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NOTE

# Isolation and Characterization of Two Amino Acid-activating Domains of Peptide Synthetase Gene from *Bacillus subtilis* 713

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**Abstract** From the sequence alignment of various nonribosomal peptide synthetases, several motifs of highly conserved sequences have been identified within each domain of peptide synthetases. We designed PCR primers based on the highly conserved nucleotide sequences to amplify and isolate a ~7.2-kb DNA fragment of the *Bacillus subtilis* 713 which was isolated and reported to produce an antifungal peptide compound. Nucleotide sequence analysis of 4.8 kb of the predicted amino acids revealed significant homology to various peptide synthetases over the whole sequence and also revealed two amino acid-activating domains with highly conserved Core 1 to Core 6 and spacer motif. This suggests that the isolated DNA fragment is part of a peptide synthetase gene for antifungal peptide.

**Key words:** Peptide antibiotics, PCR, *Bacillus subtilis* 713, nucleotide sequence

In order to decrease environmental pollution and solve the problem of widespread appearance of drug resistant pathogens, the development of new antibiotics is urgently needed. In this sense, peptide antibiotics have been a source of attention since it is possible to program a noble antibiotics by gene manipulation of modular domains of peptide synthetase genes as described by Stachelhaus *et al.* [30]. The stability of peptide antibiotics to most peptidases and proteases has made them useful in the pharmaceutical and agricultural industries [19, 20, 29]. Bacilli are the extensively studied bacteria known to produce peptide antibiotics and to be regarded as relatively safe to humans [10, 11, 14, 29]. Peptide antibiotics are also produced by many microorganisms in addition to Bacilli [20], and exhibit diversity with respect to chemical structure and biological activity. Although structurally diverse, peptide antibiotics are largely divided into two subgroups based on biosynthetic mechanisms, namely, ribosomal biosynthesis [9, 28] and nonribosomal biosynthesis.

Many of peptides are not gene-encoded, but are synthesized nonribosomally through a series of reactions catalyzed by large, often multisubunit, enzyme complexes called peptide synthetases by a thiotemplate mechanism [17, 29, 31, 32]. Each subunit of peptide synthetases has independent enzymatic activity. Isolation, sequencing, and characterization of several genes encoding multifunctional peptide synthetases of bacterial and fungal origin required for nonribosomal synthesis of peptide antibiotics have confirmed that the gene is composed of several domains for the corresponding subunits. The occurrence and specific order of domains of synthetase genes dictate the number and sequence of the amino acids incorporated into the peptide product [31]. These findings have made it possible to develop noble antibiotics. For example, Stachelhaus *et al.* [30] developed noble antibiotics by genetic manipulation of domains of the peptide synthetase genes.

Sequence alignment has also revealed six highly conserved motifs (Core 1 to Core 6) and a spacer motif in peptide synthetase genes [15, 16, 17, 31]. Cores 2 to 5 are believed to be involved in ATP-binding and hydrolysis. The Core 6 motif seems to be involved in the catalysis of the formation of thioester bonds. However, the function of the Core 1 motif is not yet known. Among the conserved regions, Core 1 and Core 2 are highly conserved even in nucleotide sequences (Fig. 1a) [3].

In this study, we designed PCR primers based on the highly conserved nucleotide sequences of Core 1 and Core 2 to isolate and characterize the peptide antibiotics synthetase genes from *Bacillus subtilis* 713 strain [12, 13]. *Bacillus subtilis* 713 strain was isolated from Korean soil and known to produce antifungal peptide

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compounds [12, 13]. Using the isolated DNA fragment as a probe, we isolated an approximately 7.2-kb DNA fragment and determined 4.8-kb of its nucleotide sequence. The predicted amino acid sequence based on the nucleotide sequence of the DNA fragment showed significant homology to various peptide synthetase genes. From the alignment with various synthetase genes, two amino acid-activating domains of peptide synthetase were detected in the 4.8-kb DNA fragment and these domains were well matched with the previous chemical analysis of the amino acid components of the antifungal peptide compound, suggesting that the DNA fragment isolated in this study is a part of the peptide synthetase gene of *Bacillus subtilis* 713.

We used *Escherichia coli* DH5αF' (Gibco BRL, Gaithersburg, U.S.A.) as the host for all plasmid constructions. Luria broth (LB) from Davis *et al.* [4] was used for routine growth of *Escherichia coli* strains and *Bacillus subtilis*. Penassay broth (Antibiotic medium 3, Difco Co., Detroit, U.S.A.) was used for growth of

**A.**

| | CORE I | | | | | | | | | | | | | CORE II | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | TTI | AAA | GCA | GGC | GGI | GCI | TAT | GTG | CCG | ATC | GAC | CC | | ATI | TAC | ACI | TCT | GGI | ACI | ACA | GGI | AAG | CCA | AAA | GG | |
| | | G | G | T | | | | | | | T | T | | | T | | C | | | | | | | | | |
| *grsA* | (328) | TTA | AAA | GCA | GGT | GGA | GCA | TAT | GTT | CCG | ATT | GAT | ATT | (363) | ——— 199 ——— | (562) | ATT | TAT | ACT | TCT | GGT | ACA | ACA | GGC | AAT | CCA | AAA | GGT | (597) |
| | | L | K | A | G | G | A | Y | V | P | I | D | I | | | | I | Y | T | S | G | T | T | G | N | P | K | G | |
| *grsB1* | (1615) | TTA | AAA | GCT | GGT | GGA | GCT | TTT | GTG | CCT | ATT | GAT | CCT | (1650) | ——— 184 ——— | (1834) | ATT | TAT | ACA | TCA | GGA | ACA | ACA | GGT | AAA | CCA | AAA | GGG | (1869) |
| | | L | K | A | G | G | A | F | V | P | I | D | P | | | | I | Y | T | S | G | T | T | G | K | P | K | G | |
| *grsB2* | (4732) | CTT | AAA | GCA | GGG | GGA | GCT | TAT | TTA | CCT | CTT | GAT | CCG | (4767) | ——— 190 ——— | (4957) | ATG | TAC | ACT | TCT | GGT | TCT | ACA | GGA | AAG | CCT | AAA | GGT | (4992) |
| | | L | K | A | G | G | A | Y | L | P | L | D | P | | | | M | Y | T | S | G | S | T | G | K | P | K | G | |
| *grsB3* | (7840) | TTA | AAA | GCA | GGA | GGA | GCA | TAT | GTG | CCT | ATC | GAT | ATA | (7875) | ——— 190 ——— | (8065) | ATT | TAC | ACT | TCT | GGT | ACA | ACC | GGA | AAG | CCA | AAA | GGT | (8100) |
| | | L | K | A | G | G | A | Y | V | P | I | D | I | | | | I | Y | T | S | G | T | T | G | K | P | K | G | |
| *grsB4* | (10981) | TTG | AAA | GCA | GGA | GGA | GCA | TAT | GTT | CCA | ATT | GAT | CCA | (11016) | ——— 190 ——— | (11206) | ATT | TAT | ACA | TCC | GGT | ACA | ACC | GGA | AAG | CCT | AAA | GGG | (11241) |
| | | L | K | A | G | G | A | Y | V | P | I | D | P | | | | I | Y | T | S | G | T | T | G | K | P | K | G | |
| *tycA* | (292) | CTT | AAA | GCA | GGC | GGA | GCC | TAT | GTG | CCC | ATC | GAC | ATC | (327) | ——— 199 ——— | (526) | ATT | TAC | ACC | TCA | GGC | ACG | ACA | GGC | AAG | CCA | AAA | GGC | (561) |
| | | L | K | A | G | G | A | Y | V | P | I | D | I | | | | I | Y | T | S | G | T | T | G | K | P | K | G | |
| *tycB1* | (1618) | TTG | AAG | GCA | GGC | GGC | GCA | TTT | GTG | CCG | ATC | GAC | CCG | (1653) | ——— 190 ——— | (1843) | ATC | TAT | ACG | TCC | GGA | ACG | ACA | GGG | CAA | CCG | AAA | GGC | (1878) |
| | | L | K | A | G | G | A | F | V | P | I | D | P | | | | I | Y | T | S | G | T | T | G | Q | P | K | G | |
| *tycB2* | (4723) | CTC | AAA | GCG | GGC | GGG | GCG | TAT | GTG | CCG | ATC | GAT | CCG | (4758) | ——— 187 ——— | (4945) | ATC | TAC | ACA | TCC | GGT | ACG | ACA | GGC | AGG | CCA | AAA | GGC | (4980) |
| | | L | K | A | G | G | A | Y | V | P | I | D | P | | | | I | Y | T | S | G | T | T | G | R | P | K | G | |
| *pcbAB1* | (1087) | TGG | AAA | TCC | GGC | GCC | GCC | TAC | GTG | CCC | ATC | GCA | CCC | (1123) | ——— 228 ——— | (1351) | ACT | TAC | ACC | TCT | GGG | ACC | ACT | GGC | TTC | CCA | AAG | GGC | (1386) |
| | | W | K | S | G | A | A | Y | V | P | I | D | P | | | | T | Y | T | S | G | T | T | G | F | P | K | G | |
| *pcbAB2* | (4369) | TGG | AAG | AGC | GGC | GGT | GCC | TAT | GTC | CCC | ATT | GAC | CCT | (4404) | ——— 208 ——— | (4612) | ATC | TAT | ACC | TCT | GGA | ACG | ACA | GGT | CGG | CCC | AAG | GCC | (4647) |
| | | W | K | S | G | G | A | Y | V | P | I | D | P | | | | I | Y | T | S | G | T | T | G | R | P | K | G | |
| *pcbAB3* | (7618) | TGG | AAG | GCT | GGT | GCA | GCA | TAC | GTG | CCC | TTG | GAT | CCG | (7653) | ——— 205 ——— | (7858) | ATC | TTT | ACT | TCA | GGC | ACT | TCC | GGT | AAG | CCA | AAG | GGA | (7893) |
| | | W | K | A | G | A | A | Y | V | P | L | D | P | | | | I | F | T | S | G | T | S | G | K | P | K | G | |

**B.**

Core I : TTI AAA(G) GCA(G) GGC GGI GCI TAT GTG CGG ATC(T) GAC(T) CC

P1

Core II : ATI TAC(T) ACI TCT(C) GGI ACI ACA GGI AAG CCA AAA GG

P2

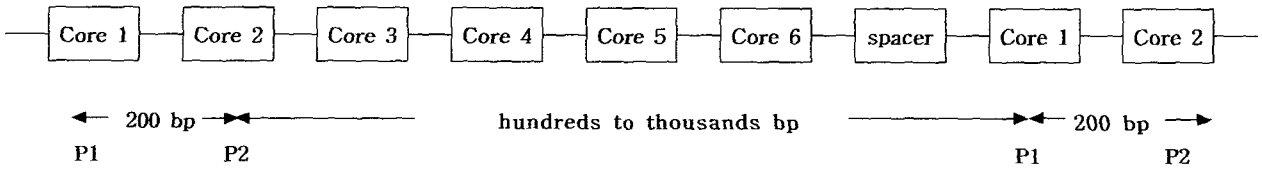





**Fig. 1.** Sequence of the primers used for polymerase chain reaction.

A. Multiple alignment of Core 1 and Core 2 region of various peptide synthetase domains. B. Primers 1 and 2 were designed based on the conserved sequence of Core 1 and the Core 2 sequence [31]. Primer 1: 5'-GGG(A) TCG(A) ATC CGC ACA TA-3' and primer 2: 5'-GGI ACI ACA GGI AAG CCA AAA GG-3'. PCR with primers 1 and 2 were supposed to give several bands ranging hundreds to thousands bp in length, because they would amplify the region from Core 2 of one domain to Core 1 of the following domain.

*Bacillus subtilis* for chromosome isolation. For all standard recombinant DNA techniques, the suggested procedures of Davis *et al.* [4] and Sambrook *et al.* [27] were used. Most enzymes including restriction enzymes, ligase, Klenow, and *Taq* polymerase were purchased from Takara (Shiga, Japan). DNA sequencing was done by the dideoxynucleotide chain termination method for double stranded and single stranded plasmid using $\alpha$-$^{32}$P-dATP (Amersham, Arlington Heights, U.S.A.) and the Sequenase version 2.0 enzyme as suggested by the manufacturer (US Biochemical, Cleveland, U.S.A.). Priming for DNA sequencing was done with custom-made oligonucleotide primers (Takara, Shiga, Japan and Bioneer, Chungwon, Korea) or with standard forward and reverse primers (US Biochemical, Cleveland, U.S.A.). Reaction conditions were as previously described [23]. Chromosomal DNA from the *Bacillus subtilis* was isolated by a modified version of the method of Ferrari *et al.* [5].

*Bacillus subtilis* 713 was isolated from Korean soil and was reported to produce antifungal compounds which seem to comprise Arg, Val, Thr, Ala, Asp (or Asn), Pro, and so on [26]. However, the exact structure of the antifungal compound has not yet been determined. In order to isolate the biosynthetic gene for peptide antibiotics, primers based on the conserved regions — Core 1 and Core 2 — were used for polymerase chain reaction. A primer set was primer 1: 5'-GGG(A) TCG(A) ATC CGC ACA TA-3' and primer 2: 5'-GGI ACI ACA GGI AAG CCA AAA GG-3'. Polymerase chain reaction condition was performed as described by Lee *et al.* [22]. Amplified products were separated by agarose gel electrophoresis. The desired band was eluted from the gel using the Qiaex II Agarose Gel Extract system

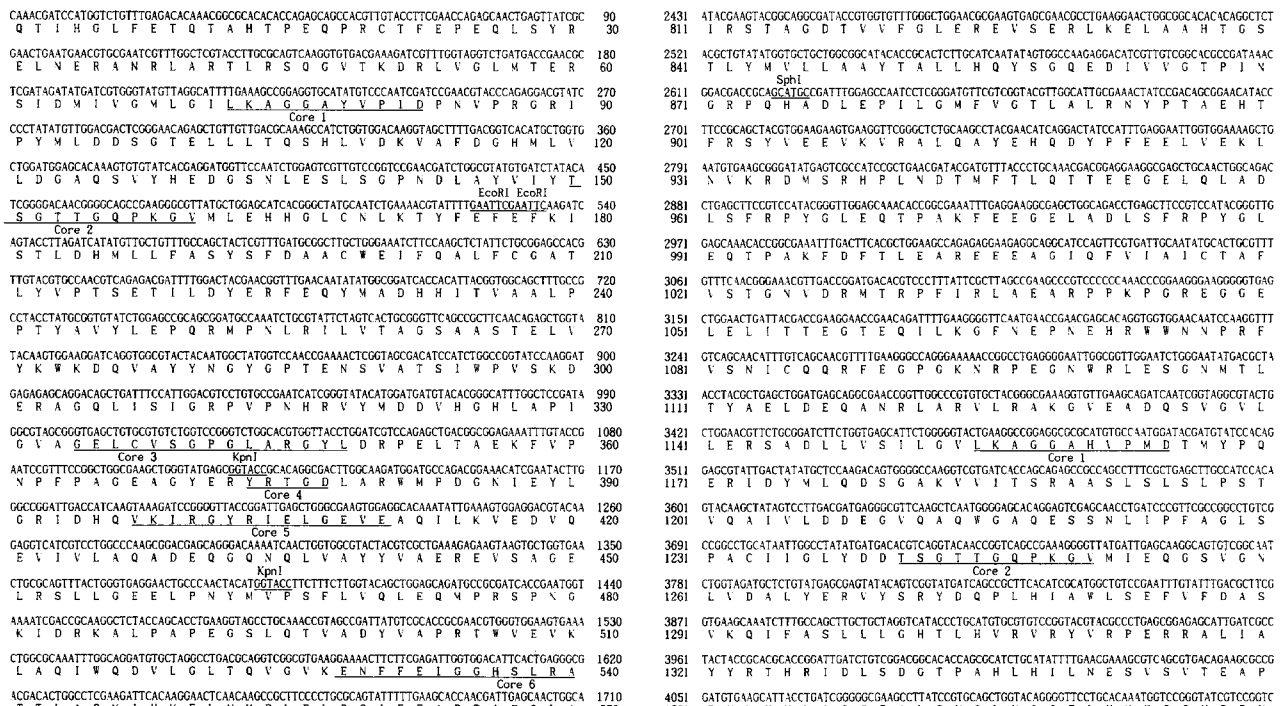

**Fig. 2.** Nucleotide sequence and their predicted amino acid sequence of DNA fragment isolated from *Bacillus subtilis* 713.
Nucleotide sequences are read in both directions. The deduced amino acid sequence is given in single letter code. Conserved peptide synthetase motifs (Core 1 to Core 6 and spacer motif) are underlined. Some restriction sites are also underlined. The nucleotide sequence has been submitted to the GenBank under accession number AF 071566.

(Qiagen, Chatsworth, U.S.A.) and then ligated into pGEM-T Easy vector (Promega, Madison, U.S.A.).

Core 1 region, whose function is not yet clear, and Core 2 region, which functions as an ATP binding site, were used [31] for designing the PCR primers (primers 1 and 2). With these primers and with 30°C as the annealing temperature, we obtained several bands including one major band of 450 bp which was used for further characterization.

In order to confirm that *B. subtilis* 713 chromosome contains the same DNA as the 450 bp PCR product, Southern hybridization was performed under medium stringent conditions using the PCR product as a probe. The probe hybridized with only one fragment for each restriction enzyme digest (data not shown), indicating that this gene exists as a single copy in the *B. subtilis* 713 chromosome.

Alignment of the predicted amino acid sequence based on the nucleotide sequence revealed that the DNA fragment is a part of the peptide antibiotics synthetase gene [22]. In order to isolate the rest of the synthetase gene from the *B. subtilis* 713, we performed Southern hybridization using the PCR product as a probe. From a mini-library containing 7~8-kb fragments of *Hin*dIII digested chromosomal DNA from *B. subtilis* 713, we isolated a 7.2-kb DNA fragment (21, Fig. 4) and characterized 4.8-kb of the fragment.

In order to determine the nucleotide sequence of the isolated DNA fragment, we subcloned the fragment into pUC18, 19 and M13mp18, 19 and used forward and reverse primers as sequencing primers. Custom-made primers were also used as sequencing primers (Fig. 4a). Once the nucleotide sequence was determined, we used the DNASIS program (Hitachi software engineering, Japan) to analyse the predicted amino acid sequence (Fig. 2) and then searched the homologous gene using the gapped advanced BLAST and original BLAST [1, 2] program through the Internet. The statistical significance of the predicted protein sequence was evaluated using the DNASIS (Hitachi software engineering, Japan) program and BLAST [1, 2] through a server system supported by NCBI. Highly related sequences usually have an optimized alignment score greater than 150 and E-value smaller than $5e^{-34}$. For multiple alignment to identify Core motifs between amino acids, the CLUSTAL V [7] program was used.

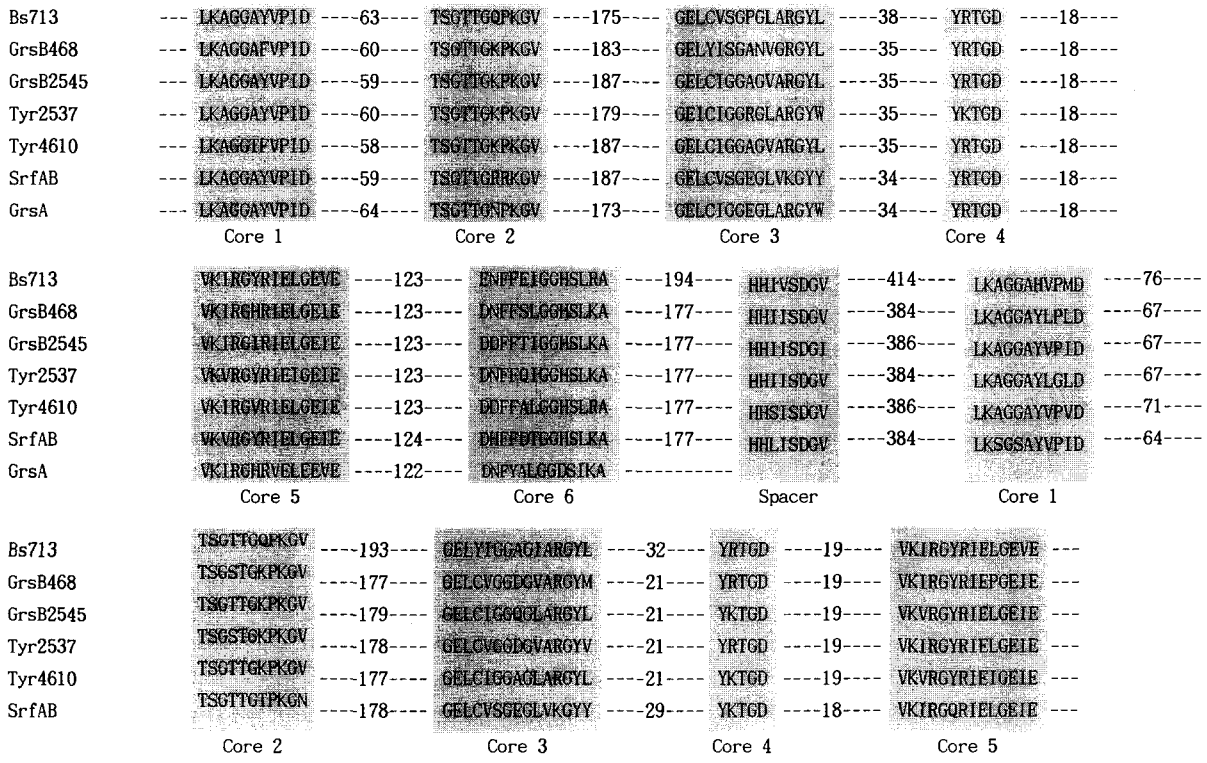


**Fig. 3.** Alignment of deduced amino acid sequences of DNA fragment from *Bacillus subtilis* 713 with other peptide synthetase domains.

Conserved regions including the 6 Core motifs and spacer motif of different peptide synthetases are presented (shaded and boxed). The distance between the conserved regions is indicated. Grs468 is from the amino acid sequence from aa 468 of gramicidine synthetase 2 including the proline and valine activating domains. GrsB2545 is from the amino acid sequence from aa 2545 of Gramicidine synthetase 2 including the ornithine and leucine activating domains. Tyr2537 is from the amino acid sequence from aa 2537 of tyrocidine synthetase including the tyrosine and valine activating domains. Tyr4610 is from the amino acid sequence from aa 4610 of tyrocidine synthetase including the ornithine and leucine activating domains.

The predicted amino acid sequence of the isolated DNA fragment showed high homology to various peptide antibiotics synthetase genes. The highest homology (41.9% identity over 1588 amino acids) was found with the Gramicidine synthetase gene [8, 18] of *Bacillus brevis*. The surfactin synthetase gene of *Bacillus subtilis* [6] and tyrocidine synthetase gene of *Bacillus brevis* also showed significant homology (39.5% identity over 1581 amino acids and 37.3% identity over 877 amino acids, respectively). These homologies are so remarkable that we might conclude that the DNA fragment we isolated was part of the peptide synthetase gene. Among the peptide synthetase genes, the regions of the proline and valine activating domains showed the highest homology. The fact that proline and valine seem to be the constituents of the peptide produced by *Bacillus subtilis* 713 [26] is very interesting in this sense. That is, the two domains identified in this study are likely to be the domains for the activation of proline and valine for peptide synthesis. This finding also supports the idea that the DNA fragment isolated in this study is a fragment of the biosynthetic gene for antifungal peptide produced by *B. subtilis* 713. However, this should be proven by further genetic and biochemical characterization.

By comparison of the deduced amino acid sequence with databases, two peptide synthetase domains containing well-conserved peptide synthetase motifs were detected (Figs. 2 and 3). We will refer to the two domains as domain I and II hereafter. Peptide antibiotics biosynthetic genes have been reported to contain the conserved regions in each domain which are involved in ATP binding (Core 2, Core 3, and Core 5), the regions involved in ATP hydrolysis (Core 4), and the region involved in 4'-phosphopantheine binding (Core 6; 15, 16).

We could locate 6 conserved Core motifs and a spacer motif in domain I, and 5 conserved Core motifs in domain II (Figs. 2 and 3). That is, two Core 1 motifs (LKAGGAYVPID and LKAGGAHVPMD) were identified in the regions of aa 72 - aa 82 and aa 1155 - aa 1165. These sequences showed 11/11 and 9/11 identity to the consensus sequence of Core 1 (LKAGGAYVPID), respectively. Two Core 2 motifs (TSGTTGQPKGV) were identified in the regions aa 150 - aa 160 and aa 1241 - aa 1251 to have 10/11 identity to consensus (YSGTTGxPKGV). Two Core 3 motifs (GELCVSGPGLARGYL and GELYIGGAGIARGYL) were identified in the regions aa 334 - aa 348 and aa 1444 - aa 1458 to have 13/15 and 14/15 identity to consensus (GELCIGGxGxARGYL), respectively. Two Core 4 motifs (YRTGD) were identified in the regions aa 373 - aa 377 and aa 1491 - aa 1495 to have 5/5 identity to consensus (YxTGD). Two Core 5

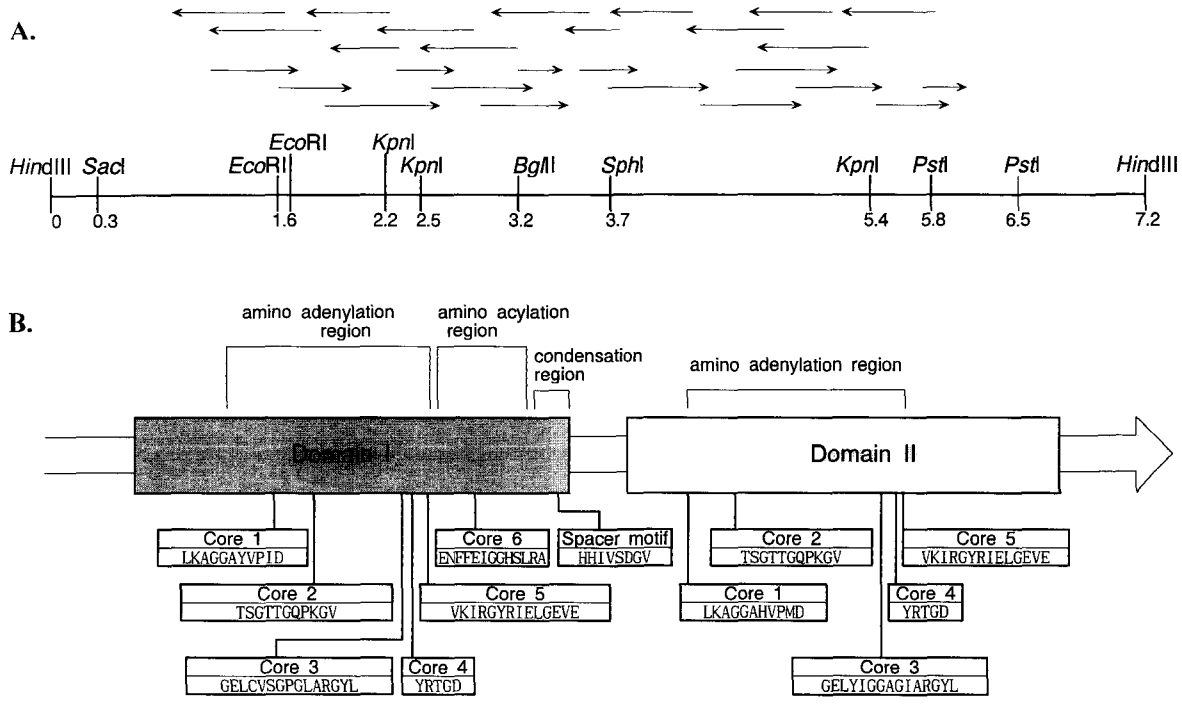


**Fig. 4.** Genetic organization of 7.2 Kb DNA fragment isolated from *Bacillus subtilis* 713.

A. Arrow indicates the direction and the length of sequence read by the sequencing reaction. Some restriction enzyme sites which were used for subcloning were indicated. The map is not on the scale. B. Schematic representation of two domains based on the sequence homology to various amino acid activating domains. Domain I and Domain II showed the highest homology to the proline activating domain and the valine activating domain, respectively.

motifs (VKIRGYRIELGEVE) were identified in the regions aa 397 - aa 410 and aa 1515 - aa 1528 to have 13/14 identity to consensus (VKIRGxRIELGEIE). One Core 6 motif (ENFFEIGGHSL) was identified in the region aa 528 - aa 538 to have 8/11 identity to consensus (DNFYxLGGHSL). The spacer motif (HHIVSDGV) was identified in the region aa 734 - aa 741 to have 6/8 identity to the consensus sequence (HHILxDGW; 31). In the fragment we characterized, however, Core 6 and spacer motif were not included in domain II. The preliminary result indicated that the spacer motif was located in the 7.2-kb DNA fragment we isolated.

In conclusion, we identified all six conserved Core motifs in Domain I and five Core motifs in Domain II including lysine in Core 2, aspartate in Core 4, and serine in Core 6 which have been known to play important roles [31]. Figure 4b shows the simplified scheme of the peptide synthetase gene fragment from *Bacillus subtilis* 713 based on the sequence homology to conserved core and spacer motifs.

In most peptide synthetase genes, the spacer motif is usually found at the end of each domain. It is also located at the N-terminal region of the domain if the domain is involved in the first step of peptide synthesis. Therefore, if the second domain has its own promoter to be the first domain for peptide synthesis, there should be two spacer motifs between the two domains. The fact that there is only one spacer motif between Domain I and Domain II in the DNA fragment we isolated suggests that these two domains are under the control of the same promoter since the spacer motif is missing at the N-terminal end of Domain II.

Interestingly, the region after the spacer motif showed high homology with *grsB* and *tyrC*, which do not have motifs for racemerization motifs [24, 25, 31], which are found in the domain for racemerized amino acids. These results indicate that the isolated peptide synthetase fragment is not involved in racemerization. This finding should give some clue as to the structure of the peptide produced by *B. subtilis* 713 which has not yet been determined.

The isolation and characterization of domains for the activation of amino acid constituents of peptide synthetase genes can be a foundation for the development of noble antibiotics. Together with the bank of peptide synthetase genes already reported, the two amino acid-activating domains identified in this study can be used for designing noble and more efficient peptide antibiotics along with a bioassay against a wide spectrum of pathogens. In this sense, a recent study by the Stachelhaus group has proven that programming new antibiotics by such gene manipulation as switching, deleting, and adding the amino acid-activating domains could create noble peptides of amino acids constituents they designed [30].

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