1	A Novel RNA Polymerase-Binding Protein Controlling Genes Involved in Spore
2	Germination in Bacillus subtilis
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11	Supporting Information
12	(SI Experimental Procedures; SI References; Tables S1-2; Figures S1-3)
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15 SI Experimental Procedures

16 Plasmid construction

17 pAH125 (*amyE*::P_{sspB}-lacZ) was constructed as previously described (Camp & Losick, 2009).

- 18 pBAT84 (*amyE*::P_{spoVT}-lacZ) was generated by cloning a *Eco*RI and *Bam*HI digested PCR
- 19 fragment containing the *spoVT* promoter into pAH124 (Camp & Losick, 2009) digested with the

same restriction enzymes. pBAT151 (*sacA::ylyA*) was constructed as previously described

21 (Traag *et al.*, 2013). pBAT260 (*sacA*::P_{sspB}-ylyA) was generated by fusing a PCR fragment

containing the *sspB* promoter and ribosome binding site (RBS) with a PCR fragment containing

the open reading frame (ORF) of *ylyA* by overlapping PCR. The resulting fragment was then

24 digested with *Eco*RI and *Bam*HI, and cloned into pSac-Cam (Middleton & Hofmeister, 2004)

digested with the same restriction enzymes. pBAT298-300 (P_{sspB}-directed overexpression of

26 yocK, yteA and dksA) were generated in the same way. pRLG10611 was generated by cloning a

27 XbaI and XhoI digested PCR fragment containing the ylyA ORF into pET28a (Novagen),

resulting in a construct for the expression of C-terminal, hexahistidine-tagged YlyA.

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30 Protein expression and purification

E. coli BL21 (DE3) derivative strains carrying plasmids pRLG10611 (see above), pDP90

32 (Kearns et al., 2005), pRL3034 (Losick lab strain collection) or pMF327 (Fujita & Sadaie,

1998), encoding hexahistidine-tagged YlyA, SinI, σ^{G} and σ^{A} , respectively, were grown at 25°C

in 1L Luria Bertani (LB) broth. When the cultures reached an OD_{600} of 0.6-0.8, protein

expression was induced by the addition of 100 μ M isopropyl β -D-1-thiogalactopyranoside

36 (IPTG). Cells were harvested and pelleted after four hours of additional growth at 25°C, and cell

37 pellets were frozen overnight at -80°C. The next day cell pellets were resuspended in lysis buffer

38 (50 mM Tris-Cl pH 8.0, 300 mM NaCl, 5 mM imidazole, 1 mM DTT, 1 mM

phenylmethanesulfonylfluoride (PMSF)), and cells were lysed by sonication. Cell debris was 39 removed by centrifugation, and the supernatants were incubated with Ni-NTA agarose beads 40 (Qiagen) at 4°C for 30 minutes. The Ni-NTA agarose-cell suspension was then applied to a poly-41 prep chromatography column (Biorad). The resulting Ni-NTA column was consecutively washed 42 43 with 10 column volumes of lysis buffer, one column volume of buffer containing 25 mM imidazole, and one column volume of buffer containing 50 mM imidazole. Proteins were eluted 44 from the column with column volume fractions of buffer containing 200 mM imidazole. The 45 46 elution fractions were run on a SDS-PAGE gel, and appropriate fractions were dialyzed at 4°C overnight against 1L storage buffer (25 mM Tris-Cl pH 8.0, 100 mM NaCl, 50% glycerol, 1 mM 47 DTT). 48

For purification of *B. subtilis* RNA polymerase core, approximately 500 bp of the 5' end 49 of rpoC, excluding the stop codon, was cloned NdeI and XhoI into pET28a, resulting in a 50 truncated rpoC gene in frame with a sequence coding for six histidine residues. This plasmid-51 borne fragment and an approximately 500 bp genomic DNA fragment downstream of *rpoC* were 52 amplified by PCR, using primers containing sequences complementary to a spectinomycin 53 54 resistance cassette. The resulting fragments and outer primers were then used to amplify a spectinomycin resistance cassette. ylyA mutant cells were transformed with this double stranded 55 linear DNA fragment, and double cross-over events were selected by plating on LB agar 56 57 containing spectinomycin. The resulting strain (RL5493) encodes a C-terminal, hexahistidinetagged β ' subunit as the only copy in the cell. This strain was grown in 1L LB broth at 37°C until 58 an OD_{600} of 1, at which point cells were harvested and pelleted. The pellet was resuspended 59 60 immediately in buffer containing 300 mM NaCl, 50 mM Na₂HPO₄, 3 mM 2-mercaptoethanol, 5

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- 61 % glycerol, and 1 mM PMSF. RNA polymerase core was purified using Ni-NTA agarose similar
- 62 to previously described (Anthony *et al.*, 2000). Fractions eluted from the Ni-NTA column were
- run on a SDS-PAGE gel, and appropriate fractions were dialyzed at 4°C overnight against buffer
- 64 containing 50 mM Tris-Cl pH 8.0, 0.1 M NaCl, 3 mM 2-mercaptoethanol, 50% glycerol. RNA
- 65 polymerase preparations were stored at -20° C.
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67 SI References

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Strain ^a	Genotype	Source or
		reference
PY79	Prototrophic derivative of <i>B. subtilis subsp. subtilis</i> 168	(Youngman
		et al., 1984)
RL5371	ylyA::erm	(Traag et al.,
		2013)
RL5372	ylyA::erm sacA::ylyA (kan)	(Traag et al.,
		2013)
RL5480	ylyA::erm sacA::P _{sspB} -ylyA (cam)	This study
RL5481	$amyE::P_{sspB}-lacZ$ (neo)	This study
RL5482	ylyA::erm amyE::P _{sspB} -lacZ (neo)	This study
RL5483	ylyA::erm sacA::ylyA (kan) amyE::P _{sspB} -lacZ (cat)	This study
RL5484	ylyA::erm sacA::P _{sspB} -ylyA (cat) amyE::P _{sspB} -lacZ (neo)	This study
RL5485	$amyE::P_{spoVT}-lacZ$ (neo)	This study
RL5486	ylyA::erm amyE::P _{spoVT} -lacZ (neo)	This study
RL5487	ylyA::erm sacA::P _{sspB} -ylyA (cat) amyE::P _{spoVT} -lacZ (neo)	This study
AHB1449	$ywrK::Tn917::amyE::P^{T7}-lacZ$ (neo) $ylnF::Tn917::amyE::P_{spoIIQ}$ -	(Camp &
	T7RNAP (spec)	Losick,
		2009)
RL5488	ylyA::erm ywrK::Tn917::amyE::P ^{T7} -lacZ (neo)	This study
	ylnF::Tn917::amyE::P _{spollQ} -T7RNAP (spec)	
RL5489	$ylyA::erm \ sacA::P_{sspB}-ylyA \ (cat) \ ywrK::Tn917::amyE::P^{T7}-lacZ \ (neo)$	This study

Table S1. *B. subtilis* strains used in this study.

	ylnF::Tn917::amyE::P _{spoIIQ} -T7RNAP (spec)	
RL5490	ylyA::erm sacA::P _{sspB} -yocK (cat) amyE::P _{sspB} -lacZ (neo)	This study
RL5491	ylyA::erm sacA::P _{sspB} -yteA (cat) amyE::P _{sspB} -lacZ (neo)	This study
RL5492	ylyA::erm sacA::P _{sspB} -dksA (cat) amyE::P _{sspB} -lacZ (neo)	This study
RL5493	ylyA::erm rpoC::rpoC-6His (spec)	This study

^aAll strains were derived from the prototrophic laboratory strain PY79.

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89 Table S2. Relative levels of germination proteins in spores from wild type, *ylyA* mutant,

90 and *ylyA* overexpression strains.

	wild type	ΔylyA	P _{sspB} -ylyA
GerAA	1	1	0.22
GerAC	1	0.85	0.13
GerBC	1	0.25	0.12
GerKA	1	1	0.25
SpoVAD	1	2.5	1
GerD	1	1	1

91 *All values are averages of results from replicate western blot analysis of two independent spore

92 preparations, and these values differed by $\leq 20\%$. Values for wild type spores have been set at 1,

93 and values for other strains are expressed relative to these values.

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Fig. S1. YlyA interacts with RNA polymerase from lysate from vegetative and sporulating cells. Western blot analysis of the co-immobilization of RNA polymerase subunits with hexahistidine-tagged YlyA. RNA polymerase was similarly co-immobilized when lysates from vegetative (left) and sporulating (right) *ylyA* mutant cells were used. Lanes: soluble protein lysate (1), flow through (2), first wash (3), final wash (4) elution fractions (5-7). Arrows indicate bands corresponding to the β/β' and α subunits of RNA polymerase which co-eluted with YlyA.

YlyA_Bamy	${\tt MNDQLTAIHTELLMMKEELQSRLFEYSCFHMSASVEPSMND-QEATLIYHIKEEL}$
YlyA_Bsub	MNDQLTAIYTELLLMKEELQSRLFEYSCFQVSTSPQAAINQKQKATLIYHIKEEL
YlyA_Blic	MNEQLAAIHTELLQMKEELEARLFEYSFFQQDSQGISSYQQATLMYHVKEEL
YlyA Bpum	MIGDLETIYTELLQMKEELQAKLFEYTSFRSPAEHVSMNEVQTATLLYHIKEEL
YlyA_Bcer	MNEMYMEIKEELQLMRKELQERLAKEVMYKYNTEFSEELGYEMKEEIKKKLLLHDIKEDL
YlyA_Bwei	${\tt MNEIYMEIKEELQLMRKELQDRLAKEVMHTYYMEFGQELGYEIKEETKKKLLLHDIKEDL$
_	* * ** *::**:: *::.:**:*
YlyA_Bamy	$\label{eq:constraint} QDVLLALSKFENNMYGYCEKTGDPIPIEKLAVLPTARTADDFYYPAQFEKKTLP-YWEPG$
YlyA_Bsub	QDVLLALSKIENGTFGYCEETGAPIPLAKLAVLPTARTANDFLYSVQFEKKTLP-IWKST
YlyA_Blic	QDVLLALSKIENGTYGICEETNQAIPLAKMTILPTARTANDFLYHAQFEKKTLP-IWAET
YlyA_Bpum	QDVSLAIAKIEQGTYGICEATGDVIPLEQMSILPTARTVDDFLYHKQYEKKAFTPYPHES
YlyA_Bcer	KDVERALFKMEIDMYGICEDTGRVISVKQMKTMPTARTIHEFFYEKVNV
YlyA_Bwei	KDVERALFKMEIDMYGICEETGRAISTKQMKTMPTARTIHEFFYEKVNV
	:** *: *:* . :* ** *. *. :: :***** .:* *
YlyA_Bamy	DYAYDQALYE
YlyA_Bsub	DIEYGQALYE
YlyA_Blic	DETFNRALYS
YlyA_Bpum	DDSHFEAFHM
YlyA_Bcer	
YlyA_Bwei	

Fig. S2. Alignment of the amino acid sequences of YlyA orthologs from Bacillus species.

ClustalW was used to align the amino acid sequences of YlyA orthologs from B.

amyloliquefaciens, B. subtilis, B. licheniformis, B. pumilus, B. cereus, and B.

weihenstephanensis. Identical residues (*), conserved substitutions (:), and semi-conserved

substitutions (.) are indicated below the alignment. The region around the predicted coiled-

coil tip is indicated with a hook above the sequence.



Fig. S3. The C-terminus of YlyA is partially dispensible *in vivo*. β-galactosidase activity (AU) was monitored for samples taken at the indicated time points after sporulation was induced by resuspension. P_{sspB} -directed *lacZ* activity was determined in *ylyA* mutant cells (triangles), *ylyA* mutant cells carrying a copy of *ylyA* expressed from the *sspB* promoter at the ectopic *sacA* locus (circles), and *ylyA* mutant cells carrying C-terminally truncated copies of the *ylyA* gene encoding YlyA residues 1-98 (*ylyA*⁹⁸; diamonds) and YlyA residues 1-71 (*ylyA*⁷¹; squares), expressed from the *sspB* promoter at the ectopic *sacA* locus. All strains carry the P_{svpB}-*lacZ* reporter construct at the *amyE* locus.