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Species Identification and Labeling Compliance in Dried Seafood Products Sold in South Korea

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ABSTRACT - In this study, we evaluated species identification and labeling compliance of 24 dried seafood products sold in South Korea. To determine the species used in these processed seafood products, sequences of cytochrome c oxidase subunit I and cytochrome b genes were analyzed and compared with reference sequences from the National Center for Biotechnology Information (NCBI) and the Barcode of Life Data Systems (BOLD system), followed by phylogenetic analysis. The identified species were *Hyporhamphus quoyi*, *Gadus chalcogrammus*, *Lophius litulon*, *Conger myriaster*, *Paramonacanthus pusillus*, *Hyporhamphus sajori*, *Gadus macrocephalus*, *Hoplobrotula armata*, *Callionymus meridionalis*, *Liparis tanakae*, *Dosidicus gigas*, *Lagocephalus cheesemanii*, and *Takifugu vermicularis*. Discrepancies between the labeled and identified species were found in 16 products (66.7%) when generic market names (e.g., unagi and squid) were included; this discrepancy rate reduced to 41.7% when generic market names were excluded. The discrepancy rate was higher for seasoned and dried seafood products (70%) than that of dried seafood products (50%). No significant correlation was observed between the country of origin and the discrepancy rate. These results provide important baseline data for the regulatory monitoring of dried seafood products, and could aid in improving the accuracy of species labeling in the seafood industry.

Key words: Processed fishery products, Food fraud, Species identification, DNA barcoding, Phylogenetic tree

Recent trends indicate a rising consumption of seafood products as a health-conscious choice, driven by increasing interest in health and sustainable dietary practices. As of 2021, the per capita consumption of seafood in South Korea reached 65.6 kg, reflecting an average annual growth rate of 2.2%[1]. Compared to meat products, seafood has a lower environmental impact in terms of climate change[2] and is a rich source of omega-3 fatty acids and essential minerals, contributing to its affordability and global demand[3]. However, the high demand for seafood has also made it particularly vulnerable to food fraud, ranking as the second most susceptible food category[4]. Food fraud, defined as the intentional adulteration of products for economic benefit, typically involves the misrepresentation of the product or related documentation[5]. The most prevalent form of food fraud within the seafood industry is mislabeling. This often occurs when generic market names (e.g., squids, clams) are substituted for specific species or scientific names, allowing lower-cost seafood to be marketed as premium products, or when the raw material's name is inaccurately represented. Such practices also include the misrepresentation of the country of origin. Previous studies monitoring domestic seafood products identified a notably high incidence of mislabeling, with rates as high as 70% for pufferfish[6] and 73% for shrimp[7] products. The growing trend of online food purchasing has further exacerbated this issue, particularly for multi-processed and convenience foods[1]. In cases where the morphological characteristics of the ingredients are obscured, the frequency of food fraud tends to be higher than in simply processed products[8].

According to the food standards and specifications outlined in the Food Code (Article 5)[9], processed fishery products are defined as those derived from seafood, with primary ingredients subjected to manufacturing and processing methods such as grinding, drying, or the addition of food additives. Within this category, dried seafood products include fish or mollusks that have undergone drying,

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cutting, or further processing and seasoning. A previous monitoring study identified a significant mislabeling rate of 73% in shrimp products, encompassing both simply and highly processed forms, including those subjected to drying, cutting, or seasoning[7]. This finding underscores the vulnerability of processed fishery products to food fraud, as they are often distributed in forms where the original shape is unrecognizable. DNA generally exhibits exceptional stability and specificity, even in foods processed under high temperatures and pressures. Consequently, a variety of polymerase chain reaction (PCR)-based analysis methods have been developed and are widely employed to verify the authenticity of seafood products. These methods include DNA barcoding, forensically informative nucleotide sequencing (FINS), microsatellite analysis, PCR-restriction fragment length polymorphism analysis, and species-specific PCR[10]. Mitochondrial DNA (mtDNA), with its higher copy number and mutation rate compared to nuclear DNA, is particularly well-suited for species identification. The DNA barcoding method analyzes standardized sequences (600-700 bp) of the cytochrome c oxidase subunit I (*CoI*) gene in mtDNA. The obtained sequences are compared with those in the GenBank database of the National Center for Biotechnology Information (NCBI) and the Barcode of Life Data Systems (BOLD system) for species identification[11]. Additionally, the cytochrome b (*Cytb*) gene of mtDNA is frequently used as a marker for species identification in seafood through FINS analysis[12]. In this study, the *CoI* and *Cytb* genes were employed for DNA barcoding and FINS analyses to identify 25 highly processed seafood products distributed in domestic online and offline markets. The objective is to assess whether the raw materials used in these products were consistent with their labeling information.

Materials and Methods

Sample collection

The 24 dried seafood products used in this study were purchased from domestic online and offline markets between May 2024 and July 2024. All products underwent multiple processing methods that obscured the morphological characteristics of the raw materials, including heating, drying, and cutting. These products were categorized into two groups: dried seafood (SD, n=4) and seasoned and dried seafood (SDS, n=20) (Table 1).

DNA extraction and quantification

For DNA extraction from processed products containing seasonings and spices, samples were thoroughly washed with distilled water and preserved in 95% ethanol, as previously described[12]. DNA was extracted from 30 mg of the edible portion of each sample using the DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. The extracted DNA was quantified with a NanoDrop ND-1000 UV-Vis spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). The purity of the extract was assessed by calculating the ratio of absorbance at 260 nm to that at 280 nm.

PCR amplification and DNA sequencing

Two mtDNA genes (*CoI* and *Cytb*) were utilized for DNA barcoding and FINS analyses. Amplification of these genes was achieved using the primer sets detailed in Table 2[13,14]. Conventional PCR was conducted in a total volume of 20 μL, comprising 10 ng of template DNA, 0.5 μM of each primer, 1×PCR Buffer, 0.2 mM deoxynucleoside triphosphates, 2.0 mM $MgCl_2$, 1 U Taq DNA polymerase (Bioneer, Daejeon, Korea), and sterile distilled water. The thermal cycling conditions employed were as follows: initial denaturation at 94°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 40 seconds, annealing at 52°C for 40 seconds, extension at 72°C for 1 minute, and a final extension at 72°C for 7 minutes, using a thermal cycler 2720 (Applied Biosystems, Foster City, CA, USA). A non-template control served as the negative control. The PCR protocol adhered to the same procedures previously described. Post-PCR, amplicons were visualized on 1% agarose gels stained with RedSafe (iNtRON, Seongnam, Korea), and their sizes were assessed against a 1 kb DNA ladder (Bioneer). The PCR products were purified with the AccuPrep PCR Purification Kit (Bioneer) and subsequently sent to Gencube Plus (Seoul, Korea) for nucleotide sequencing.

Sequence analysis and comparison with databases

The nucleotide sequences were manually edited using BioEdit software (version 7.0.5). Sequences with a quality score of less than 20 were excluded from the analysis. Forward and reverse complementary sequences of the PCR products were combined to generate a high-quality consensus sequence, following the protocol established by the Labelfish Consortium[15]. To identify species, the consensus sequences for each PCR product were compared against the NCBI GenBank database using the Basic Local Alignment Search Tool (BLASTn; https://blast.ncbi.nlm.nih.gov/Blast.cgi). Additionally, the identities of *CoI* sequences were verified using the species-level barcode records from the Barcode of Life Data Systems (BOLD; http://www.barcodinglife.org/index.php/databases). Potential species identifications were considered valid based on two stringent criteria: sequence similarity greater than 98% and query coverage exceeding 98%. The

Table 1. Commercial dried seafood products and their identification results

Sample	Commodity type*	Species declared on label	Country of origin	NCBI (Query coverage %/Identity %)		BOLD system (Similarity %)	Identified species	Labeling compliance
				CoI	*Cytb*	*CoI*		
S1	SDS	Japanese halfbeak	Vietnam	*Hyporhamphus quoyi*(99/99.12)	*Hyporhamphus quoyi*(99/100)	*Hyporhamphus quoyi*(99.69)	*Hyporhamphus quoyi*	NC
S2	SDS	Alaska pollock	Russia	*Gadus chalcogrammus*(100/99.49) *Theragra finnmarchica*(100/99.32)	*Gadus chalcogrammus*(100/99.54) *Theragra finnmarchica*(100/99.54)	*Gadus chalcogrammus*(100)	*Gadus chalcogrammus*	C
S3	SDS	Blackmouth angler	China	SF	*Lophius litulon*(100/99.54)	SF	*Lophius litulon*	NC
S4	SDS	Unagi	South Korea	*Conger myriaster*(100/99.85)	SF	*Conger myriaster*(100)	*Conger myriaster*	NC
S5	SDS	Filefish	Vietnam	*Paramonacanthus pusillus*(100/99.55)	*Paramonacanthus pusillus*(86/96.30)	*Paramonacanthus pusillus*(100)	*Paramonacanthus pusillus*	NC
S6	SDS	Japanese halfbeak	South Korea	*Hyporhamphus sajori*(100/99.85)	*Hyporhamphus sajori*(98/100)	*Hyporhamphus sajori*(100) *Rhynchorhamphus georgii*(100)	*Hyporhamphus sajori*	C
S7	SDS	Pacific cod	Russia	SF	*Gadus macrocephalus*(100/100) *Gadus ogac*(100/99.77)	SF	*Gadus macrocephalus*	C
S8	SDS	Blackmouth angler	China	SF	*Lophius litulon*(100/99.54)	SF	*Lophius litulon*	NC
S9	SDS	Armored brotula	South Korea	*Hoplobrotula armata*(100/99.22) *Neobythites stigmosus*(100/99.22) *Sirembo imberbis*(100/99.22)	*Hoplobrotula armata*(99/99.32) *Neobythites stigmosus*(99/99.09) *Sirembo imberbis*(99/99.09)	*Hoplobrotula armata*(99.64) *Neobythites unimaculatus*(99.52) *Sirembo imberbis*(99.51)	*Hoplobrotula armata*	C
S10	DS	Armored brotula	China	*Hoplobrotula armata*(100/100) *Neobythites stigmosus*(100/100) *Sirembo imberbis*(100/100) *Neobythites unimaculatus*(100/99.84)	*Hoplobrotula armata*(99/99.54) *Neobythites stigmosus*(99/99.31) *Sirembo imberbis*(99/99.31)	*Hoplobrotula armata*(100) *Neobythites unimaculatus*(100) *Sirembo imberbis*(100)	*Hoplobrotula armata*	C
S11	SDS	Bartail flathead	Vietnam	*Callionymus meridionalis*(99/99.53)	*Repomucenus meridionalis*(67/97.95)	*Callionymus meridionalis*(99.3)	*Callionymus meridionalis*	NC
S12	SDS	Cubed snailfish	China	*Liparis agassizii*(100/99.56) *Liparis tanakae*(99/99.71)	*Liparis tanakae*(87/99.48)	*Liparis tanakae*(100) *Liparis chefuensis*(100) *Liparis agassizii*(99.56)	*Liparis tanakae*	NC
S13	SDS	Squid	Peru	*Dosidicus gigas*(99/100)	SF	*Dosidicus gigas*(99/99.84)	*Dosidicus gigas*	NC
S14	DS	Alaska pollock	Russia	SF	*Gadus chalcogrammus*(100/100) *Theragra finnmarchica*(100/100)	SF	*Gadus chalcogrammus*	C
S15	SDS	Pacific cod	Russia	*Gadus chalcogrammus*(100/99.54) *Theragra finnmarchica*(100/99.54)	*Gadus chalcogrammus*(100/100) *Theragra finnmarchica*(100/100)	*Gadus chalcogrammus*(100)	*Gadus chalcogrammus*	NC
S16	SDS	Alaska pollock	Russia	SF	*Gadus chalcogrammus*(100/100) *Theragra finnmarchica*(100/100)	SF	*Gadus chalcogrammus*	C
S17	SDS	Blackmouth angler	China	SF	*Lophius litulon*(100/99.54)	SF	*Lophius litulon*	NC

Table 1. (Continued) Commercial dried seafood products and their identification results

Sample	Commodity type*	Species declared on label	Country of origin	NCBI (Query coverage %/Identity %)		BOLD system (Similarity %)	Identified species	Labeling compliance
				CoI	*Cytb*	*CoI*		
S18	SDS	Panther puffer	South Korea	*Takifugu rubripes*(99/100) *Takifugu pseudommus*(99/99.85) *Takifugu flavidus*(99/99.85) *Takifugu chinensis*(98/99.5)	*Takifugu flavidus*(100/99.75) *Takifugu rubripes*(100/99.75) *Takifugu chinensis*(100/99.24)	*Takifugu rubripes*(100) *Takifugu chinensis*(100) *Takifugu pseudommus*(100) *Takifugu flavidus*(99.56) *Takifugu obscurus*(98.17)	*Takifugu chinensis* *Takifugu rubripes* *Takifugu flavidus*	NC
S19	SDS	Pufferfish	China	*Lagocephalus cheesemanii*(98/100)	*Lagocephalus cheesemanii*(98/100) *Lagocephalus guentheri*(98/99.23)	*Lagocephalus cheesemanii*(100) *Lagocephalus spadiceus*(99.67) *Lagocephalus guentheri*(99.51)	*Lagocephalus cheesemanii*	NC
S20	SDS	Brown-backed toadfish	China	*Lagocephalus cheesemanii*(98/100)	*Lagocephalus cheesemanii*(98/100) *Lagocephalus guentheri*(98/99.23)	*Lagocephalus cheesemanii*(100) *Lagocephalus spadiceus*(100)	*Lagocephalus cheesemanii*	C
S21	SDS	Pufferfish	China	*Lagocephalus cheesemanii*(99/100)	*Lagocephalus cheesemanii*(98/99.49) *Lagocephalus guentheri*(98/98.73)	*Lagocephalus cheesemanii*(100) *Lagocephalus spadiceus*(100) *Lagocephalus guentheri*(99.54)	*Lagocephalus cheesemanii*	NC
S22	SDS	Pufferfish	China	*Lagocephalus cheesemanii*(99/100)	*Lagocephalus cheesemanii*(98/100) *Lagocephalus guentheri*(98/99.23)	*Lagocephalus cheesemanii*(100) *Lagocephalus spadiceus*(100) *Lagocephalus guentheri*(99.54)	*Lagocephalus cheesemanii*	NC
S23	DS	Pufferfish	ND	*Takifugu chinensis*(98/100) *Takifugu rubripes*(98/98.84)	*Takifugu rubripes*(99/100) *Takifugu flavidus*(99/100) *Takifugu chinensis*(99/99.49) *Takifugu pseudommus*(99/100)	*Takifugu rubripes*(100) *Takifugu chinensis*(100) *Takifugu pseudommus*(100) *Takifugu flavidus*(99.51)	*Takifugu chinensis* *Takifugu rubripes*	NC
S24	DS	Panther puffer	South Korea	*Takifugu vermicularis*(99/99.52)	*Takifugu vermicularis*(99/99.49)	*Takifugu vermicularis*(99.36)	*Takifugu vermicularis*	NC

*DS and SDS represent dried seafood and seasoned and dried seafood products, respectively.
The underlined text indicates a single species identified by the *Cytb* gene that did not meet the two stringent criteria: sequence similarity exceeding 98% and query coverage greater than 98%.
ND: not declared, SF: sequencing failed, C: compliance, NC: non-compliance.

Table 2. Primer sets used for DNA barcoding and FINS analyzes

Primer name	Target gene	Sequence (5'→3')	Size (bp)	References
LCO1490	*CoI*	GGTCAACAAATCATAAAGATATTGG	650	(13)
HCO2198		TAAACTTCAGGGTGACCAAAAAATCA		
H15149ad	*Cytb*	GCICCTCARAATGAYATTTGTCCTCA	460	(14)
L14735		AAAAACCACCGTTGTTATTCAACTA		

English common names corresponding to the finalized scientific names of dried seafood products were determined based on the common names associated with the same scientific names of seafood as specified in the List of Animal Raw Materials Usable in Food in the Food Code (No. 2023-56)[10].

Phylogenetic analysis

The *CoI* and *Cytb* sequences obtained from 24 commercial products, along with additional 22 *CoI* (*Hyporhamphus quoyi*: MW379521.1, *Gadus chalcogrammus*: MK216583.1, *Conger myriaster*: HM180545.1, *Paramonacanthus pusillus*: LC656310.1, *Hh. sajori*: NC 011173.1, *Hoplobrotula armata*: NC 086878.1, *Sirembo imberbis*: MN937450.1, *Neobythites stigmosus*: AP018427.1, *N. unimaculatus*: JQ681317.1, *Callionymus meridionalis*: PP090602.1, *Liparis chefuensis*: JQ738425.1, *La. agassizii*: HM180656.1, *La. tanakae*: GU357851.1, *Dosidicus gigas*: KY446779.1, *Takifugu pseudommus*: OP430521.1, *T. flavidus*: KJ562276.1, *T. chinensis*: OP430522.1, *T. rubripes*: OP430515.1, *T. obscurus*: OQ700678.1, *T. vermicularis*: OP430511.1, *Lagocephalus spadiceus*: KP266858.1, and *Lc. cheesemanii*: MF123933.1) and 18 *Cytb* (*Hh. quoyi*: MH714706.1, *G. chalcogrammus*: FJ264324.1, *Lophius litulon*: HE608228.2, *P. pusillus*: KF025786.1, *Hh. sajori*: AB372031.2, *G. macrocephalus*: AY946313.1, *Hb. armata*: NC_086878.1, *S. imberbis*: MN937450.1, *N. stigmosus*: AP018427.1, *R. meridionalis*: KF265088.1, *La. tanakae*: KU362835.1, *T. pseudommus*: MZ603736.1, *T. flavidus*: KJ562276.1, *T. chinensis*: AP009534.1, *T. rubripes*: AP006045.1, *T. vermicularis*: EU274421.1, *Lc. guenther*i: JQ681891.1, and *Lc. cheesemanii*: JQ681890.1) sequences retrieved from NCBI, were aligned using ClustalW in MEGA 11 software. For phylogenetic tree construction, sequences for each gene were trimmed to a uniform length (530 bp for *CoI* and 285 bp for *Cytb*). Phylogenetic analysis was conducted using the neighbor-joining algorithm in MEGA 11. The Kimura 2-parameter model was applied to estimate genetic distances and species diversity, and statistical support for tree topology was assessed with 1000 bootstrap replicates.

Results and Discussion

Species identification of dried seafood products

Upon comparison of the *CoI* and *Cytb* gene sequences derived from the analyzed dried seafood products (n=24) with those registered in the NCBI GenBank and BOLD system databases, 11 species (*Hh. quoyi*, *G. chalcogrammus*, *Lh. litulon*, *Cg. myriaster*, *P. pusillus*, *Hh. sajori*, *G. macrocephalus*, *Cn. meridionalis*, *D. gigas, Lc. cheesemanii*, and *T. vermicularis*), used in 19 products, satisfied the identification criteria and were identified at the species level (Table 1). In the analysis of samples S2, S14, S15, and S16, BLASTn searches identified two species, *G. chalcogrammus* and *Theragra finnmarchica*, both meeting the species identification criteria. However, only *G. chalcogrammus* was confirmed through the BOLD systems search. Additionally, *G. finnmarchicus* (Koefoed, 1956) is widely regarded as a junior synonym of *G. chalcogrammus* (Pallas, 1814)[16]. Therefore, *G. chalcogrammus* was selected as the final scientific name in this study, in accordance with the principle of nomenclatural precedence. Similarly, *G. ogac* (Richardson, 1836) is also considered a junior synonym of *G. macrocephalus* (Tilesius, 1810)[17] as observed in sample S7[17]. Consequently, *G. macrocephalus* was designated as the final scientific name for this study. For sample S6, the BOLD systems search identified two species, *Hh. sajori* and *Rhynchorhamphus georgii*, which contrasts with the results of the BLASTn search. However, these two species inhabit different regions. *Hh. sajori* (Temminck & Schlegel, 1846)[18] is distributed in the Northwest Pacific, including the Yellow Sea, East Sea, and the Pacific coast of Japan, whereas *Rhynchorhamphus georgii* (Valenciennes, 1847)[19] is commonly found in the Indo-West Pacific, including the Persian Gulf and the Bay of Bengal. Considering the distribution information and the country of origin indicated on the label, *Hh. sajori* was ultimately selected as the final identification (Table 1). However, five products could not be conclusively identified to a single species. For samples S9 and S10, four species (*Hb. armata*, *N. stigmosus*, *S. imber*bis, and *N. unimaculatus*) met the identification criteria in both BLASTn and BOLD system searches. In sample S12, three species (*La. tanakae*, *La. chefuensis*, and *La. agassizii*) were identified, while in samples S18 and S23, five species (*T. rubripes*, *T. flavidus*, *T. chinensis*, *T. pseudommus*, and *T. obscurus*) were detected through BLASTn and BOLD system searches.

Validation of species identified via phylogenetic analysis

To further validate the findings obtained from DNA barcode and FINS analyses, a phylogenetic analysis was conducted. The construction of the phylogenetic tree was based on a total of 40 *CoI* and 40 *Cytb* sequences, which included sequences derived from DS and SDS products and additional *CoI* and *Cytb* sequences retrieved from the NCBI GenBank database. As illustrated in Fig. 1, 13 samples (S1, S2, S4, S5, S6, S11, S13, S15, S19, S20, S21, S22, and S24), which were identified as single species based on *CoI* gene analysis (Table 1), grouped into 9 distinct clades alongside corresponding reference *CoI* sequences from the NCBI GenBank database (Fig. 1A). Similarly, 14 samples (S1, S2,

S3, S5, S6, S7, S8, S11, S12, S14, S15, S16, S17, and S24) identified as single species by the *Cytb* gene also formed 9 distinct clades in conjunction with their respective reference *Cytb* sequences from the NCBI GenBank database (Fig. 1B). Five samples (S9, S10, S18, S23, and S12) that could not be identified at the species level were grouped with their closely related species. Specifically, sample S12, labeled as cubed snailfish, was identified as *La. tanakae* based on FINS analysis using the *Cytb* gene, but with a low coverage level of 87%. Notably, the *Cytb* sequences of *La. tanakae* available in the GenBank database are 762 bp in length, whereas only 381 bp from the 3' end of these sequences aligned with our consensus *Cytb* sequence (438 bp), resulting in insufficient coverage (Table 1). Consequently, *La. tanakae* was assigned as the final scientific name for sample S12. For samples S9 and S10, labeled as armored brotula, *Hb. armata* was selected as the final scientific name, given the declared country of origin (South Korea and China) and the raw material description (English common name: 'armored brotula'). However, for samples S18 and S23, labeled as panther puffer and pufferfish, respectively, a single species could not be conclusively identified based on the genetic data alone.

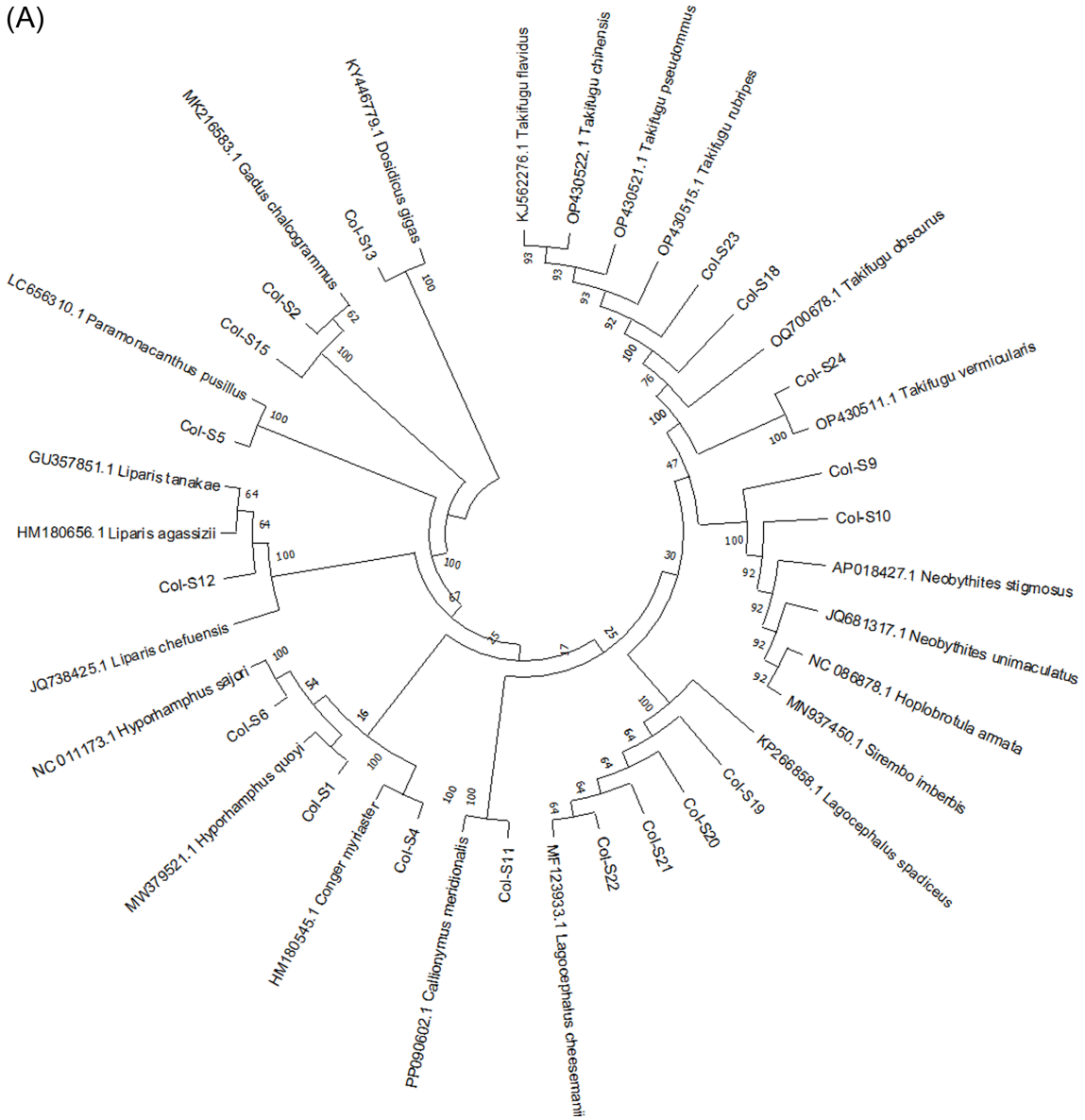

Fig. 1. The phylogenetic trees for (A) *CoI* and (B) *Cytb* sequences were constructed using the Neighbor-Joining method. These trees include 4 dried seafood (DS) and 20 seasoned and dried seafood (SDS) products as well as an additional 40 sequences retrieved from the NCBI GenBank database. The numerical identifiers (S1-S24) for the DS and SDS samples correspond to those listed in Table 1.

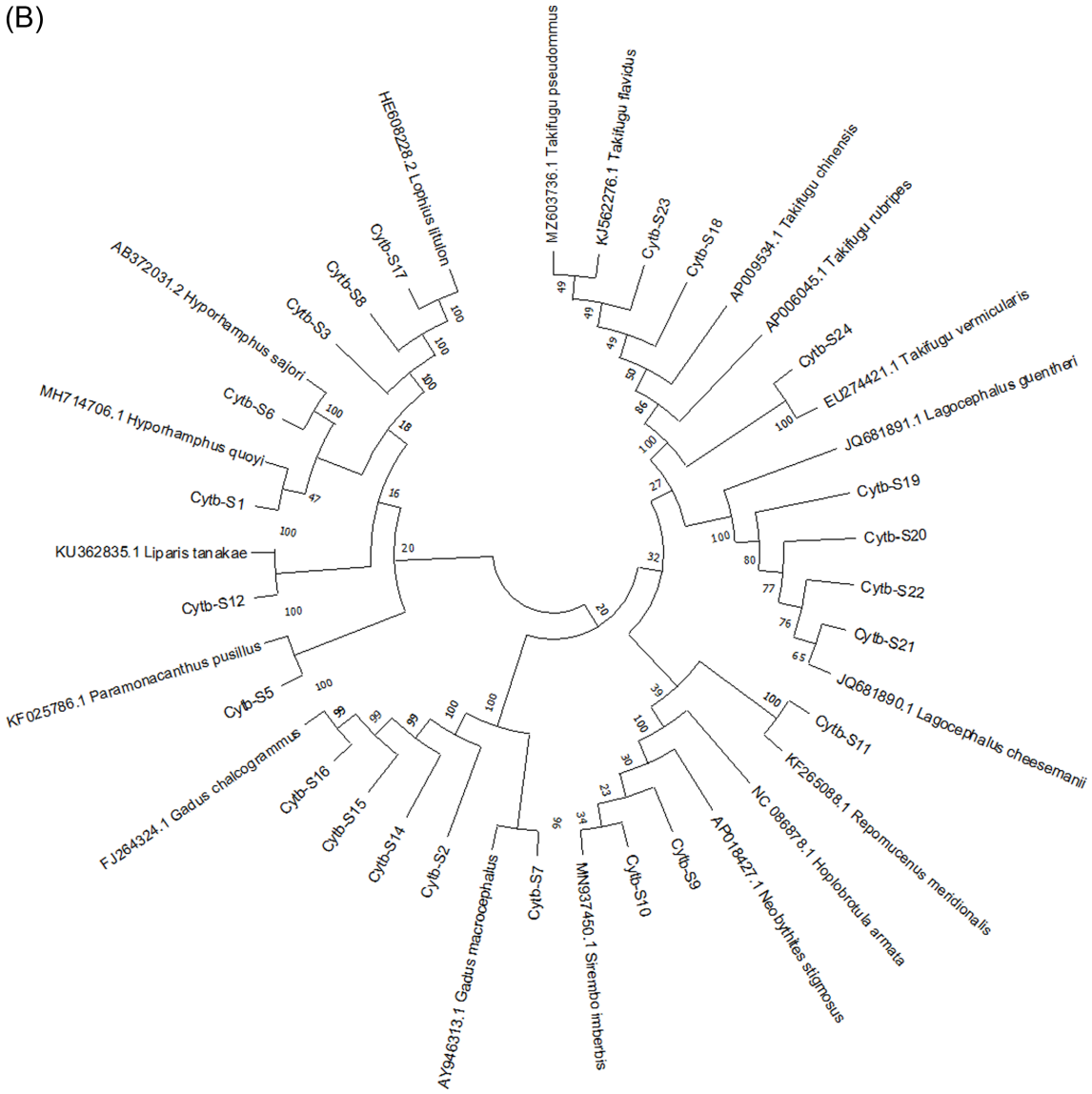

Fig. 1. (Continued) The phylogenetic trees for (A) *CoI* and (B) *Cytb* sequences were constructed using the Neighbor-Joining method. These trees include 4 dried seafood (DS) and 20 seasoned and dried seafood (SDS) products as well as an additional 40 sequences retrieved from the NCBI GenBank database. The numerical identifiers (S1-S24) for the DS and SDS samples correspond to those listed in Table 1.

Consistency between raw materials used and labeling

To evaluate labeling compliance, the raw materials listed on product labels were compared with the common names corresponding to the scientific names identified through genetic analyses (refer to *Sequence Analysis and Database Comparison*). As presented in Table 1, the raw materials listed on the labels of 24 DS and SDS products included: pufferfish (n=4), Alaska pollock (n=3), blackmouth angler (n=3), Japanese halfbeak (n=2), Pacific cod (n=2), panther puffer (n=2), armored brotula (n=2), unagi (n=1), filefish (n=1), bartail flathead (n=1), squid (n=1), cubed snailfish (n=1), and brown-backed toadfish (n=1). Among these, 8 products (33.3%; S2, S6, S7, S9, S10, S14, S16, and S20) were found to be consistent with both labeling and species identification results, including *G. chalcogrammus* (Alaska pollock, n=3), *Hb. armata* (armored brotula, n=2), *Hh. sajori* (Japanese halfbeak, n=1), *G. macrocephalus* (Pacific cod, n=1), and *Lc. cheesemanii* (brown-backed toadfish, n=1) (Fig. 2). Conversely, discrepancies were observed in 16 products (66.7%) between the labeling and species identification results. Among these, 10 products (41.7%; S3, S4, S5, S8, S13, S17, S19, S21, S22, and S23) employed generic market names, such as unagi and squid, which were inconsistent with the species identification. When including generic market names, the discrepancy rate was as follows:

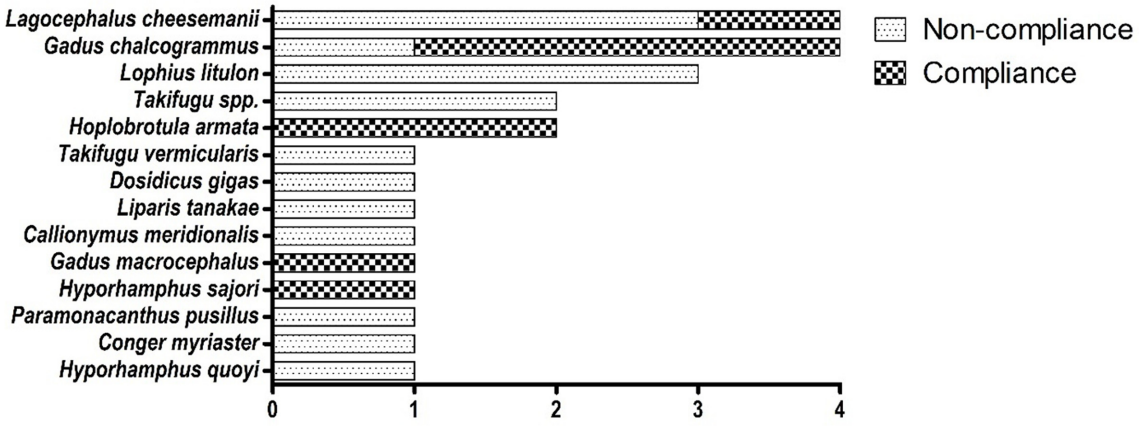

Fig. 2. Identification of species in the 4 dried seafood and 20 seasoned and dried seafood products and the corresponding compliance ratio of labeling.

Lc. cheesemanii and *Takifugu* spp. (pufferfish, n=4), *Lh. litulon* (blackmouth angler, n=3), *Cg. myriaster* (unagi, n=1), *P. pusillus* (filefish, n=1), and *D. gigas* (squid, n=1). However, excluding generic market names, the mislabeling rate reduced to 33.3%, including *Hh. quoyi* (Japanese halfbeak, n=1), *Cg. myriaster* (unagi, n=1), *P. pusillus* (filefish, n=1), *Cn. meridionalis* (bartail flathead, n=1), *La. tanakae* (cubed snailfish, n=1), *G. chalcogrammus* (Pacific cod, n=1), and *Takifugu* spp. and *T. vermicularis* (panther puffer, n=2). For the six products (S1, S11, S12, S15, S18, and S24) exhibiting labeling discrepancies, the following substitutions were noted: In the case of products S18 and S24, which were labeled as containing *T. pardalis* (Panther puffer), the actual ingredients included *Takifugu* spp. such as *T. chinensis*, *T. rubripes*, *T. flavidus*, and *T. vermicularis*. In sample S1, *Hh. quoyi* (Quoy's garfish) was used instead of the labeled *Hh. Sajori* (Japanese halfbeak). Sample S15, labeled as containing *G. macrocephalus* (Pacific cod), actually contained *G. chalcogrammus* (Alaska pollock). Additionally, in samples S11 and S12, *Platycephalus indicus* (Bartail flathead) and *La. tessellatus* (Cubed snailfish) were replaced with *Cn. meridionalis* (Whiteflag dragonet) and *La. tanakae* (Tanaka's snailfish), respectively.

The twenty-four products used in this study were categorized as DS and SDS products according to the Food Code definition, and the labeling discrepancy rate was subsequently analyzed. A discrepancy rate of 50% was observed in DS products (n=4), while SDS products exhibited a higher discrepancy rate of 70% (n=20) (Fig. 3). This elevated mislabeling rate is commonly reported in various processed seafood products, including pufferfish[6], shrimp[7], and Mi-iuy croaker[20], compared to simply processed products. These findings suggest that the difficulty in visually inspecting the morphological characteristics of raw materials in multi-processed products leads to a higher frequency of labeling discrepancies, such as mislabeling, compared to simply processed products. The countries of origin for the 24 products analyzed were China (n=9), South Korea (n=5), Russia (n=5), Vietnam (n=3), Peru (n=1), and one unlabeled product (n=1) (Fig. 4). Labeling discrepancy rates were observed to be 100% for products from Vietnam, Peru, and the unlabeled category. Products from China exhibited a discrepancy rate of 78% (S3, S8, S12, S17, S19, S21, and S22), while South Korean products showed a rate of 60% (S4, S18, and S24), and Russian products had a discrepancy rate of 20% (S15). However, due to the small sample size, no correlation between a specific country of origin and the labeling discrepancy rate could be established.

Processed fishery products are particularly prone to mislabeling and subsequent recall actions due to the difficulty of visually verifying the authenticity of the raw materials. According to recent news, the Ministry of Food and Drug Safety has suspended the sale and recalled SDS products that used squid mouths, which are prohibited as food ingredients, as well as processed seafood products that failed to disclose squid, an allergenic ingredient. In this study, we assessed the labeling compliance of 24 domestically distributed processed seafood products and found a high discrepancy rate of 66.6%. This rate significantly exceeds those reported for staple seafood products such as Mi-iuy croaker (21%)[20], snow crab (12%)[21], and cephalopod (37.5%)[22], and even surpasses the previously highest rate of 60.3% observed for pufferfish[12]. The elevated discrepancy rate is likely due to the multi-processed nature of these products, which complicates visual identification. Thus, continuous monitoring of both imported and domestic processed fishery products is crucial. The results of this study provide essential

baseline data for future monitoring and regulatory efforts concerning processed fishery products.

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국문요약

본 연구에서는 국내에서 판매되는 24개 건어포 및 조미건어포 제품의 종 판별 및 표시사항 준수 여부를 평가했다. 이러한 수산가공품에 사용된 원재료의 종판별을 위해 cytochrome c oxidase subunit I 및 cytochrome b 유전자의 염기서열을 분석하여 NCBI GenBank 및 BOLD 데이터베이스에 등록되어 있는 생물종의 염기서열과 비교 후 계통 분석을 수행했다. 분석 결과 13개 종(*Hyporhamphus quoyi*, *Gadus chalcogrammus*, *Lophius litulon*, *Conger myriaster*, *Paramonacanthus pusillus*, *Hyporhamphus sajori*, *Gadus macrocephalus*, *Hoplobrotula armata*, *Callionymus meridionalis*, *Liparis tanakae*, *Dosidicus gigas, Lagocephalus cheesemanii*, and *Takifugu vermicularis*)이 확인되었다. 일반명(장어, 오징어 등)을 포함할 경우 16개 제품(66.7%)에서 표시사항과 판별된 종 간에 불일치가 확인되었으며, 일반명을 제외할 경우 불일치 비율은 41.7%로 감소했다. 식품유형별로는 조미건어포 제품(n=20, 70%)에서 건어포 제품(n=4, 50%) 보다 높은 비율의 불일치 비율이 관찰되었다. 원산지별 분석 결과 특정 국가와 불일치 비율과의 상관성은 확인할 수 없었다. 이러한 연구 결과는 건포류 제품의 주기적 모니터링 수행 및 수산물의 국명 표시 선을 위한 기초자료로 쓰일 수 있을 것이다.

Conflict of interests

The authors declare no potential conflict of interest.

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