*a*	*b*	*a*	*b*	*a*	*b*	*b*	*b*	*b*	*s*
DA	b	b	b	b	a	a	b	a	b	a	b	b	b	b	s
RT7B	b	b	b	b	a	a	b	a	b	a	b	b	b	b	s

Conclusions and comments

1. There is no evidence of genetic variability in either of these inbred strains. All individual tested were homozygous at all genetic markers examined.

2. There is no evidence of genetic contamination in either strain. The allelic profiles obtained are consistent with previous screens and with the published literature.

3. As shown in the table, these two strains 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.