Table 1. RecA Filament Assembly and Synapsis during Replication and Homologous Recombination

Rates and Relevant Physical and Physiological Measurements		Refs
Volume of an *E. coli* cell	~1 f l (1×10^{-15} l)	[103]
E. coli genome size	4.7 Mb (4.7×10^6 bp)	[104]
Replication rate	650–800 bp/s	[105]
ssDNA generated at replication fork (average Okazaki fragment size)	1000–2000 nucleotides	[106]
Average size of daughter strand gaps	100–800 nucleotides	[107,108]
dsDNA breaks per division (average)	0.1–1	[28,109]
(maximum tolerated)	< 3	[110]
DNA crosslinks per division (maximum tolerated)	50–70	[111]
Oxidative lesions per division	~2000	[28]
Rate of RecBCD resection	1000–2000 bp/s	[14]
Average χ (Chi) frequency	1 per 4500 bp	[14]
Average length of dsDNA resection by RecBCD (*in vitro*) (*in vivo*)	30 000 bp	[14]
	10 000 bp	[15]
SSB site size per tetramer	30–70 nucleotides	[37,112]
RecA site size per monomer	3 nucleotides	[29]
Persistence length of dsDNA	~50 nm	[80]
Persistence length of ssDNA	~1 nm	[80,82]
Persistence length of RecA–ssDNA	~900 nm	[44]
Radius of gyration (R_G) for λ dsDNA (48.5 kb)	~900 nm	
RecA nucleation time (rate)[a], spontaneous RecOR-mediated RecFOR-mediated	10–60 min (1–6 nuclei/h) 5–30 min (2–12 nuclei/h) 2–10 min (6–30 nuclei/h)	[24]
RecA growth rate[a], spontaneous RecOR-mediated RecFOR-mediated	0.3–1.3 RecA monomers/s 2–6 RecA monomers/s 2–6 RecA monomers/s	[24]
RecA K_d for ATP RecA K_d for ATP (+ssDNA)	~15 μM ~2.5 μM (ssDNA)	[113]
RecA K_m for ATP (+ssDNA) (+dsDNA)	~20 μM (ssDNA) ~100 μM (dsDNA)	[114]
RecA k_{cat} for ATP (+ssDNA) for dATP (+ssDNA)	~21 per min per RecA ~33 per min per RecA	[56]
RecA–ssDNA complex salt titration midpoint[b], 0.1 mM nucleotide cofactor	255 mM NaCl ~400 mM NaCl (+ATP) 165 mM NaCl (+ADP)	[115]
RecA–dsDNA complex salt titration midpoint[c], 1 mM nucleotide cofactor	~300 mM NaCl (+ATP) 190 mM NaCl (+ADP)	[116]

[a]Nucleation and growth rates reported were measured in the presence of ATPγS (1 μM RecA, 2 mM ATPγS, pH 7.5, 37°C, ~8000 nt substrate) [24]. The numbers in Table 1 represent our best estimate for physiologically relevant nucleation and growth rates in the presence of ATP (instead of ATPγS), which is ten times slower for nucleation and two-thirds slower for growth. However, these rates are affected by temperature, pH, excluded volume, and concentrations of proteins, and monovalent, divalent, and trivalent salts in nonlinear ways. Nonetheless, these estimates are consistent with ensemble experiments with RecFOR [22] and *in vivo* imaging of RecA bundle appearance and growth [13].
[b]20 mM Tris acetate, pH 7.5, 4 mM $Mg(OAc)_2$, 25°C.
[c]20 mM MES, pH 6.2, 10 mM $MgCl_2$, 25°C.

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