A putative new peptide synthase operon in *Bacillus subtilis*: partial characterization

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Micro-organisms produce a large number of peptides, generally as secondary metabolites, which have many important activities varying from antibacterial to antiviral or antifungal, and from anticarcinogenic to immuno-suppressive. Regardless of their function, these peptides are synthesized either using the usual ribosomal system or through the action of complex multi-enzyme systems known as peptide synthases.

It is now clear that although their products can vary considerably in length and amino acid composition, all peptide synthases studied so far share remarkable similarity in their structural organization and mechanism of action (Kleinkauf & von Döhren, 1990; Cosmina et al., 1993). They are in fact organized into structural domains, each of which is responsible for the recognition and binding of a specific amino acid. Peptide synthesis takes place through subsequent reactions of thioester cleavage and amide bond formation.

*Bacillus subtilis* produces a number of peptides and lipopeptides, both linear and cyclic (Zuber et al., 1993). Of these, only surfactin has been thoroughly characterized at the genetic level (Cosmina et al., 1993; van Sinderen et al., 1993). From gene sequence analysis and a variety of biochemical studies, it was found that surfactin synthase is a multi-subunit enzyme complex in which there are seven structural domains, corresponding to the number of amino acids present in surfactin.

In this communication we report the identification in the *B. subtilis* chromosome of a large operon encoding a new peptide synthase.

The 15.4 kb fragment present in λ clone λB21 (Fig. 1), derived from a *B. subtilis* 168 chromosomal library (Ferrari et al., 1981), was mapped by PBS1 transduction (Haldenwang et al., 1980) to position 175°, approximately, on the *B. subtilis* genetic map. Using a 1.2 kb HindIII fragment of AB21 to screen the *B. subtilis* library in λFIXII (Kunst & Devine, 1991), two additional λ clones (λ1A and λ4B) were identified by DNA:DNA hybridization, the inserts of which overlap with the chromosomal fragment carried by λB21 (Fig. 1). Finally, an additional 4.3 kb overlapping fragment was isolated by chromosome walking (Glaser et al., 1993) after cloning the AB21 HindIII-Acyl fragment into the suicide vector pDIA5304. Altogether, the three λ clones and the pDIA5304 derivative contained an uninterrupted chromosomal region of approximately 25 kb.

The identity of the 25 kb region carried by the λ and plasmid vectors with the corresponding chromosomal area was confirmed by both restriction enzyme and Southern blot analyses. In particular, when λB21, λ4B and λ1A were digested with EcoRI and NotI, fragments of identical size were identified on an agarose gel. Furthermore, the large 3.0 kb EcoRI fragment of the three clones (Fig. 1) hybridized with an internal 32P-labelled probe in a Southern blot experiment (data not shown). Finally, the Southern blot analyses of the chromosomal DNA digested with a variety of restriction enzymes and hybridized with a duplicated region (see below) located within the 7270 bp NotI–EcoRI fragment of λB21 and within the 4149 bp EcoRI–NotI fragment of λ1A, respectively, gave restriction patterns consistent with the data deduced from sequence analysis.

To confirm the map location of this 25 kb segment, two fragments, the 1.3 kb EcoRI–NotI fragment located at the 5' end of the region and the 1.2 kb XhoI–ApaI fragment located at the 3' end were used as probes to screen the YAC collection of ordered *B. subtilis* DNA fragments (Azevedo et al., 1993), kindly provided by Dr D. Ehrlich.

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The EMBL accession number for the nucleotide sequence data reported in this paper is Z34883.
Hybridization experiments showed that the region maps between gltA (177') and citB (173') and its orientation is such that the EcoRI–NotI fragment is proximal to gltA and the XbaI–ApaI fragment maps next to citB. In fact, the EcoRI–NotI fragment hybridized with YAC15-19 which contains gltA whereas the other fragment hybridized with YAC15-37 which carries citB (the chromosomal fragments of the two YACs have overlapping regions).

The entire region was sequenced using a combination of two strategies. Restriction fragments covering approximately 30% of the region were subcloned in pUC vectors and their nucleotide sequence was determined using a variety of sequencing kits, including Sequenase (USB), and their nucleotide sequence was determined using a cycle-sequencing technique using the recombinant DNAs as templates (Saluz et al., 1991), but no significant homology was found between ORF1 and ORF2 and any of the protein sequences of the Swiss-Prot data bank (release 28) using the FSTSCAN (PCGENE) program.

Analysis of the three remaining ORFs, the last of which is only partially contained in the sequenced region, suggested that they are embedded in a large operon whose structure resembles the bacterial operons encoding peptide synthases (Turgay et al., 1992; Cosmina et al., 1993). The 2561 amino acid product of orf4 is preceded by a putative ribosome binding site (RBS; GGAGG), 7 bases upstream from its TTG start codon. orf5, a gene encoding a protein of identical size to that of ORF4, starts after an intergenic region of 27 bp, whereas orf6 is located only 16 bp downstream from the 3' end of orf5 and encodes a protein of at least 859 amino acids. Both the intergenic regions between orf4 and orf5 and between orf5 and orf6 contain putative B. subtilis RBSs (AAAGGTTGTTGG and ATAGGAGAGAG, respectively).

From the analysis of the sequence with the CLUSTAL and MACAW programs, it turns out that ORF4, ORF5 and ORF6 are organized into five structural domains (two in both ORF4 and ORF5, and one in ORF6) which are homologous not only to each other (with more than 20% identity) but also to the structural domains of all peptide synthases characterized so far. In particular, the 4-phosphopantetheine cofactor binding site LGG(D/H)SH(I/L), the ATP binding sites SGTTGKPRG, YGPTE, TGD and NGK, and the sequence HHILDGW delimiting the regions of the structural domains are highly conserved. Interestingly, the carboxy-terminal of both ORF4 and ORF5, spanning about 500 amino acids, shares homology with the carboxy-terminal of the SrfAORF1 and SrfAORF2 subunits of surfactin synthase, the TycA subunit of tyrocidine syn-
Fig. 2. Homology study among the structural domains of all peptide syntheses characterized so far. The dendrogram has been drawn using the CLUSTAL program and taking into account the most conserved central region (approximately 180 amino acids in length spanning from the conserved sequences PKG and GRLCY) of each domain which is supposed to be involved in amino acid recognition and binding (Cosmina et al., 1993). The domains of peptide x synthase are indicated as ppsDOM(1–5).

As far as the nature of the amino acids constituting the hypothetical peptide is concerned, Turgay et al. (1992) and Cosmina et al. (1993) have shown that in bacterial peptide synthases the domains which bind the same amino acid have specific and characteristic patterns of amino acid conservation. The comparative analysis of the central region of the five domains of the new peptide synthase with the same regions of the peptide synthases from Bacilli (Fig. 2) shows that domains 1 and 5 are mostly related to the glutamic acid binding domain of surfactin synthase, domain 2 is remarkably similar to the ornithine binding domain of gramicidin synthase and domains 3 and 4 resemble the leucine binding domain of gramicidin synthase.

Preliminary data indicate that the operon is not functional in B. subtilis 168 under normal growth conditions although two putative σ^A promoters are present 33 bp (TTGCA-17 bp-TACAAT) and 140 bp (TTCAAA-17 bp-TTTAAT) upstream from the orf4 start codon, respectively. When active promoters are inserted upstream from orf4, the expression of protein species having the expected molecular mass can be detected on SDS-PAGE (data not shown). Purification and characterization of these proteins is in progress to help elucidate the activity of this peptide synthase.

We propose to name the new enzyme peptide x synthase and the coding genes ppsorf1, ppsorf2 and ppsorf3.

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References


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