G3·Genes | Genomes | Genetics

# Double-strand break repair assays determine pathway choice and structure of gene conversion events in *Drosophila melanogaster*

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DOI: 10.1534/g3.113.010074

**Table S1 Silent mutations (mu) in DR-*white.mu***

| mu # | Distance (nt) from *Sac*I site[a] | nt change[b] | Restriction site change | mutagenic primer[c] |
|---|---|---|---|---|
| 1 | -864 | C215A | *Pst*I+ | 5’-GCAAACACCCATCTGCAGAGCATCTGAACAATGG |
| 2 | -732 | A347G | *Nhe*I+ | 5’-GTTCAGGGAGCGGCCAGCTAGCCGAGAACC |
| 3 | -693 | C386T | *Eco*RV+ | 5’-CTGGCACAATATGGATATCTTTGGGGCGGTC |
| 4 | -645 | C434T | *Hpa*I+ | 5’-GGCGGCAGCTGGTTAACCGGACACGCGGAC |
| 5 | -558 | T521C | *Sma*I+ | 5’-TTTGCGGCGTGGCCTACCCGGGCGAACTTTTG |
| 6 | -516 | A563C | *Nae*I+ | 5’-GTTCCGGTGCCGGCAAGACGACCCTGCTG |
| 7 | -471 | C608G | *Bam*HI+ | 5’-TTTCGATCGCCGCAGGGGATCCAAGTATCG |
| 8 | -423 | G656C | *Sal*I+ | 5’-GGCCAACCTGTCGACGCCAAGGAGATGC |
| 9 | -363 | C716A | *Bam*HI+ | 5’-TGACCTCTTTATCGGATCCCTAACGGCCAG |
| 10 | -327 | C752T | *Nco*I– | 5’-GATTTTCCAGGCTATGGTGCGGATGCCACG |
| 11 | -276 | G803T | *Bcl*I+ | 5’-GAGTGGCCCGCGTTGATCAGGTGATCCAGG |
| 12 | -201 | T878C | *Stu*I+ | 5’-CAGGGTGAAAGGCCTGTCCGGCGGAGAAAG |
| 13 | -150 | C929G | *Bam*HI+ | 5’-CCTCCGAGGCACTAACGGATCCGCCGCTTC |
| 14 | -63 | G1016T | *Hind*III+ | 5’-GTGCTGAAGAAGCTTTCGCAGAAGGGCAAG |
| 15 | +32 | A1110C | *Nci*I+ | 5’-TCTGATGGCCGAGGGCCGGGTAGCTTTC |
| 16 | +67 | C1145G | *Sal*I– | 5’-CCCAGCGAAGCCGTGGACTTCTTTTCCTAC |
| 17 | +118 | G1196C | *Eag*I+ | 5’-CTACAATCCGGCCGACTTTTACGTACAGG |
| 18 | +190 | A1268C | *Bgl*II+ | 5’-CGGATCGCCAAGATCTGCGACAATTTTGC |
| 19 | +236 | T1314C | *Pvu*II+ | 5’-CCGGGATATGGAGCAGCTGTTGGCCACC |
| 20 | +304 | C1382G | *Pml*I+ | 5’-CCTACAAGGCCACGTGGTTCATGCAGTTCC |
| 21 | +367 | C1445T | *Xmn*I+ | 5’-CTCAAGGAACCACTTCTCGTAAAAGTGCG |
| 22 | +397 | G1475C | *Nco*I+ | 5’-CTTATTCAGACAACCATGGTTGCCATCTTG |
| 23 | +472 | A1550C | *Hae*II+ | 5’-TGAATATCAACGGCGCCATCTTCCTCTTCC |
| 24 | +547 | G1625C | *Sac*I+ | 5’-TTCACCTCAGAGCTCCCAGTTTTTATGAGG |
| 25 | +613 | G1691A | *Mfe*I+ | 5’-CTGGGCAAAACAATTGCCGAATTGCCGC |
| 26 | +694 | A1772C | *Nae*I+ | 5’-GACTGCGGGCCGGCGTGCTGCACTTCTTC |
| 27 | +760 | A1838G | *Eco*RV– | 5’-GTGTCAACGTCCTTCGGGTATCTAATATCC |
| 28 | +859 | C1937T | *Eco*RI+ | 5’-CGGCTTCTTCTTGAATTCGGGCTCGGTGCC |

[a] Distance from I-*Sce*I site is determined by the location of the polymorphism relative to the wild-type *Sac*I cleavage site in *white* cDNA site used to create *Sce.white* (*Sac*I cleavage = 0, upstream of *Sac*I cleavage = –, downstream of *Sac*I cleavage = +).

[b] nucleotide change is determined by the nucleotide number of wild-type *white* mRNA sequence.

[c] forward primer given. Mutation is in red. Restriction site change is underlined.

A. T. Do *et al.* 3 SI

**Table S2 Total flies scored for each DSB repair phenotype**

| | | | | Total number of each phenotype (% of total) | | |
|---|---|---|---|---|---|---|
| Genotype | DSB repair assay | Exp. no. | No. progeny scored (No. of individual germlines) | y+ w– NHEJ, intersister HR, no DSB | y+ w+ intra-chromosomal HR | y– w– SSA |
| wild type | DR-*white* | 1 | 1409 (18) | 788 (55.9) | 558 (39.6) | 63 (4.47) |
| | | 2 | 891 (23) | 509 (57.1) | 349 (39.2) | 33 (3.70) |
| | | 3 | 1659 (30) | 929 (56.0) | 699 (42.1) | 31 (1.87) |
| | | 4 | 1726 (49) | 1034 (59.9) | 649 (37.6) | 43 (2.49) |
| | | **total** | **5685 (120)** | **3260 (57.3)** | **2255 (39.7)** | **170 (3.00)** |
| | | **mean % (±S.E.M.)** | | **57.2 (±0.93)** | **39.4 (±0.90)** | **3.13 (±0.59)** |
| | DR-*white.mu* | 1 | 1441 (19) | 1023 (71.0) | 365 (25.3) | 53 (3.68) |
| | | 2 | 602 (21) | 416 (69.1) | 162 (26.9) | 24 (3.99) |
| | | 3 | 1226 (28) | 850 (69.3) | 362 (29.5) | 14 (1.14) |
| | | **total** | **3269 (68)** | **2289 (70.0)** | **889 (27.2)** | **91 (2.78)** |
| | | **mean % (±S.E.M.)** | | **69.8 (±0.60)** | **27.1 (±1.18)** | **2.9 (±0.91)** |
| *spn-A*/+ | DR-*white* | 1 | 710 (18) | 398 (56.1) | 293 (41.3) | 19 (2.68) |
| | | 2 | 893 (20) | 627 (70.2) | 238 (26.7) | 28 (3.14) |
| | | 3 | 401 (14) | 246 (61.3) | 139 (34.7) | 16 (4.00) |
| | | **total** | **2004 (52)** | **1271 (63.1)** | **670 (33.3)** | **63 (3.13)** |
| | | **mean % (±S.E.M.)** | | **62.5 (±4.13)** | **34.2 (±4.23)** | **3.35 (±0.46)** |
| *spn-A/spn-A* | DR-*white* | 1 | 625 (17) | 391 (62.6) | 3 (0.48) | 231 (37.0) |
| | | 2 | 1157 (27) | 788 (68.1) | 15 (1.30) | 354 (30.6) |
| | | 3 | 631 (18) | 401 (63.5) | 5 (0.79) | 225 (35.7) |
| | | **total** | **2413 (62)** | **1580 (65.5)** | **23 (0.95)** | **810 (33.6)** |
| | | **mean % (±S.E.M.)** | | **64.7 (±1.71)** | **0.86 (±0.24)** | **34.4 (±1.94)** |