

Table 1 Numbers of SeqA foci per cell and SeqA concentration in cells with changed cell cycle parameters

Strain	τ (min)	<i>oriC/terC</i>	C* (min)	C + D† (min)	Forks/ cell‡	SeqA foci/cell	Forks/ focus	SeqA concentration§
MG1655	26	2.94 ± 0.1	41 ± 1	75	9.9	4.1	2.4	1
MG1655/ MiniR1- <i>datA</i>	26	2.42 ± 0.1	33 ± 2	68	7.3	4.2	1.7	1.1
MG1655 <i>dnaA</i> _{T174P}	28	2.18 ± 0.3	31 ± 5	67	5.4	3.5	1.5	1.2
MG1655 <i>hms206</i>	31	2.02 ± 0.1	32 ± 2	57	3.7	2.8	1.3	0.9
MG1655 Δ <i>hda</i>	36	4.74 ± 0.3	81 ± 2	104	16¶ (4–28)	3.6	4.4	1.1

Cells were grown in Glu-CAA medium supplemented with 100 μ g/mL of uridine at 37 °C (see Experimental procedures).

*Determined by $oriC/terC = 2^{C/\tau}$ in which *oriC/terC* was measured by Southern hybridization, the values are the average of three experiments (five samples for MG1655 and MG1655/MiniR1-*datA*; four samples for *dnaA*_{T174P} and *hms206* and three samples for Δ *hda*).

†Determined by analyzing rifampicin-run-out DNA histograms obtained from flow cytometry (see Supplementary Fig. S1).

‡Average number of forks calculated by using the C and D period described above.

§Measured by Western blot, the values are relative to that of wild-type MG1655 and the average of three experiments.

¶Estimated from rifampicin-run-out DNA histograms.

The standard error of the mean is shown.