

# Revised nucleotide sequence of the sporulation gene *spoVE* from *Bacillus subtilis*

Tsutomu Sato, Gunjana Theeragool<sup>1</sup>, Tatsuo Yamamoto<sup>1</sup>, Masaji Okamoto<sup>1</sup> and Yasuo Kobayashi

Department of Agricultural Chemistry, Faculty of Agriculture, Tokyo University of Agriculture and Technology, Fuchu 183, and <sup>1</sup>Faculty of Applied Biological Science, Hiroshima University, Higashi Hiroshima 724, Japan

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The nucleotide sequence of the *spoVE* gene has been determined previously by Bugaichuk and Piggot (1) and they reported that the *spoVE* gene consisted of 293 amino acid residues. However, we found that one nucleotide (thymine at no. 317 in Figure; boxed) was missing in the nucleotide sequence. The addition of thymine gave rise to a polypeptide of 40,131 daltons (366 aa). Its initiation codon (TTG) is preceded by an SD sequence having  $\Delta G$  of  $-17.8$  kcal/mol. The amino acid sequence of *spoVE* gene product is highly homologous with that of the newly identified

*E. coli* FtsW and RodA proteins functioning in cell division and cell elongation (2). It is suggested that the SpoVE protein plays an essential role not only during sporulation, but also during vegetative growth.

## REFERENCES

1. Bugaichuk, U.D. and Piggot, P.J. (1986) *J. Gen Microbiol.* **132**, 1883–1890.
2. Ikeda, M. et al. (1989) *J. Bacteriol.* **171**, 6375–6378.

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1  gggcttgct tgaagtaaa cggcagccct aatgacttta agcttgggggt gtcgattgct TTGACTACTA AAAAAACATC GCCTGATTG TTATTGGTCA
101 TCATTACGTT ATTATTATTA ACAATCGGAT TAATTATGGT GTACAGTGGC AGTGCGGTAT GGGCGGATTA TAAATTTGAC GACTCATTCT TTTTCGGAA
201 ACGGCAGCTT TTGTTTGGCG GAATCGCCGT CATTGCTATG TTTTTATCA TGAATGTGA TTATTGGACT TGGAGGACAT GGTCCAAATT GCTGATGGT
301 ATCTGCTTTT TCCTTTCGGT GCTTGTTTTG ATACCGGGCG TCGGAATGGT GCGGAACGGT TCAAGAAGCT GGATCGGAGT CGGAGCATTG AGCATAACG
401 CTTCAGAGTT TATGAAGCTT GCGATGATTG CATTCCITGC TAAATTTCTC TCTGAAAAAC AAAAAACAT CACATCGTTC AGACGGGGGT TCGTCCCTGC
501 ACTTGGCATC GTGTTTTCAG CATTITTTGAT TATCATGTGC CAGCCTGACC TCGGAACGGG GACAGTTATG GTCGGAACCT GTATTGTCAT GATTTTTGTA
601 GCCGGCCAC GGATCGECCA TTTCTCTTT CTCGGGCTGA TCGGCCTCAG CGGATTTGTC GGGCTCGTAC TATCGGCTCC ATATCGGATA AAGCGGATTA
701 CCTCATACTT AAATCCATGG GAAGACCCGC TCGGAAGCCG ATTCAGATC ATTCAAATGC TTATGTCAGT GGGGCCCGGC GGGTTGTTCC GAATGGGGCT
801 CGGACAAAGC AGACAGAAGT TCTTTTATCT GCCTGAGCCG CAAACAGACT TTATTTTCCG CATCTGTCA GAGGAGCTGG GCTTTATCGG GGAACACTT
901 ATTTTCTCC TCTTCAGCGT CCTGCTGTGG AGAGGAATCA GAATTCGCT TGGTCCGCT GATCTGTACG GAAGCTTTGT CGCAGTCGGC ATTATTTCAA
1001 TGATTGCCAT TCAAGTCATG ATAAATATCG GCGTAGTCAC GGGCCTGATT CCTGTAACAG GCATCAGCCT CCCGTTTCTG AGCTACGGAG GCTCTTCATT
1101 GACTCTAATG CTGATGGCAG TTGGTGTGCT GCTGAATGTA AGCCGCTACT CGAGGTATa acgaatgat ttccaagcct cctgtctaac atgaagcttg
1201 gaaacaattg atcgataac cctgtccaac aaaacaggggt tatcggtatg ttatagagaa acttagactg ggggaaaaaa gaa

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