

**Table 2.** Same as in table 1 except that here cells grow in M9-glucose.

Parameter	Mean	SD	CV
$\tau_c$	18.726	5.564	29.713
$\tau_g$	36.816	4.761	12.931
$\tau_g - \tau_c$	18.934	3.455	18.249
$a_1$	0.029	0.007	24.071
$a_2$	0.055	0.009	15.423
$a_h$	0.019	0.004	21.334
$L_0$	1.607	0.178	11.103
$L(\tau_c)$	2.135	0.218	10.192
$L(\tau_g)$	3.126	0.247	7.887
$D$	0.716	0.047	6.518

### Abstract

We monitor the shape dynamics of individual *E. coli* cells using time-lapse microscopy together with accurate image analysis. This allows measuring the dynamics of single-cell parameters throughout the cell cycle. In previous work, we have used this approach to characterize the main features of single-cell morphogenesis between successive divisions. Here, we focus on the behavior of the parameters that are related to cell division and study their variation over a population of 30 cells. In particular, we show that the single-cell data for the constriction width dynamics collapse onto a unique curve following appropriate rescaling of the corresponding variables. This suggests the presence of an underlying time scale that determines the rate at which the cell cycle advances in each individual cell. For the case of cell length dynamics a similar rescaling of variables emphasizes the presence of a breakpoint in the growth rate at the time when division starts,  $\tau_c$ . We also find that the  $\tau_c$  of individual cells is correlated with their generation time,  $\tau_g$ , and inversely correlated with the corresponding length at birth,  $L_0$ . Moreover, the extent of the  $T$ -period,  $\tau_g - \tau_c$ , is apparently independent of  $\tau_g$ . The relations between  $\tau_c$ ,  $\tau_g$  and  $L_0$  indicate possible compensation mechanisms that maintain cell length variability at about 10%. Similar behavior was observed for both fast-growing cells in a rich medium (LB) and for slower growth in a minimal medium (M9-glucose). To reveal the molecular mechanisms that lead to the observed organization of the cell cycle, we should further extend our approach to monitor the formation of the divisome.