

Transgenerational Effects in Mice Exposed to Continuous Low-Dose-Rate Gamma-Rays
 – Analysis of Germ Cell Mutation –

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Abstract

Transgenerational effects of continuous low-dose-rate (LDR) gamma-ray irradiation of male mice have not been well studied. To clarify incidence of copy number aberrations (CNAs) of the progeny of mice exposed to radiation, progenies of male C57BL/6J mice continuously exposed to LDR (20 mGy/22 h/day) gamma-rays for 400 days (total dose: 8000 mGy) were analyzed. Using oligo-microarray CGH (Agilent Technologies), we have, so far, analyzed a total of 333 genomes (111 progenies from 20 pairs of parents in the LDR-irradiated group and 140 progenies from 21 pairs of parents in the non-irradiated group). The results indicate that progenies from LDR-irradiated mice had significantly higher frequencies of genomic aberrations than progenies from non-irradiated mice (21.6% vs 12.1%). Mice containing more than five mutations were found only in the LDR-irradiated group.

Table 1 Results of the genomic aberrations analysis using the oligo-microarray CGH

	No. of analyzed F1 mice	No. of mice with aberrations	No. of loci with aberrations
20 mGy/22h/day irradiated group	111	24 (21.6 %)	93 (Ave. 0.84 loci /generation)
Non irradiated group	140	17 (12.1 %)	21 (Ave. 0.15 loci /generation)
		P =0.03	P <0.01



1. Mutation frequency in the 20 mGy/22h/day irradiated group is significantly higher than the non-irradiated group.
2. Multiple aberrations were found only in the 20 mGy/22h/day irradiated group.
3. Increase in copy number aberrations (CNAs) were less frequent than decreases.

Table 2 *De novo* genomic aberrations found in F1 mice

P	F1	ID	Copy	Chr	Start	size	IM	244K	♀♂	Tg
OH	5	A_67_P07597258	d	12	41196414	146136	22		♂	175
OK	5	A_67_P07881467	d	13	55020816	25412	12		♀	819
OG	2	A_67_P04226288	d	1	114741818	72062	10		♂	930
OH	5	A_67_P00568664	d	2	177113983	688713	6		♂	175
OK	4	A_67_P04816742	d	3	5533449	34160	5	72	♀	1778
OE	4	A_53_P142487	i	8	125951601	1535	1	13	♀	551
OV	2	A_67_P02587942	d	12	100883086	486	1	4	♂	1952
OG	5	A_67_P06783170	i	9	49529393	412	1	3	♀	1156
OP	3	A_67_P00830676	d	4	22048320	230	1	3	♂	2188
OF	5	A_67_P06477612	i	8	37019826	68	1	2	♀	907
OG	2	A_67_P04434755	d	2	13957250	346	1	2	♂	930
OH	1	A_67_P06382618	d	7	142916412	98	1	2	♂	1177
OH	1	A_67_P06671121	d	8	125525315	594	1	2	♂	1177
OI	3	A_67_P02693109	d	13	53303865	89	1	2	♂	2157
OL	6	A_67_P07000727	d	10	22555501	86	1	2	♀	1495
ON	5	A_67_P04221500	i	1	111527682	66	1	2	♀	1211
OO	7	A_67_P04007022	d	1	7313469	153	1	2	♀	2110
OP	3	A_67_P06620732	d	8	105555233	93	1	2	♂	2188
OP	7	A_67_P03082883	i	15	81575653	71	1	2	♀	1484
OQ	2	A_67_P08008520	d	13	117033940	66	1	2	♂	2834
OV	2	A_67_P04682955	d	2	126501011	461	1	2	♂	1952

P	F1	ID	Copy	Chr	Start	size	IM	244K	♀♂	Tg
20I	5	A_67_P02200316	d	10	98677432	744874	91		♀	1903
20E	5	A_67_P05889421	i	6	48005970	305069	58		♀	807
20R	1	A_67_P04942632	d	3	69594066	192812	43		♂	1310
20E	1	A_67_P01942010	d	9	57473630	234921	31		♂	1431
20L	5	A_67_P07898663	d	13	63501120	1E+07	19		♂	1714
20L	4	A_67_P01456795	d	6	138658494	32881	8		♂	1737
20L	2	A_67_P08087383	d	14	38727785	23540	5		♂	1839
20N	4	A_67_P05860760	d	6	34882670	10224	4	25	♂	1764
20A	1	A_67_P06933980	d	9	113994878	133572	3	18	♂	147
20G	2	A_67_P08093213	d	14	41807207	3286	2	15	♂	1703
20T	2	A_67_P08110650	d	14	52008939	11986	2	4	♀	787
20N	4	A_67_P05233855	d	4	50554508	2367	1	18	♂	1764
20G	7	A_67_P053131294	d	4	99899132	1878	1	17	♀	1069
20G	5	A_67_P04083311	d	1	44861301	948	1	9	♀	1581
20I	4	A_67_P02060678	d	10	8393959	460	1	4	♂	2190
20B	5	A_67_P02151317	d	10	68882829	1040	1	3	♀	342
20J	4	A_67_P06860168	d	9	81442835	327	1	3	♀	2020
20B	3	A_67_P05197589	d	4	33730804	94	1	2	♀	1533
20B	5	A_67_P07398579	d	11	74609783	175	1	2	♀	342
20E	3	A_67_P00341736	d	2	34273487	100	1	2	♂	1190
20G	4	A_67_P04259545	d	1	131185842	617	1	2	♀	1069
20J	4	A_67_P00912069	d	4	81088876	122	1	2	♀	2020
20L	4	A_67_P05080618	d	3	133586473	428	1	2	♂	1737
20Q	4	A_67_P06111306	d	6	149168000	108	1	2	♀	705
Multiple aberrations										
20A	2	35 loci							♂	509
20F	5	15 loci							♀	951
20H	6	10 loci							♀	1964
20L	1	5 loci							♂	1062

Mice with two *de novo* genomic aberrations are marked in red. Type of aberrations are indicated as d (deletion) or i (increase). Multiple aberrations (more than five aberrations in one mouse) are shown in the lower left side.