**TABLE 2.** Base substitutions [A, in percent; B, their mutation rates (*µ*)] among *E. coli* rifR mutants induced by 0.1 and 0.2 mM fdU.

**A**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Wild-type** | | | ***alkA−*** | | | ***xth− nfo−*** | | |
| fdU (mM) | 0 | 0.1 | 0.2 | 0 | 0.1 | 0.2 | 0 | 0.1 | 0.2 |
| A∙T→C∙G | 12 (10) | 2.9 (2) | 1.8 (1) | 22 (19) | 0 | 1.4 (1) | 10 (7) | 1.4 (1) | 2.7 (2) |
| G∙C→A∙T | 35 (30) | 12 (8) | 35 (22) | 38 (33) | 23 (15) | 15 (11) | 46 (31) | 33 (23) | 45 (33) |
| G**∙**C→C**∙**G | 3.5 (3) | 0 | 1.8 (1) | 1.2 (1) | 0 | 0 | 1.5 (1) | 1.4 (1) | 1.4 (1) |
| G**∙**C→T**∙**A | 14 (12) | 4.4 (3) | 19 (12) | 15 (13) | 4.6 (3) | 17 (12) | 13 (9) | 7.1 (5) | 26 (19) |
| A**∙**T→T**∙**A | 10 (9) | 7.4 (5) | 3.5 (2) | 7.0 (6) | 6.1 (4) | 1.4 (1) | 6.0 (4) | 4.3 (3) | 5.4 (4) |
| A∙T→G∙C | 14 (12) | 66 (45) | 40 (26) | 9.3 (8) | 62 (41) | 55 (39) | 15 (10) | 49 (34) | 11 (8) |
| BS | 88 (76) | 93 (63) | 93 (64) | 93 (80) | 95 (63) | 90 (64) | 93 (62) | 96 (67) | 91 (67) |
| Indels | 2.3 (2) | 0 | 1.5 (1) | 2.3 (2) | 0 | 0 | 1.5 (1) | 0 | 0 |
| Unknown\* | 9.3 (8) | 7.4 (5) | 5.8 (4) | 4.7 (4) | 4.6 (3) | 9.9 (7) | 6.0 (4) | 4.3 (3) | 9.5 (7) |
| Total | 100 (86) | 100 (68) | 100 (69) | 100 (86) | 100 (66) | 100 (71) | 100 (67) | 100 (70) | 100 (74) |

Number of mutants is indicated in parenthesis. BS, base substitutions; \*mutated outside the sequenced rifR region.

**B**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Wild-type** | | | | | | ***alkA−*** | | | | | ***xth− nfo−*** | | | | |
| *µ* (× 10−9) | *µ* | | *µ*0.1/*µ*0 | *µ* | *µ*0.2/*µ*0 | *µ* | | *µ*0.1/*µ*0 | *µ* | *µ*0.2/*µ*0 | *µ* | | *µ*0.1/*µ*0 | *µ* | *µ*0.2/*µ*0 |
| fdU (mM) | 0 | 0.1 | ratio | 0.2 | ratio | 0 | 0.1 | ratio | 0.2 | ratio | 0 | 0.1 | ratio | 0.2 | ratio |
| A∙T→C∙G | 0.148 | 0.0706 | 0.48 | 0.0248 | 0.17 | 0.307 | 0 | 0 | 0.0379 | 0.12 | 0.141 | 0.0327 | 0.23 | 0.0643 | 0.46 |
| G∙C→A∙T | 0.443 | 0.282 | 0.64 | 0.545 | 1.2 | 0.533 | 0.657 | 1.2 | 0.417 | 0.78 | 0.625 | 0.752 | 1.2 | 1.06 | 1.7 |
| G**∙**C→C**∙**G | 0.0443 | 0 | 0 | 0.0248 | 0.56 | 0.0161 | 0 | 0 | 0 | 0 | 0.0201 | 0.0327 | 1.6 | 0.0321 | 1.6 |
| G**∙**C→T**∙**A | 0.177 | 0.106 | 0.60 | 0.297 | 1.7 | 0.210 | 0.131 | 0.62 | 0.455 | 2.2 | 0.181 | 0.164 | 0.91 | 0.611 | 3.4 |
| A**∙**T→T**∙**A | 0.133 | 0.176 | 1.3 | 0.0496 | 0.37 | 0.0970 | 0.175 | 1.8 | 0.0379 | 0.39 | 0.0806 | 0.0982 | 1.2 | 0.129 | 1.6 |
| A∙T→G∙C | 0.177 | 1.59 | 9.0 | 0.644 | 3.6 | 0.129 | 1.80 | 14 | 1.48 | 11 | 0.202 | 1.11 | 5.5 | 0.257 | 1.3 |
| BS | 1.12 | 2.22 | 2.0 | 1.59 | 1.4 | 1.29 | 2.76 | 2.1 | 2.42 | 1.9 | 1.25 | 2.19 | 1.8 | 2.15 | 1.7 |
| Indels | 0.0296 | 0 | 0 | 0.0248 | 0.84 | 0.0324 | 0 | 0 | 0 | 0 | 0.0201 | 0 | 0 | 0 | 0 |
| Unknown\* | 0.118 | 0.176 | 1.5 | 0.0992 | 0.84 | 0.0646 | 0.131 | 2.0 | 0.265 | 4.1 | 0.0806 | 0.0982 | 1.2 | 0.225 | 2.8 |
| Total | 1.27 | 2.40 | 1.9 | 1.71 | 1.3 | 1.39 | 2.89 | 2.1 | 2.69 | 1.9 | 1.35 | 2.29 | 1.7 | 2.38 | 1.8 |