The nucleotide sequence of the *recE*⁺ gene of *Bacillus subtilis*

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The RecE protein of the spore forming, naturally competent gram positive bacterium *B. subtilis* is homologous to the RecA protein of *Escherichia coli* (1, 2). Specifically, the *recE* gene product is essential for the enhanced transcription of the genes that comprise the SOS-like or SOB global regulon (3). In addition, this protein is required for homologous recombination and for aspects of DNA repair (1, 3). However, unlike the *E. coli* model, the *recE* gene is under two distinct forms of regulation; DNA damage inducible regulation and developmental regulation when the bacteria differentiates into its natural competent state (4). The *recE* gene was previously cloned and isolated using the bacteriophage ϕ 105J23 (2). Presented in this report is the nucleotide sequence of the *recE* gene. To our knowledge, this is the first sequence of a RecA analogue from a gram positive organism that has been presented. The protein sequence was determined from the primary structure of the gene and from the translation start (position 215) following N-terminal sequencing (R.Losick and J.Roberts, personal communication). The RecE consists of 349 amino acids of which 60% are directly conserved with the RecA protein of *E. coli*. In addition, there has been an

apparent conservation of the putative single strand DNA binding domain (5), of the nucleotide binding domain (6) and of the acidic nature of the carboxyl-terminus (7).

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AATCACGCCAAGAAAAATCCGAATATGCGTTCGCTTTTTCTTGGCAATCCCTTCAAACAGGGTATAGTATATGTAAGTAAACATAAAGGAGGAAAAATAGAAAT
s d r q a a l d m a l k q i e k q f g k g s i m k l g e k t d t r i s t
GAGTGATCGTCAGGCAGCCTTAGATATGGCTCTTAAACAAATAGAAAAACAGTTCGGCAAGGTTCCATTATGAACTGGGAGAAAAGACAGATACAAGAAATTTCTAC
v p s g s l a l d t a l g i g g y p r g r i i e v y g p e s s g k t t v
TGTACCAAGCGGCTCCCTCGCTCTTGATACAGCACTGGGAATTGGCGGATATCTCGCGGACGGATTATTGAAGTATACGGTCTGAAAGCTCAGGTAAAACAACTGT
a l h a i a e v q q q g g q a a f i d a e h a l d p v y a q k l g v n i
GGCGCTTCATCGGATTGCTGAAGTTCAGCAGCAGGCGGACAGCGCGTTTTCGATGCGGAGCATGCGTTAGATCCGGTATACGCGCAAAAGCTCGGTGTTAACAT
e e l l l s q p d t g e q a l e i a e a l v r s g a v d i v v v d s v a
CGAAGAGCTTTTACTGTCTCAGCCTGACACAGGCGAGCAGGCGCTTGAATTTGCGGAAGCATTGGTTTGAAGCGGGCAGTTGACATTGTCGTTGTCGACTCTGTAGC
a l v p k a e i e g d m g d s h v g l q a r l m s q a l r k l s g a i n
CGCTCTCGTTCGAAAGCGGAAATTGAAGGCGACATGGGAGATTCCGATGTCGGTTTACAAGCAGCGTTAATGTCTCAAGCGCTTCGTAAGCTTTCAGGGGCCATTAA
k s k t i a i f f i n q i r e k v g v m f g n p e t t p g g r a l k f y s
CAATCGAAGACAAATCGGATTTTCATTAACCAAAATTCGTGAAAAAGTCGGTGTATGTTCGGGAACCCGGAACACACCTGGCGGCGGTGCGTTGAAATTCATTTC
s v r l e v r r a e q l k q g n d v m g n k t k i k v v k n k v a p p f
TTCGTCGCTCTTGAAGTGCCTGCTGAACAGCTGAAACAAGGCAACGACATTAATGGGGAACAAACGAAATCAAAAGTCGTGAAAAACAGGTGGCTCCGCGCTT
r t a e v d i m y g e g i s k e g e i i d l q t e l d i v q k s g s w y
CGGTACAGCCGAGGTTGACATTATGTACGGAGAAGGCATTTCAAAAAGAGCGAATCATTGATCTAGGAACCTGAATCTGATCGTCAAAAAAGCGGTTTCATCGTA
s y e e e r l g q g r e n a k q f l k e n k d i m l m i q e q i r e h y
CTCTTATGAAGAGAGCGCTTGGCCAAGGCGGTGAAAAATGCAAAACAATTCCTGAAAGAAAAATAAGATATCATGCTGATGATCCAGGAGCAAAATTCGCGAACATTA
g l d n n g v v q q q a e e t q e e l e f e e
CGGCTTGGATAATAACCGAGTAGTCAGCAGCAAGCTGAAGAGACACAAGAACTCGAATTTGAAGAATAAAAAATAAATAGTTTCAATGATACAAAAGGCTGA

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