NOTE

Isolation and Characterization of Histamine-Producing Bacteria from Fermented Fish Products

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Histamine is mainly produced by microorganisms that are found in fermented foods, and is frequently involved in food poisoning. Two histamine-producing bacteria were isolated from fermented fish products, anchovy sauce, and sand lance sauce by using a histidine decarboxylating medium. The species were identified as *Bacillus licheniformis* A7 and *B. coagulans* SL5. Multiplex PCR analysis showed the presence of the conserved histidine decarboxylase (*hdc*) gene in the chromosome of these bacteria. *B. licheniformis* A7 and *B. coagulans* SL5 produced the maximum amount of histamine (22.3 \pm 3.5 and 15.1 \pm 1.5 mg/L, respectively). As such, they were determined to be potential histamine-producing bacteria among the tested cultures.

Keywords: histamine, histidine decarboxylase gene (*hdc*), multiplex PCR, *Bacillus licheniformis*, *Bacillus coagulans*

Biogenic amines (BAs) are low molecular weight nitrogenous compounds that are mainly formed by amino acid decarboxylation (Brink *et al.*, 1990; Halász *et al.*, 1994). BAs most frequently involved in food intoxication is histamine, produced from the precursor amino acids histidine by the histidine decarboxylase (*hdc*) (Santos, 1996). Histamine is produced and degraded as part of normal cellular metabolism; however, high intake may cause vasoactive or psychoactive health problems, including cutaneous (primarily facial flush), gastrointestinal, haemodynamic (hypotension) and/or neurologic symptoms (Rice *et al.*, 1976; Brink *et al.*, 1990; Halász

et al., 1994). It is also of concern because they are an index of hygienic quality; the presence of high levels of histamine in food is indicative of microbial spoilage (Roig-Sagúes *et al.*, 2002). Histamine is synthesized in a variety of fermented foods, including fish (Moon *et al.*, 2010b), meat (Maijala *et al.*, 1993), dairy (Stratton *et al.*, 1991), soybean products (Chin and Koehler, 1986), wine (Lehtonen *et al.*, 1992), beer (Dumont *et al.*, 1992), and vegetables (Taylor *et al.*, 1978).

Aekjeot and Jeotkal are respectively fermented fish-sauce and fish-paste produced through the fermentation of various fishes by salts and naturally occurring microorganisms. They have been consumed for centuries in Korea as protein sources and seasoning ingredient. Those sauces and pastes contain relatively high concentrations of amino acids degraded from fishes and may be a source for histamine synthesis. The presence of histidine decarboxylase activity has been described in different microbial groups, such as *Pseudomonas* (López-Sabater *et al.*, 1994), *Vibrios* (Niven *et al.*, 1981), sporulated microorganisms (Rodriguez-Jerez *et al.*, 1994), and lactic acid bacteria (Joosten and Nunez, 1996). Despite this, insufficient research data is available on the growth of histamine-producing microorganisms in fermented fish products.

This study was performed to isolate and characterize histamine-producing bacteria in Korean fermented fish foods. In total, 24 samples of fermented fish products, which included 8 anchovy sauces, 8 sand lance sauces, 4 squid pastes, 2 clam pastes, and 4 shrimp pastes, were purchased from retail stores. All fermented fish products were immediately transported to the laboratory and kept at 4°C before analysis. Each sample (1 g) was mixed with 9 ml of sterile physiological saline [0.85% (w/v) NaCl], homogenized in a stomacher (AES Laboratoire, France) for 2 min, and then further diluted in saline at 1:10 dilution. The diluted sample solutions were spread on HD medium (Niven et al., 1981) to qualitatively assess the histamine-producing capacity of the bacterial strains. The HD medium contained 0.125% tryptone, 0.125% yeast extract, 0.75% (NH₄)₂SO₄, 0.5% NaCl, 0.1% glucose, 0.02% MgSO4·7H2O, 0.005% MnSO4·4H2O, 0.004% FeSO₄·7H₂O, 0.05% Tween 80, 0.02% cresol red, 3% agar, and 0.5% (w/v) of L-histidine monohydrochloride (Sigma Chemical Co., USA). The plates were incubated at 25°C for 7 days under anaerobic and aerobic conditions. After 7 days of incubation, halos around colonies were formed on the HD medium. Two Gram-positive, rod-shaped organisms were isolated: A7 from anchovy sauce and SL5 from sand lance sauce.

To confirm the presence of specific genes in these isolated

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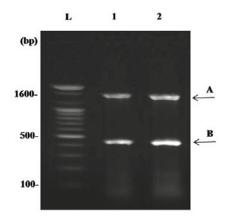


Fig. 1. Multiplex PCR-based detection of *hdc*⁺ **strains**. Lanes: L, ladder; 1, A7 isolate obtained from anchovy sauce; 2, SL5 sand lance sauce; (A) 16S rRNA (1520 bp) internal control; (B) histidine decarboxylase gene (*hdc*, 441 bp).

organisms, multiplex PCR analysis was performed for the 2 isolates using procedures described by Coton and Coton (2005). Genomic DNA was isolated from 2-mL cultures using the Genomic DNA Extraction kit (Bioneer, Korea). For the immediate detection of the *hdc* and 16S rRNA genes, 2 sets of primers were used: HDC3 (5'-GATGGTATTGTTTCKT ATGA-3') and HDC4 (5'-CAAACACCAGCATCTTC-3') for *hdc* gene fragments, the universal primers 27F (5'-AGAG

TTTGATCCTGGCTCAG-3') and 1492R (5'-GGTTACCT TGTTACGACTT-3') for 16S rRNA genes (Lane, 1991). The multiplex PCR experiments were performed using the iO5 thermal cycler (Bio-Rad, USA) using the following program: 95°C for 5 min, 32 cycles of 95°C for 45 sec, 48°C for 45 sec, and 72°C for 75 sec, and a final extension of 72°C for 5 min. PCR reactions performed on DNA from the isolates showed an amplified band of 441 bp (Fig. 1, band B), which corresponds to an hdc gene fragment. Biochemical tests of A7 and SL5 isolates were also carried out using the API 50CHB/E test kit (Biomerieux, USA), and the results indicated that the A7 isolate had 97% identity with Bacillus licheniformis, while the SL5 isolate had 96% identity with Bacillus coagulans. Subsequently, genetic identification of the strains was performed by sequencing the 16S rRNA and hdc genes of the 2 isolates. Species identification of the isolates was accomplished by comparing the isolated sequences with those of related reference strains in the DNA Data Bank of Japan (DDBJ, http://www.ddbj.nig.ac.jp) using the Fasta program. The sequence of the A7 isolate showed 99% homology to *B. licheniformis*, and the sequence of the SL5 isolate showed 99% homology to B. coagulans. The 16S rRNA gene sequences of strains A7 and SL5 have been deposited in the DDBJ under accession numbers AB553280 and AB557590, respectively. In addition, the partial hdc sequences of B. licheniformis A7 and B. coagulans SL5 were deposited in the DDBJ under accession numbers AB553282 and AB553281, respectively.

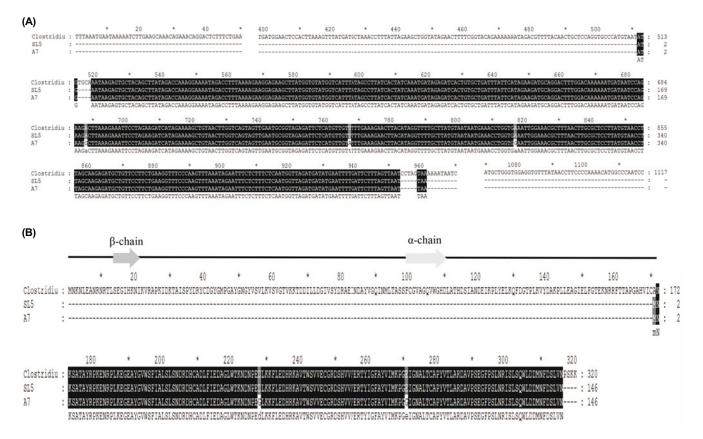
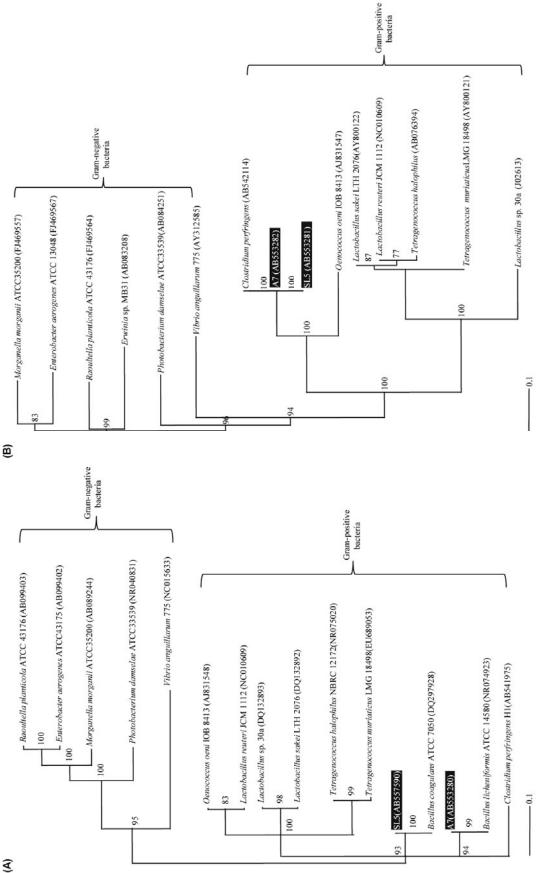


Fig. 2. Partial alignments of hdc gene sequences (A) and amino acids (B) of B. licheniformis A7, B. coagulans SL5, and C. perfringens using the GeneDoc program.





Sequence analysis of amino acids showed that 2 *hdc* partial genes from isolates were similar to the previously reported pyruvoyl-dependent *hdc* of *Clostridium perfringens* ATCC 13124 (Fig. 2A). Notably, the amplification of 2 *hdc* partial genes from the isolates was located at the N-terminus of the α -chain. The above result shows that a molecular method using PCR can be used for detection and identification of histamine-producing bacteria instead of or simultaneously with the conventional culture technique.

Phylogenetic trees of the isolated strains based on the newly determined sequences of partial hdc genes and 16S rRNA sequences were compared (Fig. 3A and 3B). The bootstrap scores observed for all the nodes are indicated. The phylogenetic tree of the hdc genes show that the A7 and SL5 isolates are genetically closely related with C. perfringens ATCC 13124 and Oenococcus oeni IOB8413 (Fig. 3B). Overall, the phylogenetic tree determined by the partial hdc gene was similar to that determined by the 16S rRNA sequence. In both trees, groups of Gram-negative and Gram-positive strains showed high bootstrap values (99% and 98% on 16S rRNA and partial *hdc* gene trees, respectively). The phylogenetic distance matrix tree of hdc showed that the hdc fragment evolved similarly to the 16S rRNA gene and may provide a basis for identification of Gram-positive histamine producers. Along with three known bacterial hdc-Tetragenococcus muri-

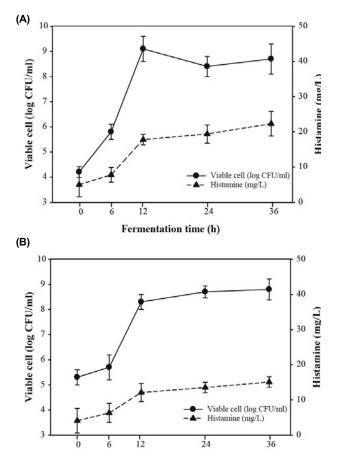


Fig. 4. Synthesis of (A) histamine by *B. licheniformis* A7 and (B) histamine by *B. coagulans* SL5 in decarboxylating broth containing 0.5% histidine.

aticus LMG 18498(EU689053), O. oeni IOB 8413(AJ831548), Lactobacillus 30a (DQ 132893), and C. perfringens ATCC 13124-partial hdc (J02880) sequences from the 4 strains contained the conserved sequence a-chain (Phe-Cys-Gly-X-Val-Ala-Gly-Gln) in the pyruvoyl group (detected as glutamine). These sequence similarities suggest that the 4 enzymes have evolved from a common ancestral protein with similar catalytic mechanisms. While the hdc gene cannot be used for the universal phylogenetic analysis of gram-positive bacteria, the partial hdc sequence is sufficient for identifying grampositive histamine producers that have hdc, similar to the phylogenetic trees generated from 16S rRNA. These data are in agreement with the findings of studies on the evolution of pyruvoyl-dependent decarboxylases (Konagaya et al., 2002). Significant and extensive similarities of pyruvoyldependent decarboxylases suggest an ancient and common origin for all pyruvoyl-dependent decarboxylases.

Histamine production ability of the isolated microbial cells was confirmed via qualitative and quantitative assays as shown in Fig. 4. The isolates, *B. licheniformis* A7 and *B. coagulans* SL5, were cultivated in decarboxylating medium containing 0.5% histidine, and the HPLC unit (Waters 2695) equipped with a Waters 2996 photodiode array detector was utilized for histamine analysis (Garcia-Garcia *et al.*, 2000). After 36 h of cultivation, A7 and SL5 isolates produced the maximum amounts of histamine (22.3 \pm 3.5 mg/L and 15.1 \pm 1.5 mg/L, respectively). Meanwhile, *Clostridium perfringens* H1, which was cultured as a positive control for histamine production (Moon *et al.*, 2010a) produced 25.4 \pm 2.8 mg/L, while *Leuconostoc mesenteroides* ATCC 8293, which is a negative control for histamine production, produced no detectable amount of histamine.

It is well known that *Bacillus* species (often *Bacillus subtilis* spp.) continue to be the dominant microbial participant in food fermentations, particularly for protein-rich soya ; they contribute to important biochemical changes, pH, and flavor development. While the occurrence of *B. cereus* in foods at numbers of 10^3-10^5 CFU/g or mL is considered unsafe due to the ability of *B. cereus* to cause food poisoning, *B. subtilis* and *B. licheniformis* generally are regarded as safe by European Food Safety Authority (EFSA, 2005). However, food-borne *B. licheniformis* outbreaks have been reported to be predominantly associated with cooked meats and vegetables (Rosenkvist and Hansen, 1995), and a toxin-producing *B. licheniformis* was isolated from raw milk and baby food products (Salkinoja-Salonen *et al.*, 1999).

B. coagulans is often used in veterinary applications, especially as a probiotic in pigs, cattle, poultry, and shrimp. There are many references to the use of this bacterium in humans, especially for improving vaginal flora, improving abdominal pain and bloating in Irritable Bowel Syndrome (IBS) patients, and increasing the immune response to viral challenges (Hun *et al.*, 2009). Our results indicate that *B. licheniformis* and *B. coagulans* are potential histamine producers. Potential histamine-producing bacteria have been isolated from various salted fish products, including salted sardines, salted Spanish anchovies, and fish sauce; they were *Staphylococcus* spp., *Vibrio* spp., and *Pseudomonas* III/IV-NH (Yatsunami and Echigo, 1991, 1992), *S. epidermidis, S. xylosus, Klebsiella oxytoca, Enterobacter cloacae, P. cepaciae*,

and *Bacillus* spp. (Rodriguez-Jerez *et al.*, 1994; Hernandez-Herrero *et al.*, 1999), and *T. muriaticus*, halophilic lactic acid bacterium (Kimura *et al.*, 2001).

The existence of contaminating microorganisms in fermented foods may be considered an indicator of the quality or grade of sanitation of the raw material applied during food production (Halász et al., 1994). Foods can also be contaminated during raw material preparation, particularly during the natural incubation period. These data suggest that safe starter strains and hygienic conditions should be used for the production of fermented fish products. The starter strains frequently used in commercial products should be tested for the absence of *hdc* genes in their genome and the inability to produce histamine during growth in amino acid-rich medium. Application of the culture-dependent and independent methods used in this study will permit broad monitoring of histamine-producing bacteria in various fermented foods. The molecular information presented here opens the way to further studies on developing more sophisticated molecular methods for detecting and identifying these bacteria.

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