Effects of the scid mutation on X-ray-induced deletions in the brain and spleen of gpt delta mice

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Abstract

Background: DNA-dependent protein kinase (DNA-PK), consisting of a Ku heterodimer (Ku70/80) and a large catalytic subunit (DNA-PKcs), plays an important role in the repair of DNA double-strand breaks via non-homologous end-joining (NHEJ) in mammalian cells. Severe combined immunodeficient (scid) mice carry a mutation in the gene encoding DNA-PKcs and are sensitive to ionizing radiation. To examine the roles of DNA-PKcs in the generation of deletion mutations in vivo, we crossed scid mice with gpt delta transgenic mice for detecting mutations.

Results: The scid and wild-type (WT) gpt delta transgenic mice were irradiated with a single X-ray dose of 10 Gy, and Spi− mutant frequencies (MFs) were determined in the brain and spleen 2 days after irradiation. Irradiation with X-rays significantly enhanced Spi− MF in both organs in the scid and WT mice. The MFs in the brain of irradiated scid mice were significantly lower than those in WT mice, i.e., 2.9 ± 1.0 × 10−6 versus 5.0 ± 1.1 × 10−6 (P < 0.001), respectively. In the spleen, however, both mouse strains exhibited similar MFs, i.e., 4.1 ± 1.8 × 10−6 versus 4.8 ± 1.4 × 10−6. Unirradiated scid and WT mice did not exhibit significant differences in MFs in either organ.

Conclusions: DNA-PKcs is unessential for the induction of deletion mutations in the spleen, while it plays a role in this in the brain. Therefore, the contribution of DNA-PKcs to NHEJ may be organ-specific.

Keywords: DNA-PKcs, scid mice, Non-homologous end-joining, Spi− assay, Deletion, X-irradiation

Introduction

The repair of DNA double-strand breaks (DSBs) is critical for the maintenance of genomic integrity. In mammalian cells, DSBs are repaired by the homologous recombination and/or the nonhomologous end-joining (NHEJ) pathways [1–3]. However, DSBs induced by ionizing radiation (IR) are mainly repaired through NHEJ pathway. This is particularly true in non-dividing cells and in G1 cells due to the absence of sister chromosomes, the preferred substrate for homologous recombination. Although defects in NHEJ result in genomic instability and cancer predisposition, NHEJ often leads to deletion mutations, with or without short length insertions, when DNA ends can’t be directly ligated [4]. IR and chemical treatments usually induce modified DSBs with ends that are incompatible for direct ligation. Therefore, NHEJ can be regarded as a double-edged sword; while it prevents cell death and gross chromosome rearrangements, it often induces deletions and insertions during ligation of incompatible ends.

DNA-dependent protein kinase (DNA-PK) consists of three components, the catalytic subunit DNA-PKcs and the heterodimeric Ku70 and Ku80 proteins, and is involved in NHEJ of DNA DSBs and V(D)J recombination [5–9]. In general, when DNA DSBs are induced, Ku70/80 proteins bind to the ends and interact with other...
proteins including DNA PKcs and Artemis for end-resection, DNA polymerase μ and λ for addition of nucleotides, and the DNA ligase IV complex for ligation of the ends. However, different proteins are recruited to the site of DNA damage to participate in the repair of DSBs each time, depending on the end configurations i.e., blunt ends, 5′- or 5′-overhands or ends containing modified bases [10].

The scid (severe combined immune-deficiency) mice bear a naturally occurring mutation in the DNA-PKcs gene that results in an 83-amino acid truncation of the C-terminal end [11–14]. These mice, and cells derived from them, are hypersensitive to IR, display defects in joining of IR-induced DNA DSBs [12, 15], and are defective in coding joint formation during V(D)J recombination [16, 17]. However, scid cells can form signal joints in V(D)J recombination [18], which involve the joining of the ends created after the excision of intervening DNA during V(D)J recombination and the formation of circular DNA molecules. In contrast, Ku-deficient mice and embryonic stem cells exhibit defects in both coding and signal joint formation [19–22]. Therefore, it appears that DNA-PKcs is only needed to resolve a subset of DSBs and that NHEJ may proceed in a DNA-PKcs-independent manner, as well as DNA-PKcs-dependent, manner.

We previously developed the gpt delta transgenic mouse for the detection of mutations in vivo [23–25]. In gpt delta mice, about 80 copies of lambda EG10 DNA, which carries red and gam genes, are integrated into each chromosome 17 in a C57BL/6J background [26, 27]. A feature of the mutation assay is its ability to efficiently detect certain types of deletions by Spi− (sensitive to P2 interference) selection, as well as point mutations, i.e., base substitutions and frameshifts, by 6-thioguanine selection [28, 29]. Spi− selection takes advantage of the restricted growth of the lambda phage in P2 lysogens [30]. Only mutant lambda phages that are deficient in the functions of both red and gam genes can grow well in P2 lysogens and display the Spi− phenotype. Simultaneous inactivation of the two adjacent genes is usually induced by a deletion in the region, or frameshifts that interfere with the translation of both genes. Spi− selection detects deletions ranging from single nucleotide (−1) frameshifts to 10 kb in size [29]. In this procedure, the lambda EG10 is rescued from the mouse genome by in vitro packaging reactions, and P2 lysogens are infected with the rescued phages to identify Spi− plaque. We have demonstrated that the Spi− mutant frequency (MF) is substantially increased by IR and chemical treatments, and suggested that NHEJ repair plays an important role in the induction of Spi− deletion mutants [28, 31, 32].

Since NHEJ may proceed in DNA PKcs-dependent and independent manners, it may be possible that DNA PKcs plays a significant role in deletion formation in one organ while it plays only a negligible role in another one. It is reported that MF of unirradiated Ku80−/− mice is higher than that of WT mice in the spleen while the MFs are similar between two strains of mice in the liver [33]. To examine the possible variation of the roles of DNA PKcs in deletion mutations in mammalian organs, we crossed scid mice with gpt delta mice (hereafter, the offspring from this cross will be referred to as scid mice, and gpt delta mice as wild-type (WT) mice). We irradiated scid and WT mice with X-rays and compared Spi− MFs in the brain and spleen, which are representative organs with quiescent and proliferating cells, respectively. The results indicated that X-ray irradiation significantly induced deletion mutations in both organs of scid and WT mice. Although scid mice exhibited significantly lower MFs than WT mice in the brain, both mouse strains exhibited similar MFs in the spleen. Possible mechanisms of DNA-PKcs-independent NHEJ of DNA DSBs are discussed.

Materials and methods
Treatment of animals
C.B-17 scid mice, maintained in CLEA Japan, were crossed with C57BL6/J lambda EG10-homozygous gpt delta mice [26]. The heterozygous F1 mice were mated with the same offspring carrying the scid mutation and lambda EG10 transgene, which resulted in F2 mice. The scid genotype of each experimental animal was confirmed by PCR, according to a previously reported method [13]. The existence of the transgene was also confirmed using a previously reported method [26]. Eleven- to twelve-week-old WT (wt/wt) and scid (scid/scid) mice were whole-body irradiated with X-rays; a total dose of 10 Gy. X ray-irradiation (200 kVp, Softex-Rigaku) was delivered at a dose rate of 1 Gy per min. Each group consisted of a total of 6–10 male and female mice. The mice were sacrificed 2 days following irradiation. The brain and spleen were collected and quickly frozen in liquid nitrogen and stored at −80 °C. Genomic DNA was extracted from the organs using the phenol/ chloroform method and lambda EG10 phages were rescued using TranspackR Packaging Extract (Agilent Technology, Japan) as described previously [24].

Spi− mutation assay
The Spi− mutation assay was performed as described previously [24]. The rescued phages were used to infect E. coli XL1-Blue MRA (P2) cells. The infected cells were mixed with molten soft agar, poured on lambda-trypticase agar plates, and incubated at 37 °C. The Spi− candidate plaques detected on the plates were suspended in 50 μL of SM buffer. The suspension was spotted on the plate where the XL1-Blue MRA (P2) cells were
spread. The plates were incubated at 37°C; the mutants that produced clear spots were counted as confirmed Spi− mutants. The rescued phages were also used to infect E. coli XL1-Blue MRA cells to determine the number of rescued phages. The Spi− MF was calculated as described previously [24]. Phage lysates of the Spi− mutants were used as templates for PCR analysis. The PCR primers were:

- primer 001 (5′-CTCTCCTTTGATGCGAATGCGAGC-3′)
- primer 002 (5′-GGAGTAATTATGCAGACAGATCATGC-3′)
- primer 005 (5′-CGTGGTCTGAGTGGATACAGAGG-3′)
- primer 006 (5′-GTTATGCGTTGTTCCATACAACCCTC-3′)
- primer 012 (5′-CGGTGAGGGACCTAATAACTTG-3′).

The appropriate primers for DNA sequencing were selected based on the results of PCR analysis. The sequencing primers have been described previously [34–36]. The entire sequence of lambda EG10 is available at http://www.nihs.go.jp/dgm/dgm3/eg10v20.txt. DNA sequencing was performed with BigDye™ Terminator Cycle Sequencing Kit (Applied Biosystems, Foster City, CA) and ABI PRISM™ 310 Genetic Analyzer (Applied Biosystems).

Statistical analysis
All data were expressed as mean ± standard deviation (SD). A Tukey-test was used to determine if the differences between two groups were statistically significant. A P value of < 0.05 was considered statistically significant.

Results
Spi− MFs in the brain and spleen of X-ray-irradiated mice
WT and scid mice were exposed to X-ray irradiation at a dose of 10 Gy and Spi− MFs were determined in the brain and spleen (Fig. 1, Supplementary Table 1 and 2). X-ray irradiation significantly enhanced Spi− MFs in both organs in WT and scid mice. The MFs in the brain of scid mice were significantly lower than those of WT mice, i.e., 2.9 ± 1.0 × 10−6 versus 5.0 ± 1.1 × 10−6, P < 0.001. In the spleen, however, both mouse strains exhibited similar MFs after irradiation (4.1 ± 1.8 × 10−6 vs 4.8 ± 1.4 × 10−6, P = 0.77). Unirradiated scid and WT mice did not exhibit significant differences in MFs in either organ (0.85 ± 0.67 × 10−6 vs 1.0 ± 0.64 × 10−6 in the brain and 1.4 ± 0.31 × 10−6 vs 2.6 ± 1.3 × 10−6 in the spleen).

Deletion mutation spectra in the brain of WT and scid mice
Since MFs in the brain were significantly lower in scid mice than in WT mice, we were interested in whether the spectra of deletions were different in the two strains of mice. Therefore, we sequenced the Spi− mutants recovered from the brain of X-ray-irradiated and unirradiated WT and scid mice (Tables 1 and 2). The specific MFs of each type of deletion were calculated by multiplying the MF by the ratio of the number of each class of mutations to the total number of deletion mutations.

In WT mice, the frequency of 1 base pair (bp)-deletions increased 3.0-fold by irradiation (0.82 to 2.50 × 10−6), while the frequency of deletions of more than 2 bps in size, increased 20.3-fold (0.12 to 2.43 × 10−6). Among the sequenced 35 deletions of more than 2 bps in size, 37% (13/35) were deletions of more than 1 kb and 60% (21/35) had microhomologous sequences of 1

![Fig. 1](image-url) The Spi− MFs in the brain and the spleen of WT and scid mice with or without X-ray-irradiation. Error bars mean ± SD of the MFs in each group; n = 10 for WT (0 Gy), n = 8 for WT (10 Gy), n = 6 for scid (0 Gy) and n = 7 for scid (10 Gy). * P < 0.01, relative to the unirradiated groups. ** P < 0.01, relative to the WT mice. A Tukey-test was used to determine if the differences between two groups were statistically significant.
to 4 bps at the junction. The average length of microhomology was 1.8 bps. Six % (2/35) had an inserted base at the junctions.

In scid mice, the frequency of 1 bp-deletions increased 2.4-fold by irradiation (0.64 to 1.52 × 10−6), while the frequency of deletions of more than 2 bps in size, increased 11.1-fold (0.11 to 1.22 × 10−6). Among the sequenced 40 deletions of more than 2 bps in size, 35% (14/40) were more than 1 kb and 63% (25/40) had microhomologous sequences at the junction. With the exception of one mutation that had a 12-bp microhomology, the average length of microhomology was 1.7 bp. Five mutations containing a 1 bp-insertion, not accompanied by deletions, were observed in irradiated scid mice, whereas no such mutations were observed in irradiated WT mice.

There was no significant difference in the mutation spectra between unirradiated WT and scid mice. One bp-deletions in the repetitive sequences were the most dominant type of mutation. Three hotspots were observed in unirradiated mice: 1) AAAAA to AAAA at position 227–231, 2) GGGG to GGG at position 286–289 and 3) AAAAAA to AAAAA at position 295–300 in the gam gene.

**Discussion**

Although it is well known that the scid mice are severely sensitive to killing effects of irradiation, little is known about the roles of DNA PKcs in irradiation-induced deletion mutations in various organs of mice. In this study, the WT and scid mice were irradiated with X-rays and deletion mutations were analyzed in the brain and the spleen. In the X-ray-irradiated WT mice, the Spi− MFs in the brain and spleen were significantly higher than those of unirradiated mice. Sequencing analysis of the Spi− mutants in the brain showed that X-ray irradiation preferentially induced large deletions of up to 10 kbps (Table 1). Specific MFs of deletions of more than 2 bps in size increased 20.3-fold upon irradiation, in contrast to the MFs of deletions of 1 bp that increased 1.9-fold. Among the sequenced 35 deletions of more than 2 bps in size, 60% (21/35) had microhomologous sequences of 1–4 bps at the deleted junction (Table 2). These data confirmed that deletions of more than 2 bps in size in this study are largely generated through NHEJ of DNA DSBs [3, 29].

In irradiated scid mice, the Spi− MFs were significantly increased 3.2- and 2.9-fold in the brain and spleen, respectively, compared with those of unirradiated scid mice. In the brain, the specific MF of deletions of more than 2 bps in size increased 11-fold by irradiation, in contrast to the MF of 1 bp-deletions that increased 1.9-fold (Table 1). Sequencing analysis of the Spi− mutants showed that 63% (25/40) of the deletions of more than 2 bps in size had microhomologous sequences of 1–12 bps at the deleted junction. These characteristics of the X-ray-induced deletions in scid mice were similar to those of WT mice, suggesting that X-ray-induced DSBs are repaired by NHEJ even without DNA-PKcs. It is possible, however, that the defective protein encoded by the murine scid allele retains enough residual function to support NHEJ. Bogue et al. examined V(D)J recombination in DNA-PKcs-deficient SLIP mice and found that the effects of this mutation on coding and signal joint formation are identical to the effects of the scid mutation [18]. These data are incompatible with the notion.

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**Table 1 Spi− mutation spectra in the brain of X-ray-irradiated WT and the scid mice**

|         | WT 0 Gy |         | WT 10 Gy |         | scid 0 Gy |         | scid 10 Gy |         |
|---------|---------|---------|----------|---------|-----------|---------|------------|---------|
|         | No. %   | MFx10−6 | No. %    | MFx10−6 | No. %     | MFx10−6 | No. %      | MFx10−6 |
| 1 bp deletion |         |         |          |         |          |         |            |         |
| In run  | 18 72 0.74 | 30 42 2.08 | 6 75 0.64 | 40 42 1.22 |
| Other   | 2 8 0.08 | 6 8 0.42 | 0 0 0.00 | 10 11 0.30 |
| > 2 bp deletion |         |         |          |         |          |         |            |         |
| With microhomology | 0 0 0.00 | 21 29 1.46 | 0 0 0.00 | 25 26 0.76 |
| Without microhomology | 3 12 0.12 | 12 17 0.83 | 1 13 0.11 | 11 12 0.33 |
| Insertion | 0 0 0.00 | 2 3 0.14 | 0 0 0.00 | 4 4 0.12 |
| Insertion | 2 8 0.08 | 0 0 0.00 | 0 0 0.00 | 5 5 0.15 |
| Complex  | 0 0 0.00 | 1 1 0.07 | 1 13 0.11 | 0 0 0.00 |
| Total    | 25 100 1.03 | 72 100 5.00 | 8 100 0.85 | 95 100 2.89 |

Specific MFs were calculated by multiplying the total MF by the ratio of each class of mutants.

In unirradiated WT mice, total 26 mutants (suppl. Table 1) were obtained. They were sequenced and 25 deletion mutations (Table 1) were identified. In 10 Gy-irradiated WT mice, total 172 mutants were obtained. Eighty seven mutants were sequenced and 72 deletion mutations were identified. In unirradiated scid mice, total 9 mutants were obtained. All were sequenced and 8 deletion mutations were identified. In 10 Gy-irradiated scid mice, total 67 + 89 mutants were obtained. One hundred and twenty five were sequenced and 95 deletion mutations were identified. In 10 Gy-irradiated scid mice, 89 mutants were obtained by additional plating for sequencing analysis, but they were not used for calculation of MF because no additional plating was conducted for control groups.

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**Note:** The table above shows the mutation spectra for the brain of X-ray-irradiated WT and scid mice. The data were compiled to understand the effects of irradiation on the mutation frequencies and types in these mice. The table includes the number of mutations, their frequency, and the MF (mutation frequency) for each class of mutations. The data are presented for both WT and scid mice irradiated with 0 and 10 Gy, respectively.
### Table 2 Summary of Spi− mutations in the brain of X-ray-irradiated WT and scid mice

| Types of deletions | Position in gam | Position in lambda EG10 | Sequence Change | Sequence at junction | No. of mutants |
|--------------------|----------------|-------------------------|----------------|----------------------|----------------|
| One base pair deletions | | | | | |
| In run sequences | | | | | |
| 141–142 | | | GG→G | | 1 |
| 188–190 | | | CCC→CC | | 1 |
| 199–201 | | | AAA→AA | | 1 |
| 227–231 | | | AAAAA→AAAA | | 5d 1 |
| 238–241 | | | CCCCC→CCC | | 2d 1 |
| 286–289 | | | GGGGG→GGG | | 5d 1 |
| 290–291 | | | CC→C | | 1 |
| 295–300 | | | AAAAAA→AAAAA | | 1 |
| 316–318 | | | TTT→TT | | 1 |
| 334–336 | | | TTT→TT | | 2 |
| 377–378 | | | CC→C | | 1 |
| 380–381 | | | TT→T | | 1 |
| 387–388 | | | CC→C | | 1 |
| 390–391 | | | CC→C | | 1 |
| Other 1 bp deletion | | | | | |
| 131 | | | ttAtt→tttt | | 1 |
| 175 | | | cacTac→cacac | | 1 |
| 183 | | | caGct→cact | | 1 |
| 203 | | | gAgg→ggg | | 1 |
| 218 | | | agAcg→agcg | | 1 |
| 236 | | | ccTgc→ccgc | | 1 |
| 268 | | | tcGat→tcat | | 1 |
| 276 | | | tttG→tttt | | 1 |
| 277 | | | ttgCaac→ttgaac | | 2d |
| 285 | | | Cgggg→gggg | | 1 |
| 294 | | | Caaaaaaa→aaaaaa | | 1 |
| 301 | | | aaaaaaT→aaaaaaa | | 1 |
| 320 | | | ttgAt→tttgt | | 1 |
| 328 | | | tGt→ttt | | 1 |
| 332 | | | gAg→gg | | 1 |
| 341 | | | ggAg→ggg | | 1 |
| 392 | | | ccAgg→ccgg | | 1 |

> 2 bp deletions

| Deleted sizes (bp) | | |
|-------------------|----------------|----------------|
| 2 | 153 → 156 | tgag tcag 1 |
| 2 | 251 → 254 | tgtt aatc 1 |
| 2 | 349 → 352 | atgg gaac 1 |
| 3 | 355 → 359 | gaac tccg 1 |
| 4 | 182–184 | agcaGCtccgt 1 |
Table 2  Summary of Sp1<sup>−</sup> mutations in the brain of X-ray-irradiated WT and scid mice (Continued)

| Types of deletions | Position in gam | Position in lambda EG10 | Sequence Change<sup>a</sup> | Sequence at junction<sup>b,c</sup> | No. of mutants |
|--------------------|----------------|-------------------------|-----------------------------|----------------------------------|---------------|
|                    |                |                         |                             |                                  |               |
| 187–189            | 4              | 222 → 227               | cgac aaaa                   |                                  | 1             |
|                    | 4              | 239–240 → 244–245       | tgcctCacct                  |                                  | 1             |
|                    | 4              | 247–249 → 251–253       | caacctTgaat                 |                                  | 1             |
|                    | 4              | 295–300                 | cagTAatcca                  |                                  | 1             |
|                    | 4              | 304 → 309               | tcca cgct                   |                                  | 1             |
|                    | 5              | 300–301 → 306–307       | aaaaTccc                    |                                  | 2             |
|                    | 7              | 147–149 → 155–157       | tcgCTcaga                   |                                  | 1             |
|                    | 7              | 349–351 → 357–359       | atggaCAatccg                |                                  | 1             |
|                    | 8              | 175 → 184               | cact ctcg                   |                                  | 1             |
|                    | 10             | 196–198 → 207–209       | gaagaAGaact                 |                                  | 1             |
|                    | 10             | 323 → 334               | atga tttc                   |                                  | 1             |
|                    | 10             | 335 → 346               | agtt atgg                   |                                  | 1             |
|                    | 10             | 375–379 → 386–390       | tgaaACCoicc                 |                                  | 1             |
|                    | 12             | 221–222 → 234–235       | acgaCctgc                   |                                  | 1             |
|                    | 12             | 313 → 326               | cggtg atgt                  |                                  | 1             |
|                    | 13             | 376–379 → 389–392       | gaagaCCAggtt                |                                  | 1             |
|                    | 14             | 165–167 → 180–182       | ctggCagtcg                  |                                  | 1             |
|                    | 17             | 154–155 → 172–173       | gaggCAccta                  |                                  | 1             |
|                    | 17             | 239–240 → 257–258       | ctgcCgcta                   |                                  | 1             |
|                    | 17             | 251 → 269               | tgtt atca                   |                                  | 1             |
|                    | 19             | 212–215 → 232–235       | aactGCCCtgc                 |                                  | 1             |
|                    | 22             | 288–289 → 311–312       | cggtgCtgcg                  |                                  | 3             |
|                    | 26             | 268 → 285               | atcg cggg                   |                                  | 2<sup>f</sup> |
|                    | 28             | 307 → 336               | atta tcag                   |                                  | 1             |
|                    | 28             | 338 → 367               | ttca atgg                   |                                  | 1             |
|                    | 32             | 189–190 → 222–223       | cgccCatggg                  |                                  | 1             |
|                    | 34             | 346–348 → 381–383       | cgcaTgtcga                  |                                  | 1             |
|                    | 41             | 380 → 422               | ccatt aatgg                 |                                  | 1             |
|                    | 49             | 206 → 257 (1 bp ins.)   | aggc Ccgct                  |                                  | 1             |
|                    | 67             | 246–247 →               | gcacCgttt                   |                                  | 1             |
| Types of deletions | Position in gam | Position in lambda EG10 | Sequence Change at junction | No. of mutants |
|-------------------|----------------|------------------------|-----------------------------|----------------|
|                   |                |                        |                             |                |
| 314–315           |                |                        |                             |                |
| 76                | 189 → 266     |                        |                             |                |
| 86                | 252–253 → 339–340 |                |                             |                |
| 107               | 91–92 → 199–200 |                        |                             |                |
| 124               | 208 → 333     |                        |                             |                |
| 127               | 273–276 → 401–404 |                        |                             |                |
| 151               | 24,867–24,870 → 25,019–25,022 |                |                             |                |
| 432               | 24,828–24,830 → 25,261–25,263 |                |                             |                |
| 449               | 24,683–24,684 → 25,133–25,134 |                |                             |                |
| 596               | 24,446–24,450 → 25,043–25,047 |                |                             |                |
| 654               | 24,719 → 25,374 |                        |                             |                |
| 1248              | 24,524–24,536 → 25,767–25,779 |                |                             |                |
| 1436              | 24,563 → 26,000 |                        |                             |                |
| 1557              | 24,222 → 25,802 (22 bps ins.) |                |                             |                |
| 1616              | 23,938–25,555 (2 bps ins.) |                |                             |                |
| 1856              | 23,960–23,961 → 25,817–25,818 |                |                             |                |
| 1874              | 24,161–24,162 → 26,009–26,010 |                |                             |                |
| 2124              | 23,141 → 25,266 (1 bp ins.) |                |                             |                |
| 2388              | 23,000–23,004 → 25,389–25,393 |                |                             |                |
| 2388              | 24,000–24,002 → 28,232–28,234 |                |                             |                |
| 2441              | 24,034–24,035 → 26,476–26,477 |                |                             |                |
| 2842              | 24,247–24,248 → 27,090–27,091 |                |                             |                |
| 3628              | 25,062 → 28,691 |                        |                             |                |
| 3701              | 24,560 → 28,262 |                        |                             |                |
| 3707              | 21,458–21,459 → 25,166–25,167 |                |                             |                |
| 3979              | 22,200–22,204 → 26,180–26,184 |                |                             |                |
| 4144              | 22,585–22,586 → 26,730–26,731 |                |                             |                |
| 4689              | 23,611–23,612 → 28,301–28,302 |                |                             |                |
| 4698              | 24,423–24,424 → 29,122–29,123 |                |                             |                |
| 4841              | 21,691–21,692 → 26,533–26,534 |                |                             |                |
| 5037              | 21,355 → 26,393 |                        |                             |                |
| 5251              | 19,712–19,713 → 24,964–24,965 |                |                             |                |
| 5422              | 22,340 → 27,760 (3 bps ins.) |                |                             |                |
| 5562              | 19,997 → 25,560 |                        |                             |                |
| 5727              | 19,335 → 25,063 |                        |                             |                |
| 6900              | 24,036 → 30,037 |                        |                             |                |
| 7303              | 23,917 → 31,221 |                        |                             |                |
| 9030              | 21,854–21,857 → 30,885–30,888 |                |                             |                |
that signal joint formation in scid mice results from residual DNA-PKcs function and support the idea that DNA-PKcs is not an essential factor for NHEJ in mice. The analysis of DNA-PKcs knock-out mice also supports this idea [37]. Hence, we suggest that DNA-PKcs-independent NHEJ is responsible for deletions associated with X-ray exposure in the spleen and, in part, in the brain.

How can NHEJ proceed without DNA-PKcs in the brain and spleen? DNA-PKcs interacts with the C-terminal part of Ku80, a component of DNA-PK. When Ku binds to DNA ends, the interaction with DNA PKcs increases substantially, which leads to autophosphorylation of DNA PKcs and activation of the endonuclease activities of Artemis [38]. This endonuclease appears to play a role in the removal of 5′- and 3′-overhangs in DNA ends, which seems to be a necessary step for the efficient ligation of broken DNA ends. It is estimated, however, that more than half of IR-induced DSBs are repaired even without the activities of Artemis [39, 40]. This suggests that nucleases other than Artemis, such as Apratoxin and PNKP-like factor (APLF), flap endonuclease (FEN1), DNA replication helicase/nuclease 2 (DNA 2) and exonuclease 1, may play roles in the resection of broken DNA with incompatible DNA ends [3]. We speculate, therefore, that DNA PKcs-independent nucleases may play roles in NHEJ in the brain and spleen while the canonical DNA PKcs-dependent Artemis is involved in NHEJ in the brain. Obviously, further work is needed to reveal exact mechanisms by which NHEJ proceeds without DNA PKcs in the organs.

Unirradiated scid and WT mice did not exhibit significant differences in MFs in the brain and spleen (Fig. 1). In addition, the spectra of deletions were similar between the two strains of mice, where 1 bp-deletions in the repetitive sequences were the most dominant. These deletions, however, are mostly generated by slippage of DNA polymerases during DNA replication and not during DNA repair of DSBs [29]. It is reported that spontaneous lacI MFs were similar between scid and WT mice in the brain, spleen and liver [41]. Spontaneous MF of expanded simple tandem repeat (ESTR) in male germline was higher in the scid mice than in the WT mice although the frequency was not enhanced by irradiation [42].

Lee et al. report that DNA-PK activity fluctuates in a cell cycle-dependent manner, and propose a model in which two illegitimate recombinational repair pathways exist in mammals, one of them being DNA-PK dependent and restricted to the G1/early S phase and the other being DNA-PK independent and restricted to the late S/G2 phase of the cell cycle [43]. They showed that the DNA DSB repair activity in the scid pre-B cells was greatly reduced during the G1/early S phase resulting in increased X-ray hypersensitivity but was indistinguishable from that in WT cells during the late S and G2 phases. In the spleen, in which cell division is active, DNA-PK independent repair may work well during the late S and G2 phases and neutralize the effect of the scid mutation. In the context, the scid mutation may lead to a reduced activity of DSB repair and the induction of deletion mutations. In the mutation spectra of Spi− mutations recovered from the brain of the irradiated scid mice, there were 4 mutations having insertion sequences at the deleted junctions and 5 mutations having +1 insertions. This was observed in 9.5% (9/95)
of the analyzed samples (Table 2). In the irradiated WT mice, there were 2 mutations having insertion sequences at the deleted junctions and no mutations having +1 insertions. This was observed in 2.8% (2/72) of the analyzed samples. The higher frequency of mutations with insertions that was observed in the irradiated scid mice raises the possibility that DNA-PKcs-independent NHEJ may incorporate more nucleotides compared with DNA-PKcs-dependent NHEJ during DNA DSBs repair. Other characteristics of the mutation spectra in the brain of irradiated mice were similar between scid and WT mice.

Conclusions
X-ray-induced deletions are predominantly generated by NHEJ in the brain and spleen of irradiated mice. NHEJ proceeds in DNA-PKcs-dependent and DNA PKcs-independent manners. DNA-PKcs contributes to NHEJ in the brain while it is dispensable in the spleen. This study suggests the organ specificity of the roles of DNA PKcs in deletion induction and raises a question of how NHEJ proceeds in the absence of DNA PKcs in mammalian organs.

Supplementary information
Supplementary information accompanies this paper at https://doi.org/10.1186/s41021-020-00158-y.

Additional file 1: Table S1. Spi” mutant frequency in the brain of X-ray-irradiated mice. Table S2. Spi” mutant frequency in the spleen of X-ray-irradiated mice.

Abbreviations
DNA-PK: DNA-dependent protein kinase; DNA PKcs: The catalytic subunit of DNA PK; scid: Severe combined immunodeficient; WT: Wild type; MFs: Mutant frequencies; NHEJ: Non-homologous end-joining; DSBs: Double-strand breaks; IR: Ionizing radiation; Spi: Sensitive to P2 interference; SD: Standard deviation; bp: Base pair; APLF: Apratoxin and PNKP-like factor; FEN1: Flap endonuclease; DNA 2: DNA replication helicase/nuclease 2; ESTR: Expanded simple tandem repeat

Acknowledgements
We acknowledge Ms. Makiko Hoshino, Showa Pharmaceutical University, for technical assistance for mutant analyses. We thank Drs. Otoya Ueda and Hiroshi Suzuki, Exploratory Research Laboratory, Fuji Gotemba Research Laboratory, Chugai Pharmaceutical Co., Ltd., for generation of the scid/gpt delta mice.

Authors’ contributions
MK and TN designed the experiments and MK conducted most of the experiments. FY irradiated the mice with X-ray and MO and HN characterized the scid mice. TN wrote the draft and all the authors confirmed the final manuscript.

Funding
This study was financially supported by the budget for Nuclear Research of the Ministry of Education, Culture, Sports, Science and Technology, Japan, based on the screening and counselling by the Atomic Energy Commission. This work was also supported by the Japan Health Science Foundation and the Tsuchikawa Memorial Fund for Study in Mammalian Mutagenicity.

Availability of data and materials
All data generated or analysed during this study are included in this published article and its Supplementary Table 1 and 2.

Ethics approval and consent to participate
All animal care and experimental procedures were conducted in compliance with the internal regulation for animal use at the National Institute of Health Sciences.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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Received: 7 February 2020 Accepted: 16 May 2020
Published online: 24 May 2020

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