A *Bacillus subtilis* gene cluster similar to the *Escherichia coli* phosphate-specific transport (pst) operon: evidence for a tandemly arranged pstB gene

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We have determined the complete nucleotide sequence of the *Bacillus subtilis* homologues of the *Escherichia coli* phosphate-specific transport (pst) genes in the framework of the international *B. subtilis* genome sequencing project. The pst genes in *E. coli* form an operon arranged in the order *pstS, pstC, pstA, pstB* and *phoU*. In the case of *B. subtilis*, there are also five ORFs presumably forming an operon. The deduced amino acid sequences of the products of these ORFs show striking similarities to their *E. coli* counterparts. Comparison of the organization of the pst operon of *B. subtilis* with that of *E. coli* revealed that the gene corresponding to *phoU* is missing, while there are two genes homologous to *pstB* in *B. subtilis*. The pst operon is located at 222° on the *B. subtilis* chromosome.

**Keywords:** *Bacillus subtilis*, genome sequencing project, phosphate-specific transport operon, pstB, tandem genes

The phosphate-specific transport (Pst) system of *Escherichia coli* comprises four distinct subunits encoded by the *pstS, pstA, pstB* and *pstC* genes (Amemura et al., 1985; Surin et al., 1985). These genes, together with the *phoU* gene, form the pst operon, which maps at about 84 min on the *E. coli* chromosome (Bachmann, 1990). The nucleotide sequences of all five genes have been determined, and the amino acid sequences of the corresponding proteins have been deduced (Amemura et al., 1985; Surin et al., 1985). Apart from transporting phosphate, the Pst system plays an important role in the regulation of a number of coordinately regulated genes collectively referred to as the phosphate regulon (Wanner, 1987; Wanner & Letterel, 1980).

As part of the international *Bacillus subtilis* sequencing project, we report here the cloning and sequencing of *B. subtilis* homologues of the *E. coli* pst gene products.

A λ phage library of *B. subtilis* strain JH642 (trpC2 pheA1)

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Abbreviations: Pst, phosphate-specific transport; RBS, ribosome-binding site.

The DDBJ accession number for the nucleotide sequence reported in this paper is D58414.
Fig. 1. For legend see facing page.
Nucleotide sequence of *B. subtilis* pst operon

The deduced amino acid sequence of ORF108 shows 20.7% identity to the PstS protein, which is a phosphate-binding protein located in the periplasmic space (Gerdes & Rosenberg, 1974). The ORF72 product has 26.1% identity to the PstC protein, and the protein encoded by ORF73 has 27.2% identity with the PstA protein. The PstA and PstC proteins are hydrophobic and likely to form the transmembrane portion of the Pst system (Amemura et al., 1985; Surin et al., 1985). The hydropathy plots of the ORF72 and ORF73 products show significant similarities to those of their *E. coli* counterparts (data not shown). Interestingly, the ORF74 and ORF75 products show 58.6% identity with each other and 57.3% identity to the PstB protein (Fig. 2). The PstB protein is hydrophilic and is likely to interact on the cytoplasmic side with the PstA and PstC proteins. Two key residues (Gly-48 and Lys-49) have been shown to be required for phosphate transport by the Pst system (Cox et al., 1989) and are located in the conserved sequence associated with a nucleotide-binding site (Higgins et al., 1985). Importantly, these two residues are also conserved in the ORF74 and ORF75 products (Fig. 2).

Comparison of the organization of the *pst* operon of *B. subtilis* and that of *E. coli* is represented schematically in Fig. 3. It is very interesting that the gene corresponding to *phoU*, which is involved in the regulation of the phosphate regulon in *E. coli* (Wanner, 1987), is not present in the *B. subtilis* *pst* operon, while there are two genes homologous to *pstB* in *B. subtilis*. The location of *phoU* gene homologue in *B. subtilis* is not known at present.
ACKNOWLEDGEMENTS

We are grateful to Dr Naotake Ogasawara for helpful comments and suggestions. We thank Dr Mitsugoro Itaya for the kind gift of NotI linking clone, pNEXT27. This work was supported by a Grant-in-Aid for Creative Basic Research 'Human Genome Analysis' from the Ministry of Education, Science and Culture, Japan.

REFERENCES


Received 6 February 1996; revised 22 March 1996; accepted 29 March 1996.