

Genetic Monitoring of laboratory mice using highly informative STR-marker panels

Application Note:

Genetic background validation of inbred animals

Unclear or misclassified genetic background of laboratory rodents or a lack of strain awareness causes a number of difficulties in performing or reproducing scientific experiments.

More than 240 highly informative STR markers (Short Tandem Repeats, microsatellites) covering the 19 autosomes as well as X and Y chromosomes have been identified. Inbred strains and substrains can be differentiated with a large number of informative marker, mixed genetic profiles can be easily detected. The markers can be used for validation of strains, their substrains and parentage lines to ensure consistency with consensus alleles of reference strains.

Method: Genotyping with GVG standard panel of STR loci, comparison with strain- or substrain-specific consensus alleles
 Determination of Y-chromosome STR-haplotype
 Checking for presence of C57BL/6-specific mutations

Typically, analysis of 3 DNA samples (at least 2 males) per strain to assess the variation between animals

Fast results, customer-friendly presentation of analysis data:

Genotyping results within 10 working days
Analysis data in customer-friendly tabular form

Example: Characterization of C57BL/6-derived inbred mice

Service 1: Genotyping of key-markers (Small panel)

Combination of C57BL/6-specific markers with Y-chromosomal STR haplotype allows fast assignment of inbred mice to strains and substrains. Mixed genetic background of C57BL/6J and C57BL/6N can be detected easily.

Service 1 provides no further information about other chromosomal regions (see Service 2).

<i>Crb1</i> ^{rd8}		DIP 686		DIP 1606			<i>Nnt</i>		<i>Snca</i>		<i>Dock 2</i>		
wt	mut	wt	mut	wt	mutA	mutB	wt	mut	wt	mut	wt	mut	
	x	x				x	x		x		x		NTac, NRj
	x	x			x		x		x		x		NCrI, NJ
	x	x			x		x		x			x	NHsd
x			x		x			x	x		x		J (Jax), JRj
x			x		x		x			x	x		JOlaHsd
x			x		x		x		x		x		JBomTac, JRccHsd
x		x		x			x		x		x		non-C57BL/6

Identification of C57BL/6 strain- and substrain-specific markers

	DYS101	DYS102	DYS201	DYS204	DYS301	DYS601
JCrI	21-24	24	28	20	16	14-16
JRj	21-23	24	28	20	16	14-16
JOlaHsd	21-24	23	28	20	16	14-16
JRccHsd	21-24	24	28	21	15	15-16
JBomTac	21-24	24	27	20	16	0-0
NCrI	21-24	22	28	21	16	14-16
NHsd	21-24	23	28	21	16	14-16
NTac	24-24	23	28	21	17	14-16
NRj	21-24	23	28	21	17	14-15

Y-chromosomal STR loci. Each substrain has its characteristic haplotype (combination of alleles)

Service 2: Genotyping of key markers and full STR-genotyping (Large panel)

Combination of key markers with full STR-genotyping (246 markers) allows reliable estimation of the complete genetic background. Mixed profiles are identified, mixture ratio can be calculated.