

# 9<sup>th</sup> MEETING OF THE SCIENTIFIC COMMITTEE

Held virtually, 27 September to 2 October 2021

SC9-Doc17

Republic of Korea Annual Report

Republic of Korea

# KOREA ANNUAL REPORT ON FISHING, RESEARCH ACTIVITIES, AND OBSERVER IMPLEMENTAION IN THE SPRFMO CONVENTION AREA IN 2020

August 2021



# **CONTENTS**

1.	DESCRIPTION OF FISHERIES	2
1.1	Trawl fishery	2
1.2	Jigging fishery	2
2.	CATCH, EFFORT AND CPUE SUMMARIES	3
2.1	Pelagic trawl fishery	3
2.2	Bottom trawl fishery	4
2.3	Jigging fishery	4
3.	FISHERIES DATA COLLECTION AND RESEARCH ACTIVITIES	6
3.1	Fisheries catch & effort data collection system	6
3.2	Research activities	6
	.2.1 Development of SNP markers for jumbo flying squid using genotyping-by-sequencing (GBS)	6
4.	OBSERVER IMPLEMENTATION REPORT	9
4.1	Observer program design and training	9
4.2	Observer coverage and data collection	10
4.3	Biological sampling and length composition of catches	11
5.	ECOSYSTEM APPROACH CONSIDERATIONS	13
5.1	Seabird mitigation measures	13
5.2	Observed interactions with other species of concern	13
RF	FERENCES	15

# 1. Description of Fisheries

### 1.1 Trawl fishery

Korea has been conducting trawl fishing targeting on jack mackerel (*Trachurus murphyi*) since 2003 when Korean research trawl vessel *Tamgu No.1* operated pristinely in the SPRFMO Convention Area. The number of active Korean trawl vessels has been changed from 1 to 3 in the last 15 years (Table 1). Since 2020, Korea has not conducted any trawl fishing in the Convention Area due to the COVID-19.

Table 1. Summary of the number and size of Korean trawler in the SPRFMO Convention Area.

Year	Number of	Gross registered Tonnage (GT)					
Tear	vessels	2,000-2,999	3,000-3,999	4,000-4,999	5000<		
2004	3	1	1	1	-		
2005	2	1	1	-	-		
2006-2008	3	1	1	1	-		
2009	2	-	1	1	-		
2010-2012	2	-	1	-	1		
2013-2014	1	-	1	-	-		
2015-2016	2	-	1	-	1		
2017	1	-	1	-	-		
2018-2019	2	-	1	-	1		
2020	0	-	-	-	-		
2021	0	-	-	-	-		

### 1.2 Jigging fishery

Korea jigging fishery targeting on jumbo flying squid (*Dosidicus gigas*) has been commercially operating in the Convention Area since 1990. The number of jigging vessels fluctuated in a range of 0-50 in the last 30 years (Figure 1). In the 1990s, the numbers of vessels peaked at 50 in 1995 and decreased rapidly since then. Only the number of vessels remained smallest in the 2000s. In 2020, only 13 vessels operated in the Convention Area.

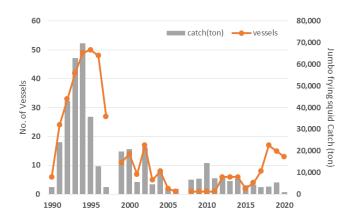


Figure 1. Trends in effort (the number of jigging vessels fishing) and total catch of jumbo flying squid (*Dosidicus gigas*) in the SPRFMO Convention Area from 1990 to 2020.

# 2. Catch, Effort and CPUE Summaries

### 2.1 Pelagic trawl fishery

The annual trawl fishing effort and catch by Korean vessels targeting on mainly jack mackerel (*Trachurus murphyi*) in the SPRFMO Convention Area is summarized in Table 2. The number of fishing days fluctuated between the range of 40-249, depending on the change of the number of vessels between 1 to 3 in the last 17 years except in 2020. No trawl fishing was conducted in the convention area due to the COVID-19 pandemic.

Jack mackerel is the main target species, and has made up more than 85% of the total catch with tonnages ranging from 1,235 to 13,759 tons. Chub mackerel (*Scomber japonicus*) is the second most dominant species in the catch which ranged from 21 to 1,460 tons. Other species that have been significant in the catch include Blue fathead (*Cubiceps caeruleus*), Pacific pomfret (*Brama japonica*), and jumbo flying squid (*Dosidicus gigas*), and the catches of these species were included in "Other species" category in Table 2.

The CPUE trend of jack mackerel is relatively stable in the range of 4 to 6 (ton/hour) except for 2009 when the highest CPUE (10.5 ton/hour) was reported (Figure 2). The total catch in 2019 increased substantially, and the catch of jack mackerel increased by more than twofold of the last year. However, the CPUE did not increase as much as the catch.

Table 2. Annual fishing effort (number of vessels and tow) and fisher-reported catch (tones) of two main fishing species and others by weight (CJM: jack mackerel, MAS: chub mackerel) by Korean trawlers in the SPRFMO Convention Area.

Year	No. Vessels	*No. Fishing days	No. Tows	Total towed hours	CJM (ton)	MAS (ton)	Other species (ton)	Total catch (ton)
2004	3	205	?	?	7,438	708	0	8,146
2005	2	170	?	?	9,126	381	0	9,507
2006	3	232	?	?	10,474	1,460	0	11,934
2007	3	237	?	?	10,940	1,240	0	12,180
2008	3	249	?	?	12,600	968	0	13,568
2009	2	182	?	?	13,759	716	59	14,534
2010	2	136	?	?	8,183	84	0	8,267
2011	2	205	?	?	9,253	24	100	9,377
2012	2	117	?	?	5,492	0	0	5,492
2013	1	140	?	975	5,267	111	0	5,378
2014	1	86	?	652	4,078	21	0	4,099
2015	2	104	?	900	5,749	82	3	5,834
2016	2	182	?	1,581	6,430	486	16	6,931
2017	1	40	?	225	1,235	191	3	1,429
2018	2	138	209	882	3,717	246	86	4,049
2019	2	111	249	1,427	7,444	82	96	7,622
2020	0	0	0	0	0	0	0	0

No. of fishing days: only days of fishing activity occurred.

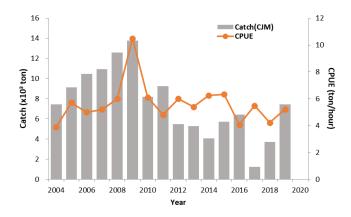


Figure 2. Annual catch and CPUE (ton/hour) of jack mackerel in the SPRFMO Convention Area.

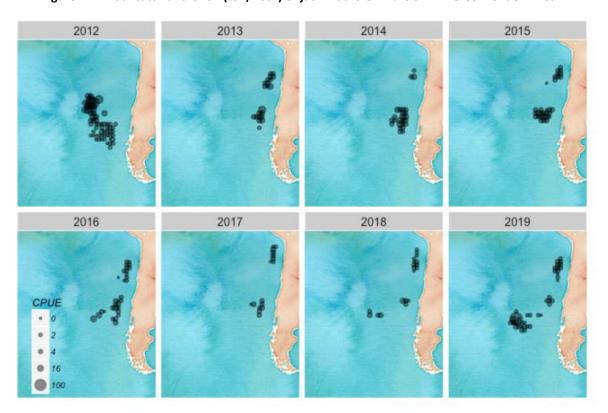


Figure 3. Distribution of CPUE (ton/hour) of jack mackerel in the SPRFMO Convention Area during 2012-2019

### 2.2 Bottom trawl fishery

Korean bottom trawl fishery, mainly targeting on orange roughy (*Hoplostethus atlanticus*), has not fished in the SPRFMO Convention Area since 2008 (Refer to SC6-Doc27).

### 2.3 Jigging fishery

The annual fishing efforts (fishing days) and catches by Korean jigging vessels are summarized in Table 3. The fishery mainly targets on jumbo flying squid. The annual fishing effort and catch varied over time. The highest catch on jumbo flying squid was over 69 thousand tons in 1994, and the largest number of jigging vessels operated in 1995. The catch trend shows a continuous decrease since the highest catch was observed (Figure 1). The CPUE ranged from 3.6 to 28.2 ton/day in the recent 9 years. The CPUE shows a decreasing trend since

2015. In 2020, thirteen fishing vessels operated in the Convention Area from 9 to 49 days only. The catch and CPUE stayed low, accordingly (Figure 4).

Table 3. Annual fishing efforts (number of vessels and fishing days) and catches of jumbo flying squid by Korean jigging fisheries in the SPRFMO Convention Area.

Vacu	No.	No.	Avg.	Total catch
Year	Vessels	Fishing days	fishing days/vessel	(ton)
1990	6	?	?	3,465
1991	24	?	?	24,015
1992	33	?	?	43,022
1993	42	?	?	62,887
1994	49	?	?	69,664
1995	50	?	?	35,719
1996	48	?	?	12,896
1997	27	?	?	3,359
1998	0	0	0	0
1999	11	?	?	19,728
2000	14	?	?	20,822
2001	7	?	?	5,797
2002	17	?	?	21,759
2003	5	?	?	4,722
2004	8	?	?	10,787
2005	2	?	?	2,519
2006	1	?	?	2,485
2007	0	0	0	0
2008	1	?	?	6,775
2009	1	?	?	7,221
2010	1	?	?	14,506
2011	1	?	?	7,410
2012	6	580	97	7,991
2013	6	365	61	6,034
2014	6	397	66	7,261
2015	2	151	76	4,263
2016	4	409	102	4,388
2017	8	456	57	3,460
2018	17	1,003	59	3,651
2019	15	1,037	69	5,577
2020	13	212	16	1,003

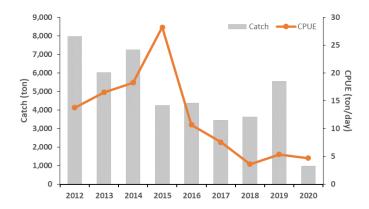


Figure 4. Annual catch (ton) and CPUE (ton/day) of jumbo flying squid in the SPRFMO Convention Area.

### 3. Fisheries Data Collection and Research Activities

### 3.1 Fisheries catch & effort data collection system

The data collection system implemented for Korean high seas fishing vessels has been changed since 2015. Before 2015, the system was operated in a dualized manner: total catches of high seas fishing vessels were collected by Korea Overseas Fisheries Association (KOFA) while fishing logbook was collected and managed by National Institute of Fisheries Science (NIFS). Since September 2015, detailed tow-by-tow catch and effort data of all high seas fishing vessels is being reported through Electronic Reporting System (ERS) to Korea Fishery Monitoring Center (KFMC). The catch and effort data from all fishing vessels operating in the Convention Area is submitted to the Secretariat in accordance with the data standards of SPRFMO.

### 3.2 Research activities

In 2020, Korea conducted a preliminary study on developing single nucleotide polymorphism (SNP) markers for jumbo flying squid for population genetic analysis in the Convention Area.

### 3.2.1 Development of SNP markers for jumbo flying squid using genotyping-by-sequencing (GBS)

GBS can be used as a fast and cost-effective tool in population genetics, QTL (quantitative trait locus) discovery, high-resolution mapping, and genomic selection. In this study, SNP (single nucleotide polymorphism) markers were developed using genotyping by sequencing (GBS) without relying on the reference genome sequence for population analysis of jumbo flying squid. The muscle tissue samples of jumbo flying squid were collected by scientific observers dispatched on board Korean jigging vessels in 2019. Genomic DNA of jumbo flying squid was extracted using the modified cetyltrimethylammonium bromide (CTAB) method. The extracted 96 genomic DNAs was used as GBS library constructions (Figure 5).

The genomic DNA was digested with Pstl (5'-CTGCA/G-3') & Mspl (5'-C/CGG-3') restriction enzymes (New England Biolabs) using a protocol modified from Elshire et al., (2011). The DNA fragments from each sample were ligated to unique barcoded Pstl adapters and Mspl Y-adapters for identification to allow pooling of samples for DNA sequencing and analysis. The GBS libraries were sequenced on the Illumina HiSeqX with the length of 150bp PE reads.

After sequencing, raw reads were de-multiplexed according to the barcode sequences were trimmed using inhouse python script. The de-multiplexed reads were trimmed using the Solexa QA package v.1.13. We trimmed either end of the reads when the Phred quality score dropped below Q = 20 (or 0.05 probability of error). In addition, we also trimmed all 5' and 3' stretches of ambiguous 'N' nucleotides. Poor quality sequence reads along with reads shorter than 25 bases were discarded.

To align the clean reads to the assembled transcripts (Axon\_rRNA\_Depleted (accession: SRX3391198) & Axoplasm (accession: SRX3391197)) the Burrows-Wheeler Aligner (BWA, 0.6.1-r104) program were applied. The BWA default values for mapping were used, except for seed length (-I) = 30, maximum differences in the seed (-k) = 1, number of threads (-t) = 16, mismatch penalty (-M) = 6, gap open penalty (-O) = 15, and gap extension penalty (-E) = 8. Mapped reads were extracted from the resulting BAM file using SAMtools (v.0.1.16) for further analyses. The high mapping quality ensures reliable (unique) mapping of the reads, which is important for variant calling. Using the varFilter command, SNPs were called only for variable positions with a minimal mapping quality (-Q) of 30. The minimum and maximum of read depths were set at 3 and 765, respectively. In-house script considering biallelic loci was used to select significant site in the called SNPs positions. Depending on ratio of SNP/InDel reads to mapped reads, variant types are classified into three categories: homozygous where SNP/InDel is greater than 90%, heterozygous where SNP/InDel is greater than 40% and less than or equal to 60%, and Etc for any remaining reads. To control the quality of markers, missing proportion (MSP) < 0.4 and minor allele frequency (MAF) > 0.05 was selected.

Sequencing of the GBS library yielded total 705 million reads in 96 samples. Out of 96 samples, we found SNP in 87 samples except 9 samples that failed to produce 300,000 reads. A total of 15,390 informative SNPs were identified throughout jumbo flying squid genome. The final set of SNPs was obtained by applying additional

population-level filtering criteria (MAF >5%) in terms of polymorphisms and missing genotypes (missing data < 40%). This resulted in a set of 1,076 filtered SNPs for further analysis.

The evolutionary history was inferred using the Neighbor-joining method with 1000 replications. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. All ambiguous positions were removed for each sequence pair. There were a total of 1,071 positions in the final dataset. Evolutionary analyses were conducted in MEGA6.

The principal component analysis (PCA) was conducted based on 1,071 SNPs using 87 individual samples (Figure 6). The top two principal components (PC1 and PC2) explain 14.64% of the genetic variation (R package SNPRelate).

Population structure was analyzed using the Bayesian method implemented in STRUCTURE 2.3.4 software, assuming an admixture model and correlated allele frequency. After the initial burn-in period of 10,000 iterations for each K value (ranging from 1 to 10), ten replicate runs of 10,000 Markov Chain Monte Carlo iterations were performed. The STRUCTURE 2.3.4 results were summarized using the Structure Harvester. The number of groups was estimated using the Evanno's  $\Delta K$  based method. The most reasonable biological interpretation was showed at K =2 and K=4 (Figure 7). The population structures by each sampled location seem different in north and south when K=2 (Figure 8), but the further study is in progress.

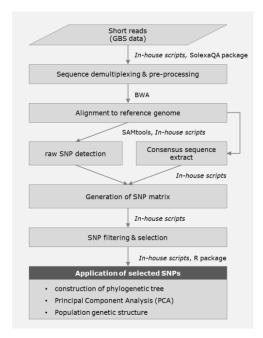


Figure 5. Flowchart of developing single nucleotide polymorphism (SNP) markers for jumbo flying squid using genotyping-by-sequencing (GBS).

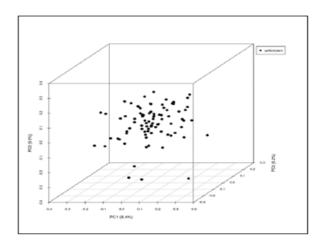


Figure 6. PCA-3D plot of 87 individual *D. gigas*.

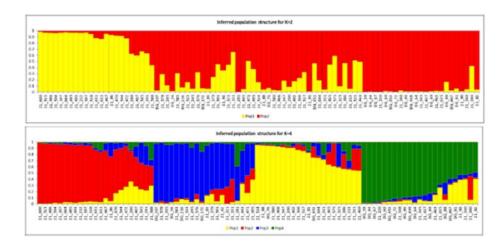


Figure 7. Population structures of 87 individual *D. gigas* when K=2 and K=4.

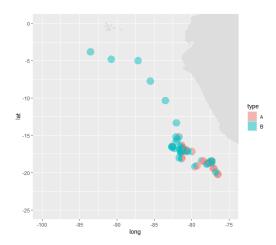


Figure 8. The population structures (K=2) by each sampled location.

# 4. Observer Implementation Report

### 4.1 Observer program design and training

Korean scientific observer program for distant-water fisheries has been in place since 2002. According to "Enforcement decree of the distant water fisheries development act," the Korean scientific observer program is operated by two organizations: 1) National Institute of Fisheries Science (NIFS) and 2) Korea Fisheries Resources Agency (FIRA). NIFS is in charge of the scientific investigation including the briefing/debriefing, management of observer data, data verification, and training of observer on the RFMOs' Conservation and Management Measures (CMMs), while FIRA is in charge of the management of the program except for NIFS's responsibilities.

The observer trainings provided by the Korean scientific observer program can be classified into four types: 1) candidate training for recruitment, 2) regular training for all observers, 3) self-development training, and 4) pre-survey training.

The process to recruit observers is as follow. Candidates are selected by reviewing their applications and CVs based on the qualification criteria: a person who is a college graduate whose major field is nature science; or else, a high school specialized fisheries graduate who accompanies at least 1-year experience on board with having a certificate of qualification to deck officer. The candidates who pass the review process are subject to an in-person interview. In the interview, the candidates are asked of their basic knowledge on fisheries, English speaking skill, availability to be on board, etc. The candidates who passed the in-person interview can attend the <u>candidate training</u> course. The trainees who pass the final test can be selected to be deployed to the vessels.

Biannual <u>regular training</u> sessions are provided for all selected observers who are on off-duty. The training includes updated RFMOs' CMMs, safety trainings, protected species (marine mammals, seabirds, VMEs), and other subjects including integrity courses.

Due to the limitation in gathering as a group and providing a group training, the <u>self-development training</u> focuses on individual observer's free will in improving their skills of English, computer, and more. All observers can be provided approximately \$300/year for their self-development training.

NIFS trains observers before dispatching them to each RFMOs convention area. The <u>pre-survey training</u> includes the CMMs of each RFMO, the method to collect the data and biological samples by specific tasks to be done, and the detailed information on writing the survey reports.

Table 4. Types of observer training process by the Korean scientific observer program

Type of training	Candidate training	Regular training	Self-development training	Pre-survey training
Organization	FIRA	FIRA	FIRA	NIFS
Period	Only once	Biannual	Time of need	Before every dispatching
Materials	An overview of the	Scientific research,	English,	Update on RFMO's CMMs,
	observer program,	Protected species	Computer skill,	Scientific survey process,
	Gear-specific observer	(seabirds, mammals),	and	How to write logbook,
	duties,	Identification on VMEs,	Physical training	Sample collection method,
	Identification and	Safety education,		and
	measurement for target	and		Preparation of survey
	species,	Integrity education		report
	Observation of			
	sharks/whales/seabirds,			
	Observation of Vulnerable			
	Marine Ecosystems			
	(VMEs),			
	Hand-on computer			
	program training,			
	Marine species			
	identification,			

Introduction of RFMOs,		
Systematic management of		
fishing information,		
Catch product processing,		
Marine meteorology,		
At-sea safety training		
English (maritime		
everyday),		
Organizational structure		
and culture of a ship,		
and		
Fish dissection LAB		

Currently, Korean scientific observer program is on the process of Accreditation Assessment based on CMM 16-2021.

### 4.2 Observer coverage and data collection

Korean observers collect a wide range of data from both target and bycatch species to inform scientific analyses. The lists of data collected by observers are based on SPRFMO CMM 02-2020 Annex 7.

The observer coverage of Korean vessels is summarized in Table 5. In 2008, two trawlers operated in the Convention Area, and one observer was deployed on two vessels for 9 days. No observer was dispatched in 2009-2010. One observer was aboard in one trawler in 2011 and 2012, and the coverages were 6.8% and 58.1% respectively. The observer coverage for trawl fishing has been 100% since 2013. No Korean trawler fished in the Convention Area in 2020, so there was no observer activity.

The first placement of scientific observers on Korean commercial jigging vessels was in 2015. In 2020, one observer embarked and collected scientific information with a coverage of 20% over the total fishing days.

Table 5. Scientific observer coverage on Korean vessels in the SPRFMO Convention Area.

Year	Gear types	Vessel name	Observer onboard days	Coverage rate of the vessel (total coverage of the fishing method)
2008	Trawl	Insungho	3	4%
	Trawl	Kwangjaho	6	
2011	Trawl	Kwangjaho	14	6.8%
2012	Trawl	Kwangjaho	68	58.1%
2013	Trawl	Kwangjaho	140	100% (100%)
2014	Trawl	Kwangjaho	86	100% (100%)
2015	Trawl	Kwangjaho	120	100% (100%)
	Trawl	Sejong	10	100% (100%)
	Jigging	No.705 Amor	75	100% (50%)
2016	Trawl	Kwangjaho	179	100% (100%)
	Trawl	Sejong	28	100% (100%)
2017	Trawl	Kwangjaho	88	100% (100%)
2018	Trawl	Kwangjaho	134	100% (100%)
	Trawl	Sejong	37	100% (100%)
	Jigging	No.703 Amor	93	100% (17%)
	Jigging	No.101 Agnes	82	100% (17%)
2019	Trawl	Kwangjaho	194	100% (100%)
	Trawl	Sejong	17	100% (100%)
	Jigging	No.705 Amor	88	84% (18%)
	Jigging	No.316Sunhae	99	86% (18%)
2020	Jigging	No. 5 Sae In	*103	86%(20%)

<sup>\*</sup> the observer embarked from the domestic port due to COVID-19 and sailed to the Convention Area

### 4.3 Biological sampling and length composition of catches

There is no update on the biological information of jack mackerel since there was no trawl fishering in 2020. Following information is analogous to that provided in the last annual report.

Yearly length frequencies and length-weight relationship of jack mackerel is shown in Figure 9 and 10. The ranges of annual sampling size are from 1,108 to 9,789 for the length measurement, and from 231 to 5920 for the length and weight measurement. A comparison among the range of the annual fork length measurements taken from 2012 to 2019 suggests that a trend having a single mode in the earlier part of the sampling year has been changed to have multiple modes in the later sampling period. In 2019, the strongest mode appeared around 23cm in fork length of jack mackerel.

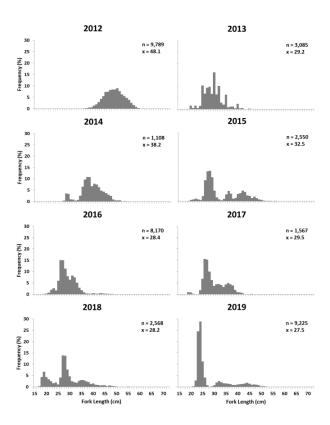


Figure 9. Length frequency distributions for jack mackerel from 2012 to 2019 collected by scientific observers in the SPRFMO Convention Area.

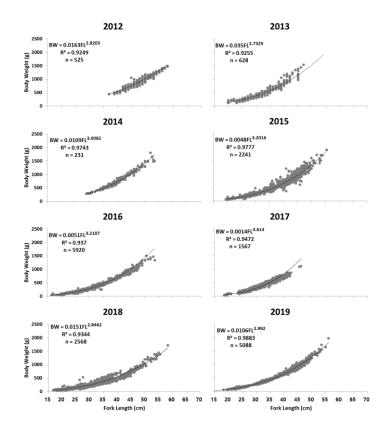


Figure 10. Length-weight relationships of jack mackerel from 2012 to 2019 collected by scientific observers in the SPRFMO Convention Area.

The yearly length frequencies of jumbo flying squid from 2018 to 2020 is shown in Figure 11. The ranges of annual sampling size are from 782 to 4,901. The bimodal distributions were appeared through the years with different intensity. In 2020, the most distinct bimodal mode appeared among the years around 55 and 80cm in dorsal mantle length of jumbo flying squid.

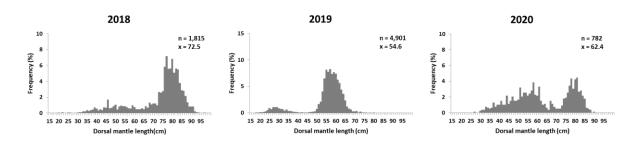


Figure 11. Length frequency distributions for jumbo flying squid from 2018 to 2020 collected by scientific observers in the SPRFMO Convention Area.

# 5. Ecosystem Approach considerations

### 5.1 Seabird mitigation measures

All Korean trawl vessels fishing in the SPRFMO Convention Area are required to comply with seabird mitigation methods specified in CMM09-2017. The requirements include deployment of streamer (tori) lines or bird bafflers where it is not operationally feasible to use streamer lines and management of discharge of biological material. Trawl vessels are prohibited to discharge biological material during shooting and hauling. There is no update on the description on seabird mitigation method since no trawl fishing was conducted in 2020.

### 5.2 Observed interactions with other species of concern

All scientific observers executed daily observation of seabirds at least once every set or haul for more than 15 minutes. Observers were instructed to observe whether the seabirds were dipping their beak or head into the water near the net to feed on during fishing. The quantitative information on seabird observation was submitted by observers. Total of 24 species of seabirds were observed on trawl vessels in the last 8 years, and 8 species were observed on jigging vessels in the last 2 years (Table 6). There were no injured, struck or dead seabirds observed or reported in the last 8 years. In 2020, the most abundant seabird species observed by a scientific observer on a jigging vessel were PRX (72%) and OCO (14%).

Table 6. A list of observed seabirds by scientific observers in the SPRFMO Convention Area.

Observed fishing vessel	FAO species code	Scientific name	English name
Trawl	CSK	Catharacta skua	Great skua
Trawl, Jigging	DAC	Daption capense	Cape petrel
Jigging	DAQ	Phoebastria albatrus	Short-tailed Albatross
Trawl	DCR	Thalassarche chlororhynchos	Yellow-nosed Albatross
Trawl	DIB	Thalassarche bulleri	Buller's albatross
Trawl	DIC	Thalassarche chrysostoma	Grey-headed albatross
Trawl, Jigging	DIM	Thalassarche melanophrys	Black-browed albatross
Trawl	DIU	Thalassarche cauta	Shy albatross
Trawl, Jigging	DIX	Diomedea exulans	Wandering albatross
Trawl	DMP	Diomedea melanophris	Black browed albatross
Trawl	DSL	Thalassarche salvini	Salvin's albatross
Trawl	DSQ	Sula dactylatra	Masked Booby
Trawl, Jigging	FGZ	Fregetta spp	Storm petrels nei
Trawl	FUG	Fulmarus glacialoides	Southern fulmar
Trawl	MAH	Macronectes halli	Hall's giant petrel
Trawl	MAI	Macronectes giganteus	Southern giant petrel
Trawl, Jigging	OCO	Oceanites oceanicus	Wilson's storm petrel
Trawl	PCI	Procellaria cinerea	Grey petrel
Trawl	PFG	Puffinus griseus	Sooty shearwater
Trawl	PHE	Phoebetria palpebrata	Light-mantled albatross
Trawl	PHE	Phoebetria palpebrata	Light-mantled Sooty Albatross
Trawl, Jigging	PRO	Procellaria aequinoctialis	White-chinned petrel
Jigging	PRX	Procellariidae	Petrels nei
Trawl	PWX	Pachyptila spp	Prions nei
Jigging	SZV	Sula variegata	Peruvian booby
Trawl	-	Phaethon spp	Tropicbird

Trawl - Pteroderma externa Juan Fernandez petrel

There was no incidental catch of species of concern by Korean fishing vessels in 2020. Previous incidental catches on species of concern are described in Table 7. To encourage the reporting on incidental captures of species of concern and non-target species (CMM02-2020) by jigging vessels, a poster to aid the identification of bycatch species was provided to all jigging vessels (Figure 12).

Table 7. Summary of species of concern from the Korean vessels in the SPRFMO Convention Area.

Year	Fishing vessels	Species	Amount caught	Datasets
2015	trawl	Porbeagle shark	7 (62kg)	FA, Obs
2016	trawl	Porbeagle shark	8 (97kg)	FA, Obs
2017	trawl	Porbeagle shark	2 (53kg)	FA, Obs
2018	jigging	Porbeagle shark	1 (no info)	Obs
2019	trawl	Porbeagle shark	20 (276.2kg)	Obs

FA: Fishing activity Data, Obs: Observer data

# 상태명 양지역수산관리기구(SPRFMO)해역 채낚기 부수어획종 및 우려종 제낚기 부수어획종 W라기 보수이획종 및 우려종 W라기 보수이획종 W라기 보스 Common dichiarida and annu den a

Figure 12. A poster for the identification of bycatch species provided to Korean jigging vessels in the SPRFMO Convention Area.

### REFERENCES

Cox, M. P., Peterson, D. A. and Biggs, P. J. (2010) SolexaQA: At-a-glance quality assessment of Illumina second-generation sequencing data. *BMC Bioinformatics* 11(1), 1-6.

Earl, D A. (2012) STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* 4 (2), 359-361.

Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., and Mitchell, S. E. (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE* 6(5), e19379.

Eun, M. H., Han, J. H., Yoon, J. B., and Lee, J. (2016) QTL mapping of resistance to the Cucumber mosaic virus P1 strain in pepper using a genotyping-by-sequencing analysis. *Hortic. Environ. Biotechnol.* 57 (6), 589-597.

Evanno, G., Regnaut, S., and Goudet, J. (2005) Detecting the number of clusters of individuals using the software STRUCTURE: A simulation study. *Mol Ecol.* 14(8), 2611–20.

Ibáñez, C. M., Cubillos, L. A., Tafur, R., Arguelles, J., Yamashiro, R., and Poulin, E. (2011). Genetic diversity and demographic history of *Dosidicus gigas* (Cephalopoda: Ommastrephidae) in the Humboldt Current System. *Marine Ecology Progress Series* 431: 163-171.

Kang, Y. J., Lee, B. M., Nam, M., Oh, K. W., Lee, M. H., Kim, T. H., Jo, S. H., and Lee, J. H. (2019) Identification of quantitative trait loci associated with flowering time in perilla using genotyping-by-sequencing. *Mol Biol Rep.* 46(4), 4397-4407.

Kim, J. E., Oh, S. K., Lee, J. H., Lee, B. M., and Jo, S. H. (2014) Genome-wide SNP calling using next generation sequencing data in tomato. *Mol Cells*. 37(1):36-42.

Li, H., and Durbin, R. (2009) Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25:1754-1760.

Li, H., Handsaker, B., Wysoker, A. Fennell, T. Ruan, J., Homer, N., & Durbi, R. (2009). The sequence alignment/map format and SAMtools. *Bioinformatics*. 25(16):2078-2079.

Sanchez, G., Tomano, S., Yamashiro, C., Fujita, R., Wakabayashi, T., Sakai, M., and Umino, T. (2016). Population genetics of the jumbo squid *Dosidicus gigas* (Cephalopoda: Ommastrephidae) in the northern Humboldt Current system based on mitochondrial and microsatellite DNA markers. *Fisheries Research* 175: 1-9.

Sandoval-Castellanos, E., Uribe-Alcocer, M., and Díaz-Jaimes, P. (2009). Lack of genetic differentiation among size groups of jumbo squid (*Dosidicus gigas*). *Ciencias Marinas* 35(4): 419-428.

Sandoval-Castellanos, Uribe-Alcocer, M., and Díaz-Jaimes, P. (2010). Population genetic structure of the Humboldt squid (*Dosidicus gigas* d'Orbigny, 1835) inferred by mitochondrial DNA analysis. *Journal of Experimental Marine Biology and Ecology* 385(1-2): 73-78.

Zheng, X., Levine, D., Shen, J., Gogarten, S., Laurie, C. and Weir, B. (2012) A High-performance Computing Toolset for Relatedness and Principal Component Analysis of SNP Data. *Bioinformatics*, 28(24):3326-3328.