1 Supporting information for

² Single-stranded DNA uptake during gonococcal

- 3 Christof Hepp, Heike Gangel, Katja Henseler, Niklas Günther, Berenike Maier*
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6 Supporting Figures



Fig. S1. Mid-labeling confirms that the import efficiency of ssDNA is increased by
dsDUS. Gonococci (Δ*pilV*, Ng005) were incubated for 1 h with DNA fragments containing a
single dye molecule at the center of the fragment. Subsequently they were treated with DNase
I. The fragments consisted of dsDNA, ssDNA, or ssDNA with 16 b complementary
oligonucleotide containing DUS. Average fluorescence intensity of individual cells. (N > 500
for each condition)

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Fig. S2 Decay of imported dsDNA and dsDUS DNA. Gonococci (Δ*pilV*, Ng005) were incubated for 1 h with DNA fragments containing a single dye molecule at the center of the fragment. Single cell fluorescence intensity was monitored starting immediately after DNA removal. Cells were not treated with DNase. Grey: dsDNA, red: dsDUS. Full lines are exponential fits to the data.

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28 Tables

Strain	Relevant genotype	Source/Reference
MS11 Ng001	wild type	
GV1 (<i>ApilV</i>) Ng005	recA6ind(tetM) pilVfs (G-1)	(31)
<i>∆pilQ∆pilV</i> Ng055	pilQ::m-Tn3cm recA6ind(tetM) pilVfs	(21) (24)
<i>∆pilT∆pilV</i> Ng056	pilT::m-Tn3cm recA6ind(tetM) pilVfs	(21) (43)
<i>MS11 Δnuc</i> Ng164	nuc::kan	This study
<i>∆nuc∆pilV</i> Ng058	nuc::kan recA6ind(tetM) pilVfs	This study
<i>∆pilQ∆nuc∆pilV</i> Ng163	pilQ::m-Tn3cm nuc::kan recA6ind(tetM) pilVfs	This study
<i>∆pilT∆nuc∆pilV</i> Ng162	pilT::m-Tn3cm nuc::kan recA6ind(tetM) pilVfs	This study

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30 Table 1 Bacterial strains used in this study

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	Sequence	
Cy5-ssDNA-end	5'-Cy5-CTCCTGACTGTTCGCGCCCAGAATAAAATCCATCGCTGACTGC	
	GTATCCAGCTCACTCTCAATGGTGGCGGCATACATCGCCTTCACATTC	
	AGACGGCAT-3'	
Atto647-ssDNA-mid	5'-CTCCTGACTGTTCGCGCCCAGAATAAAATCCATCGC[T-	
	Atto647N]GACTGCGTATCCAGCTCACTCTCAATGGTGGCGGCATACATC	
	GCCTTCACATTCAGACGGCAT-3'	
oligo Watson-DUS	5'-ATGCCGTCTGAATGTG-3'	
oligo control	5'-TGTGAAGGCGATGTATG-3'	
HG1	5'ATGGCTAAAATGAGAATATCACCGGAATTGAAAAAACTG3'	
HG2	5'CTAAAACAATTCATCCAGTAAAATATAATATTTTTTTTTT	
	CAG 3'	
HG3	5'ATGCCGTCTGAAGTCCCTGAACGAAGTGTCCGGTTTG 3'	
HG4	5'CAGTTTTTTCAATTCCGGTGATATTCTCATTTTAGCCATCTCTGAACC	
	GGATTTCAGACGGCATC 3'	
HG5a	5'CTGATTGGGAGAAAATAAAATATTATATTTTACTGGATGAATTGTTT	
	TAGAGACACCGCACGGCCTTGAACG 3'	
HG6	5'ATGCCGTCTGAACCCGAGTTGGCGATCAGTGCC 3'	
HG11	5'ACTGCCCGTGGAAGCCGTCG 3'	
HG12	5'GGACGAAAAACGGAAACCACACATACG 3'	
ngch_L01	5'CGCGGTAATCAGGGTGGCGACCTCTTGGCTGGCGAGCATTTTTTCAA	
	AACGTGCTTTTTCGACGTTCAAAATTTTACCTTTGAGCGGCAAAATCG	
	CTTGGAATTTGCGGTCGCGGCCCTGCATGGCGGAACCGCCTGCGGAGT	
	TGCCCTCGACGAGGTAGAGTTCAGACAGGGCAGGGTCTTTTTCTTGGC	
	AGTCGGCGAGTTTGCCGGGCAGTCCCAAGCCGTCCATCACGCCTTTGC	
	GGCGGGTGATTTCGCGGGGCTTTGCGGGCGGCTTCGCGTGCGCGGGCGG	
	CTTCAGACGGCAT	
kh33	5'ATGCCGTCTGAAGCCGCCCGCGCACGC	
kh34	5'CGCGGTAATCAGGGTGGCGAC	