ICES STOCK IDENTIFICATION METHODS WORKING GROUP (SIMWG)

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Contents

i Executive summary

The Stock Identification Methods Working Group (SIMWG) reviews new methods for the definition and investigation of stock structure and provides recommendations to other ICES expert groups on how to interpret patterns of population structure.

In 2023, SIMWG has continued providing annual updates on recent applications of stock identification methods to species assessed by ICES and on advances in stock identification methods. Based on the wide expertise of SIMWG members, we provide reviews of recent literature on genetics, growth marks in calcified structures, life history parameters, morphometrics/meristics, tagging, otolith shape, otolith chemistry, parasites and interdisciplinary approaches.

A key activity of SIMWG is to address requests by ICES working groups for technical recommendations on issues of stock identity. In the current term, we reviewed two working documents on the stock definition of a) Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4), and b) flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4).

Moreover, SIMWG members co-chaired and participated in the Workshop on the Evaluation of NEA Mackerel Stock Components (WKEVALMAC) and the Second Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC2).

SIMWG contributes to the general understanding of the biological features of the north Atlantic ecosystem through its work to describe fish population structure. Additionally, SIMWG’s annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. SIMWG expert reviews on questions of stock structure for particular ICES species are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. We see an important role for SIMWG in the future as ICES copes with the shifting distributions of fishery resources and questions regarding the appropriate definition of fish stocks. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated and SIMWG will continue to work with ICES expert groups to address pressing stock identification issues.

ii Expert group information

Expert group name	Stock Identification Methods Working Group (SIMWG)
Expert group cycle	Multiannual
Year cycle started	2023
Reporting year in cycle	1/3
Chair	Christoph Stransky, Germany
Meeting venue and dates	By correspondence in 2023

1 Review recent advances in stock identification methods

Over the past years, there has been a wide use of applications of stock identification methods to ICES stocks, as well as several notable advances in stock identification methods with many results relevant to ICES science and advice. SIMWG has committed to providing annual updates on recent applications of stock identification methods to ICES species and on advances in stock identification methods. The group has focused on summarizing research in the focal areas listed below:

a) Genetics
b) Growth marks in calcified structures
c) Life history parameters
d) Morphometrics/meristics
e) Tagging
f) Otolith shape
g) Otolith chemistry
h) Parasites
i) Simulation approaches
j) Interdisciplinary approaches
k) Emerging issues

SIMWG's annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. This review activity has served as a valuable contribution to the field and has formed the foundational material for two editions of the book "**Stock Identification Methods: Applications in Fishery Science**". This book was published first in 2005 and again in 2014. SIMWG members S. Cadrin, L. Kerr and S. Mariani edited the 2nd edition and several SIMWG members contributed chapters to this book. A 3rd edition is planned for 2024/2025, again involving several SIMWG members.

The details of annual reviews of advances in stock identification methods are summarized in Annex 3.

2 Technical reviews and expert opinion on matters of stock identification

SIMWG provides ICES expert groups and working groups expert feedback on questions of stock structure for ICES stocks. In 2023, SIMWG has contributed to ICES advisory needs by providing expert feedback on the status of stock structure of a) Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4), and b) flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4). The detailed reviews are provided in Annex 5.

SIMWG expert reviews on questions of stock structure for ICES stocks are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated and SIMWG will continue to work with ICES expert groups to address pressing stock identification issues. We see an important role for SIMWG in the future as ICES copes with the shifting distributions of fishery resources and questions regarding the appropriate definition of fish stocks.

SIMWG's recommendations have been well received by the requesting groups and there are a growing number of requests from different groups which speaks to the service that SIMWG provides to the ICES community. SIMWG's expertise should be continued to be used to address on specific questions of stock structure and should be considered in the advisory process in the context of whether the stock units are appropriate for accurate assessment and sustainable management of ICES fishery resources.

Moreover, SIMWG members co-chaired and participated in the Workshop on the Evaluation of NEA Mackerel Stock Components (WKEVALMAC) and the Second Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC2). Summaries of those workshops are provided in Annex 4.

Annex 1: List of participants

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Annex 2: SIMWG resolution

The **Stock Identification Methods Working Group** (SIMWG), chaired by Christoph Stransky, Germany, will work on ToRs and generate deliverables as listed in the Table below.

	MEETING DATES	VENUE	REPORTING DETAILS	COMMENTS (CHANGE IN CHAIR, ETC.)
Year 2023	By correspondence		Interim report by August 2023	
Year 2024	June	Faro, Portugal	Interim report by August 2024	
Year 2025	By correspondence		Final report by August to ACOM & SCICOM	

ToR descriptors

TOR	DESCRIPTION	BACKGROUND	SCIENCE PLAN CODES	DURATION	EXPECTED DELIVERABLES
a	Review recent advances in stock identification methods.	a) Tracks best practices in stock ID b) Promotes new technologies relevant to all ICES species	1.4, 1.8, 5.2	3 years (and continued)	EG report, revised stock ID book chapters
b	Provide technical reviews and expert opinions on matters of stock identification, as requested by specific Working Groups and ACOM.	Ad hoc advice requests to be addressed at short notice	1.4, 1.8, 5.2	3 years (and continued)	EG report, contribution to ASC
c	Review and report on advances in mixed stock analysis, and assess their potential role in improving precision of stock assessment.		1.4, 1.8, 5.2, 5.4	3 years (and continued)	EG report
d	Review of the suggested splitting of the West Greenland inshore stock (cod) into two separate stock units, based on available biological (tagging), catch trends and survey trends.	Advisory requirement	1.4, 1.8, 5.2	1 year	Bief review report provided to NWWG and ACOM (clear response required) Chapter in EG report

Summary of the Work Plan

Year 1	Address terms of reference through work by correspondence in 2023
Year 2	Organise a physical meeting for SIMWG for summer 2024
Year 3	Address terms of reference through work by correspondence in 2025

Supporting information

Priority	Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock level can be contemplated. SIMWG liaises with ICES expert groups and working groups on stock identification issues and continues to review new methods as they develop.
Resource requirements	SharePoint website and clear feedback from expert groups.
Participants	The Group is normally attended by some 15–20 members and guests.
Secretariat facilities	Standard EG support.
Financial	None
Linkages to ACOM and groups under ACOM	ACOM
Linkages to other committees or groups	SIMWG has recently worked closely with a range of ICES working groups including HAWG, WGBIE and WGHANSA; benchmark workshops including WKELASMO, workshops on cod stock structure (WKNSCodID, WK6aCodID). In previous years, SIWMG connected with many more ICES groups to fulfill requests.
Linkages to other organizations	There are no obvious direct linkages, beyond the SIMWG members' affiliation and commitment to their own employers. Depending on the request, SIMWG's scope might expand beyond the ICES area to address straddling stocks e.g. in the NAFO, NEAFC, CECAF and other RFMO areas.

Annex 3: Review recent advances in stock identification methods (ToR a)

Advances in Stock Identification Methods in 2023

In 2023 (review period mid-2022 to mid-2023), there were several notable advances in stock identification methods and a proliferation of applications, with many results relevant to ICES science and advice. Here, we summarize advances and results accounting for research in genetics, life history parameters, growth marks in calcified structures, morphometrics, tagging, otoliths, parasites, simulation approaches, and interdisciplinary approaches.

Genetics (Contributors: Florian Berg, Rita Castilho, Stefano Mariani, David Murray, Christophe Pampoulie, Naiara Rodríguez-Ezpeleta)

From the data gathered, we can observe different trends regarding papers published using microsatellites, SNPs, and emerging markers such as copy number variations (CNVs) over the years. In particular, microsatellite papers suffered a noticeable upward trend between 2000 and 2015, peaking at 166 papers in 2018. Following that peak, the numbers fluctuated with a notable decline in recent years, particularly in 2023 when the number dropped to 68 papers. On the other hand, at the beginning of the millennium, the number of papers focusing on SNPs was almost negligible. However, there has been a substantial increase in the number of SNP-related papers since 2011, with a peak in 2022 at 108 papers. This indicates a growing academic interest and likely advancements in SNP-related methodologies and applications. Papers using emerging markers such as CNVs started from single counts in 2001 but numbers are still low compared to the two other marker types and not common. Yet, it is expected that with the raise of available genomes (see section below), these markers will become easily to identify and to incorporate into future studies.

In summary, while microsatellite-based research publications saw a rise and then began to taper off in the recent years, SNP-related research has been gaining traction, especially in the past decade. The advent of reference genomes and the decrease of cost for obtaining genomic sequences anticipates a future increase in the use of alternative markers such as copy number variations and other structural variant types. The data paints a picture of the evolving landscape of the use of different genetic marker types for population structure analyses for stock identification.

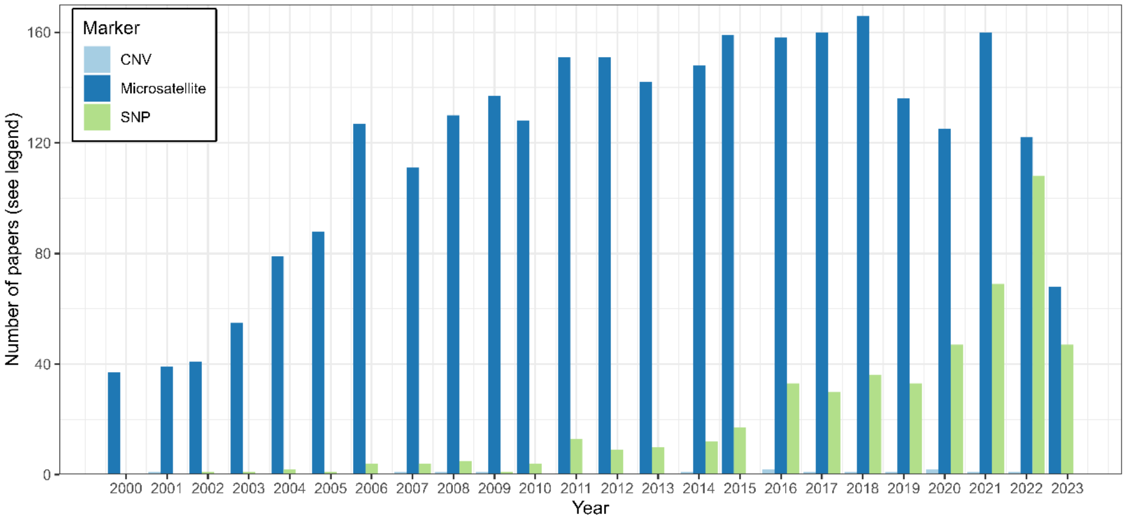

Figure A4.1. Scientific publishing trend since 2000, comparing outputs of studies using microsatellite, SNPs and CNVs, as listed in the Clarivate Analytics Web-of-Science. The search criteria were: "fish* AND gene* AND (population OR stock) AND 'molecular marker*', where 'molecular marker*' means "Microsatellite*", "SNP*" or "CNV*". Search link for microsatellite (https://www.webofscience.com/wos/woscc/summary/b5c80b49-662b-4525-b4c1-865c22f99b20-a52e48cd/relevance/1); SNP (https://www.webofscience.com/wos/woscc/summary/c4da2151-03b7-4ed7-b153-12deb40c9041-a52f4b87/relevance/1); CNV (https://www.webofscience.com/wos/woscc/summary/7ee22b70-0976-4fe3-9098-4da0373aa33b-a52f88dd/relevance/1). Only papers in the following Web of Science categories were considered: 'Fisheries', 'Environmental Sciences', 'Ecology', 'Biodiversity Conservation', 'Marine & Freshwater Biology' and 'Oceanography'. Data for 2023 only represent papers published through to the present date (September 2023).

Herring and cod

In last year's report, the availability of a reference genome for these two species was highlighted. As a consequence, a series of studies have been published on the use of genetic information retrieved from these reference genomes to identify stock structure and dynamics. Bekkevold *et al.* (2023) and Farrell *et al.* (2022) provide two examples where genetic stock identification has been applied for herring based on SNPs. Both have established population baselines and assigned unknown individuals against them. Similarly, Henriksson *et al.* (2023) have used SNPs to identify cod populations along the Swedish coast. Furthermore, Atmore *et al.* (2022) have used ancient DNA to study population dynamics of herring in the central and western Baltic Sea. Petterson *et al.* (2023) have investigated the hybridization between Atlantic and Pacific herring in northern Norway. Pampoulie *et al.* (2023) provide a thorough review how the genetic work of the last years as improved our understandings of cod stock structure.

Other species

Bourret *et al.* (2023) used genome-wide markers (>10 000 SNPs) to assess genomic differences between Atlantic mackerel of a northern and a southern contingent in the northwest Atlantic. Small but significant genetic differentiation was observed between the northern and southern contingents. Genetic assignments to reference samples from the two contingents were performed with predictive accuracy > 85%.

Jones *et al.* (2023) assembled a reference genome for northern sand lance (*Ammodytes dubius*) and then used low-coverage whole genome sequencing to quantify genetic differentiation between geographic regions based on SNPs. They found strong separation between *A. dubius* from locations north and south of the Scotian Shelf coinciding with a clear break in winter sea surface temperature, suggesting that differential offspring survival, rather than limited transport, causes a break in realized connectivity.

Fuentes-Pardo *et al.* (2023) analyzed whole-genome sequencing to study the population structure and genetic basis of local adaptation of Atlantic horse mackerel (*Trachurus trachurus*). Their genomic approach indicated low population structure with a major split between the Mediterranean Sea and the Atlantic Ocean and between locations north and south of mid-Portugal. Populations from the North Sea are the most genetically distinct in the Atlantic. Most population structure patterns are driven by a few highly differentiated putatively adaptive loci. Only 17 highly informative SNPs can genetically discriminate the North Sea and North African samples from neighboring populations. This study provides the basis for more accurate delineation of the horse mackerel stocks and paves the way for improving stock assessments.

Fully annotated and assembled genomes to support fisheries management

From a fisheries management perspective, having a fully annotated and assembled genome provides substantial resolution for selecting population markers and therefore, assisting with determining biologically relevant stock units (Andersson *et al.*, 2024). For example, cod, herring and horse mackerel genomes have provided greater insight into the biological connectivity, and boundaries, of populations throughout the northeast Atlantic, see the following for examples: Bekkevold *et al.* (2023), Fuentes-Pardo *et al.* (2023), Pampoulie *et al.* (2023). Furthermore, the availability of an organism's entire genome can highlight potential responses of populations to environmental impacts, such as heatwaves and climate change (Benestan *et al.*, 2016). However, despite the importance of these tools to fisheries management questions, the majority of species are without a fully annotated and assembled genome.

Recently, collaborative networks have formed to assist with using genomic data to understand and explore the biology of organisms, their place within ecosystems and develop tools to assist in their management and conservation. The Darwin Tree of Life (DToL, https://www.darwintreeoflife.org) and European Reference Genome Atlas (ERGA, https://www.erga-biodiversity.eu) are part of a global initiative, known as the Earth BioGenome Project (https://www.earthbiogenome.org), that are working together to sequence the genome of every species on earth. Relative to terrestrial organisms, there is an inherent difficulty in collecting tissue samples from marine species and as such there is an under representation of genomes for aquatic organisms.

The Centre of Environmental, Fisheries and Aquaculture Science (Cefas) in England/UK signed a memorandum of understanding with DToL to assist with collecting marine species. By tying 'blue sky science' with fisheries management issues, this collaboration hopes to assist DToL with sequencing UK marine species by providing hard to obtain samples for sequencing. Concurrently, the resulting open access assembled and annotated genomes will be used by Cefas to determine biologically relevant populations for species such as sole (*Solea solea*), plaice (*Pleuronectes platessa*) and sardine (*Sardina pilchardus*). In this instance, DToL provides a variety of services, such as sampling equipment, postage of samples and sequencing the genome free of charge.

Future fisheries management related research projects seeking to utilize genomes should contact ERGA and DToL (or other local initiatives) as early as possible to explore mutually beneficial collaboration between applied and pure science.

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Growth marks in calcified structures (Contributors: Florian Berg and Richard McBride)

Calcified structures in fish, particularly the ear bones (otoliths), but also scales, spines, and fish rays, are used for identifying stock structure as well as for a variety of research applications (Brophy, 2014). Notably, for well over a century, they have been used to age fish when interpreting daily and annual rings (annuli). The utilization of growth marks in calcified structures for stock identification has decreased during the last years and were mainly replaced by studies involving their shape or chemical composition.

During the review period (mid-2022 to mid-2023), there were no studies published using growth marks in calcified structures for stock identification. However, García-Fernández *et al.* (2022) published a study where they used daily growth analysis of European hake (*Merluccius merluccius*) otoliths to determine their spawning dynamics which identified several spawning components within the stock. Their results showed that daily growth of hake females decreased during the spawning period because they allocate less energy to somatic growth in favor of the production of gametes. Daily growth trends showed a "spawning pattern" in 28% of medium and large females, suggesting an individual spawning period of one to two months, with 4–5 valleys of narrow daily increments, likely associated to batch release. This is the first time that individual spawning frequency in European hake was estimated based on individual data. Finally, the spawning pattern is detected only once per year, indicating that a single female participates only in one spawning peak per year, supporting the hypothesis of the existence of two or more spawning components in the stock.

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Life history parameters (Contributors: Richard McBride and Florian Berg)

The stock structure of Atlantic cod (*Gadus morhua*) in US waters was recently re-evaluated using life history traits, namely: geographic distribution and abundance, size at age 2, and median size and age at maturity, as recorded by a standardized bottom trawl survey during the period 1970-2017 (McBride *et al.*, 2022). The original number and boundaries of the Gulf of Maine and Georges Bank management units, established in the 1970s, had considered life history data available at that time. However, by the 2000s, there was growing pressure to re-evaluate this using an interdisciplinary approach. Regarding life history traits, there were two long-term trends: 1) size at age differences between the two management units has narrowed considerably, and 2) both length and age at maturity had declined but coherent spatial clusters were still identifiable. Spatially, life history data suggested minor deviations in the boundaries between the two management units, as well as notable variations within the Georges Bank management unit. This life history re-analysis was embedded within a larger, interdisciplinary working group that considered early life history traits, genetic traits, natural markers, tagging studies, and fishermen's ecological knowledge (McBride and Smedbol, 2022). This 'Atlantic Cod Stock Structure Working

Group' rejected the existing 2-stock model and instead proposed 5 stocks for best representing the biological population structure of cod in US waters. This recommendation has already led to multiple US cod stock assessments along a data-limited to data-rich gradient. However, because one new area is composed of a mixed-stock fishery, and there is no operational way to separate these stocks in the catch, the recent (July 31-August 3, 2023) Atlantic Cod Research Track Assessment Peer Review presented a 4-stock model, one of which was a mixed stock of winter and spring spawners.

A general rule of thumb for life history attributes relative to population structure is that long-distance dispersal of early life stages and movements of adults leads to high levels of connectivity. Larval drift simulations of Antarctic toothfish (*Dissostichus mawsoni*) indicate such long-distance dispersal, on the scale of months and many degrees longitude, and tagged adults have been recaptured at distances as great as 4000 km from their release location (about the distance from Boston, USA, to Reykjavík, Iceland. Indeed, Maschette *et al.* (2023) found very low (0.1%) genetic diversity attributed to location of toothfish when they examine genetic population structure across its range, using thousands of single nucleotide polymorphisms from over 700 fish. The success of this study was such that the authors do not recommend further work on Antarctic toothfish genetic stock structure in isolation of other disciplines. They point to complementary value of further interdisciplinary research to continue dispersal modelling, or new work to incorporate stable isotopes or trace elements to examine different scales of connectivity. These findings had direct relevance to the toothfish fishery, in terms of how they confirmed existing subareas and divisions for managing this species.

At a much finer scale, Mueller *et al.* (2023) investigated the spawning dynamics as well as life-history and reproductive traits of Atlantic herring (*Clupea harengus*) throughout the spring spawning season from February to April on a coastal spawning ground along the west coast of Norway. The oocyte diameter of females was measured as an indicator of reproductive investment over the spawning season in combination with life-history traits and genetic spawning time assignment. The aim was to study potential mixing of herring with different reproductive strategies during the spring spawning season on this coastal spawning ground. Their results indicate that mixing between ripe spring and autumn spawners occurred on the spawning ground during spring, with ripe autumn spawners being generally smaller but having larger oocytes than spring spawners. Within spring spawners, large variability was found in reproductive traits indicating two groups with different reproductive investment. Comparisons with other herring populations along the Norwegian coastline suggest that the high variability can be explained by the co-occurrence of groups with different reproductive investments potentially resulting from stationary or migratory behavior. The complexity observed in Mueller *et al.* (2023) is representative for many locations along the Norwegian coast where herring with different reproductive strategies as well as migration behaviors are thought to co-occur during spawning.

Clain *et al.* (2023) report that several life history traits of largehead hairtail (*Trichiurus lepturus*) are different in south-eastern Australia than elsewhere, for this relatively well-studied, globally-distributed species. These traits include larger maximum length, larger size at maturity, a different (summer) spawning season, and spatially explicit sex ratios. The authors point to these possible causes: 1) lower fishing pressure in this particular region for what is otherwise a heavily exploited species, 2) genetic population structure arising from geographic isolation, 3) different environmental variables affecting ecophenotypes, and 4) sampling artifacts of past studies possibly confusing species identifications or the current study not collecting smaller sizes of fish. These life history traits are all new to this region and will form the basis of a developing management plan for largehead haritail in New South Wales and elsewhere in south-eastern Australia.

In the better-late-than-never category, we call attention to Artetxe-Arrate *et al.* (2021) – published two years ago rather than in the most recent year – as this paper reviewed the stock structure of three tropical tunas (skipjack *Katsuwonus pelamis*, yellowfin *Thunnus albacares* and bigeye *Thunnus obesus*) in the Indian Ocean. Analyses of fishery data have suggested two or more stocks of skipjack and yellowfin tuna, but only one stock bigeye tuna. The life history data examined included geographic distribution, abundance, and size composition from the catch. Other stock identification methods available include morphometric and meristic characters, parasites, genetics, otolith microchemistry, and mark-recapture. Recent stock assessments on all three species assume unit stock structure in the Indian Ocean, without exchange with other ocean basins. This is largely based on tagging results showing rapid and large-scale movements. However, it is noted that the fishery and genetic data available suggest more fragment population structure for these species, which has not been resolved.

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Morphometrics/meristics (Contributor: Emma White)

A review of the papers published on studies using morphometric and meristic methods between June 2022 and June 2023 was conducted to collate the most recent application of these stock identification techniques.

El Idrissi El Awad and El Ouizgani (2022) investigated geographically distinct populations of anchovy, *Engraulis encrasicolus*, from the Moroccan Atlantic coast. A total of 22 morphometric measurements and 4 meristic variables were collected from fish caught at five different locations along the coast of Morocco. Morphological differences changed from north to south along the coast with two exceptions, and varied with port, age and sex. Environmental and genetic factors were attributed to the variation in anchovy off the Moroccan coast.

The yellow striped goatfish was sampled from three locations along the Indian coast in order to identify different stocks from the east and west coast (Nama *et al.*, 2022). Truss measurements were calculated from 13 anatomical landmarks on the body of the fish. The stepwise discriminant function analysis classified two separate stocks, one from the east coast of India and the other from the west coast of India. The use of truss morphometric variables helped determine the stock structure of this species around the coast of India and highlights the need for separate stock assessments for better management of this species.

Chesalin and Nikolsky (2023) compared the Azov anchovy, *Engraulis encrasicolus maeoticus*, and the Black Sea anchovy, *Engraulis encrasicolus ponticus*, using morphometric analysis. Twelve anatomical landmarks were used to measure 23 morphometric variables. Similarities and differences in the body shape were identified between the two subspecies of anchovy using a multivariate principal component analysis. The result of the discriminant analysis was 83%, showing a strong differentiation between the subspecies.

Morphometric and meristic analyses were applied to samples of sardines, *Sardina pilchardus*, collected from three locations along the Moroccan Atlantic coast (Mounir *et al.*, 2022). This study used 6 meristic counts and 15 morphometric variables collected from the sardines and applied univariate and multivariate analysis to discriminate between the three populations. The study showed significant differences across the areas and the differences increased from north to south along the coast.

Goldstripe ponyfish, *Karalla daura*, were sampled from four sites along the Pakistan coast to investigate intraspecific variability of this species (Kashani and Panhwar, 2023). Anatomical landmarks were used to created morphometric measurements and truss measurements across the body. A Canonical Discriminant Function Analysis was used to show variability among the four populations sampled. The morphometric methods used for this species allows an easily accessible, fast and inexpensive method of identifying different stocks of goldstripe ponyfish along the Pakistan coast.

The pearlspot chiclid, *Etroplus suratensis*, is an estuarine fish species found around the coast of India. Samples were collected from five different locations and the fish were processed for morphometric measurements and meristic counts (Chandrasekar, 2022). Using multivariate analysis of the morphometric variables, including Principal Component Analysis (PCA), allowed the authors to conclude that only one of the five locations showed a distinct stock. The other four locations showed similarities that resulted in them being classified as one stock. The two stocks identified in South Indian waters are separated geographically on the east and west coast of the country.

Using geometric morphometrics, the body shape of five populations of brown trout, *Salmo trutta*, were compared in order to determine differences in the populations in Iran (Salehi *et al.*, 2022). A total of 16 anatomical landmarks were selected on the body and used in a Generalised Procrust

Analysis, which removes non-shape data, including position, direction and scale. Further analysis included Principal Component Analysis (PCA), Canonical Variant Analysis (CVA) and Cluster Analysis. The study showed significant morphological variation in the populations sampled, which the authors have suggested may be due to the influence of habitat on body shape. These results can be used for the management of these stocks, among other things.

Halasan and Lin (2022) applied traditional lineal morphometrics with meristics, landmark-based truss morphometrics and geometric morphometrics to two genetic lineages of yellowstripe scad, *Selaroides leptolepis*, from the Tropical Western Pacific. Principal Component Analysis (PCA) showed an overlap between the two populations for all three morphometric techniques. Discriminant Function Analysis (DFA) was able to identify Asian individuals accurately but showed poor identification of the Australian individuals. Despite these individuals being genetically distinct, morphological techniques could not distinguish the two genetic lineages accurately enough for use in the management of this economically important species.

Parenrengi *et al.* (2022) used morphometric analysis to differentiate between male and female tiger shrimp, *Penaeus monodon*, in Aceh waters. Traditional morphometric measurements and truss measurements were used and analysed using multivariate analysis. The authors were successful in discriminating male and female tiger shrimp using these methods.

Three stock identification methods were used in a study of Atlantic Bonito (*Sarda sarda*) in the Black Sea; morphometrics, meristics and genetics (Kasapoğlu *et al.*, 2022). A total of 10 meristic counts and 22 morphometric measurements were collected from this species in Turkish waters. The meristic counts were compared with previous studies and found similarities and differences in counts. The morphometric measurements showed sex-based differences within the species, with females being larger than males. The genetic analysis conducted was able to establish a difference between samples collected from three locations. Using the three methods in combination provides more information on this species in Turkish waters.

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Tagging (Contributors: Douglas Zemeckis and Steve Cadrin)

Introduction

Conventional and electronic tagging studies published since the last SIMWG report in 2022 have focused on investigating movement patterns and interdisciplinary stock identification analyses in combination with other methods. The following summarizes recent tagging studies focusing on those with relevance to stock identification.

Movement Patterns

Tagging technologies and methods continue to advance with further development of electronic tags, but recent conventional tagging studies also continue to provide valuable information on movement patterns for application in stock identification, often conducted over decades with many releases and recaptures.

For example, Vihtakari *et al.* (2022) compiled mark-recapture data from 1952-2021 to gain insight into the spatial population structure of Greenland halibut (*Reinhardtius hippoglossoides*) across the North Atlantic. A total of 5466 of 168 130 tagged fish (3.3%) were recaptured. Their results indicated that fish tagged at <50 cm body length migrated at higher rates than larger fish. There was evidence of migrations across management units with indication of two regional offshore populations: (a) one in the Northeast Atlantic, where the West Nordic and Northeast Arctic stocks likely belong to a single population despite currently being managed separately, and (b) one in the Northwest Atlantic where migration occurred between the Newfoundland and Labrador stock and the Northwest Arctic stock.

Citizen science tagging programs with conventional tags also provide valuable information on fish movements. In the northeast USA, Musick *et al.* (2022) collected data for recreationally important marine fishes in cooperation with trained volunteers through the Virginia Game Fish Tagging Program. More than 380 000 fishes have been tagged since 1995 and contribute data on fish movements and site fidelity patterns for stock identification and assessment, as well as fisheries management. Cooperative citizen science tagging off eastern Australia by Hughes *et al.* (2022) investigated movement patterns of mulloway (*Argyrosomus japonicus*), which is an important recreational species. There were 677 recaptures of more than 4300 tag releases. Most recaptures (81%) came from within the same estuary with 31% of all individuals being recaptured within 1 km of their release location. This spatial scale of movements was much smaller than the scale of management in the region (~1000 km) and suggests that assessment and management should be re-examined to better represent their movement patterns.

Cadrin *et al.* (2022) reviewed and reanalyzed conventional and archival tag of Atlantic cod off the northeast USA, including nearly 200 000 tag releases and nearly 12 000 recaptures. Their review showed persistent patterns of residence and fidelity to spawning areas in the western Gulf of Maine and the Bay of Fundy, moderate spawning site fidelity on eastern Georges Bank with some post-spawning dispersal, and greater dispersal from the "Cape Cod" spawning grounds.

de Pontual *et al.* (2023) tagged European seabass (*Dicentrarchus labrax*) with DSTs in the North Sea, the English Channel, and the Bay of Biscay from 2014–2016 to better understand their ecology and spatio-temporal population structure. There were 482 recaptures out of 1220 deployed DSTs (40%). Approximately half of the tagged fish included a period of potential spawning migration. European seabass were confirmed to be a partial migratory species with individuals exhibiting either residence or long-distance migrations where they showed fidelity to summer feeding areas and winter spawning areas. Their results suggested a spatial structure of the Atlantic population that differs from the stock structure currently considered for assessment and management, which they recommend be explored by regional fisheries managers.

Several recent studies used electronic tagging to study the movements of Atlantic bluefin tuna (*Thunnus thynnus*). Aarestrup *et al.* (2022) studied bluefin tuna in Nordic waters, which is an area where this species has returned after being rare for more than half a century. Eighteen bluefin tuna were tagged with pop-up satellite archival tags (PSATs) and demonstrated different migration routes, with individuals migrating into the western Atlantic Ocean and others staying exclusively in the eastern Atlantic and entering the Mediterranean to spawn. Evidence of some potential skipped spawning was inferred from behavioural analyses. Their results supported the hypothesis that bluefin tuna migrating to Nordic waters return to the same general feeding area within the region on an annual basis and they recommended careful management of the bluefin tuna returning to Nordic waters so that their resurgence in this region is not short-lived.

Rouyer *et al.* (2022) used PSATs to study bluefin tuna (n = 8) tagged on the Maltese spawning ground in the central Mediterranean Sea. Their results showed that larger fish (> 200 cm) exhibited large-scale migrations outside of the Mediterranean but stayed within the northeast Atlantic, whereas smaller fish did not migrate out of the Mediterranean. Additional tagging was delayed during the COVID-19 pandemic, but efforts are ongoing to provide more information about bluefin tuna movements from this important spawning ground that will further aid in stock identification and fisheries management given the relevance of this area to a large segment of the international fishery.

A new spawning area for Atlantic bluefin tuna has been described in the Slope Sea region off New England, USA, but the movements of fish spawning in that area are not well understood. Aalto *et al.* (2023) used data from archival data storage tags (DSTs) and PSATs from the Stanford University TAG A Giant program that were from bluefin tuna tagged primarily in the Gulf of St. Lawrence, Canada (n = 290) and coastal waters off North Carolina, USA (n = 968). A total of 24 tagged fish were identified as being present in the Slope Sea during the spawning season (June-August) with tag data showing temperatures and behaviour consistent with spawning. Similar spatial ranges were observed during the spawning season as observed for spawning fish in the Mediterranean-spawning bluefin tuna and some individuals spawning in the Slope Sea displayed distinct behaviours that were first identified in Gulf of Mexico-spawners. Bluefin tuna in the Slope Sea might represent a disproportionate share of the West Atlantic catch, and these insights into behaviour and movement patterns are valuable for stock identification and multi-stock management of this highly migratory species.

Baden *et al.* (2022) investigated spawning migrations of turbot (*Scophthalamus maximus*) and European flounder (*Platichthys flesus*) in a fjord off Denmark using acoustic telemetry. The turbot are stocked fish in this estuary and the European flounder are a naturally occurring population.

The two species exhibited different migration behaviours towards the spawning season. The turbot remained in the low salinity southern parts of the estuary and the majority of the European flounder migrated towards more marine waters prior to spawning. The insights provided into movement patterns and spawning ground utilization of two different species are valuable to understanding recruitment dynamics, stock structure, and stocking strategies for turbot.

Conventional and electronic tagging data can also be used for estimating natural mortality, which aids in movement rates analyses and investigating stock structure. For example, Whitlock *et al.* (2022) used data from acoustic telemetry and PSATs to estimate the instantaneous annual natural mortality rate of Atlantic bluefin tuna. Continued advancement in tagging technology, such as the newly developed acoustic data storage tag (ADST) (Goossens *et al.*, 2022), will encourage further innovation in research approaches employing electronic tags. Furthermore, several tagging studies are being conducted to answer other questions related to changes in marine ecosystems, such as offshore wind energy development and climate change related impacts, and information from these studies will also improve our understanding of the stock structure of marine fishes for application in stock identification.

Interdisciplinary Analyses

Results from tagging studies are often combined with findings from other stock identification approaches for interdisciplinary analyses of stock structure. For example, Marshall *et al.* (2023) combined spatial data on Atlantic halibut (*Hippoglossus hippoglossus*) migration paths and spawning locations obtained through electronic tagging with fish harvesters' knowledge reported at public meetings and semi-structured interviews to recognize ocean management concerns. Harvesters' input in combination with halibut movement data helped to identify and anticipate potential conflicts between halibut management, other fisheries, and other ocean industries (e.g., oil and gas drilling). The authors demonstrated that using complementary data from electronic tagging and fish harvesters' knowledge can bring additional value to tagging data given that stakeholder input provides the perspectives on how the ecological data fits into the greater context of marine resources.

Le Luherne *et al.* (2022) analysed adult spawning site fidelity and natal homing of European sea bass using archival DSTs and otolith microchemistry to help address remaining uncertainties regarding the structure and connectivity of European seabass populations where ecological evidence was missing to support current stock delineation between northern and southern French stocks. Movements inferred from DSTs were used to assign a spawning area during each winter spawning season. The elemental composition was measured in both larvae and adult otolith increments corresponding to the winter spawning season. Their results demonstrated that 64% of the seabass expressed spawning site fidelity and there was geographic variability with the highest proportions of fidelity in the northern and southern limits of their study area. They were not able to prove natal homing, but discuss that their results were suggestive that natal homing behaviour does occur in this highly mobile species with structured populations that warrant attention in management to mitigate the potential of localized depletion within spawning areas.

These recent contributions demonstrate how information on movement patterns from conventional or electronic tags can complement information from other approaches to stock identification. Similar to the open data access being enjoyed by geneticists, providing data from past tagging studies can facilitate compilation of large sample sizes over a long time period and a wide range of conditions for re-analysis in the context of new information or new analytical methods.

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Otolith shape (Contributors: Florian Berg, Christoph Stransky)

From June 2022 to June 2023, there were 14 papers dedicated to the otolith shape. For marine organisms, especially for fish, the otolith is the main calcified structure used to identify the stock structure.

Otolith shape as tool for stock identification

Species/stocks in the ICES area

Neves *et al.* (2023) conducted a comparative analysis of the performance of two shape descriptors (Elliptic Fourier descriptor, and Discrete Wavelet descriptor) in reconstructing the population structure and connectivity patterns in a small pelagic fish species with a wide geographical distribution and fast growth rate, the European sardine (*Sardina pilchardus*), for the first time. A combination of each otolith shape descriptor and shape indices was explored using multivariate statistical methods. The two otolith shape descriptors showed similar, although limited, overall classification success associated with the population dynamic characteristics of the species. Both descriptors point to migration among adjacent areas, such as northern Atlantic locations, eastern Mediterranean and even across well-defined physical obstacles, such as the Strait of Gibraltar, among Atlantic and western Mediterranean locations. Both descriptors supported the division of the populations of Mediterranean waters into three main groups but slightly differed in the group limits of the Atlantic waters.

Morales-Nin *et al.* (2022) aimed to assess the discrimination capability of otolith shape and microchemistry at two geographical scales within the Mediterranean: (1) the official geographical subareas (GSAs), and (2) three larger units previously suggested by genetic markers. Two complementary analyses were completed because shape is more easily analyzed than chemistry. First, a large sample of juvenile hake (n = 1656) from 40 Mediterranean GSAs subunits was used for shape analysis. Second, a subsample of those fish (n = 154) from 10 GSAs was analyzed for both otolith shape and microchemistry. Irrespective of the type of data (shape and/or chemistry) and geographical scale (GSAs versus the 3-units), between-unit differences were always statistically significant. However, according to the large within-unit variability, discrimination capability was always poor but better at the GSA scale, and even better when both shape and microchemistry were combined. Overall, these results are fully compatible with the hypothesis of a continuous gradient, within which discrete spatial units cannot be safely recognized.

Khan *et al.* (2022) examined the variability in the shapes of the body and sagitta otoliths to identify the different European anchovy stocks in the Black Sea and adjacent regions, i.e., the Sea of Marmara and the Aegean Sea. Shape indices and elliptic Fourier analysis were used to evaluate the shape of the sagitta otoliths. The data were analyzed using multivariate and univariate analysis of variance, discriminant function and principal component analysis. The differences in sagitta otolith shape revealed the existence of four distinct stocks with an overall leave-one-out cross-validated correct classification of 46.5%–69.3%. The elliptic Fourier analysis revealed two main stocks of anchovy from the Black Sea as the Eastern–Middle Black Sea stock and the Western Black Sea stock. Based on the elliptic Fourier analysis, the differences in the sagitta otoliths increase in magnitude with increasing geographic separation, first manifested at the otolith anterior notch, followed by changes in the otolith width. The findings affirmed the existence of distinct stocks that should have important implications for effective management of this pelagic fish in the Black Sea and adjacent regions.

Moura *et al.* (2023) studied the structure of the European eel population in the Minho River (Portugal) using otolith shape analysis, showing complete discrimination between the two main types of habitats studied (tributaries and estuaries). Otoliths of eels from the estuary were rectangular and elliptic, whereas in the tributaries, they presented a more round and circular form. Eels collected in both habitats were mostly yellow-stage eels with a similar age range, but the eels from the tributaries showed smaller length-at-age and lower body condition than those collected in the estuary. Additionally, the sex ratio was skewed towards males in the tributaries and females in the estuary. This study revealed that there are at least two distinct groups of eels in this basin, likely with different development characteristics.

Species/stocks outside the ICES area

Vu *et al.* (2022) analyzed the Caroun croaker (*Johnius carouna*, Cuvier, 1830) shape of sagittae from several areas along the Vietnamese coast. The morphometric characters of the otoliths were used to identify stock among the fish of different geographic areas. A multivariate statistics analysis of otolith shapes was applied to estimate the differences between three regions. Based on the shape indices, wavelet transformed and Elliptic Fourier Descriptors (EFD) have signals for division into three groups of otolith shapes according to the three locations. This study inferred that two distinct stocks were identified, namely Cat Ba and Tho Chu. The individuals from the central zone may be a mixing zone between the north and the south, with two possible populations of Cat Ba and Tho Chu.

Mounir *et al.* (2023) investigated the applicability of the otolith shape analysis of the European sardine, *Sardina pilchardus* to help in stock discrimination off the Moroccan Atlantic coast. Discriminant analysis was achieved by an otolith-based morphometrics assignment of otolith shape; 360 specimens of *S. pilchardus* were collected from three localities (Larache, Safi and Dakhla). Otolith shapes were described from otolith measurements and elliptic Fourier descriptors. This analysis showed the presence of three different morphotypes in the studied locations. The existence of three morphotypes is probably related to the variation of oceanographic conditions impacting the feeding regime and fish growth. This study proved that otolith shape analysis could become an accurate marker for *S. pilchardus* population discrimination.

In the study of Morawicki *et al.* (2022), silverside (*Odontesthes argentinensis*) from nine locations in the Argentinian Sea were investigated for spatial stock structure, using otolith shape analysis. A combination of elliptic Fourier descriptors, Wavelet coefficients and otolith shape indices were explored by multivariate statistical methods. The combination of wavelet, Fourier and shape indices were the most effective variables to discriminate between sampling sites (7.42 % total error). PERMANOVA analysis of otolith shape revealed multivariate significant differences between northern versus southern locations ($p < 0.0001$). The results show that the spatial structure of *O. argentinensis* presents a North–South gradient with marked differences between the extreme localities of the north (Mar del Plata, Quequén) with more elliptical shapes than those in the south (San Blas, San Antonio Este) and an isolated group conformed by Puerto Lobos.

Otolith 3D shape as tool to stock identification

Andrialovanirina *et al.* (2023) studied the presence of asymmetry in otolith shape depending on the inner ear side (i.e., left versus right inner ears) was tested by comparing the approaches of 2D and three-dimensional (3D) sagittal otolith shape analyses. Eighty-two red mullet adults (*Mullus barbatus*) from three locations in the eastern part of the Mediterranean Sea were studied. Fourier harmonic descriptors computed from 2D outlines and spherical harmonic descriptors computed from 3D meshes were used to evaluate otolith shape variation. The results of a multivariate mixed-effects model from 2D images showed that there was no asymmetry effect of inner ear side on the otolith shape in any location. There was, however, a significant geographical effect for the 2D otolith shape between the Adriatic Sea and the Levantine Sea. In contrast, 3D information showed that both side effects and geographical differences were significant. This is the first study comparing 2D and 3D data showing different results on the same sample of red mullet. These results demonstrate the importance of 3D otolith shape analysis for stock discrimination.

Otolith shape combined with other descriptors for stock identification

De Souza Corrêa *et al.* (2022) used otolith silhouette and morphometric analysis (n = 103) in addition to chemical signatures (n = 20) to test the hypothesis of a single stock unit of skipjack tuna (*Katsuwonus pelamis*) in the Southwest Atlantic Ocean (20–34°S). No significant differences were found between sexes, enabling analyses for all study specimens to be grouped. Cluster analysis using Fourier coefficients (30 first harmonics) differentiated three otolith morphotypes within South (28–34°S) and Southeast (20–28°S) regions of the study area. Harmonic principal component analysis using the first two significant axes showed no pattern of spatial separation by region. Among the seven shape descriptors examined, only circularity and form factor showed significant differences between the morphotypes (A and B). Microchemistry analysis (LA/ICP-MS) applied to the core portion of fish otoliths showed significant differences in Ba, Mn and Mg concentrations between the two regions and morphotypes ($p < 0.05$). These results support that the *Katsuwonus pelamis* population in the Southwest Atlantic Ocean belong to a single stock unit with a probable common area of origin. Specimens captured in the South and Southeast regions of Brazil had heterogeneous phenotypic attributes regarding otolith shape, probably determined by a temporal equilibrium selection process.

Gunton *et al.* (2023) investigated connectivity and population structure of a fishery-important monacanthid, *Nelusetta ayraud*, using otolith-based methods to compare among three locations (220–540 km apart) along the coast of New South Wales (NSW), Australia. Otolith elemental signatures sampled with laser-ablation inductively-coupled plasma mass spectrometry (LA-ICP-MS) revealed differences between two of the three locations during a recent period before capture, as well as differences between the two times examined, although spatial differences were consistent across these times. In contrast, elemental signatures in the juvenile core of the otolith did not differ among locations. Sr:Ca increased linearly with age, and Ba:Ca initially increased to age 1+ before declining in older age classes, consistent with previous observations of an ontogenetic movement into deeper offshore waters for *N. ayraud*. No differences in otolith shape were detected among locations using Elliptical Fourier Analysis. Our findings suggest there may be spatial structuring of the *N. ayraud* stock over an intermediate scale (100s km) within NSW, which will inform the design of a larger nation-wide investigation.

Otolith shape as tool for species identification

Moore *et al.* (2022) examined the efficacy of using otolith shape to differentiate between the morphologically similar grenadiers *Macrourus caml* and *M. whitsoni* and validate species identifications by fishery observers within and adjacent to the Ross Sea region, Antarctica. Otolith shape information was collected from 610 *M. caml* and 329 *M. whitsoni* otoliths from research collections, where confidence in species identification was high, and 2558 samples collected by fishery observers from commercial longline catches. Univariate and linear discriminant analyses of research-collected samples revealed consistent differences in otolith shape between the two species, with otoliths of *M. caml* being larger and more elongate than those of *M. whitsoni*. No significant effect of collection depth or fishing season on otolith shape was evident for either species, and no significant effect of sampling location on otolith shape was evident for *M. caml*. Otolith shape of *M. whitsoni* varied slightly among sampling regions, although the extent of these differences was less than those between species. To validate observer identifications, a random forest (RF) model was trained using otolith shape data of 75% of the research collection samples, validated on the remaining 25%, and used to predict the species of fishery observer-collected samples. The RF model achieved high classification success for individuals from the research collections, with an Out-Of-Bag error rate of 5.97% for the training dataset. Overall classification success of individuals in the validation dataset was 96.2%, with 96.8% of *M. caml* and 94.8% of *M. whitsoni* correctly classified. Using this model, 90.6% of *M. caml* and 85.7% of *M. whitsoni* sampled by fishery observers were predicted as being correctly identified. Individual observer identification success ranged from 50.5% to 98.2%. The reliable and predictable differences in otolith shape observed between the two species indicates that our approach can be applied to ongoing or archived otolith collections to confirm species identification of fishery-sourced samples to improve the accuracy of fisheries monitoring, facilitate assignment of previously collected material to species level, develop high-confidence datasets for further biological analyses, and to understand and prioritize observer training needs.

Marval-Rodríguez *et al.* (2022) conducted a population-based study concerning otolith shape and genetic analyses to evaluate if *Lutjanus campechanus* and *L. purpureus* are the same species. Samples were collected from populations in the southwestern Gulf of Mexico and the Venezuelan Caribbean. Otolith shape was evaluated by traditional and outline-based geometric morphometrics. Genetic characterization was performed by sequencing the mtDNA control region and intron 8 of the nuclear gene FASD2. The otolith shape analysis did not indicate differences between species. A nested PERMANOVA identified differences in otolith shape for the nested population factor (fishing area) in morphometrics and shape indexes and otolith contour. An AMOVA found the genetic variation between geographic regions to be 10%, while intrapopulation variation was 90%. Network analysis identified an important connection between haplotypes from different regions. A phylogenetic analysis identified a monophyletic group formed by *L. campechanus* and *L. purpureus*, suggesting insufficient evolutionary distances between them. Both otolith shape and molecular analyses identified differences, not between the *L. campechanus* and *L. purpureus* species, but among their populations, suggesting that western Atlantic red snappers are experiencing a speciation process.

Arroyo-Zúñiga *et al.* (2022) used lapilli for species ID of sea catfishes of the family *Ariidae* from the north-eastern Pacific, as representatives of Siluriformes, a taxon with increased taxonomic complexity. The lapillus otolith shape obtained by geometric morphometrics showed high discrimination potential both at the genus and species levels with an overall classification accuracy of approx. 93% (K = 0.92). Due to the strong species delimitation exhibited by lapillus otolith shape, the descriptions and identification keys provided in this study are the most useful materials to recognize the eight sea catfish species evaluated. The shared similarities in lapillus otolith shape among species seem to be more influenced by phylogenetic relationships than other factors such as habitat.

Chen *et al.* (2023) evaluated many commonly used machine learning techniques to identify juvenile fish from four species (*Chionodraco rastrospinosus*, *Krefftichthys anderssoni*, *Electrona carlsbergi*, and *Pleuragramma antarcticum*) based on their otolith shape in the Southern Ocean. Eventually, by introducing a triplet loss function (function used to reduce intraspecific variation and increase inter-specific variation), the discrimination confusion caused by the allometric growth of otoliths was reduced. The classification results show that the neural network model with the triplet loss function achieves the best classification accuracy of 96%. The proposed method can help improve otolith classification performance, especially under the context of limited sampling effort, which is of great importance for trophic ecology and the study of fish life history.

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Otolith chemistry (Contributors: Lisa Kerr, Patrick Reis-Santos, Susanne Tanner, Zach Whitener)

Farias *et al.* (2022) used otolith chemical composition of the black scabbardfish (*Aphanopus carbo*) to investigate discrimination among different capture areas, identify potential birth areas and study life-time spatial migration patterns. Otolith edge composition allowed discrimination among capture locations and provided evidence of separation between the northern and the southern distribution areas. Otolith core chemical composition clustered into two different groups suggesting the existence of two natal sources. Chemical composition of longitudinal profiles in otoliths also supported the separation into two groups. Overall, results provide evidence of both southern and northern spawning grounds and of migratory movements along the NE Atlantic in northward and southward directions. These findings may result in changes to the large-scale clockwise migration hypothesised for this species which ultimately may be translated into different stock boundaries and fisheries management of *A. carbo*.

Bassi *et al.* (2023a) used otolith chemical composition to assess the population structure and investigate potential small-scale connectivity of Greenland halibut (*Reinhardtius hippoglossoides*) in the Estuary and the Gulf of St. Lawrence (EGSL) as recent genomic studies revealed genetic differentiation between this area and the remainder of the Northwest Atlantic. Otolith edge elemental signatures were used to infer spatial differentiation and using quadratic discriminant analysis 59% of fish were correctly classified to their capture location. Otolith core signatures indicated three chemically distinct juvenile sources, suggesting high connectivity in the EGSL and supporting the St. Lawrence Estuary as a main nursery. Results suggest that one of the three distinct juvenile sources showed lower contribution compared to the other sources.

Bassi *et al.* (2023b) used otolith chemical composition to determine the migration patterns among nurseries of Greenland halibut (*Reinhardtius hippoglossoides*) in the Gulf of St. Lawrence. Using margin-core transects and marginal elemental fingerprints of Mg, Mn, Sr, and Ba, they inferred the migratory behaviour between two sites, with correct classification rates of 77%. Most fish (82.5%) were from a single source, belying the source-sink dynamic and the estuary being the main nursery in the St. Lawrence system.

Labonne *et al.* (2022) used whole otolith elemental signatures of hake (*Merluccius merluccius*) and sardine (*Sardina pilchardus*) collected in 10 locations along the Moroccan coast to assess population structure. The study area is part of one of the most productive marine eastern boundary upwelling systems, but knowledge of population structure of exploited fish species remains scarce. Correct classification of fish based on otolith chemical composition and using linear discriminant function analysis was 88% and 71% for hake and sardine, respectively. Spatial variation in otolith elemental compositions of both species was significant and a major split occurred for both species in the same area (28º–29ºN) which coincides with the transition zone between the northern temperate mud-shelf ecosystem and the arid ecosystem in the south. Drivers of this separation likely involve complex oceanographic processes that act as a barrier to larval dispersal. Results confirm previous findings on sardine population structure and provide evidence for a similar structure in hake which should be considered in fisheries management to ensure matching biological and management units.

Samson *et al.* (2022) used otolith chemistry to investigate its application to identify two parapatric flounder (*Platichthys flesus* and *Platichthys solemdali*) to the species level, since the two species can only be distinguished based on egg and sperm characteristics and genetic analyses. Otolith chemical composition was used to test for species-specific differences in two species and investigate spatial consistency of differences for early life stages in three areas of the central Baltic Sea (ICES SD 24–28), where the distribution of both species overlaps. Otolith core signatures (obtained through maternal transfer) and post-hatch signatures were not significantly different among species, with species-specific differences limited to one survey area. Classification of age-0 juveniles to survey areas was more successful than classification to species which is related to a spatial trend in otolith Sr:Ca following the salinity gradient and higher Mn:Ca and I:Ca values in the most eastern survey area. Overall, otolith chemistry of early life flounder reflects spatial variability in environmental conditions in the Baltic Sea but fails to differentiate among the two flounder species.

Logan *et al.* (2023) used stable isotope analysis to infer foraging habitats and pre-spawning habitat use of Atlantic bluefin tuna (ABFT) from the eastern and western stocks. Specifically, they used bulk nitrogen and compound-specific stable isotope analysis to estimate the percent of ABFT that occupied shelf or open ocean foraging habitats before capture in spawning grounds in the eastern and western Atlantic (Gulf of Mexico, and Morocco coast, Strait of Gibraltar, Balearic Sea, and Adriatic Sea, respectively). Linear discriminant analysis was used to classify isotopic signatures from ABFT to isoscapes created from shelf and open ocean habitats in the North Atlantic. Overall, western Atlantic spawners mainly used shelf habitats as past foraging grounds (91 %), while eastern Atlantic spawners primarily used open ocean and/or Mediterranean Sea habitats to fuel spawning migrations (from 79% in the strait of Gibraltar to 100 % in the Adriatic sea). This suggested that most Gulf of Mexico spawners travelled from the western Atlantic shelf and slope while Mediterranean Sea spawners used local or similar habitats in the eastern Central Atlantic Ocean. Whilst this paper does not explicitly investigate stock structure, results provide key insight into the foraging habitats that support eastern and western Atlantic spawning assemblages.

Arai *et al.* (2023) used otolith carbon and oxygen stable isotopes ($\delta^{13}C/\delta^{18}O$) to predict geographic origin of Northwest Atlantic mackerel (*Scomber scombrus*) which is comprised of northern (spawning off Canada) and southern components (spawning off US) that seasonally overlap in the US fished regions. To do so they developed a new framework integrating nominal and continuous assignment approaches by (1) developing a machine-learning multi-model ensemble classifier using Bayesian model averaging (nominal); and (2) integrating nominal predictions with continuous isoscapes to estimate the probability of origin across the spatial domain (continuous). The nominal approach yielded high contingent classification accuracy (84,9%) of known origin samples and unknown-origin samples showed temporally highly variable contingent mixing levels (12.5–83.7%). Mackerel-specific otolith oxygen isoscapes were developed based on the nominal predictions which allowed identifying geographic nursery hotspots in known spawning sites, as well as detecting shifts over 4 decades. The presented framework is applicable to other marine fish species.

Combined use of otolith chemistry with other markers

Morales Nin *et al.* (2022) examined the population structure of European hake (*Merluccius merluccius*) in the Mediterranean Sea using otolith shape and microchemistry. Whilst 40 official geographical subareas (GSA) were analysed for otolith shape, only a subsample from 10 GSA were analysed for microchemistry. Linear discriminant analysis was used to test the discrimination capability of otolith markers, independently and together with otolith shape, at GSA and at three larger unit scales (Western, Central and Eastern Mediterranean). Overall, classification success was limited and dependent on the number of units considered, but the combination of shape and microchemistry improved the classification success. Classification accuracy using otolith chemistry varied between 29% (10 subareas, chemistry only) to 60% (3 units, chemistry and shape combined). Unsupervised clustering methods (i.e., groups are not defined a priori) also failed to find clear structuring. Results support the hypothesis of a continuous gradient, within which discrete spatial units cannot be safely recognized. The authors advocate for the continuous impulse of dynamic spatial management plans to ensure hake’s sustainability in the Mediterranean.

Le Luherne *et al.* (2022) coupled Data Storage Tag (DST) data with otolith chemistry to investigate population structure and connectivity of European seabass (*Dicentrarchus labrax*) between the northern (southern North Sea, English Channel and Celtic Sea) and southern stocks (Bay of Biscay). DST-based trajectory reconstructions were used to assign a spawning area to each spawning winter record and chemical composition was determined in both larvae and adult otolith increments corresponding to a winter spawning event. DST and otolith chemistry data were used to build a Random Forest model capable of assigning spawning areas based on otolith chemistry only. Results showed considerable spawning site fidelity (64%) with higher site fidelity found in the northern and southern areas of the study area. Significant ontogenetic effects on otolith chemistry prevented the use of the assignment model across cohorts to study adult natal homing, however the patterns of difference were similar for larval and adult Zn, Sr and Ba between the two spawning areas, suggesting a homing behaviour.

Stounberg *et al.* (2022) conducted a comparison of chemical composition of Baltic cod otoliths and eye lenses in a methods paper, analysing many isotopes. The authors found few similarities between otolith and lens chemistry, however Sr-88 values showed strong correspondence between growth rings of the lens and otolith periodicy. Albeit, no other elements showed similar patterning, thus the authors conclude different uptake pathways between otoliths and lenses. Although this paper did not explicitly investigate stock structure, it describes the utility of LA-ICPS to "provide a baseline study identifying elements in corresponding eye lenses and otoliths that show potential for unravelling the environmental and biological conditions experienced by fish" that may be used for stock discrimination in the future.

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Parasites (Contributor: Ken Mackenzie)

Seven publications on the use of parasites as biological tags for population studies of marine fish were published in the year from June 2022 to July 2023, covering a wide variety of host and parasite taxa over a wide geographical range. The target hosts included three demersal species, two small pelagics and one elasmobranch. Study regions were the Eastern Pacific, the Southwest Atlantic, West Africa, Australia and the Black Sea. One publication reviewed the use of parasites as biological tags over the past century.

Gonzalez-Poblete *et al.* (2022) analysed the parasitofauna of southern hake, *Merluccius australis*, in the Patagonian Fjord and Channel System of southern Chile to determine if more than one ecological population might be present in their study area. Samples totalling 219 hake were taken between spring 2004 and winter 2005 from three locations along a north-south gradient from Chiloé to north and south of the Strait of Magellan (north and south Magellanes). Criteria used to select potential tag parasites were: 1) those with a prevalence of >5%, 2) those that accumulated through time (host body length) and 3) variability in their abundance between sampling locations. Univariate analyses were carried out using the Kruskal-Wallis test to determine differences in abundance of each parasite taxon between sites, then whole parasitofaunas were compared by the multivariate correspondence analysis without tendency (DECORANA). Statistical analyses of parasites with prevalences >5%, including fish of all length groups, showed significant differences between sampling sites. Analyses of fish of the first maturity length category showed no significant difference between the two Magellanes locations, but both were significantly different to the Chiloé samples. Based on these analyses, seven endoparasites and one ectoparasite are proposed as potential biological tags for future monitoring of ecological stocks of hake in the study area.

Irigoitia *et al.* (2022) surveyed the metazoan parasite fauna of the skate *Dipturus brevicaudatus* in Argentine coastal waters with a view to selecting parasites that may be useful for stock identification. This skate is extremely vulnerable to overfishing and is frequently caught as a by-catch in fisheries targeting teleosts and shrimp, so a knowledge of its stock structure is extremely important for its conservation. Parasite tagging has rarely been applied to elasmobranchs because of the dominance of adult stages in their parasite faunas; these are generally short-lived and thus considered to be less useful for stock identification. Skate were sampled from three areas along a north-south gradient: Buenos Aires (BA) in the north, and North and South Patagonia (NP and SP). Three parasite guilds were recognized among the parasites infecting *D. brevicaudatus* – ectoparasites, short-lived endoparasites and long-lived endoparasites. Since only three taxa of long-lived parasites were found, all of them anisakid nematode larvae, analyses were also carried out on the entire parasite infracommunities, including short-lived species. Analyses of prevalence and abundance data on the two most common of the long-lived parasites, *Anisakis simplex s.l.* and *Pseudoterranova cattani*, showed statistically significant differences between NP and both BA and SP, while analyses of entire parasite assemblages varied between BA and the two other areas in species richness and relative abundance of parasite guilds. The results suggested the existence of three stocks in the study area. Three different species of the *Anisakis simplex* complex are known to occur there, so specific molecular identification of these species could add further refinement to the application of parasite tagging in future studies.

López-Moreno *et al.* (2023) documented the metazoan parasite fauna of the Pacific thread herring, *Opisthonema libertate*, in the Gulf of California by examining fish caught at six localities along the eastern part of the Gulf – a distance of about 1000 km - during a single research vessel cruise. The aims were to determine latitudinal changes in parasite infection levels and to assess the potential of the parasites as biological tags for host stock structure in the study area. Six parasite taxa were identified, of which by far the most common at all sampling localities were two adult digeneans in the gastrointestinal tract. Differences in prevalence and intensity of infection of the two digeneans between localities, as well as separation of localities indicated by a multivariate analysis of the entire parasite assemblage, suggested a discontinuous distribution of both digeneans along the Gulf - possibly a result of latitudinal variations in oceanographic conditions and the availability of intermediate hosts. Based on these differences, it is possible to hypothesize that thread herring have limited movement between certain geographical areas within the Gulf. The authors point out, however, that this is not a solid conclusion because these parasites do not satisfy all of the selection criteria for their use as good biological tags. In future, they suggested continuing with parasite surveys while also considering possible drivers such as seasonality together with host traits such as diet and ontogeny.

Ogbon *et al.* (2023) carried out the first study of the parasite fauna of the small clupeoid *Sardinella maderensis* along the coasts of Benin and Ghana in West Africa. In addition to documenting the parasite fauna, they also aimed to identify those parasite taxa with the potential to be used as biological tags for stock identification of the host in this area. Fish samples were collected from commercial catches landed at two ports, Elmina in Ghana and Cotonou in Benin, 100 fish from each port, and examined for parasites. Five metazoan parasites were found with the most common being an adult digenean parasitising the stomach. Two parasite taxa, the nematode *Anisakis* sp.(p) and the cestode *Tentacularia coryphaenae*, were selected as potentially useful biological tags for stock identification of *S. maderensis* along the coast of West Africa. Both are present in *S. maderensis* as long-lived larval stages that can survive as "resting stages" for several years, and possibly for as long as the host lives. As the genus *Anisakis* comprises a group of nine species, each with its own cetacean host preferences, it is crucially important to identify the species present using molecular methods. This can then be related to the occurrence of cetacean species in the study area. This approach cannot be used for *T. coryphaenae* because of its wide host specificity, but significant differences in its prevalence and abundance in different parts of the study area may indicate different dietary compositions between stocks of *S. maderensis.*

Porter *et al.* (2023) evaluated spatial and temporal variability in parasite communities of the commercially important teleost black-spotted croaker *Protonibea diacanthus* to examine its population structure off the coast of the Northern Territory, Australia. A total of 228 fish were collected from four sampling stations, two nearshore close to river mouths and two offshore off islands with no major river systems. Fish were caught during three seasonal sampling periods over a period of two years. Fifteen parasite taxa were identified from the gills and gastrointestinal systems, of which two taxa were excluded from the analysis based on their having a prevalence of <10% in at least one of the sampling locations. Linear discriminant analyses (LDFA) were conducted to provide a statistical and visual indication of the similarities of the parasite communities between samples at the regional spatial scale, and across seasons. Analysis of parasite prevalence and mean intensity across the three sampling seasons suggested that fish from the four sampling sites represented distinct host populations. Across time, parasite assemblages at the four sites were distinct during the mid-dry and build-up seasons, but during the wet season there was substantial overlap at three sites, indicating that some host population mixing may be occurring at that time. Parasite assemblages at one nearshore site remained distinct across spatial and temporal scales. The results support the utility of parasite tags for elucidating the population structure of host species and stress the necessity of taking spatial and temporal variability into account when performing stock discrimination analyses.

Timi and Buchmann's (2023) review of a century of the use of parasites as biological tags in fisheries is divided into seven sections, each dealing with a different aspect of the topic. The first section is an introduction and a compilation of the literature showing the gradual evolution of the methodological criteria or guidelines for the selection of appropriate tag parasites. Most parasite tag studies have been carried out on teleost fishes of commercial importance, but the second section questions why parasites have not been used more as tags for elasmobranchs and invertebrates. The third section discusses the long-established criteria or guidelines used to select the most appropriate parasites for use as tags and how some recent studies have tested these criteria and confirmed their validity. The fourth section discusses the effects of host traits on the application of parasite tags and recommends that more attention should be paid to differences among host length classes when using parasite tags for resources with temporally and spatially variable migratory patterns, especially when different cohorts are being compared. Section five stresses the value of integrative multidisciplinary studies that simultaneously apply different, but complementary, techniques, including parasite tags, to studies of stock structure. Section six looks in depth at the use of genetic data and methodologies and the importance of applying genetic identification methods to specifically identify parasites, such as species in the nematode genus *Anisakis*, in order to achieve higher taxonomic resolutions of the parasites. The final section discusses the use of parasites as indicators of the success of marine protected areas (MPAs), where several studies have evaluated the success of MPAs using parasites as biological indicators. Most of these studies recorded increased abundance, species richness and/or diversity for different parasite taxa resulting from the protection measures. Overall, this is an excellent review of the current status and future use of parasites as biological tags or indicators.

The paper by Yuryshynets *et al.* (2023) demonstrates a different use of parasites as tags for stock identification by using parasites as a means of clarifying the possible origin of populations of an invasive host species. The black-striped pipefish *Syngnathus abaster* is a euryhaline Atlanto-Mediterranean species with a tolerance to fresh water that has allowed it to spread up all rivers in the Black Sea basin. The aims of this study were to describe the current range of *S. abaster* in Ukrainian waters and to obtain parasite biological tag data for different populations. Fish were sampled from five different localities – one marine, two deltaic and two freshwater. The entire parasite fauna consisted of 21 protozoan and metazoan taxa, the most numerous of which were ciliates of the genus *Trichodina.* The majority of parasites were present as larval stages, with just two digeneans and an isopod found as adults. The formation of the parasite component community depends entirely on environmental factors, with the parasite communities of different populations forming according to 1) Presence of "marine" protistan parasites, mainly ciliates, in marine localities; 2) Presence of metazoan parasites in localities with conditions that allow completion of complex life cycles, such as trematodes and cestodes. Overall, the parasite fauna of *S. abaster* shows two main parasite community formation strategies in their newly acquired ecosystems: 1) Parasite release (very poor communities in freshwater) and 2) Acquisition of local parasite taxa which have overcome the filters of encounter and adaptation.

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Simulation approaches (Contributors: Lisa Kerr and Steve Cadrin)

Simulating complex population structure continues to provide an informative tool for integrating information on stock identity, learning about general implications of population structure from heuristic simulations, and testing the performance of spatial alternatives for stock assessment and fishery management from more precisely conditioned simulations representing fish and fisheries. Several case studies, a general review, and an international workshop were published in the last year. These recent examples applied to a diversity of species and demonstrated a range of technical approaches. Spatial simulation is a promising approach to considering information from stock identity and is being applied to species conservation, marine protected areas, climate change scenarios, shifting spatial distributions and offshore wind farms.

Wilson *et al.* (2022) simulated generic metapopulations under various conditions to evaluate recovery of endangered species. Results were largely determined by spatial patterns of disturbances, such as unevenly impacted subpopulations. Recovery was slower with low dispersal or connectivity among habitats, high local heterogeneity in demographics, and synchronous variability of population processes. Although the simulations were loosely conditioned to represent a wide range of metapopulations, results were generally confirmed with case study information for Chinook salmon, sea otters, and snail kites.

Mendoza-Portillo *et al.* (2023) modelled the effects of climate change on three allopatric populations of Almaco jack with a combination of genotype–environment association, spatial distribution models, and demogenetic simulations. Their results indicated a loss of suitable habitat and range contractions under most climate scenarios, and less population connectivity caused by fishing. In combination, fishing and climate change are expected to impact genetic diversity.

Krueck *et al.* (2022) developed bio-physical simulations to represent several species inhabiting coral reefs in Indonesia to consider larval dispersal for siting marine protected areas. Larval export was measured as the contribution of larvae from candidate protected areas to total larval settlement in surrounding areas. Some protected area designs doubled catches and tripled fish biomass compared to scenarios with no protected areas.

A series of papers describe an initiative to evaluate the effects of offshore wind farm development on surf clam populations using spatial simulations. Monroe *et al.* (2022) developed a spatially explicit model of surfclams conditioned on observed stock distributions and fleet characteristics, with fishing behavior. Scheld *et al.* (2022) extended the model to include costs and revenues and simulated offshore wind farm scenarios that restrict fishing and transit to 1-5% increased fishing costs and 3–15% decreased revenues. Stromp *et al.* (2023) applied the model to five scenarios of spatial overlap of surf clams and wind farms and found that scenarios with fewer spatial constraints on the fishery had higher catch but greater costs and reductions in revenue compared to no wind farms. Although the application is less relevant to stock identification, the operating models and methods could be applied to evaluating the implications of spatial distribution and heterogeneity on stock assessment and fishery management.

Goethel *et al.* (2023) recommended simulation testing and MSE in their review of good practice for spatial stock assessment. They provide details on good practice, including the specification of operating models that have the same or higher spatiotemporal resolutions than candidate assessment models. They demonstrated that simulation testing can help to develop assessment models with the minimum complexity required to meet management needs. As an extension of the 2021 World Fisheries Congress symposium on spatial population modelling (Goethel *et al.* 2022), an international workshop was organized as a series of webinars and a meeting in New Zealand to consider best practices in spatial model development, evaluate performance of assessment software that supports spatial structure, and compare general performance of non-spatial, spatially-implicit, spatially-stratified, and fully spatiotemporal assessment models (Berger 2023). Preliminary results were presented at the Tuna Stock Assessment Good Practices Workshop with recommendations for iterative spatial model development to move away from unit population assumptions using a stepwise approach (Berger *et al.* 2023).

Jacobsen *et al.* (2022) applied MSE was developed to international management of Pacific hake. Operating models had spatially complex populations and alternative hypotheses about climate-induced changes in movement rates to test three candidate harvest control rules. They found that movement rates and annual catch variability increased with climate change and demonstrated the value of spatial management.

ICCAT (2022) developed a spatial MSE to adopt a fishery management procedure for Atlantic bluefin tuna populations. Despite typical stock assessment information (e.g., catch, catch rates, and size composition by fishing area) as well as movement observations from conventional and electronic tagging and information on stock composition from genetics and otolith chemistry, developing a reliable multi-population spatially-structured stock assessment remains a challenge. As an alternative, a wide range of operating models with two populations and seasonal mixing were conditioned on the available information, with alternative scenarios of movement, relative population abundance, stock-recruitment, and natural mortality to test alternative management procedures for meeting management objectives (Carruthers 2022). ICCAT accepted a management procedure in 2022 for implementation this year that is expected to conserve both populations and meet fishery objectives.

A spatial MSE is also being developed for New England cod populations. After an interdisciplinary review identified five genetically distinct populations off New England (McBride & Smedbol 2022), a research track stock assessment working group developed four new spatial stock assessment units, with the western Gulf of Maine stock comprised of sympatric winter and spring spawning populations (Kerr *et al.* 2023a). A MSE is underway based on a five-population operating model conditioned on the revised stock assessments to test performance of alternative spatial management procedures (Kerr *et al.* 2023b). The New England Fishery Management Council is considering alternative spatial management units of cod as a priority for 2024.

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Interdisciplinary approaches (Contributors: Manuel Hidalgo, David Secor, Steve Cadrin and Lisa Kerr)

The incorporation of the spatial population structure in stock assessment models is still rare, while the concern and awareness that it must be progressively implemented in the near future is considerably high. In Goethel *et al.* (2023), the authors reviewed the types of spatial assessment models available, summarizing the options to parameterize population structure, offering a guidance to promote the development of the most appropriate candidate spatial assessment models for application in management procedures, and provide a pragmatic guide for choosing a spatial assessment model given observed spatial structure, data limitations, and management concerns. This publication is expected to be a reference document to guide the implementation of spatial stock assessment.

Darnaude *et al.* (2022) identified the knowledge needed to account for marine connectivity to support transition to a sustainable blue economy, including a connectivity-based approach to improve the sustainability of harvested marine resources within an ecosystem approach. This is framed in a perspective article around the Cost Action Sea-Unicorn project '*Unifying Approaches to Marine Connectivity for improved Resource Management for the Seas* (2020-2025)', which stresses that the connectivity among marine populations and habitats facilitates the persistence and resilience of vulnerable species and ecosystems and controls the spread of invasive species. Constructing effective networks of restoration or conservation areas, spatial assessment and management, and promoting sustainable harvesting requires integrative advanced knowledge of connectivity.

Integrating genetic information with oceanographic modelling is becoming a common approach to stock identification of diverse taxa and is being continuously and rapidly improved. Fitz *et al.* (2022) combined the genetic isolation-by-Distance and connectivity matrices by running a Lagrangian particle tracking tool to assess whether genetic patterns of Anemonefish, *Amphiprion biaculeatus*, in central Philippines can be used for estimating dispersal, or whether the influence of ocean currents can provide a better explanation. Results show that currents were a better explanation for genetic distance at large spatial extents (sites greater than 150 km apart), while geographic distance remained the best explanation for spatial extents less than 150 km, evidencing the need of combining IBD patterns with oceanographic simulations to understand connectivity in marine environments. Horoiwa *et al.* (2022) combined the same two techniques to assess the potential and realized dispersal of crown-of-thorns sea star, *Acanthaster cf. solaris*, between Ogasawara and other Japanese regions associated to Kuroshio current. The study aimed also to explain a populations outbreak observed in 2018. The oceanographic dispersal indicated that larvae are mostly self-seeded in Ogasawara populations and have difficulty reaching Ogasawara from the Kuroshio region within one generation, showing a gradual larval dispersal migration from the Kuroshio region to Ogasawara in a stepping-stone manner over multiple years. These results also suggest that the 2018 outbreak was likely the result of self-seeding, resulting in a likely inbreeding. Marino *et al.* (2022) used the same combination of genetic results and Lagrangian simulations to assess connectivity patterns of the marbled crab, *Pachygrapsus marmoratus*, a high dispersal species, in the Adriatic and Ionian basins, including existing or planned Marine Protected Areas (MPAs). The integration of results suggest that suggest that the observed genetic homogeneity may be the consequence of a high realized connectivity among sites, which might result from a regional metapopulation dynamics, rather than from direct exchange among populations of the existing or planned MPAs. Also, Van der Rois *et al.* (2022) applied identical integrative approach to assess the population connectivity of the deep sea lobster, *Metanephrops challenger*, around New Zealand, a species with low dispersal capacity, including the early life stage due to a short pelagic larval duration. Genetic differentiation evidenced three groups (eastern, southern and western) displaying a clear source-sink dynamics. The direction of gene flow inferred from the genomic data largely reflected the hydrodynamic particle modelling of ocean current flow around New Zealand. The modelled dispersal during pelagic larval phase highlights the strong connectivity among eastern sampling locations and explains the low genetic differentiation detected among these sampled areas. Quingley *et al.* (2022) assessed population connectivity of New Zealand green-lipped mussels, *Perna canaliculus*, comparing outputs of Lagrangian particle tracking experiments with published multi-locus microsatellite data of observed population genetic structure. This study also showed that common discrepancies between genetic and biophysical data often observed in combined studies may be explained by the different timescales of connectivity described by the two methods and the impact of localized ecological conditions and corresponding adaptations in genetic structure not captured by the biophysical model as no evidence was found for an oceanographic barrier to gene flow. Jahnke *et al.* (2022) used this integrative combination of techniques to resolve questions at smeller spatial scale related to how the adaptive responses of the shore crab, *Carcinus maenas*, larvae overcome tidal barriers of different amplitude using samples of different locations around the North Sea and Skagerrak coast. Dispersal and recruitment success of larvae was assessed with a Lagrangian biophysical model, which showed a strong effect of larval behaviour on long-term connectivity, and dispersal barriers that, in general, coincided with different tidal environments. Indeed, the genetic population structure showed a subdivision of the samples into three clusters representing micro-, meso-and macrotidal areas. This study evidence that tidal regime acts as a strong selection force on shore crab population structure in this area, consistent with the larval behaviour effect on dispersal and recruitment success. Finally, Legrand *et al.* (2022) expanded this integrated approach to a multispecies level, using 58 population genetic studies of 47 phylogenetically divergent marine sedentary species over the Mediterranean basin to assess how genetic differentiation is predicted by isolation-by-distance, single-generation dispersal and multigeneration dispersal models. This study found that almost 70 % of observed variance in genetic differentiation is explained by coalescent connectivity (i.e., associated to implicit links among siblings from a common ancestor) over multiple generations, significantly outperforming other models.

Of particular interest are few studies integrating up to three methods in novel integrative frameworks. Wilcox *et al.* (2023) developed a novel approach that integrates estimates of spatial genetic structure with representation of regions of high dispersal potential, incorporating elements of pelagic larval and benthic adult life history. They applied the circuit theory as an inverse function oceanographic- and habitat-based resistance to movement by combining genetic information to habitat suitability predictions and oceanographic models. They applied this method to four species broadly distributed in the Northwest Atlantic (cod, American lobster, Atlantic sea scallop and European green crab). This study shows that estimates of resistance to gene flow revealed multiple connectivity barriers not observed in oceanographic or habitat models. Comparison of isolation-by-distance versus isolation-by-resistance revealed genetic variation was best explained by seascape resistance in three of four species, supporting the resistance-based assessments of connectivity.

Beyond the increasing frequency of research combining genetics with oceanographic modelling, there are other studies combining genetics with other techniques and data. This is the case, for instance, of Knutsen *et al.* (2022) who combines genetic information of two coastal species with contrasting life history in terms of spawning behavior, larval stage and juvenile settlement (broadnosed pipefish, *Syngnathus typhle*; corkwing wrasse, *Symphodus melops*; black goby, *Gobius niger*) along the coast of Norway with observations from long-term coastal surveys of juveniles (ca. 30-year). The rapid decline in spatial correlations in abundance with distance as short as ~2 km in the habitat attached species, pipefish, contrasts with the other two species that show a wider spatial scale of connectivity and weaker genetic isolation-by-distance, except where both species experienced a strong barrier to gene flow. This study supports that a fragmented habitat and absence of a pelagic larval stage promote genetic structure, while presence of a pelagic larvae stage increases demographic connectivity and gene flow, except in the presence of extensive habitat gaps. Mendoza-Portillo *et al.* (2023) integrate genetic information of loci under selection (genotype–environment association), species distribution models and information of fishing impact to investigate the potential responses of population structure and genomic diversity to climate change and fishing pressure in an important pelagic fish, Almaco jack (*Seriola rivoliana*), in the central Pacific Ocean, to model the effects of climate change under three pathway scenarios. Their results show that most of the outlier loci identified were related to biological and metabolic processes potentially associated with temperature and salinity. Future projections suggest a loss of suitable habitat and potential range contractions for most scenarios, while fishing pressure decreased population connectivity, suggesting that climate change and fishing pressure will affect the genomic structure and genotypic composition of many species.

Oceanographic modelling, on the other hand, has been also combined with other techniques and data. Nolasco *et al.* (2022) combined Lagrangian models with recruitment observations of stalked barnacle *Pollicipes pollicipes* of rocky shores in 3 regions around the Iberian Peninsula (Asturias and Galicia in Spain, and southwest Portugal). The study assessed three migrating scenarios emerging from cross-correlation analysis: passive, surface-dwelling and ontogenetically migrating. They showed that none of the scenarios produced a substantially better fit than the others, and all three produced estimates of average realized dispersal and larval retention that were numerically similar. These estimates indicate high levels of connectivity, either during larval life or via steppingstone processes, within and between the 3 regions. Vaz *et al.* (2022) used the queen conch, *Aliger gigas*, an endemic marine gastropod of the wider Caribbean harvested for thousands of years, to investigated whether and how exploitation can drive changes in the population connectivity. They combine spatiotemporal observations of the species, with simulated larval dispersal and demographic models to assess how the population connectivity of conch changes with spatially variable patterns of fishing exploitation comparing the potential connectivity under an unexploited and a contemporary exploited reproductive scenario. Their study confirms that the existence of self-sustained metapopulations of queen conch throughout the Wider Caribbean and suggests that replenishment through larval dispersal occurs primarily within subregional spatial scales.

The integrative studies with other stock identification methods are comparatively less abundant this year, but used to respond questions beyond stock boundaries or develop novel analytical frameworks. Xuan *et al.* (2022) combined signatures of strontium (Sr) and calcium (Ca) in the otoliths of estuarine tapertail anchovy (*Coilia nasus*) from the Yangtze River Estuary (China) using electron probe microanalysis with gonad maturity stages to disentangle different patterns of reproductive ecology within the same species: the long freshwater early life history type and a bluish pattern. Their results of the otolith microchemistry indicated that both types originated in spawning/hatching sites far from and close to the estuary, respectively. The mature gonads of blueish fish indicated that they may breed in areas close to the estuary, whereas the immature gonads of long freshwater fish indicated that they may breed in areas far from the estuary. Finally, Arai *et al.* (2023) used long-term spatiotemporal otolith microchemistry information (1975-2019) of Northwest Atlantic mackerel (*Scomber scombrus*) across the gradient of distribution in US and Canada coasts in the Northwest Atlantic to develop a novel framework that integrates nominal and continuous assignment approaches by (1) developing a machine-learning multi-model ensemble classifier using Bayesian model averaging (nominal); and (2) integrating nominal predictions with continuous isoscapes to estimate the probability of origin across the spatial domain (continuous). The combined approach identified geographic nursery hotspots in known spawning sites, but also detected geographic shifts over multi-decadal time scales.

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Emerging issues (Contributors: David Murray and Steve Cadrin)

Stock ID and mismatches with data collection and assessment

There is a current drive within ICES to delineate biologically relevant population structures across a broad range of marine species, with the aim of producing stock assessments that more accurately account for boundaries and connectivity among populations across the northeast Atlantic. For example, recent cod (*Gadus morhua*) stock ID benchmarks (ICES, 2020, 2022) determined the presence of four sub-stocks within the North Sea commonly referred to as Dogger/West of Scotland, Viking, southern North Sea and Inshore west of Scotland. Most of these sub-populations have a degree of connectivity with stocks from adjacent areas making it difficult to determine exact geographical boundaries among components (ICES, 2020, 2021). While such work provides estimations of connectivity and boundaries among stock units, Fisheries Scientists require data to be disaggregated or reaggregated based on these boundaries to feed into assessments. Unfortunately, this reaggregation is where data limitations and mis-match issues are emerging.

For decades, data managers have provided stock assessors fishery dependant and independent data from ICES divisions defined during the 1970's. The historical time-series of data is a powerful tool for estimating stock productivity, current status, and ICES advice. However, the spatiotemporal resolution of some data cannot support compilation into revised stock boundaries based on biologically relevant population units, with complex connectivity components into assessments. Using cod as an example again, in response to the North Sea cod stock ID workshop (ICES, 2020), the 2021 benchmark assessment workshop attempted to compile fishery data to support the recommended spatial units, but there were unexplained discrepancies between the spatially disaggregated and aggregated data as used during previous assessment (ICES, 2021). After the expanded review of cod stock ID in the North Sea and west of Scotland (ICES, 2022), WKBCOD 2023 acknowledged mixing of the Dogger and Viking cod sub-stocks in most Quarters, except Quarter 1 (ICES 2023). The multi-stock model utilised for cod assessments used whole stock landings fractions, which the group acknowledged may not apply to sub-stocks and which they believe impacted the model fit for the report (WKBCOD, section 13.1); (ICES 2023). Although WKBCOD 2023 stated that this was not a serious concern, the ongoing problems cod stock assessors face in gathering regionally specific data based on sub-stock structures can be seen as a forewarning to ICES for other species.

The challenge of spatially re-aggregating fishery data is by no means specific for North Sea and west of Scotland cod. The increasing frequency of ICES stock ID workshops suggest that more species will require data with specific regional resolution beyond what current data collectors are able to provide. Therefore, on a species-by-species basis ICES may need to adapt data requests to assist assessors cope with the avalanche of future stock ID benchmarks currently being organised. Long term conversations regarding where, when and how data is collected may also be necessary, as time and again SIMWG is recommending that ICES advisory units reflect biologically relevant population scenarios but data suppliers may not be able to provide re-aggregated data for assessment purposes.

As best practices for spatial specification of stock assessments develop, such practical limitations need to be identified and confronted. The 2022 FAO/CAPAM workshop on Stock Assessment Good Practices identified low spatial resolution of some data as a constraint for improved spatial specification of assessments (CAPAM 2022). Although fishery-independent surveys and electronic fishery monitoring usually have the spatiotemporal resolution needed to support re-aggregation of data to revised stock boundaries, historical fishery monitoring data were usually collected for broad reporting areas. Potential solutions include:

1) continued advancement of monitoring technologies (e.g., vessel monitoring systems for fisheries; Gerritsen and Lordan, 2011);
2) attempt to estimate stock composition of broad reporting areas using discriminant analysis of archived samples (e.g., Bierman *et al.*, 2010) or spatiotemporal patterns in fishery-independent data (e.g., ICES 2023);
3) 3), refine the ICES Transparent Assessment Framework to support more flexible data preparations for alternative spatiotemporal aggregation (C. Millar, CAPAM 2022 discussion); and
4) integrated assessment models that fit directly to spatially aggregated data (e.g., historical fishery data) as well as spatially disaggregated data (e.g., recent fishery data and survey data) to evaluate current status with appropriate spatial specification while also accounting for historical productivity (Cadrin *et al.*, 2023).

SIMWG accepts the validity of data challenges for re-defining ICES advisory units and the investments needed for suggested solutions are not trivial but also recognizes that these solutions may be necessary to improve stock assessments and ICES advice.

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Annex 4: Summaries of WKEVALMAC and WKSIDAC2

Workshop on the Evaluation of NEA Mackerel Stock Components (WKEVALMAC; Chairs: Richard Nash & David Secor), London/hybrid, 12-16 June 2023

The objective of WKEVALMAC was to review information on stock identification of Northeast Atlantic (NEA) mackerel and develop a consensus understanding of the Atlantic mackerel population structure and key uncertainties. The data and studies covered the distribution and movements of different life-stages of mackerel, including changes over time. The data and studies that were evaluated centred on genetic, tagging, otolith, dispersal models (e.g. of mackerel eggs and larvae/juveniles, commercial landings and perceptions from the industry). The motivation was the continued consideration of the mackerel stock consisting of three 'components' and the advice sheet referring to separate recommendations for at least one of the 'components' (the North Sea).

Genetic studies concentrating on the structure of the fish occurring in the Northeast Atlantic, in the vicinity on the North Sea and including populations in the western Atlantic and the Mediterranean did not find clear evidence for supporting recognizable 'stock components' in the Northeast Atlantic mackerel population. At the species-level, a comprehensive study concluded that the populations in the Northeast Atlantic, Northwest Atlantic and the Mediterranean are indeed discrete.

The historical tagging data shows that there is mixing from the southern and western NEA areas throughout most of the year and their cohabitation in the western spawning grounds cast doubts on the reliability of the assumption of separate spawning components in these two areas.

The survey data from the triennial egg survey gave no clear pattern which would suggest 'components' in the spawning distribution. In addition, there was no clear boundary between Divisions 6a and 4a, indicating that spawning in the North Sea is an eastward extension of the principal spawning of the NEA mackerel stock. An extension to the survey results on egg distributions is that there is support for the hypothesis that dynamics in the spawning migration of mackerel is state-dependent, i.e. influenced by the age, size, condition of the individual fish. Evidence from tagging surveys, acoustic surveys and egg surveys, and catch data all supported this premise. With regard to the assessment and catch data, ICES has undertaken a combined assessment (one stock) since 1996. The assessment WG accepts that the entire NEA mackerel fishery is on a mixed stock. Regarding potential data for investigating demographic differences between what were considered as 'components', limited data exists in Q2 (North Sea) when potential components are spawning, and the catch is generally not well sampled. Information remains unavailable on size and age structure and maturity stages to support separation of this component. Further, mackerel catches cannot be allocated to specific spawning areas based on any biological discrimination technique. However, by convention, catches from the Southern and Western components are separated according to the area where they are taken (ICES, 2016). Lastly, the industry's perception is that this is one single stock; there is no evidence for components. There are spatial differences in abundance and morphometrics, but these changes can be quite dynamic over spatial and temporal scales. This is to be expected of a highly migratory stock.

The conclusions of the workshop were:

1. The workshop acknowledges that there are spatial and temporal patterns in demography (e.g., size and age) which are primarily related to the highly migratory and dynamic nature of the stock, and not due to separate components.
2. Recent directed genetics, tagging, otolith chemistry investigations; ongoing surveys, catch data, fisher perspective and preliminary modelling studies, all failed to support the three-component concept for NEA mackerel.
3. The workshop therefore rejected the current three-component structure and accepted a single NEA mackerel stock concept to advance towards assessment, management and advice.
4. Given conclusion 3, the workshop recommends that the current 'headline advice' based on a single stock assumption should continue.
5. The advice sheet should give no reference to components within the Northeast Atlantic mackerel stock.

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Second Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC2; Chairs: Richard Nash & Florian Berg), Copenhagen, Denmark, 19-23 June 2023

Stock identification plays an important role in the assessment of Atlantic herring (*Clupea harengus*). Several morphological/traditional methods have been applied in the past to split catches (both within survey and commercial samples) and to identify herring stocks. However, in recent years, advances in genomics have provided a robust and precise method to genetically identify herring stock (Han *et al.*, 2020; Farrell *et al.*, 2022; Bekkevold *et al.*, 2023). WKSIDAC2 reviewed the current status of genetic stock identification for herring and outstanding issues affecting identification accuracy/success. The genetic methods using single nucleotide polymorphism (SNP) as genetic markers to identify herring population are considered appropriate. Depending on the region of interest, different sets of markers are used to identify herring populations. The differences in the set of markers have only minor influence on the stock identification and can be negligible. However, it is recommended to choose sets of markers which will allow a direct comparison between institutes. Furthermore, the review concluded that 26 different herring spawning populations can be currently identified using genetic methods in the northeastern Atlantic. However, future genetic studies may increase the number of identified populations and also provide a greater resolution for the spatial distributions. For example, using the current known genetic markers, we are not able to genetically differentiate between Icelandic summer spawners, Faroese autumn spawners, and Norwegian autumn spawners. These three potential populations are currently combined as a single genetic unit. Future work, such as whole genome sequencing, is recommended to investigate this issue in more detail. In addition, the 26 identified genetic populations cannot directly and uniquely be mapped to any one particular stock (management unit). Baseline samples of these 26 populations have been analyzed based on different sets of markers. Therefore, the baseline information cannot be shared directly between institutes. Again, it is recommended that a common method for analyzing baseline samples, as well as storing the genotypes in an open and public database is agreed. During WKSIDAC2, a general description of prerequisites for the implementation of stock identification of herring was discussed and several options have been presented. A series of presentations provide potential solutions on how to implement stock identification in current stock assessment models or during survey estimates. However, analyses of the optimal baseline requirements for stock assessment purposes, both for specific surveys as well as commercial catches, is to be the subject of a new workshop (WKSIDAC3), proposed for 2024. The aim of the workshop is to establish a simulation framework for estimating stock compositions based on genetics 1) to investigate differences between random or stratified sampling, and 2) to investigate inter-haul variability in surveys.

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Annex 5: Responses to requests from ICES working groups (ToR b)

Stock definition of Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)

Background

The working document (WD) "Review and update of the stock definition of Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)" by Sven Stötera and Holger Haslob (see Annex 6) examines dab stock identification in the North Sea, Skagerrak, Kattegat and the Baltic Sea. Current ICES advice is provided for dab27.3a4 (North Sea, Skagerrak and Kattegat) and dab 27.22-32 (encompasses the Baltic Sea). The authors have provided spatio-temporal distribution (survey and fishery data) and biological (maturity and length-weight data) evidence to suggest that dab from the Kattegat area (27.3a.21) should be included within the ICES dab 27.22-32 and not ICES dab27.3a4.

SIMWG review

The spatio-temporal distribution data provided originates from two international surveys: The International Bottom Trawl Survey (IBTS), which covers the North Sea (Subarea 4) and the transition areas of Skagerrak (3a.20) and Kattegat (3a.21) and is conducted twice per year in quarter 1 and 3, and the Baltic International Trawl Survey (BITS) which covers the entire Baltic Sea, as well as Kattegat (3a.21) in Q1 and Q4. Figures 5, 6, 7 and 8 within the WD show the CPUE's of different trawls and different quarters during selected time periods with the authors suggesting that the intensity of CPUE's highlight linkages between Baltic Sea and Kattegat dab. In general, the CPUE's reveal a continuous catch of dab from the Baltic Sea into Kattegat, particularly 27.3c.22 and 27.3.b.23 (see Figures 5,6 and 7 within WD for example). However, there is also CPUE evidence linking Kattegat, Skagerrak and the North Sea (for example, see Fig. 8 Q3 2017). It is not clear from the working document why certain years have been selected for analysis and not others. For example, Figure 5 (Q1, BITS) shows CPUE's from 2007 to 2022 at 5-year intervals, while Figure 7 (Q4, IBTS) is 9/10 year intervals from 1994 to 2022.

The next piece of evidence is averaged landings data from 2019 until 2022. In general, the main landings (tonnes) show the highest amount of dab landings occurring in 27.3.c.22 (Belt Sea, part of the Baltic Sea dab stock) with few landings being registered within the Kattegat region (4-6 tonnes). The authors point out that there is potential misreporting of dab landing data, either dab being caught and landed in different areas or dab being assigned as 'mixed flatfish' limiting the inferences that can be made regarding stock identification.

The final evidence provided is life history parameters, including maturity, growth, and length/weight relationships (see Table 1 and Figure 10). As sampling on the IBTS does not provide age reading, North Sea dab maturity at age data was replaced by analyses of southern North Sea dab (Rijnsdorp *et al.*, 1992). Table 1 shows that dab in the southern North Sea mature at a much older age (2–3 years) compared to Kattegat (1 year) and Baltic Sea (1 year). There are also differences in the length at maturity among female dab within the North Sea (10 cm) and Kattegat (12 cm), while female Baltic Sea dab appear to mature at the same length to Kattegat conspecifics (see Table 1). Finally, Figure 10 shows the length-weight relationship among Baltic Sea, Kattegat and North Sea dab from the Q1 surveys (IBTS and BITS) from 2022. According to the figure, Baltic and Kattegat dab have a similar length-weight relationship compared to North Sea dab.

SIMWG conclusions

This WD provides initial stock unit evidence utilising spatio-temporal trends and life history data of dab within the North Sea, Skagerrak, Kattegat and Baltic Sea. Overall, the data shows linkages among dab CPUE's within Kattegat and the Baltic Sea, but also Skagerrak and the North Sea. Despite an apparent large temporal data set to work with, the figures offer a mis-match of comparable Q1, Q3 and Q4 years without any explanation. Perhaps a more robust and informative visual assessment of CPUE's would have included the same years for each quarter to accurately assess survey trends over time. A single figure for each quarter, containing an averaged total CPUE of all available data would have also been informative. The biological data (e.g., maturity and length/weight relationships) again highlights similarities between Kattegat and Baltic Sea dab and dissimilarities among Kattegat and North Sea dab, but this is only from a single time point with no statistical tests to investigate the significance of these relationships. With the temporal coverage that the IBTS and BITS data provides, a time-series of life history parameters could be statistically examined to further assess the position of Kattegat dab within either the North Sea or Baltic dab.

Unfortunately, there is not enough evidence provided within this WD to place Kattegat dab solely within the Baltic Sea stock (dab 27.22-32). As a data-limited species, more work is required to understand key life history traits of this species. For example, where do they spawn? Do they exhibit spawning or feeding site fidelity? Do they exhibit intra- or inter-season migration patterns, and if so how far? Studies utilising tagging, otolith microchemistry and/or genetics could investigate the biological (genetics) and geographical (otolith microchemistry/ tagging) linkages of dab across the relevant regions and would lead to a more accurate assessment of biologically relevant stock units.

Although there is a drive within ICES to align stocks to biological units, there must be a threshold of evidence to do so. Without this, there is a growing risk of delineating stocks without the necessary assessment data to ensure sustainability. This point has been discussed in recent ICES Stock Identification Benchmarks for Sea bass (not yet published), North Sea and west of Scotland Cod (ICES, 2020, 2022).

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Stock definition of flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)

Background

Current ICES advice is provided for fle.27.3a4 (North Sea, Skagerrak and Kattegat) and fle.27.22-23 (southern Baltic Sea). The working document (WD) "Review and update of the stock definition of flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)" by Sven Stötera and Holger Haslob (see Annex 6) reviews the stock structure of flounder in the western Baltic and North Sea. The authors have provided spatio-temporal distribution (survey and fishery data), biological (maturity and length-weight data) and genetic evidence to suggest that flounder from the Kattegat area (27.3a.21) should be included within the southern Baltic Sea (fle 27.22-23) and not the North Sea (fle27.3a4).

SIMWG review

The spatio-temporal distribution data provided originates from two international surveys: The International Bottom Trawl Survey (IBTS) which covers the North Sea (Subarea 4) and the transition areas of Skagerrak (3a.20) and Kattegat (3a.21) and is conducted twice per year in quarter 1 and 3, and the Baltic International Trawl Survey (BITS) which covers the entire Baltic Sea, as well as Kattegat (3a.21) in Q1 and Q4. Figures 5-9 within the WD show the CPUE's of different trawls and different quarters during selected time periods with the authors suggesting that the intensity of CPUE's highlight linkages between Baltic Sea and Kattegat flounder while showing low connection between North Sea and Kattegat. It is evident that highest flounder concentration is in the adjacent ICES Subdivision (SD) 24 and when this is removed from the analyses highest concentration is in southern Kattegat, sometimes hotspots are also in Belt Seas and Öresund. Much less flounder is caught in Skagerrak. It is not clear from the WD why certain years have been selected for analysis and not others. It is also not clear if white areas of the map designates no flounder or no data.

The fishing pattern revealed by averaged landings data from 2019 until 2022 show that the major part of the landings in Kattegat is taken close the border to SD 22 & SD 23 while majority of landings in Skagerrak is in the western part emphasizing the conclusions from the trawl surveys that there is little connection between Norths Sea-Skagerrak and Kattegat while there is evidence for connection between Kattegat and southern Baltic Sea. It is also mentioned in the background data that the > 90 % of flounder landings in the fle27.3a4 is from area 4, i.e less than 10% is from the Skagerrak/Kattegat area.

Analyses of life-history parameters from the BITS 2022 (length at maturity, growth, and L_{inf}) show no difference between samples from North Sea, Kattegat and Baltic Sea and gives no guidance for stock separation. It is mentioned that samples from the Kattegat are few and therefore this conclusion is weak.

The authors present genetic evidence that there are two types, or even species, of flounder in the Baltic Sea: pelagic spawning European flounder (*Plathichthys flesus*) and demersal spawning Baltic Sea flounder (*Platichthys solemdal*) (cf. Momigliano 2017). From the references provided, and if in fact there are two species of flounder, those present within North Sea, Skagerrak, Kattegat and western Baltic Sea belong to *P. flesus* (Momigliano *et al.*, 2017).

The authors argue that none of the genetic studies so far conducted show any differentiation between Kattegat and Belt Sea, hence supporting the conclusion of a large homogenous flounder population in the Kattegat and western Baltic Sea (Hemmer-Hansen *et al.*, 2007; Florin and Höglund, 2008; Momigliano *et al.*, 2017; Jokinen *et al.*, 2019; Kuciński *et al.*, 2023). However, Momigliano *et al.* (2017) found evidence supporting 3 populations in this region, with a putative 'North Sea' population emerging from Skagerrak, Kattegat and Sound samples. Using allele frequency data this population could be distinguished from flounder from the eastern Baltic region and at the very least highlights some evidence of biological connectivity between Skagerrak and Kattegat. Additionally, Florin and Hoglund (2008) found no significant genetic differentiation between ICES division 3a20 flounder compared to those collected from ICES subdivisions 23 and 24. Unfortunately, none of the genetic studies mentioned within the WD contained robust enough experimental designs to make accurate inferences on the current or newly proposed stock identification boundaries for flounder. For example, not a single study referenced collected genetic samples from ICES division 4a-b to compare them to flounder from Skagerrak, Kattegat or Baltic Sea.

SIMWG conclusions

This WD provides a review and initial stock unit evidence utilising spatio-temporal trends, life history data and genetics of flounder within the North Sea, Skagerrak, Kattegat and western Baltic Sea. Overall, the data shows linkages among flounder CPUE’s within Kattegat and the western Baltic Sea while at the same time show low connection between Kattegat and North Sea (via Skagerrak).

The biological data (e.g., maturity and growth) and genetic data again highlights similarities between Kattegat and Western Baltic Sea. However, the biological and genetic data presented do not suggest a separation between the suggested unit (fle 21-23) and neither Skagerrak/North Sea nor southern Baltic Sea.

This WD gives some evidence that from spatio-temporal distribution and exploitation pattern, Kattegat flounder is better lumped with western Baltic Sea, analogous to plaice and sole. However, from a biological viewpoint, there is neither evidence supporting current stock unit nor evidence for the proposed stock structure.

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Annex 6: Working Documents

Review and update of the stock definition of Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)

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Table of Content

Summary

European dab is a marine flatfish species that usually inhabits the deeper parts of sea basins. Presently, dab in the Kattegat is considered a part of the North Sea stock. The adjacent Baltic Sea dab stock covers the areas of the Belt Sea and teSound (SD 22-23), Arkona Sea (SD24) and parts of the Bornholm Sea (SD25). Only occasional catches of dab occur in the more eastern parts of the Baltic Sea.

We provide evidence that the management areas may require a change. Distribution maps from scientific surveys strongly suggest that there is no spatio-temporal separation between dab in the Kattegat and the western Baltic (Belt Sea and the Sound) and that dab in the Kattegat have negligible links to dab in the North Sea. The Danish Straits are highly dynamic connecting channels between the southern Kattegat and Kiel and Mecklenburg Bight south of Denmark that make a stock separation between the Belt Sea and Kattegat highly unlikely. No distinct differences were found in biological life history parameters (i.e. maturity and growth) between dab from SD 21 and SDs 22-23, while dab in the North Sea displays a different growth and maturation pattern than dab in SD 21 and SD22-32.

Thus, a stock comprising dab from the management areas SD 21-32 would realistically reflect the dab population in the Baltic Sea.

Proposal

We propose to update the stock definition and boundaries of the dab stocks in the North Sea and Baltic Sea by removing Kattegat (Area 9, Subdivision SD 21) from the North Sea stock and adding it to the dab stock of the Baltic Sea to realistically reflect the dab population in the Baltic Sea. Similar analyses already resulted in the inclusion of Kattegat to the western Baltic plaice stock (ple.27.21-23) and of Kattegat and Skagerrak to the Baltic sole stock (sol.27.20-24), making a similar scenario for other flatfishes very likely.

The updated dab stocks *„dab.27.21-32"* (Baltic Sea) and *„dab.27.3an4*" (North Sea) could be part of the benchmark "WKMSYSPICT3" by ICES in late 2023/early 2024 where the new stock ID and the respective changes in data can be implemented for stock assessment and stock status evaluation.

Current status

North Sea

Dab and flounder in the North Sea have been assessed under a shared TAC until 2017. Since 2018, dab in the North Sea is assessed as one stock (*dab.27.3a4*), covering Subarea 4 (North Sea) and Division 3.a. (Skagerrak and Kattegat) and is no longer subject to a TAC. Instead, a catch advice is given as long as dab and flounder remain largely bycatch species, with the main fleets catching dab and flounder continuing to fish the target species (plaice and sole) sustainably within the F_{MSY} ranges provided by ICES. If this situation changes, or dab is no longer within safe biological limits, this advice would need to be reconsidered (ICES 2023a).

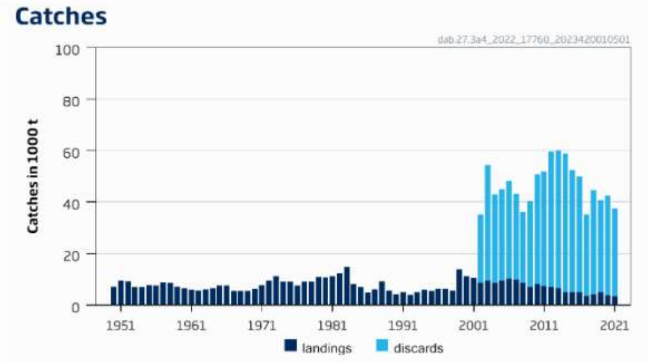


Figure 1: Official landings (1950–2001) and ICES estimates of landings and discards (2002–2021).

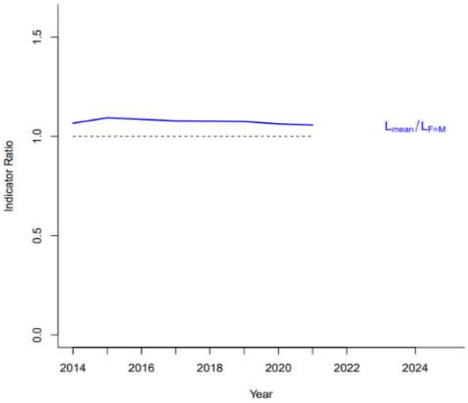


Figure 2: Index ratio L_{mean} /$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023a). The exploitation status is below the F_{MSY} proxy (dotted line) when the index ratio value is above one.

Catch advice is given for three years and was last given in 2022 (for 2023, 2024 and 2025, updated advice in May 2023). Dab is mainly a bycatch species in the mixed demersal fisheries for North Sea plaice and sole, with a high discard rate (>90% on average, included in the assessment since 2002). Division 3.a. contributes <10% of total landings.

The stock is categorized as "data limited", following the ICES framework for category 3 stocks (ICES, 2023a). The most recent advice is based on the *chr* rule to provide MSY advice (ICES, 2023b). A survey combined biomass index is used as an indicator of stock development. An additional index ratio L_{mean} /$L_{F=M}$ from the length-based indicator (LBI; ICES, 2022a) method is used for the evaluation of the exploitation status. In former years, a SPiCT assessment has been performed to evalaute the stock and give advice (ICES 2023b)

Baltic Sea

Dab in the Baltic Sea is assessed as one stock (*dab.27.22-32*) covering Divisions 3.b., 3.c. and 3.d. (ICES Subdivisions 27.3.c.22-27.3.d.32). Catch advice was given between 2016 and 2018. Since 2019, ICES has not been requested to provide advice on fishing opportunities (ICES, 2023c). Instead, a stock status update is given every three years. The last “advice” was given in 2023 for 2024, 2025 and 2026 (ICES 2023c). Dab is mainly caught in a mixed flatfish fishery and was as a bycatch species in the mixed demersal fisheries for Baltic Sea plaice and cod, with a high discard rate (>40% on average, included in the assessment since 2012).

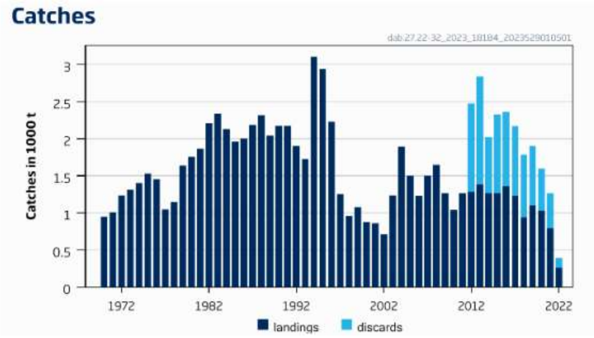


Figure 3: Official landings (1971–2001) and ICES estimates of landings and discards (2012–2022).

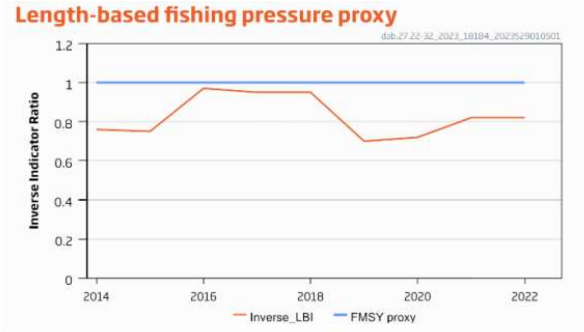


Figure 4: inversed Indicator ratio from the length-based indicator method (LBI; ICES, 2023c). The exploitation status is below the F_{MSY} proxy (dotted line) when the inverted index ratio value is lower than one.

The stock is categorized as “data limited”, following the ICES framework for category 3 stocks (ICES, 2023c). The advice is based on the *chr* rule to provide MSY advice (ICES, 2023d). A survey combined biomass index is used as an indicator of stock development. An additional index ratio (inversed indicator ratio) from the length-based indicator (LBI; ICES, 2023c) method is used for the evaluation of the exploitation status. Dab catches in the Baltic Sea are not currently regulated by a TAC.

Spatio-temporal distribution

Surveys

The data of scientific trawl surveys were used to generate distribution maps and overviews for dab in the north-eastern North Sea, Skagerrak and Kattegat, as well as the western Baltic Sea. The aim was to investigate spatio-temporal distribution patterns and changes since the start of the time series and between seasons.

The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the Transition area (Division 3.a. including the Skagerrak 3.a.20 and Kattegat 3.a.21) and is conducted two times per year in Quarter 1 and 3 (Q1, Q3). The Baltic International Trawl Survey (BITS) covering the entire Baltic Sea and Kattegat (3.a.21) and is conducted also twice per year, in Q1 and Q4. Both surveys are conducted using the same sampling protocols and data are publicly available at the International Survey database DATRAS, hosted by ICES (https://datras.ices.dk). For the maps used in this document, the datasets of both surveys were merged and combined CPUE data were calculated using the respective method of the sampling manual of WGBIFS (ICES 2023d).

Although the Baltic Sea dab stock virtually covers the entire Baltic Sea, the focal point of its distribution is the western part of the Baltic. Only very few dab are found east of the Arkona basin (SD 24) and almost no dab are found east of Bornholm (Figure 5). These areas were therefore excluded for the survey overviews.

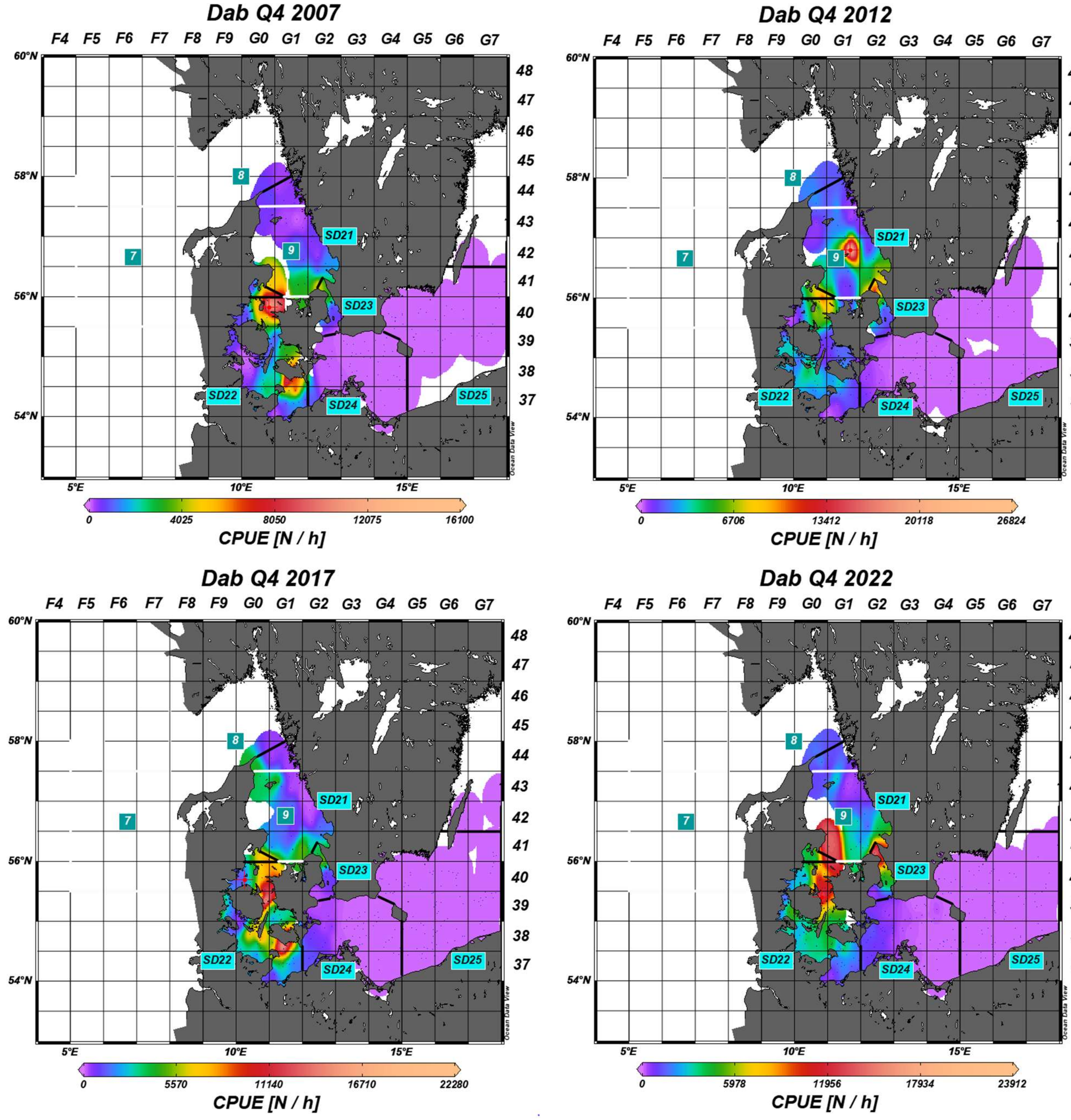
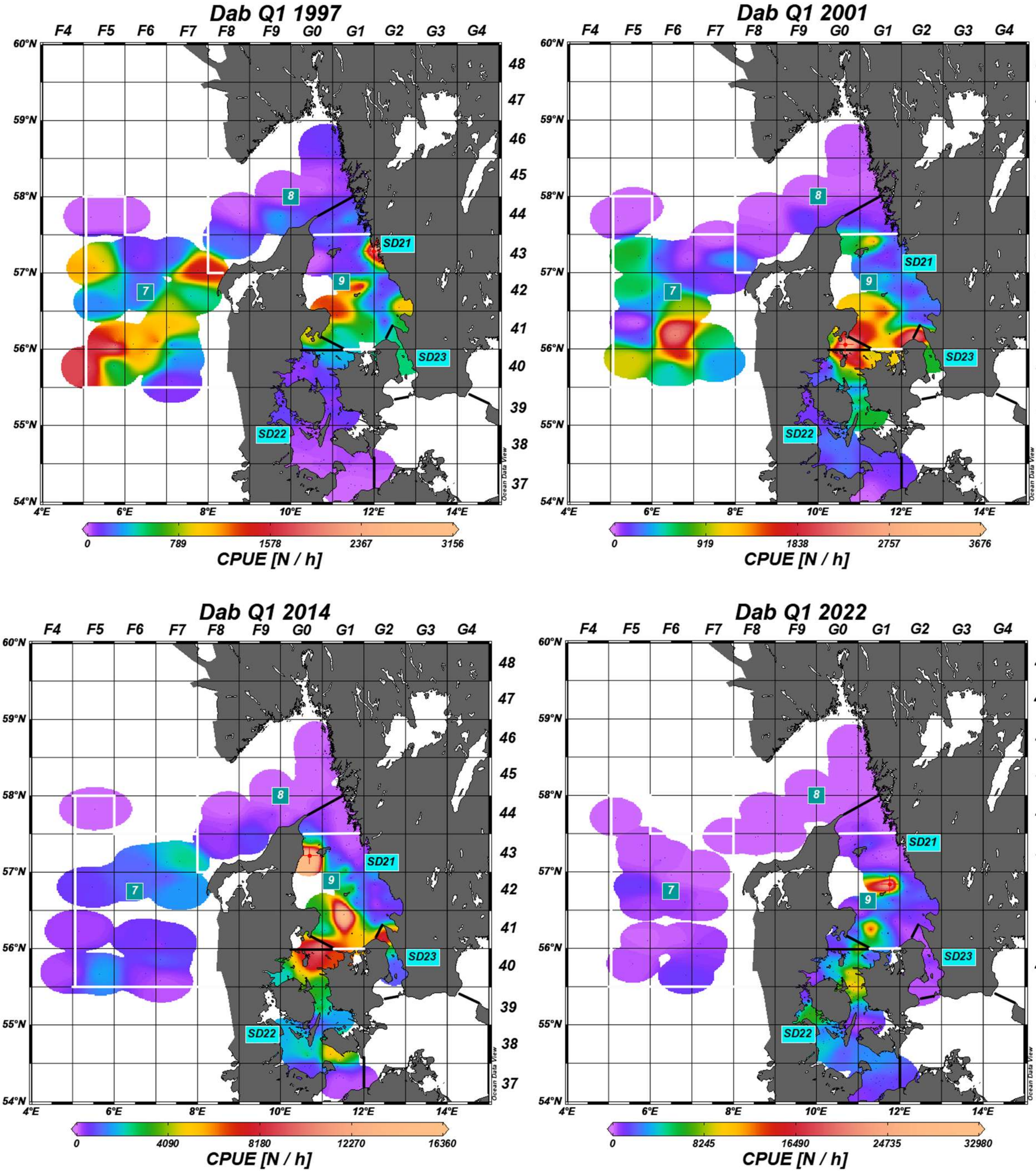


Figure 5: distribution area of dab in the Baltic Sea and Kattegat (Q1 BITS survey index) including SDs 24 and 25 (Arkona and Bornholm Sea.

Combined Survey indices of quarter 1 (Q1) surveys from 1992-2023 in IBTS areas 7, 8, and 9 and the Western Baltic Sea (SDs 22, 23) showed that the main distribution area of dab in Division 3.a. and the Baltic Sea was found in the northern part of the Belt Sea and southern Kattegat around Sjælland (Figure 6, Annex 1.1). That is, the Danish archipelago is the centre of distribution of dab in the region.

In the northern Kattegat, a smaller aggregation of dab around Læsø was present in the early 2000’s and some years in the 2010’s. In most years, a clear connectivity between all three areas (SD 21, 22 and 23) through the Danish straits was displayed, whereas the link to Skagerrak and the North Sea is negligible with a CPUE of 0 in central Skagerrak. Only very few dab were found in the region between Skagerrak and Kattegat (Figure 6, Annex 1.1).


Dab Q1 1997

Dab Q1 2001

Dab Q1 2014

Dab Q1 2022

Figure 6: Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-23, BITS)

The Q4 BITS and IBTS Survey showed a similar distribution with high accumulations of dab around Sjælland, connecting all three areas (SDs 21, 22 and 23) with each other (Figure 7, Annex 1.2). The IBTS indicated a very high CPUE of dab in the Subareas 7 and 8 until 1994. In 1995 and 1996, the spatial distribution was similar to the Q1 distribution pattern. However, IBTS has only been conducted in Q4 until 1996.

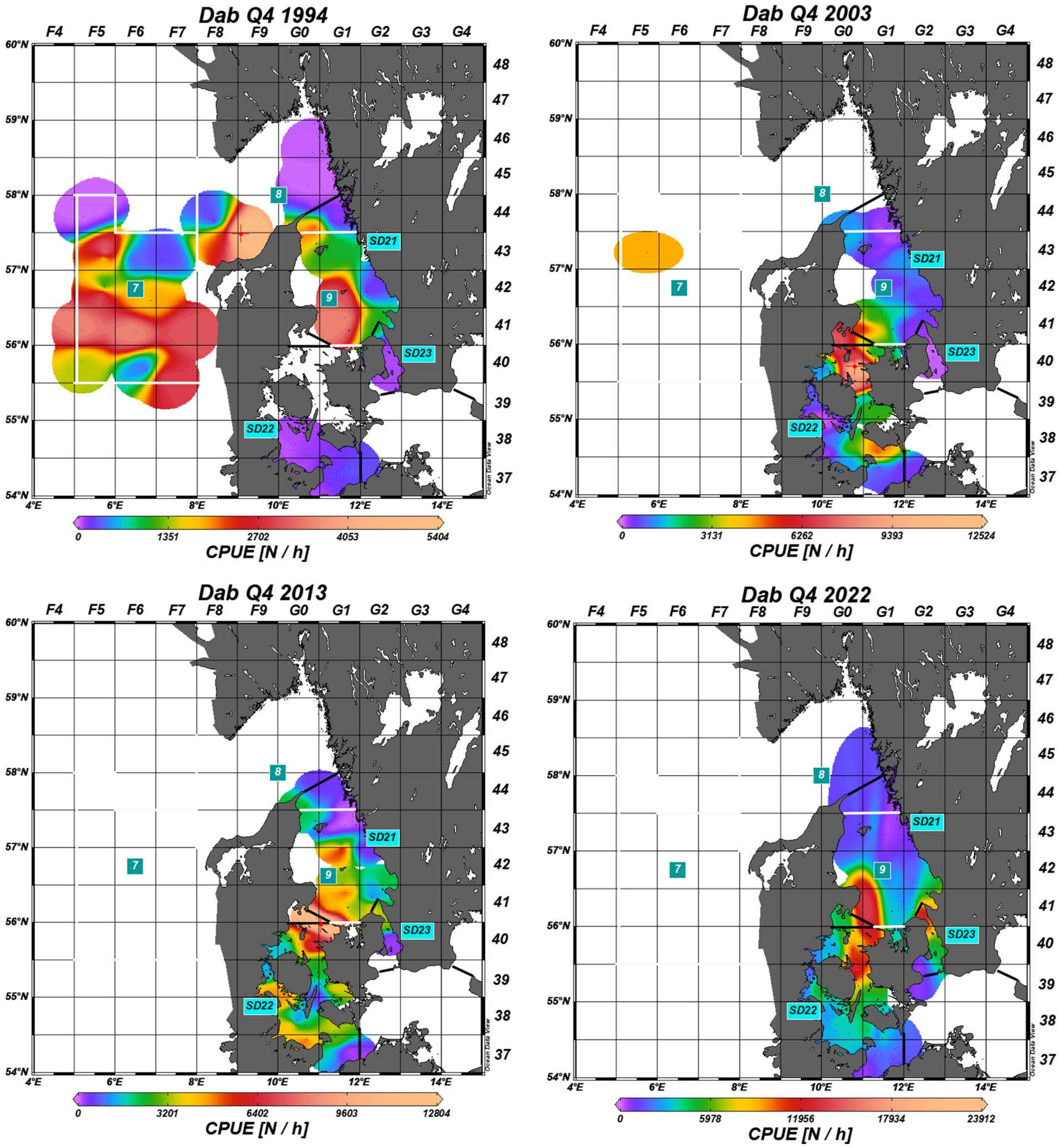


Figure 7: Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-32, BITS)

Additionally, the Q3 IBTS index of dab displayed a similar distribution pattern (Figure 8) with high abundances of dab in the North Sea (Area 7,) and southern Kattegat, exceeding the border to SD 22 and reaching into the Baltic Sea. There is connection of the high abundances in North Sea and Kattegat via the Skagerrak where the abundance of dab was as low as seen in Q1 and Q4 surveys. Only a small aggregation of dab was present along the Northern Danish coast.

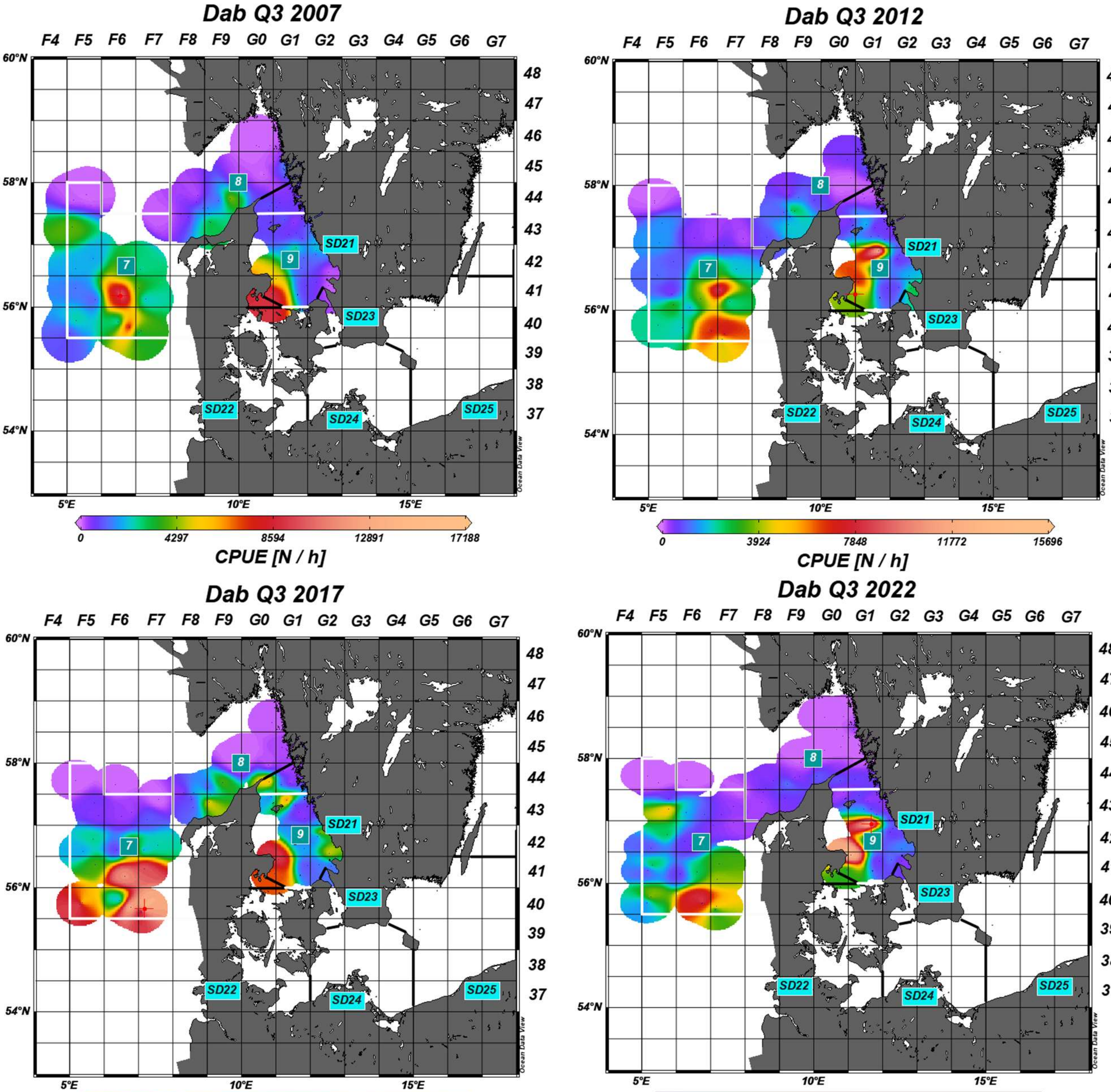


Figure 8: Survey-based CPUE distribution of dab in North Sea (Areas 7,8,9) during the Q3 IBTS survey

Fishery

The fishing pattern in Division 3.a. showed a similar species distribution as seen in the survey indices, with the major parts of dab landings originating from southern Kattegat and western Skagerrak (Figure 9, Annex 1.3). However, dab is also caught and landed close to the two major harbours in northern Denmark, Hirtshals and Skagen, where the survey index indicates low abundances.

Aside these two hotspots close to the harbours, only occasional and very low (<1t/year) landings are registered in the central part of Division 3.a., indicating a low link between the stock components, presently considered to be part of one North Sea stock.

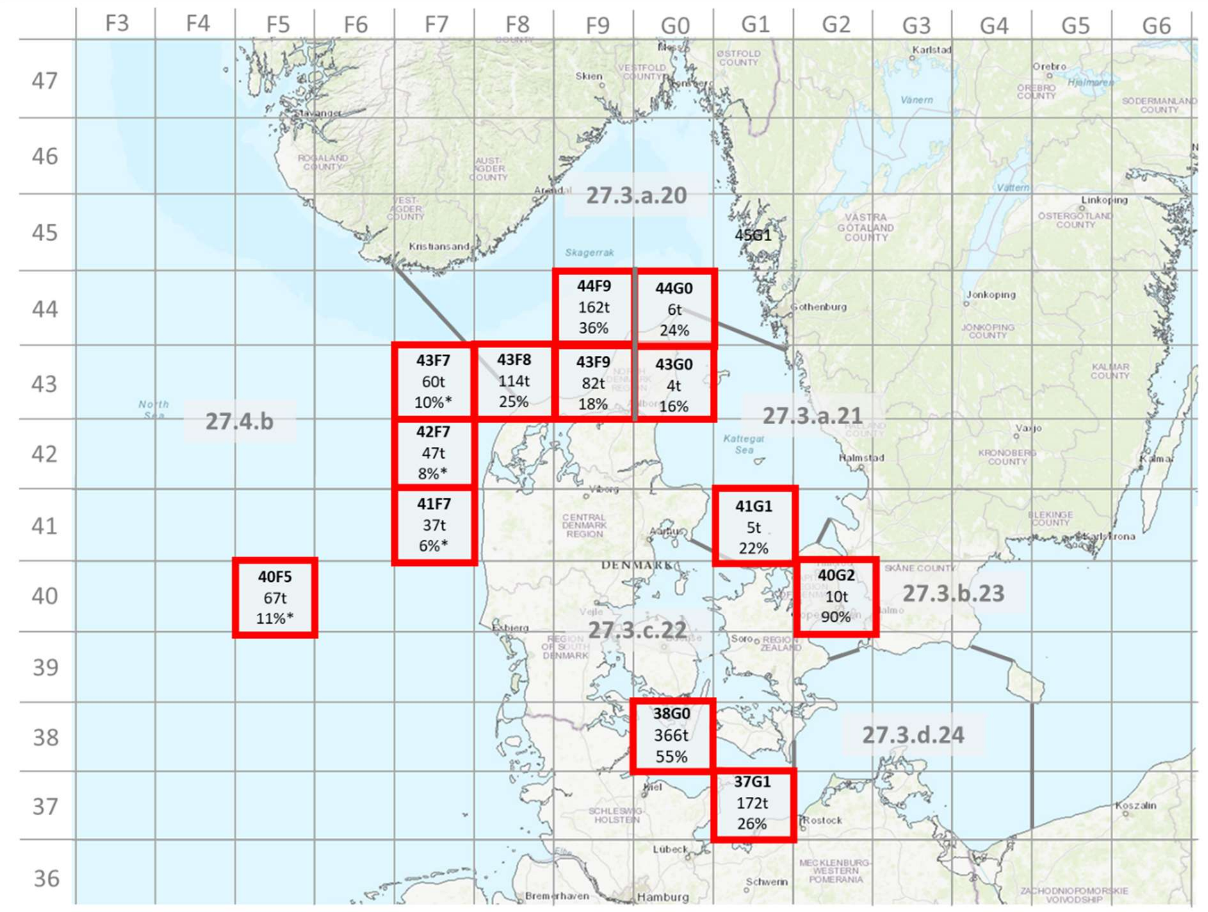


Figure 9: Landings of dab in the North Sea (27.4.b), Transition area (27.3.a) and the Baltic Sea. Averaged (2019-2022) contribution of ICES statistical rectangles that provide >75% of landings per Area.

* 2% (~10t) of Dab landings in the North Sea are not allocated to a statistical rectangle and were not used for the calculation

Generally, Kattegat has very low landings of dab (around 17-25t/year), where the species is mainly caught as bycatch in Nephrops-directed fisheries and thus usually discarded. Landings are registered mainly in the southern part of the Kattegat (ICES rectangles 41G0, 41G1 and 42G1) and between Læsø island and Skagen in northern Kattegat (44G0 and 43G8).

Dab landings in Skagerrak are higher, with around 400t/year, mostly along the northern Danish coastline of western Skagerrak, with 44F9 and 43G8 contributing most (>60%) of the landings. However, given the low abundance in the IBTS surveys in Q1, Q3 and Q4 it is likely that these dab landings were taken in the North Sea and rectangles were assigned afterwards, using the landings harbours in Skagerrak. WGNSSK also states that species misreporting has been an issue in dab fisheries in former times as it was caught as “mixed flatfish” along with flounder (ICES 2023a).

Regionally estimated discards are not available for Kattegat nor Skagerrak, as these are estimated along with Division 4 (North Sea).

The fishery on dab in the Baltic Sea is concentrated on the Belt Sea (SD 22). On average, >90% of the annual landings originate from the Belt Sea, mainly by Germany and Denmark. Average landings have been around 1000t/year, except for 2022 where a strong decline in fishing activity (caused by Western Baltic cod TAC restrictions and limited fishing opportunities) also decreased landings to around 250t (Figure 3). The major part of the landings is taken in two ICES statistical rectangles (38G0 and 37G1, Figure 9).

Life history parameters

Different life history parameters were obtained from Q1 surveys (IBTS, covering North Sea) and BITS (covering Kattegat and Baltic Sea.). The maturation is very similar between dab in Kattegat and Baltic Sea, where females mature at 12cm total length.

Dab in the North Sea displayed a slower growth than those caught in Kattegat and the Baltic (Figure 10, Table 1), the latter two being very similar in length-weight relationship.

Table 1: life history parameter of dab caught in Q1 Surveys in 2022 in the North Sea (IBTS), Kattegat (BITS) and Baltic Sea (BITS)

	North Sea	**Kattegat**	**Baltic Sea**
Maturity age	2-3 years*	1 year	1 year
(Lmat) length	10cm (F), 11cm (M)	12 cm (F), 11cm (M)	12cm (F), 11cm (M)
Growth intercept	0.004	0.0089	0.0084
slope	3.262	3.148	3.155
N	1133	125	978

** No age reading conducted on IBTS for dab; From Rijnsdorp et al. (1992) for the Southern North Sea*

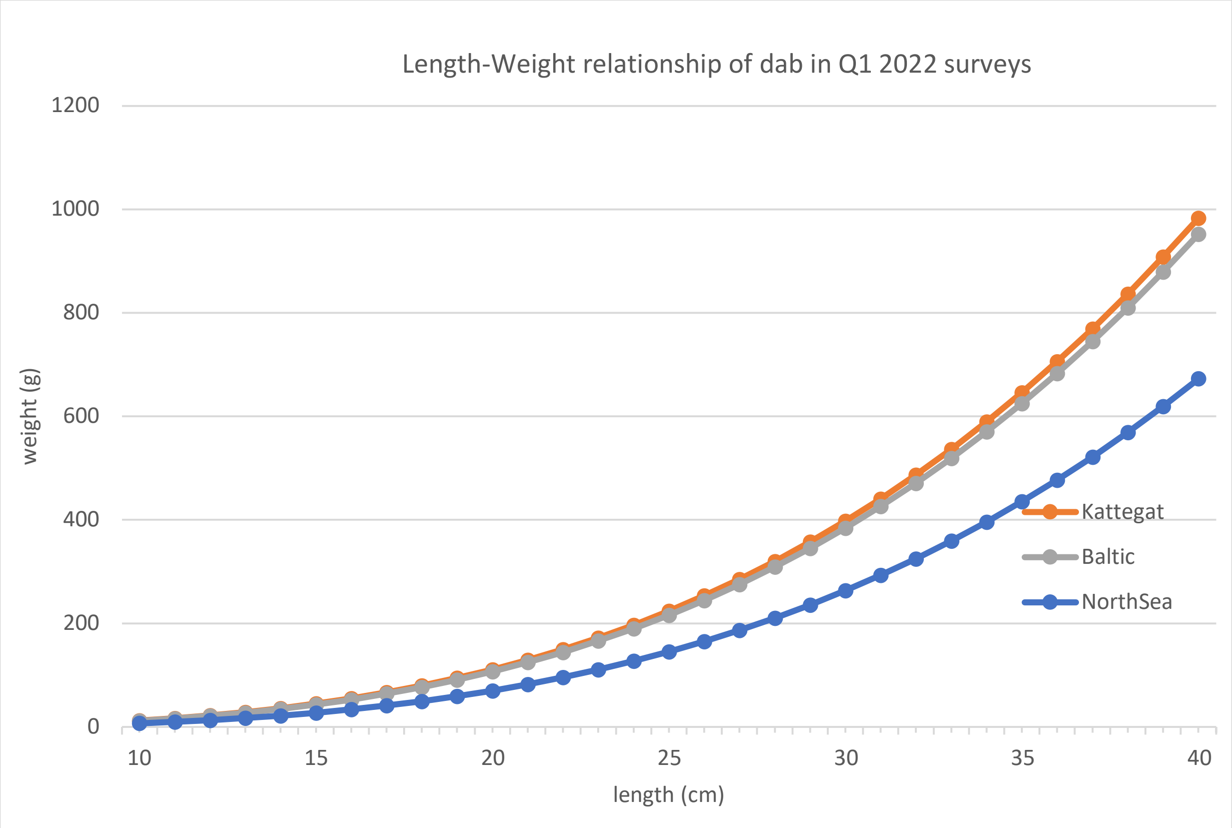


Figure 10: length-weight correlation of dab in the North Sea (blue line), Kattegat (red line) and Baltic Sea (green line). Data obtained from Q1 Surveys (IBTS and BITS)

Genetics

No genetic studies were found that investigate stock boundaries of dab in the Baltic Sea and North Sea.

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ICES (2023a). ICES Advice 2023 – dab.27.3a4 – https://doi.org/10.17895/ices.advice.22793633

ICES (2023b). Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak (WGNSSK). ICES Scientific Reports. 5:39. 1072pp.https://doi.org/10.17895/ices.pub.22643143

ICES (2023c). ICES Advice 2023 –dab.27.22-32 – https://doi.org/10.17895/ices.advice.21820503

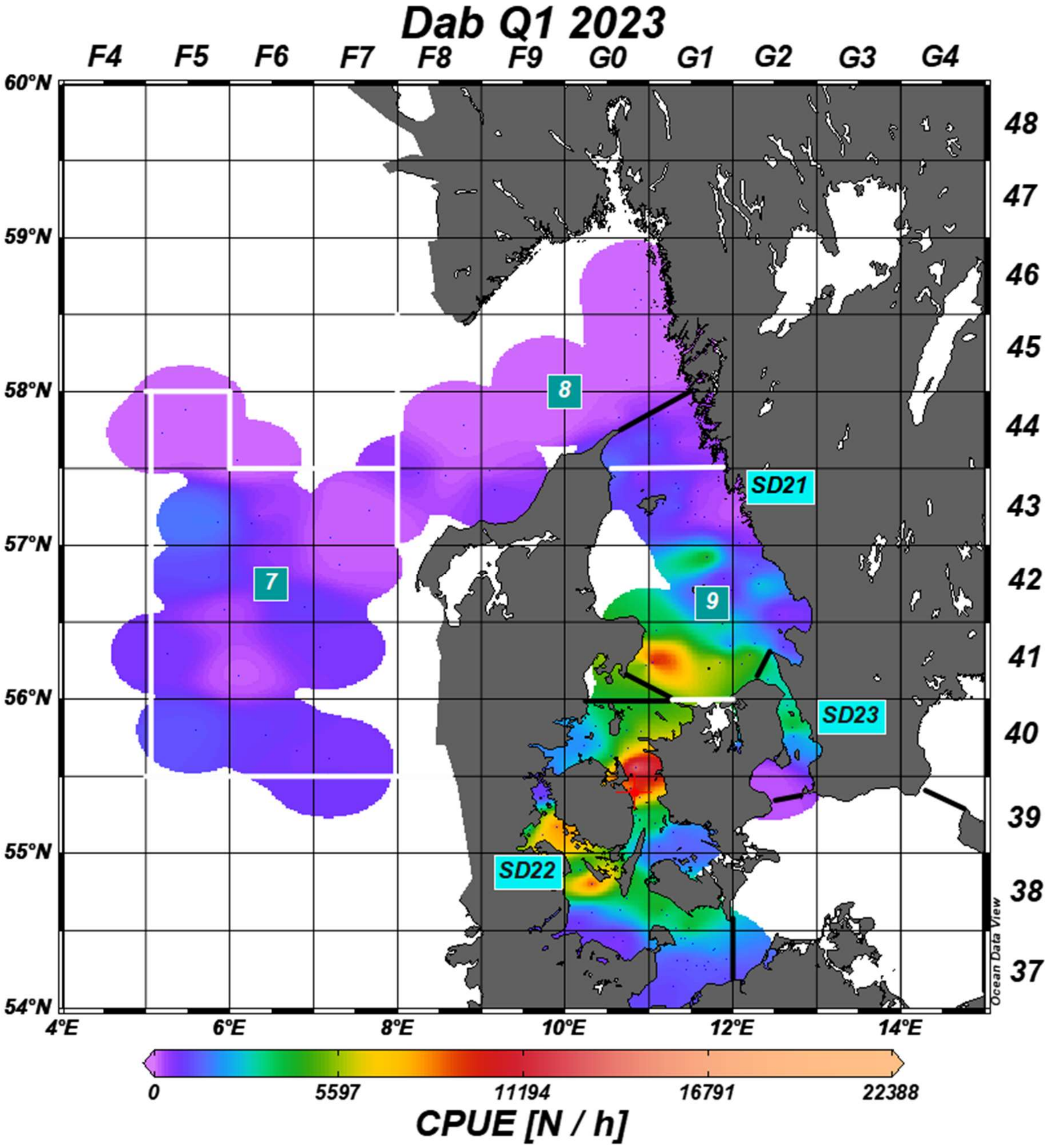
ICES (2023d). Baltic Fisheries Assessment Working Group (WGBFAS). ICES Scientific Reports. 5:58. 606 pp. https://doi.org/10.17895/ices.pub.23123768

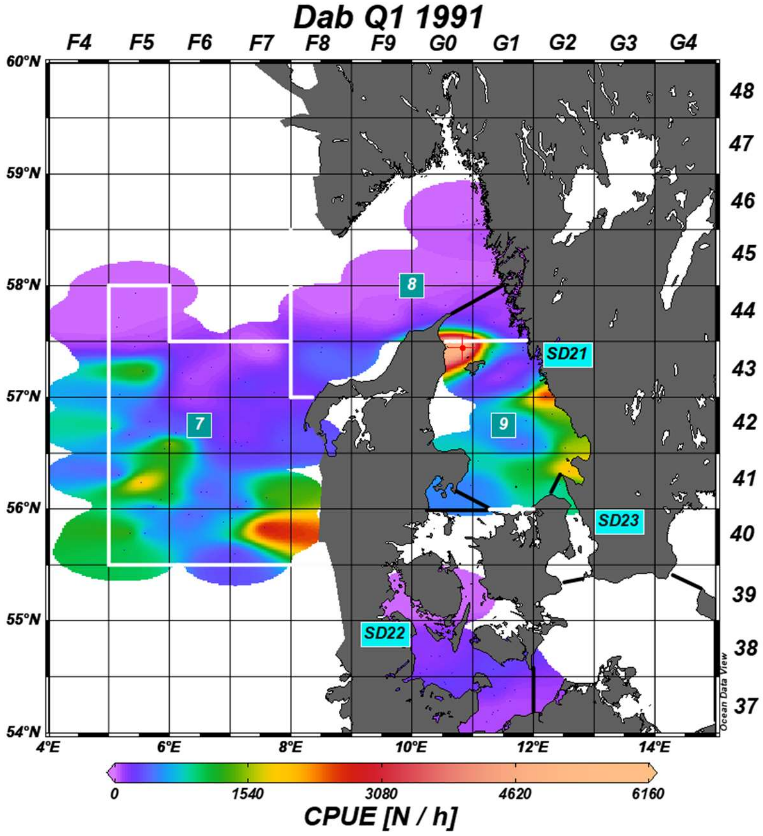
Rijnsdorp, A.D., Vethaak, A.D., van Leeuwen, P.I. (1992). Population biology of dab *Limanda limanda* in the south-eastern North Sea. Mar. Ecol. Prog. Ser. 91, 19-35

ANNEX 1.1

Combined **Quarter 1 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.




Dab Q1 1991
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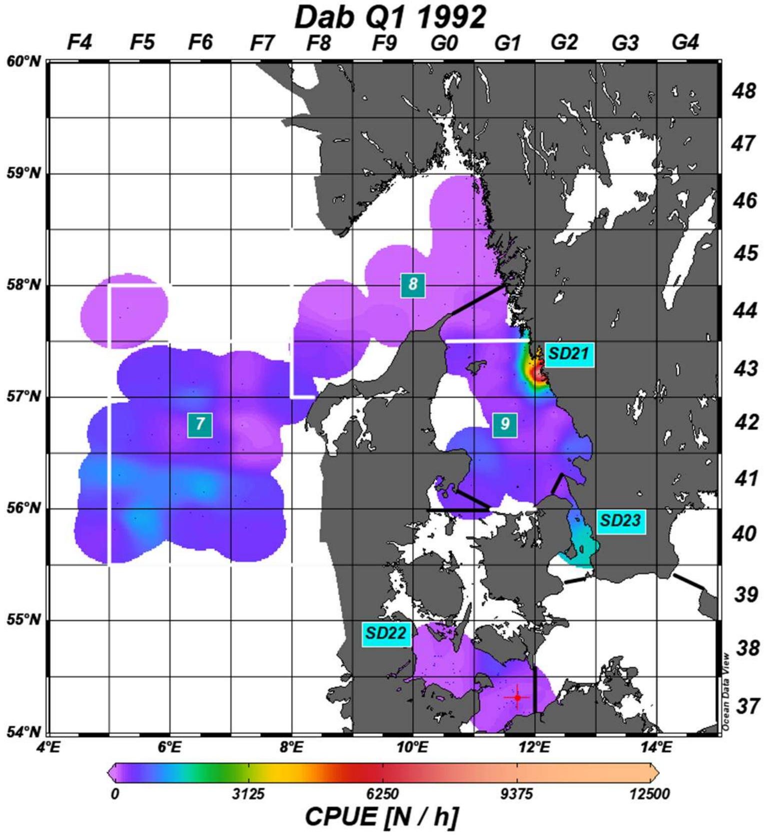
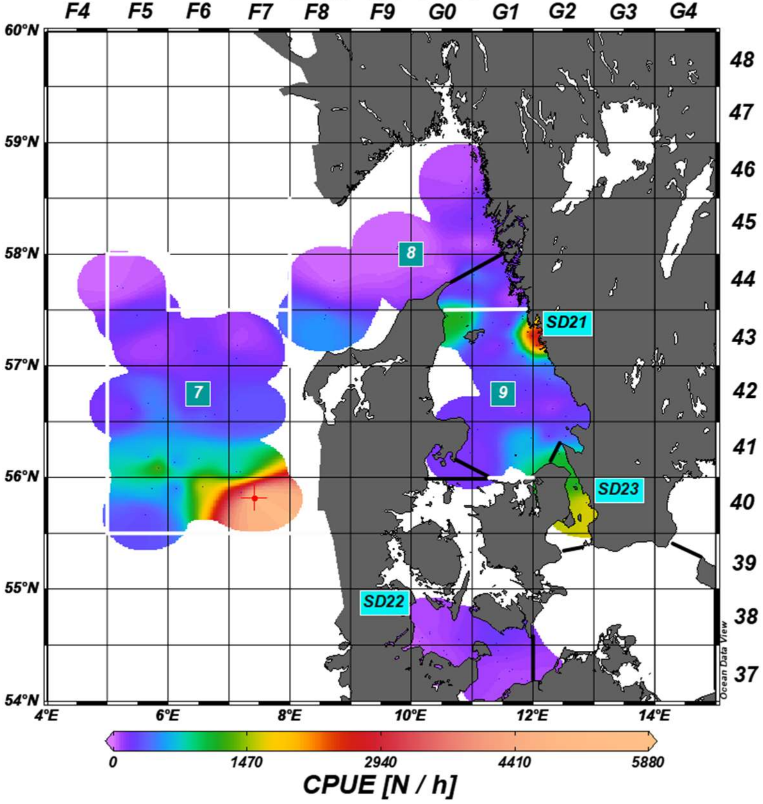
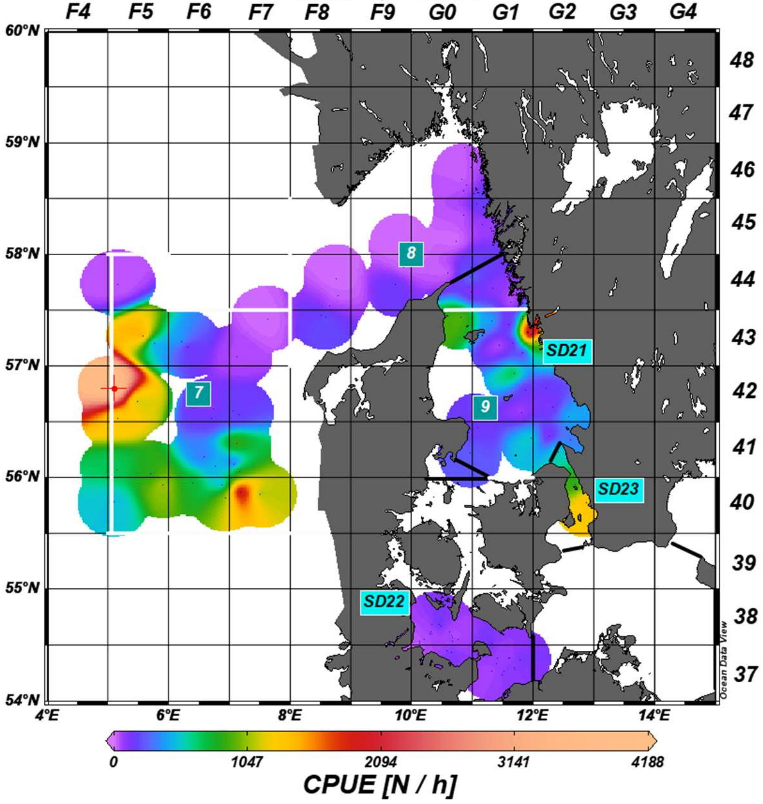
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
1540
3080
4620
6160
CPUE [N / h]


Dab Q1 1992
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
3125
6250
9375
12500
CPUE [N / h]



Dab Q1 1993



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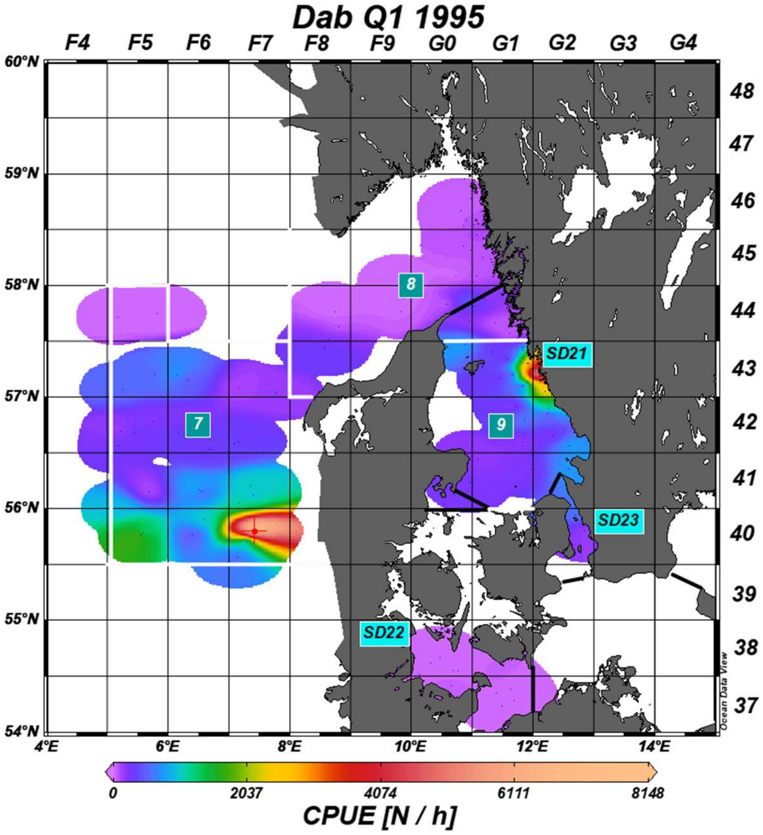
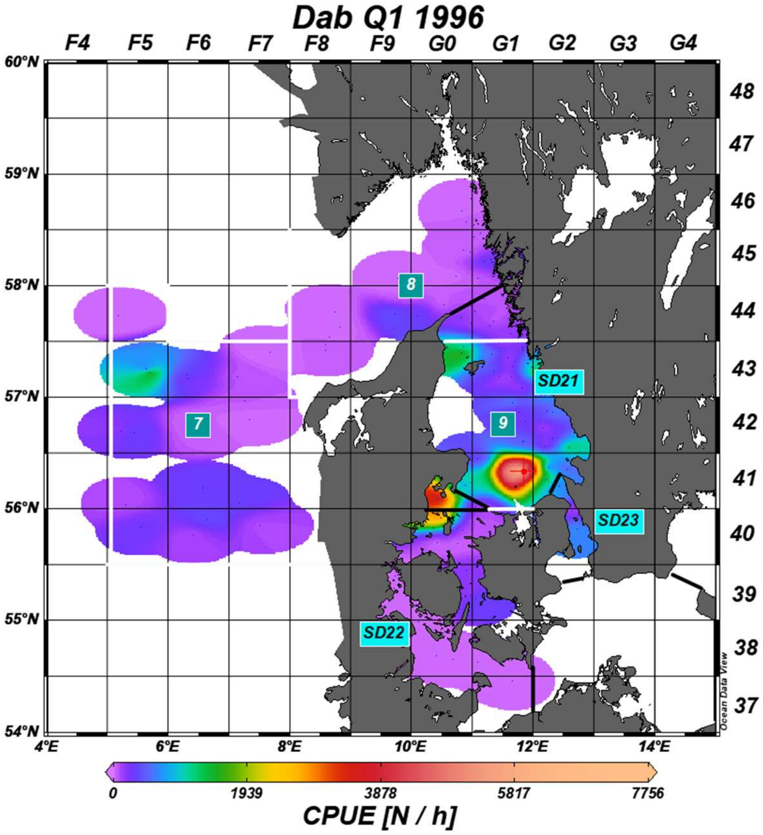
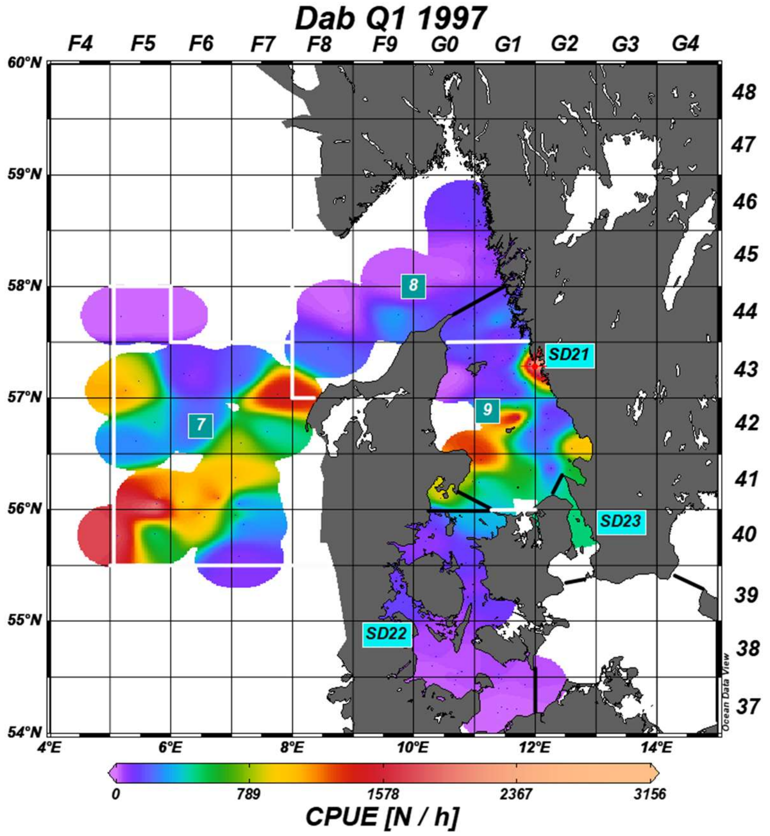
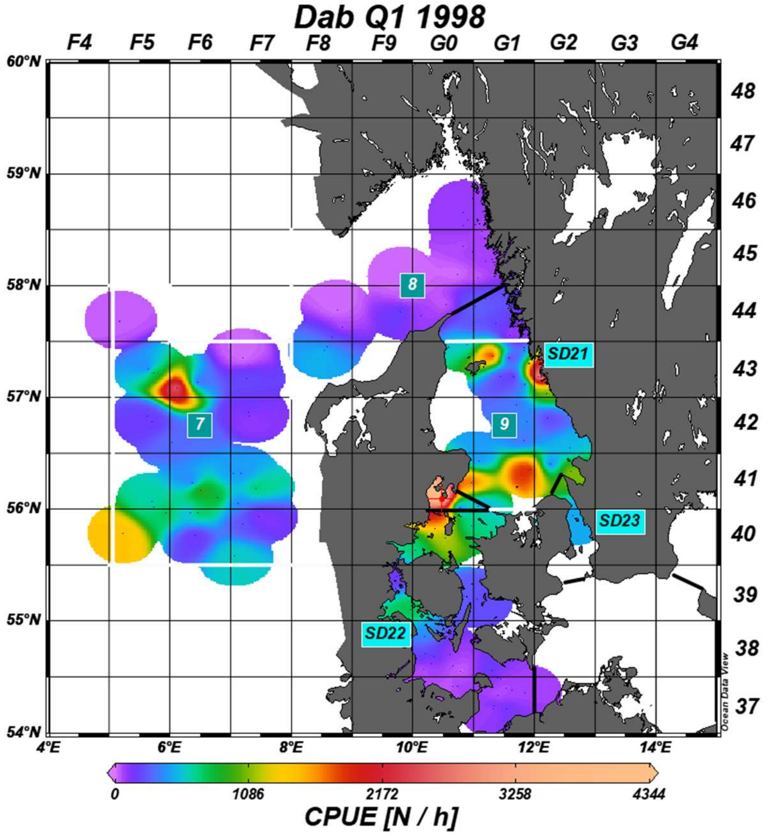
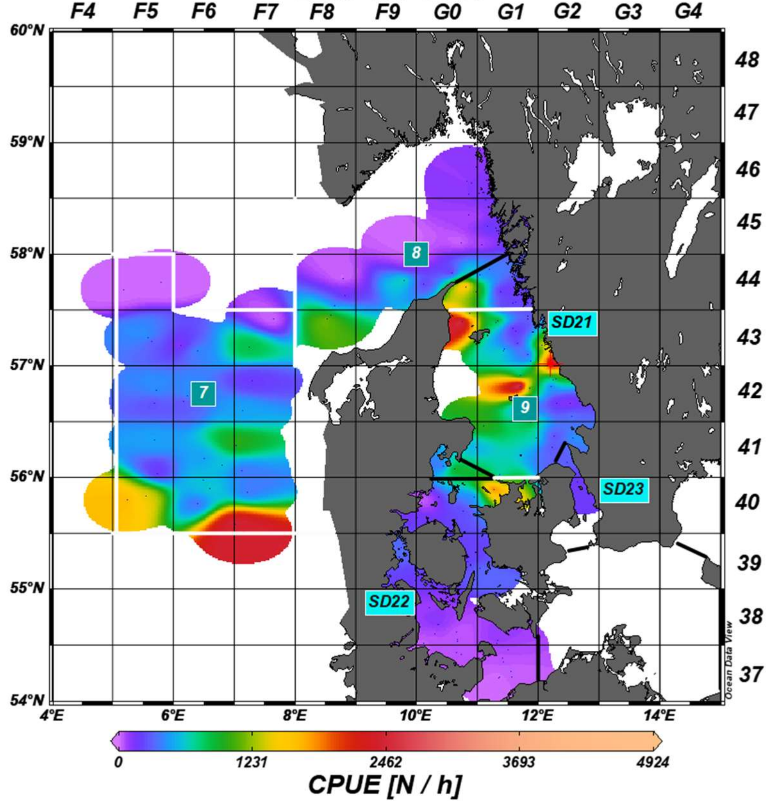

Dab Q1 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
2037
4074
6111
8148
CPUE [N / h]

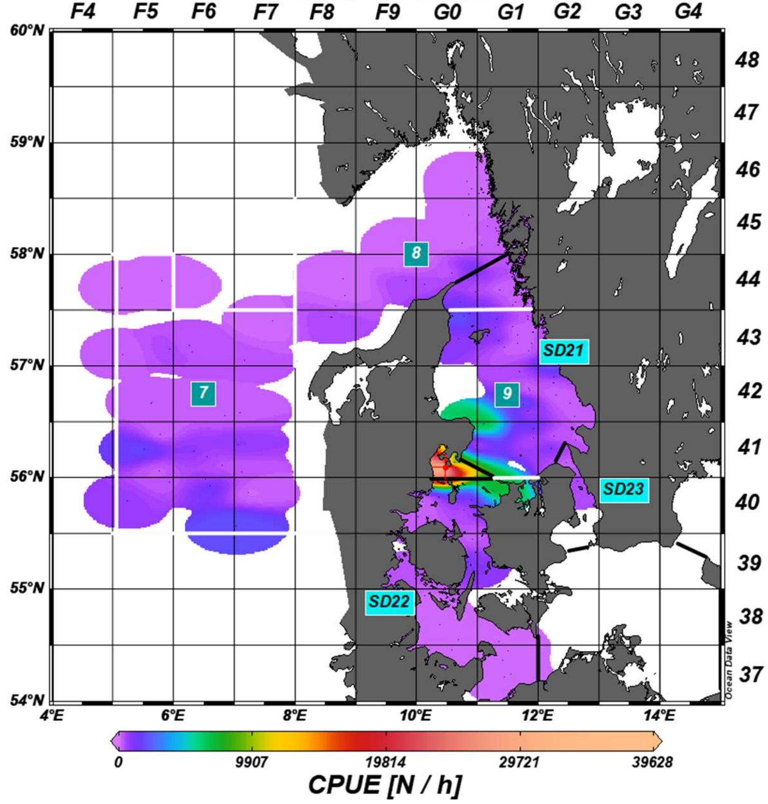

Dab Q1 1996
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
1939
3878
5817
7756
CPUE [N / h]


Dab Q1 1997
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 789 1578 2367 3156
CPUE [N / h]

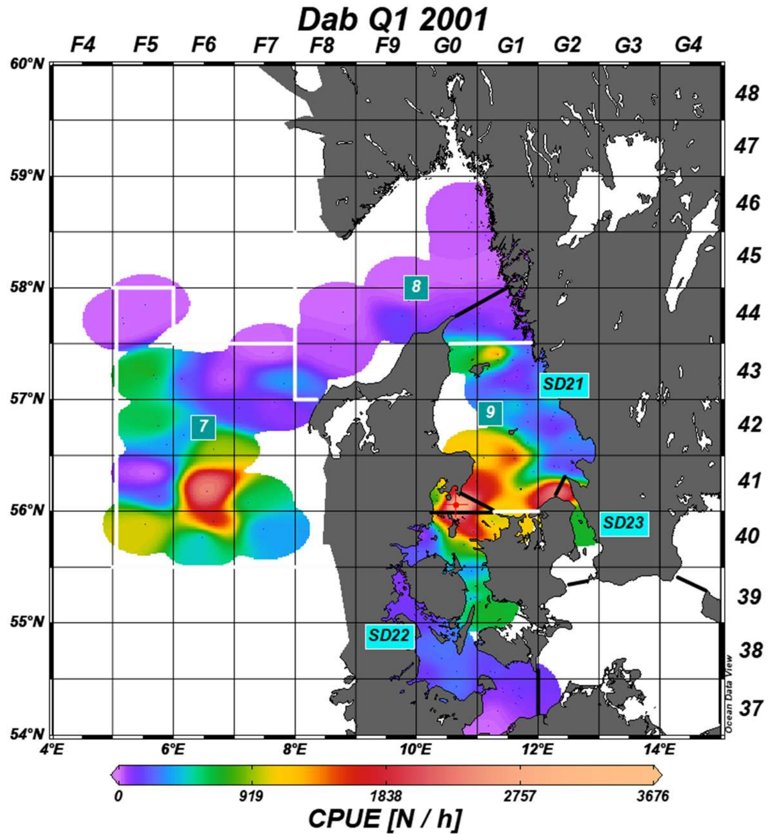

Dab Q1 1998
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 1086 2172 3258 4344
CPUE [N / h]



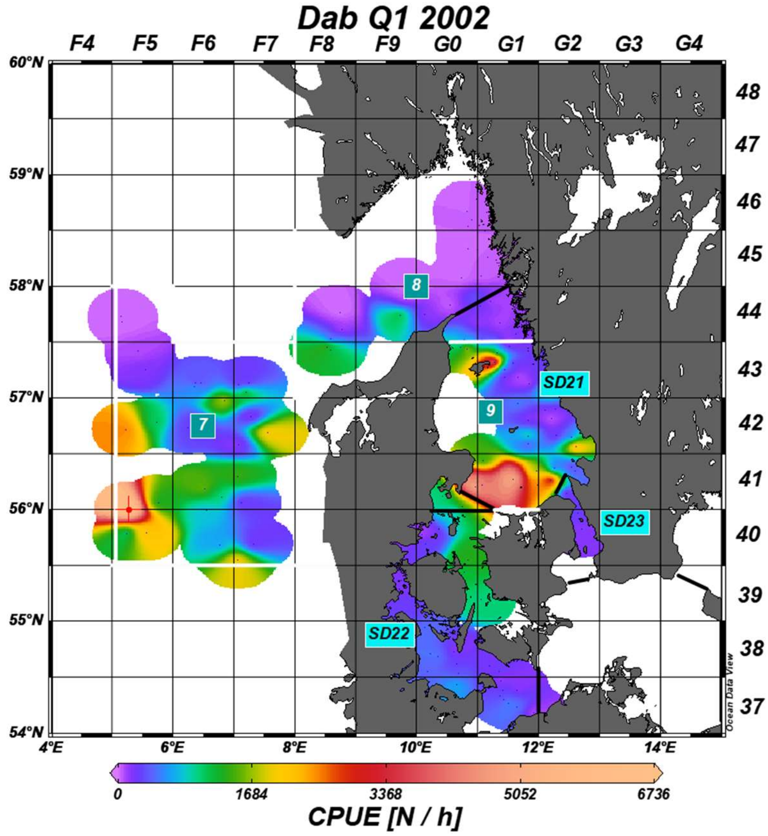
Dab Q1 1999



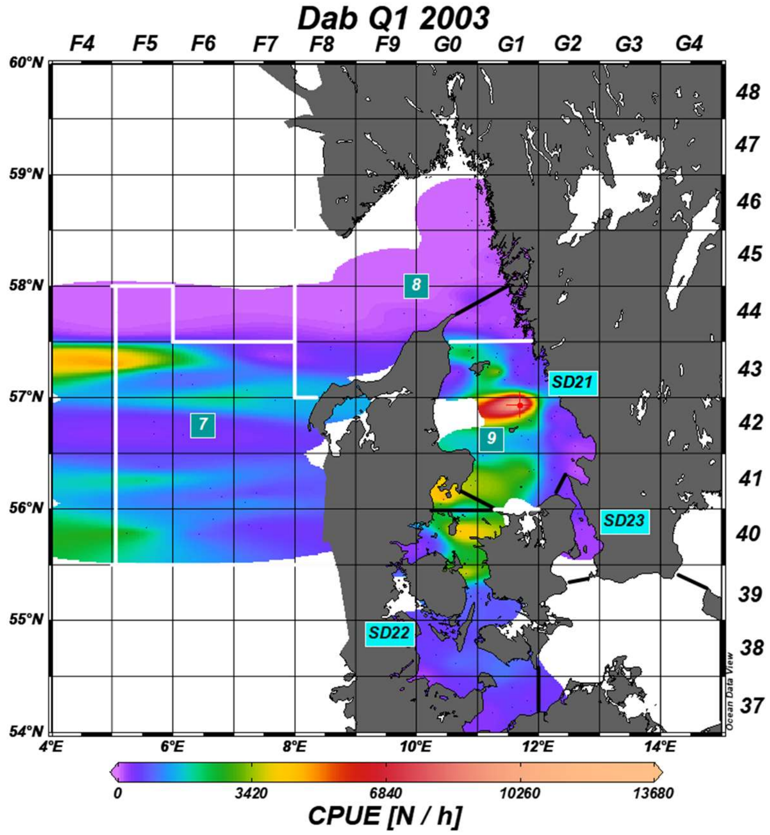
Dab Q1 2000



Dab Q1 2001



Dab Q1 2002


Dab Q1 2003
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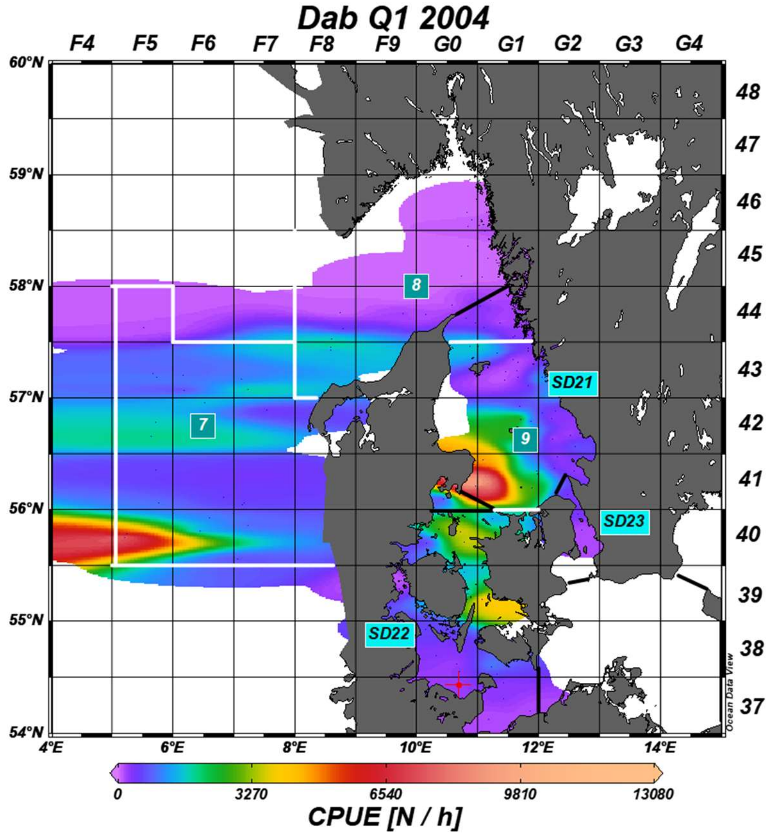
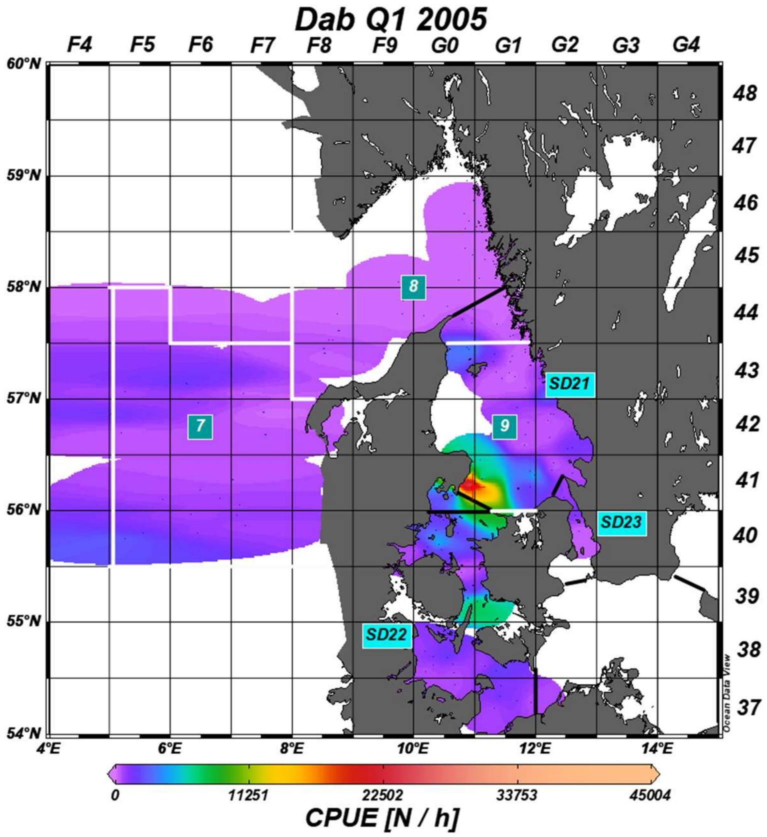
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 3420 6840 10260 13680
CPUE [N / h]


Dab Q1 2004
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0 3270 6540 9810 13080
CPUE [N / h]


Dab Q1 2005
F4
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G4
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59°N
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SD21
SD23
SD22
Ocean Data View
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11251
22502
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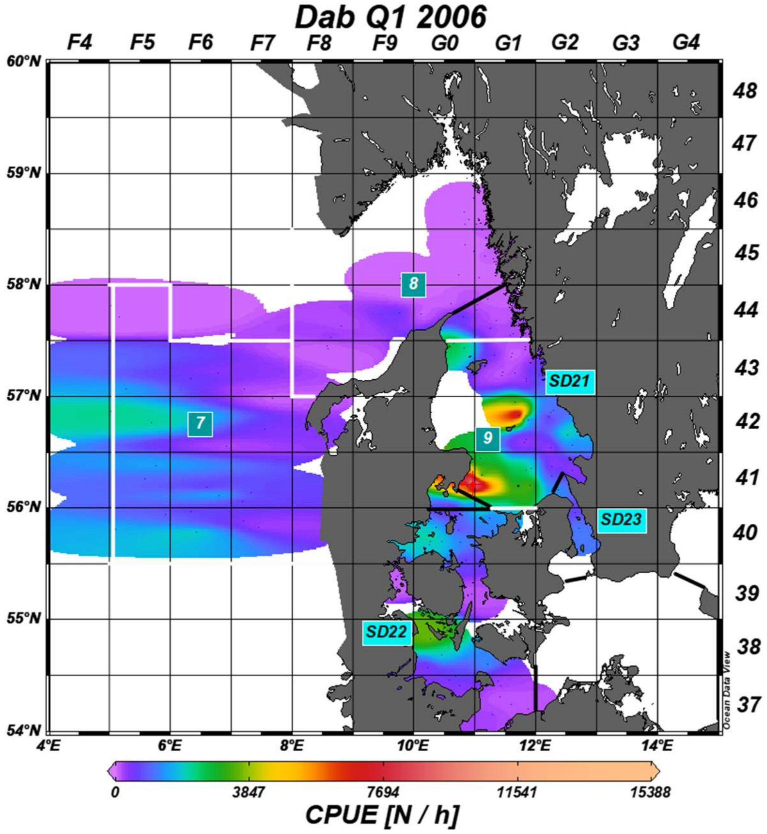
45004
CPUE [N / h]


Dab Q1 2006
F4
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60°N
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58°N
57°N
56°N
55°N
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4°E
6°E
8°E
10°E
12°E
14°E
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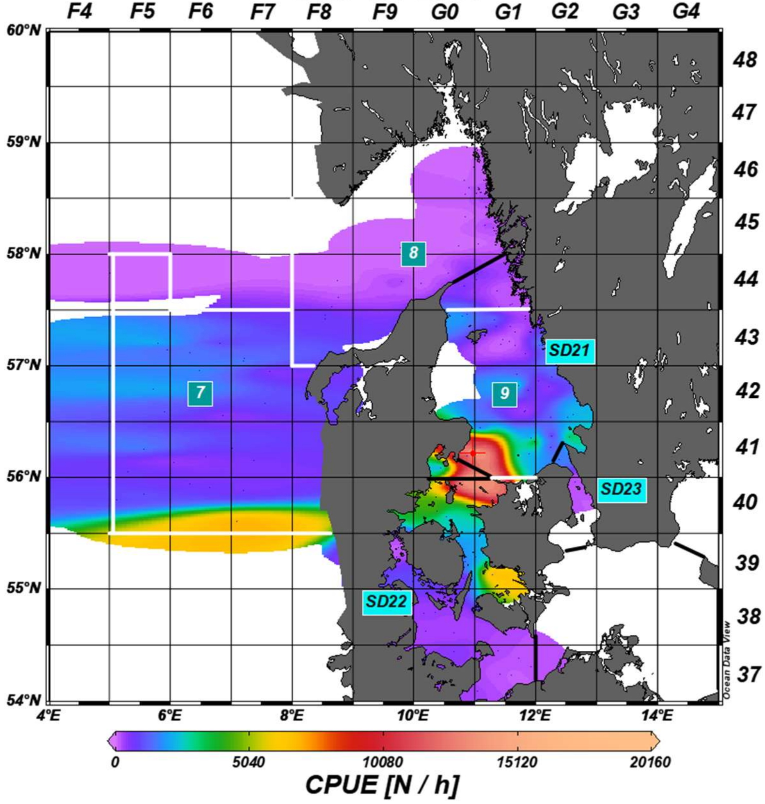
SD21
SD23
SD22
Ocean Data View
0
3847
7694
11541
15388
CPUE [N / h]

Dab Q1 2007



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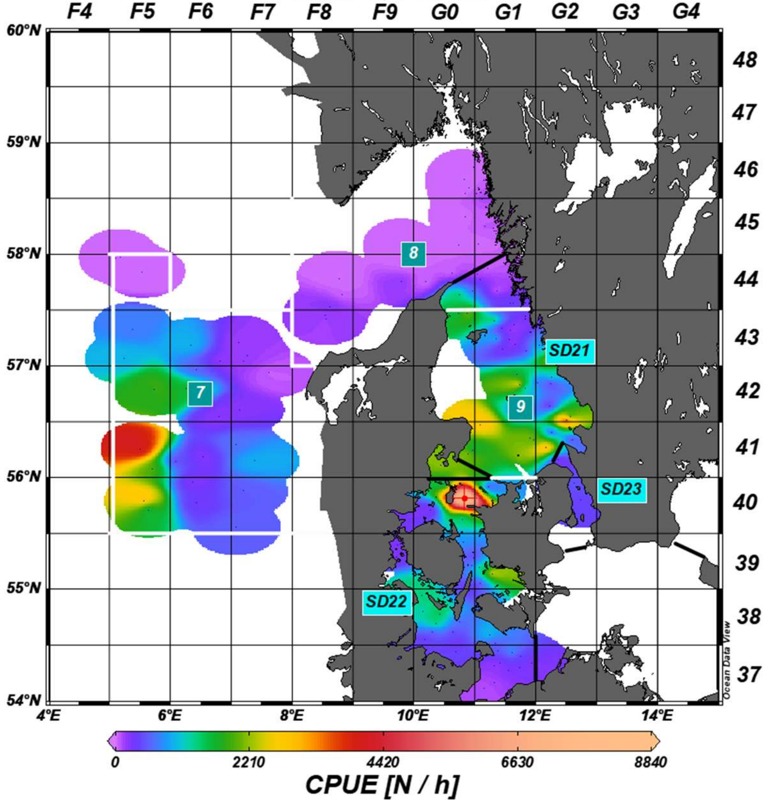
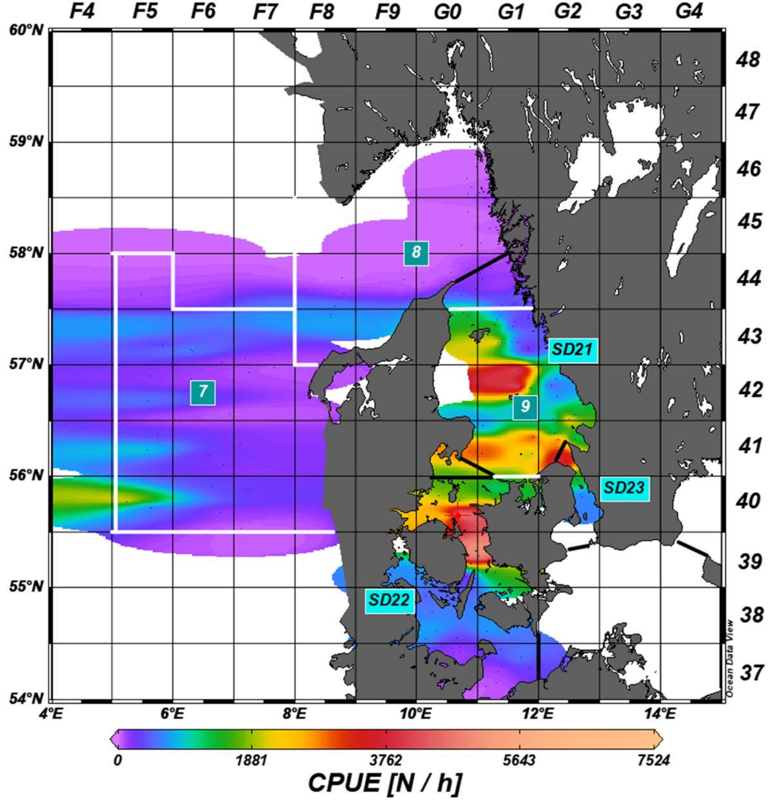
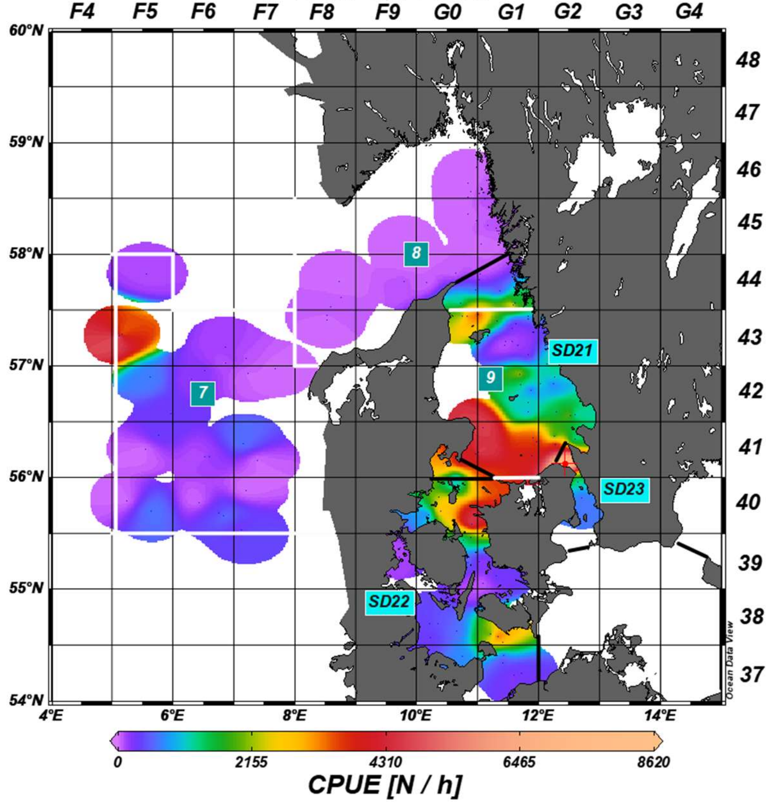



Dab Q1 2009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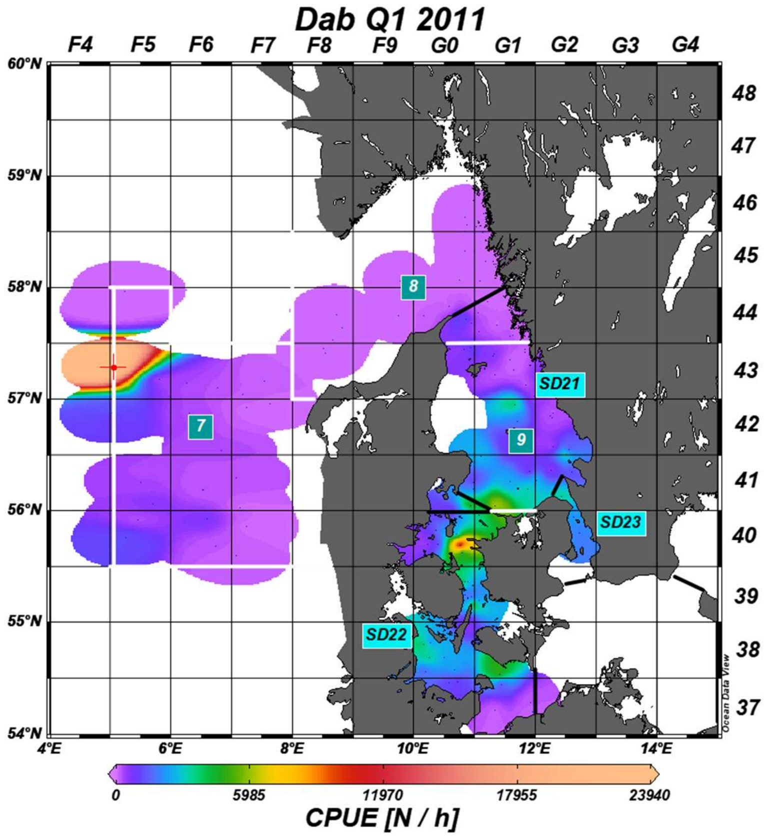

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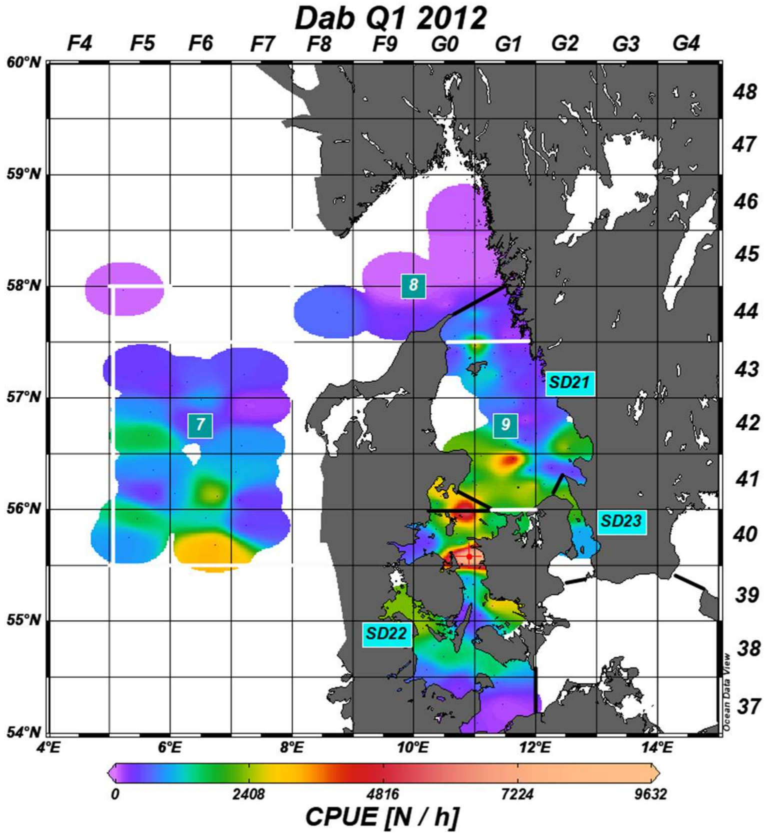

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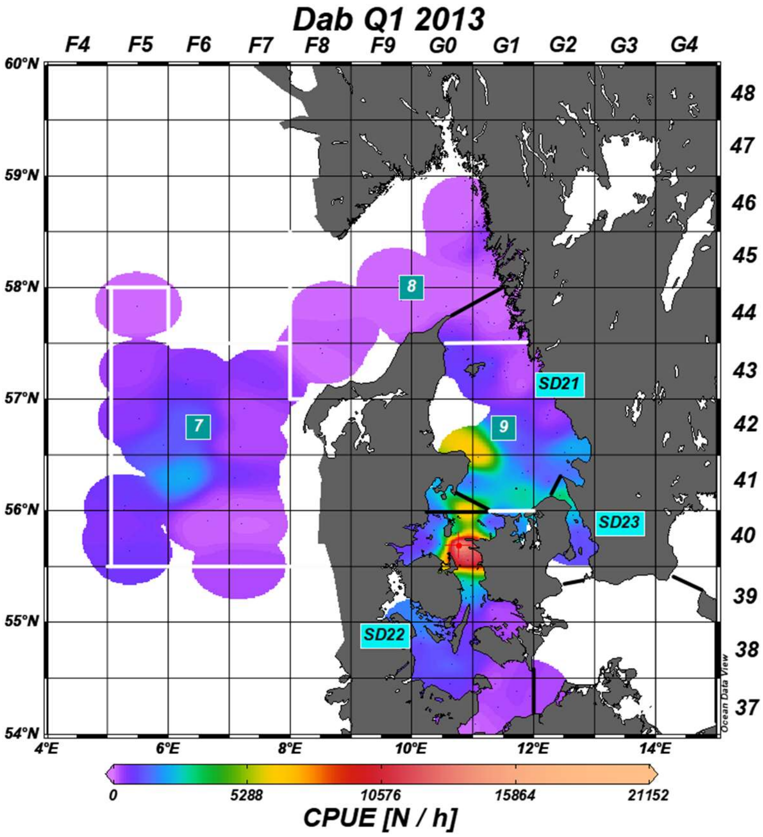
Dab Q1 2013
F4
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F6
F7
F8
F9
G0
G1
G2
G3
G4
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57°N
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14°E
48
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37
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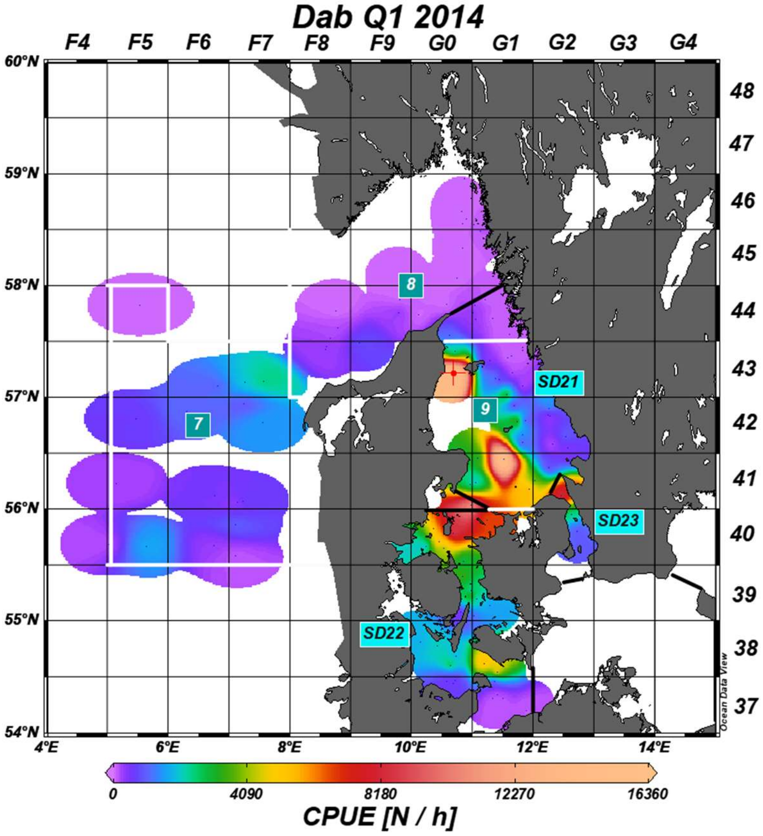
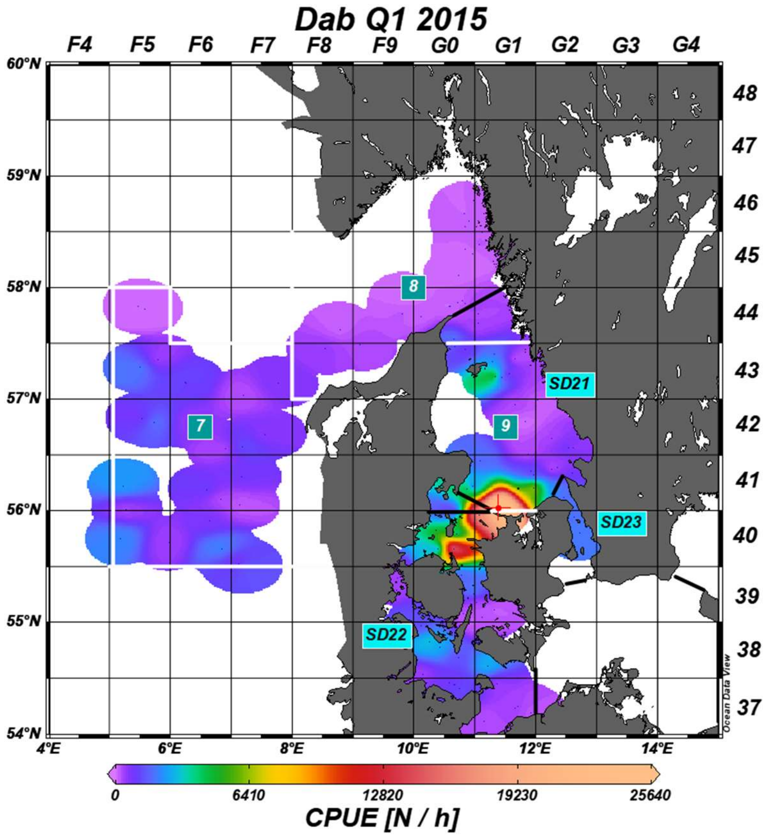
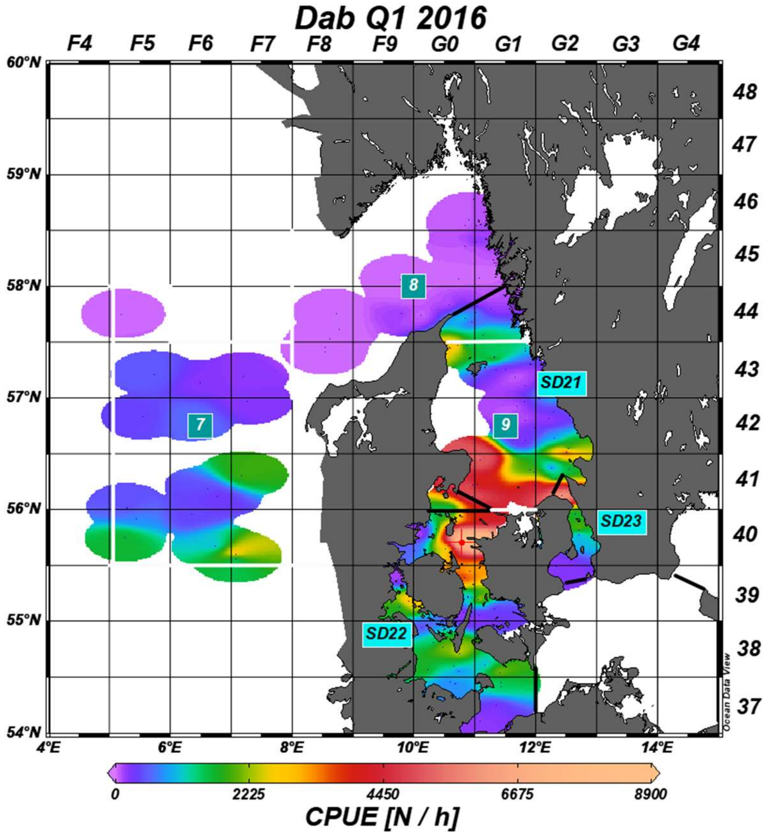
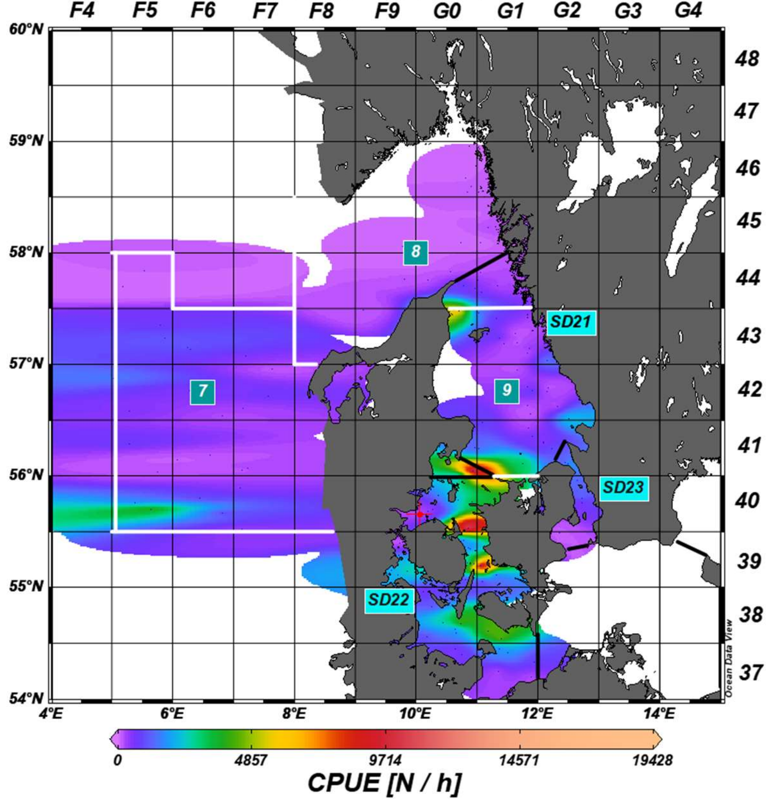
8
9
SD21
SD22
SD23
Ocean Data View
0
5288
10576
15864
21152
CPUE [N / h]


Dab Q1 2014
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
7
8
9
SD21
SD22
SD23
Ocean Data View
0
4090
8180
12270
16360
CPUE [N / h]

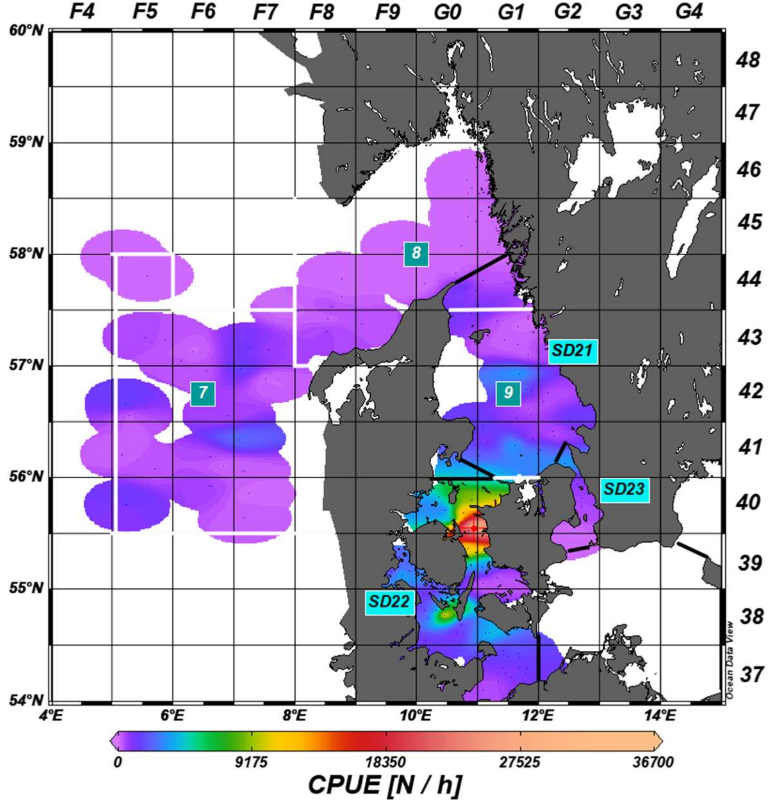

Dab Q1 2015
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
Ocean Data View
0 6410 12820 19230 25640
CPUE [N / h]

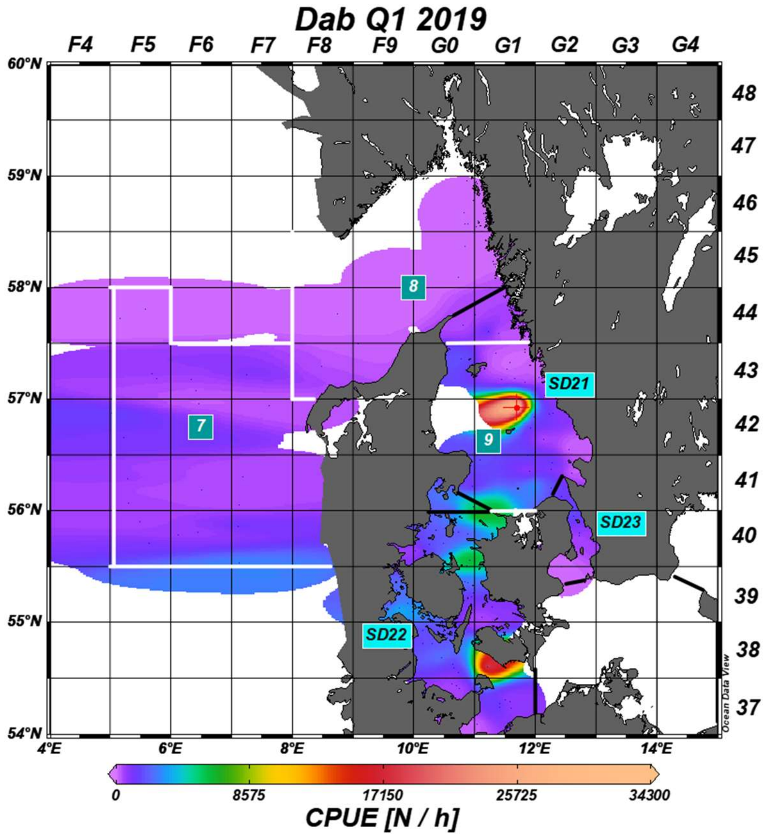

Dab Q1 2016
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E 6°E 8°E 10°E 12°E 14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD23
SD22
Ocean Data View
0 2225 4450 6675 8900
CPUE [N / h]

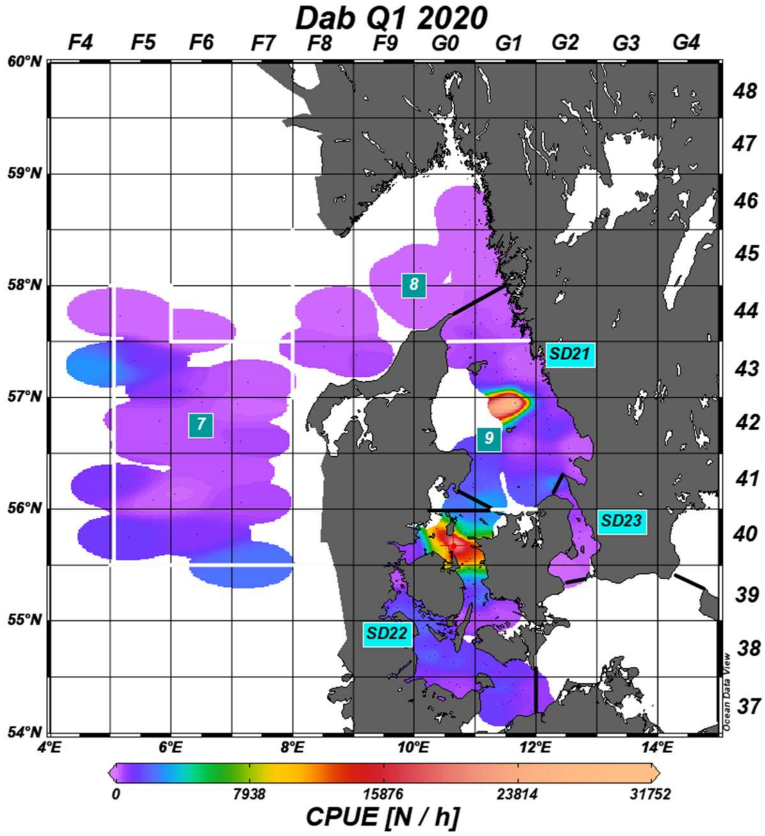
Dab Q1 2017

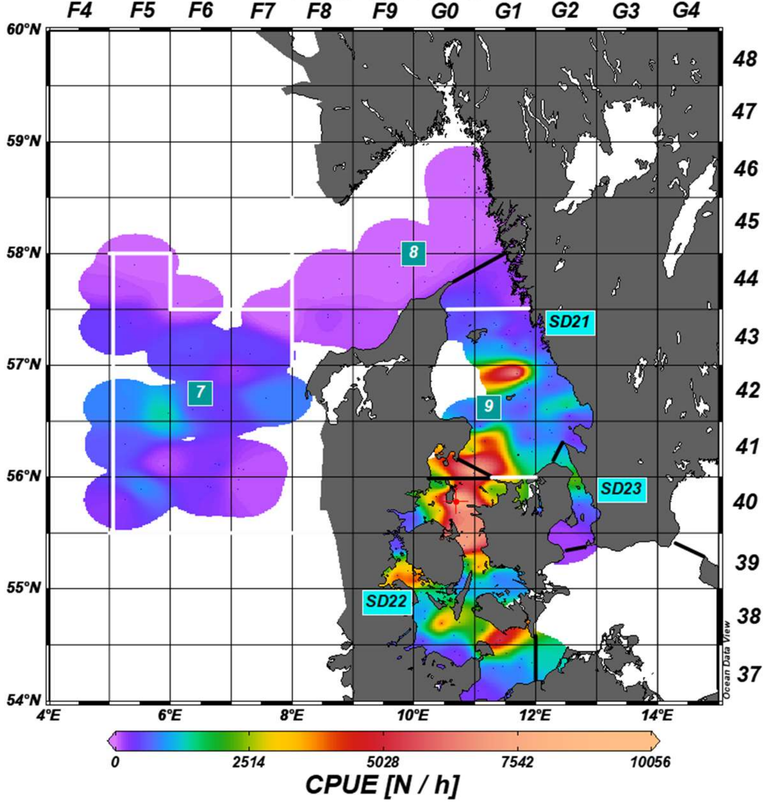


Dab Q1 2018

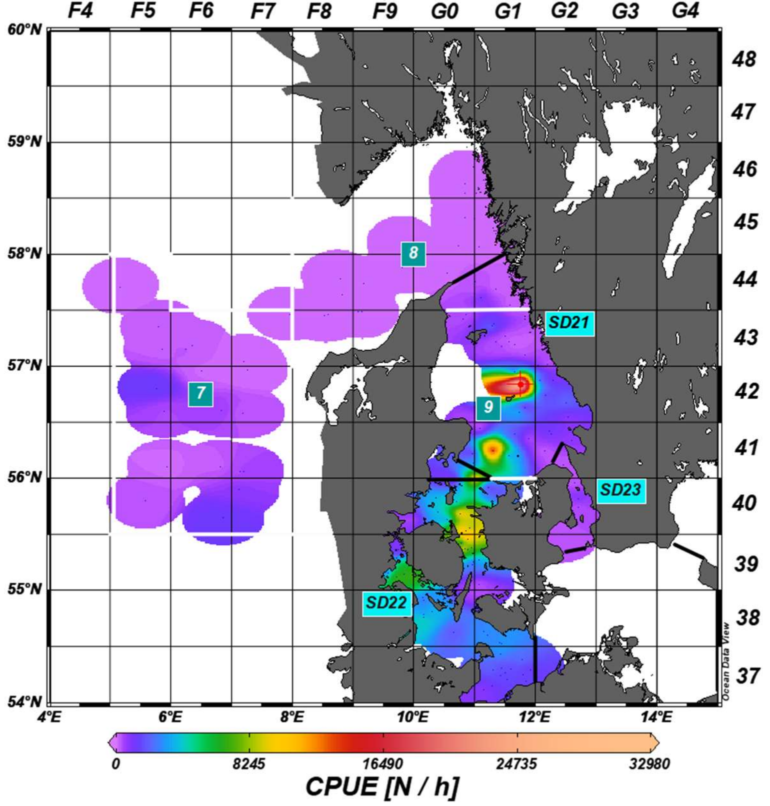



Dab Q1 2019
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
8575
17150
25725
34300
CPUE [N / h]


Dab Q1 2020
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
7938
15876
23814
31752
CPUE [N / h]



Dab Q1 2021

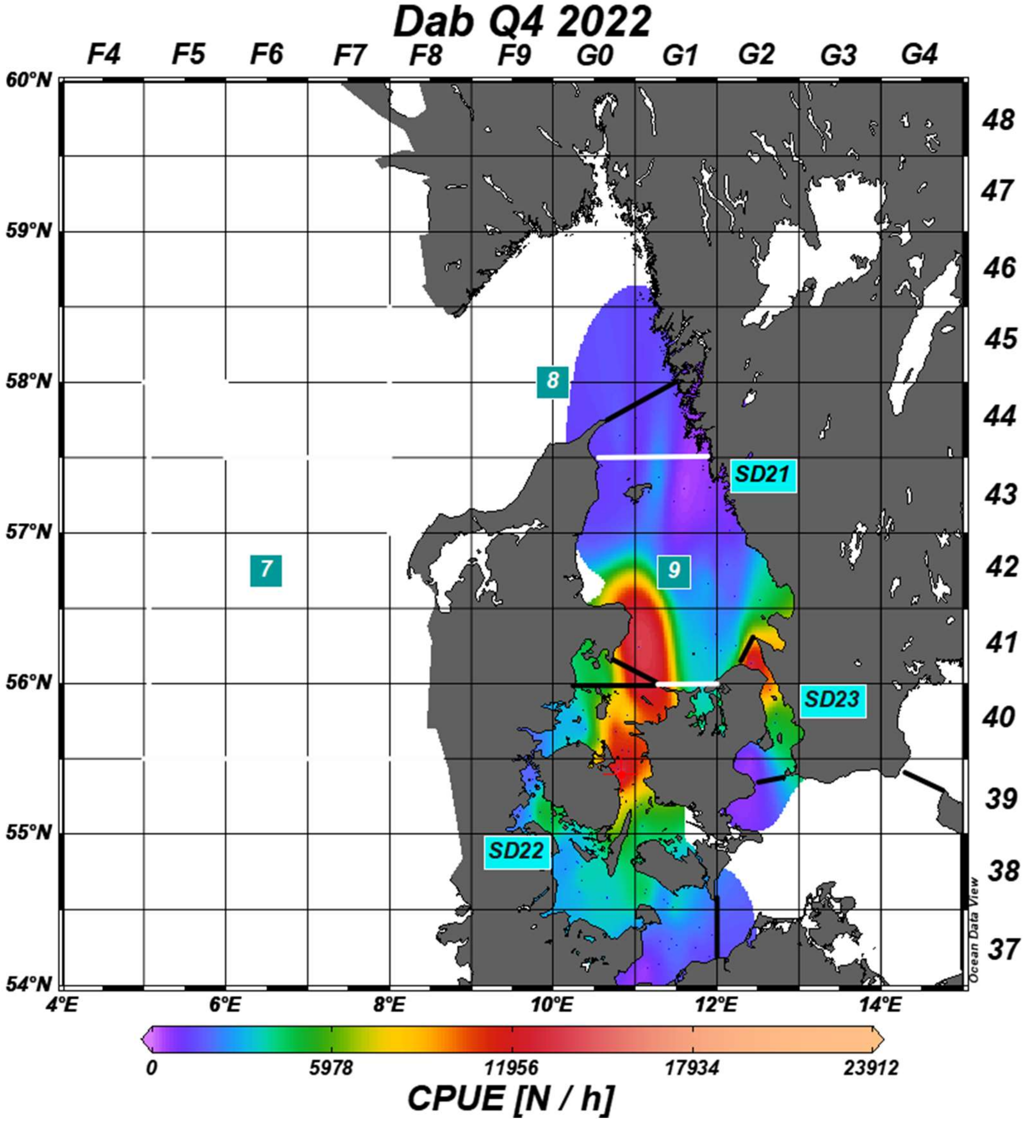


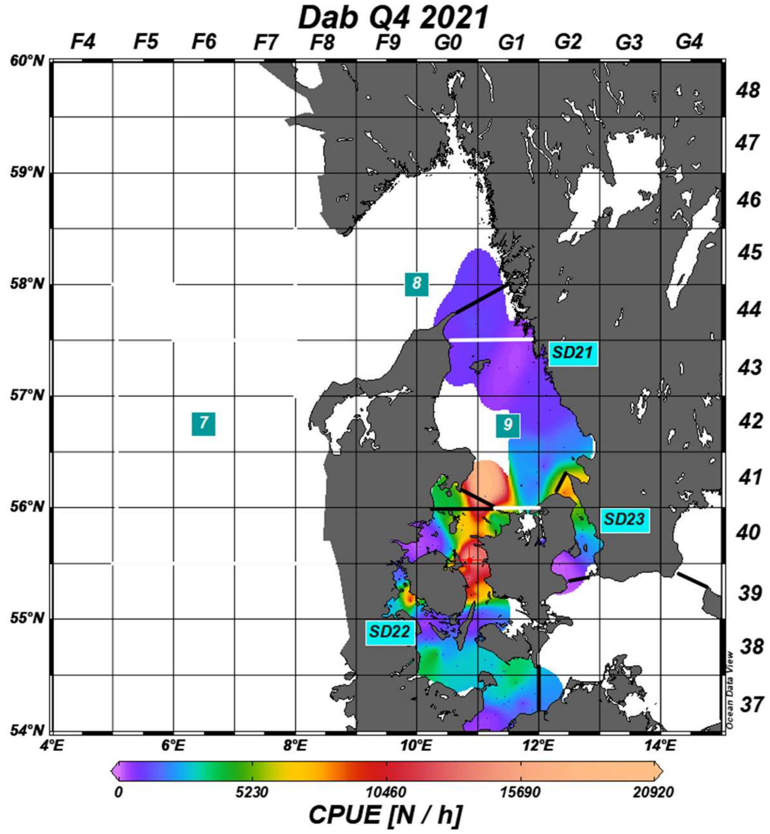
Dab Q1 2022

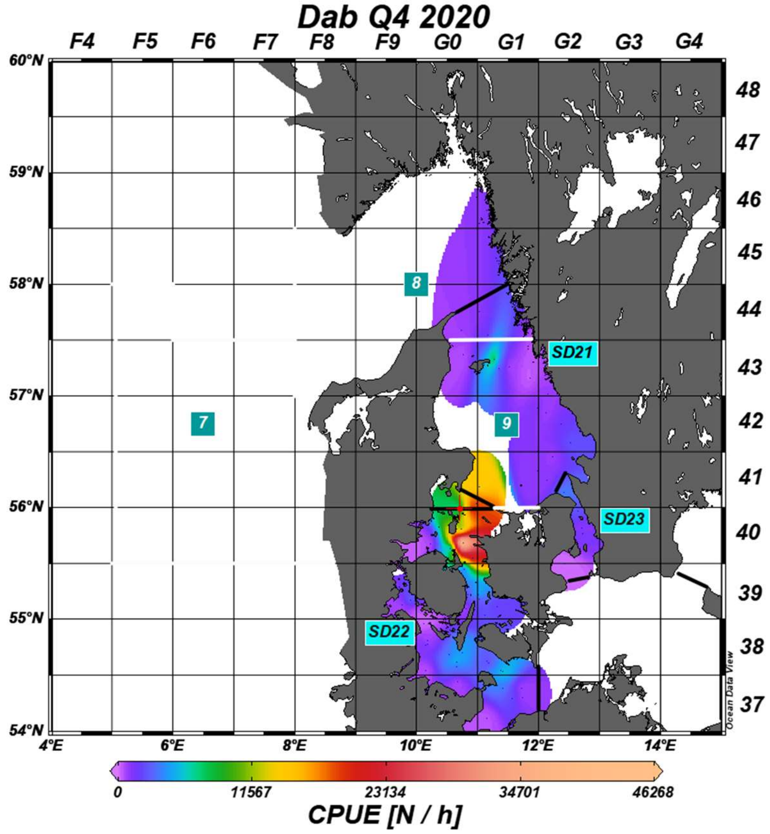
ANNEX 1.2

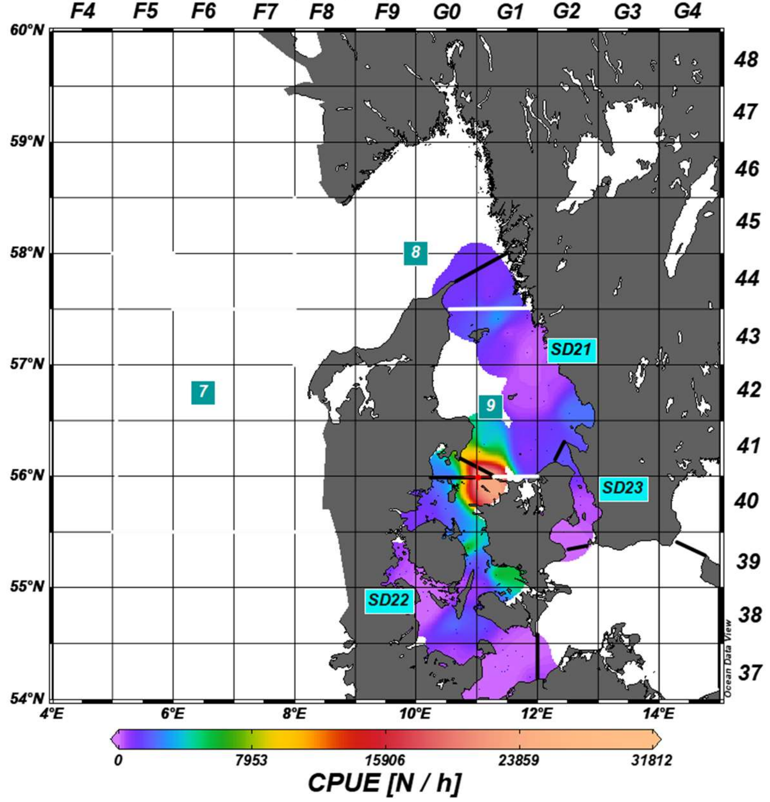
Combined **Quarter 4 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23. IBTS has not been conducted in Q4 since 1996.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.

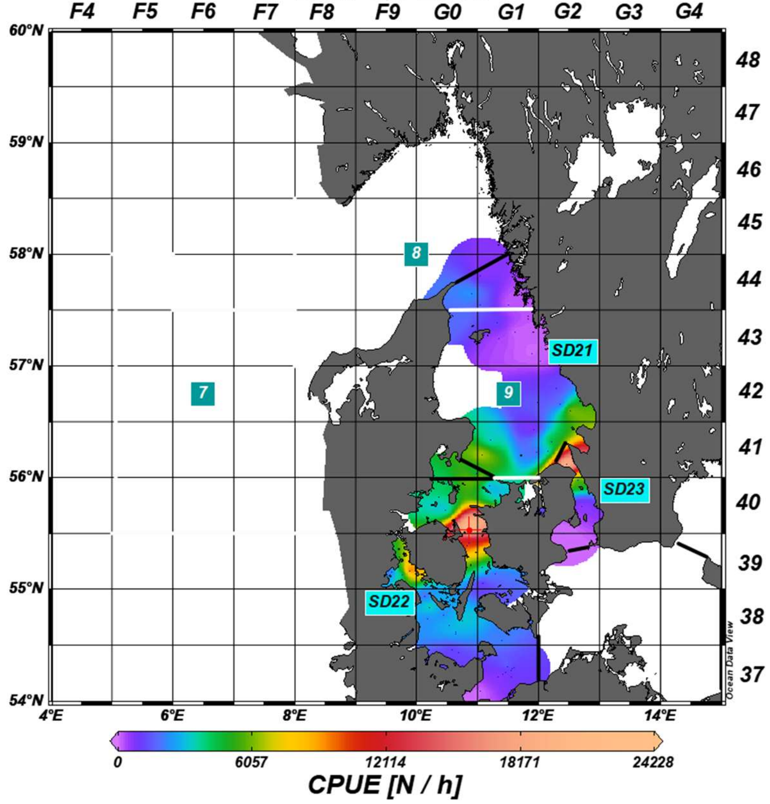



Dab Q4 2021
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
5230
10460
15690
20920
CPUE [N / h]

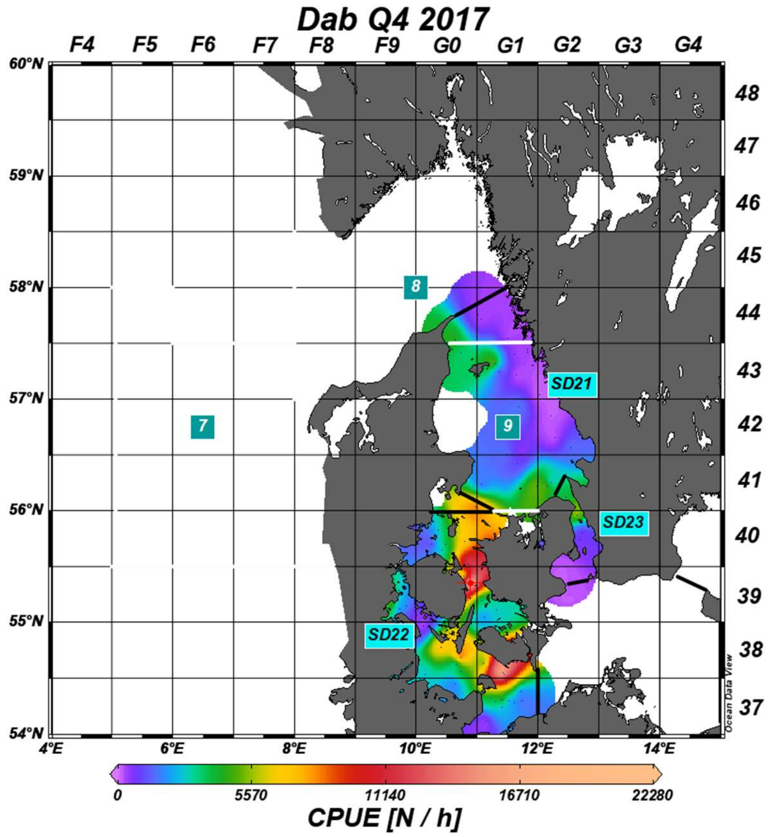

Dab Q4 2020
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
11567
23134
34701
46268
CPUE [N / h]



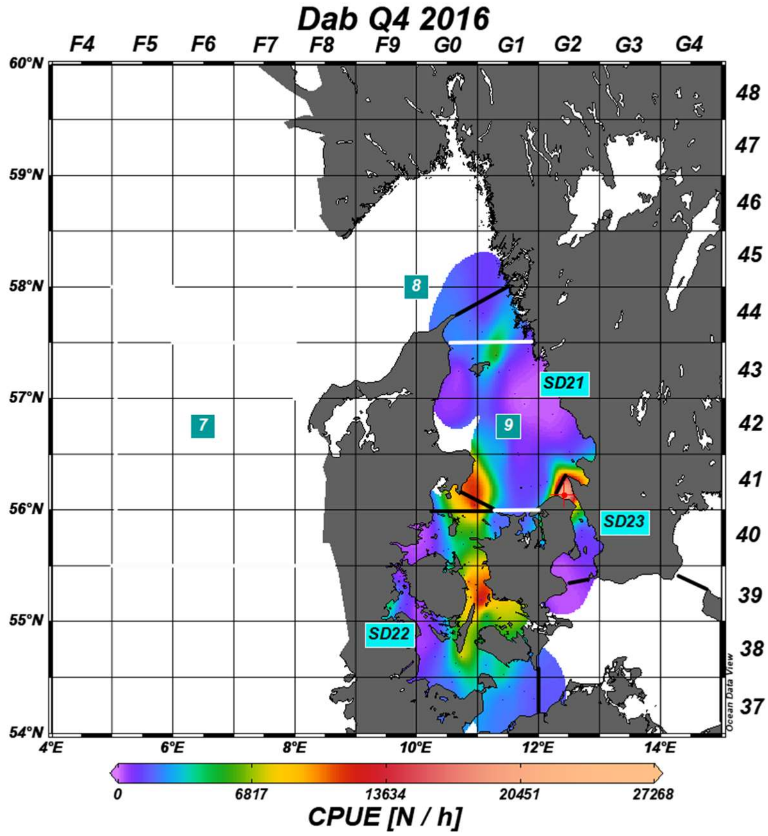
Dab Q4 2019



Dab Q4 2018

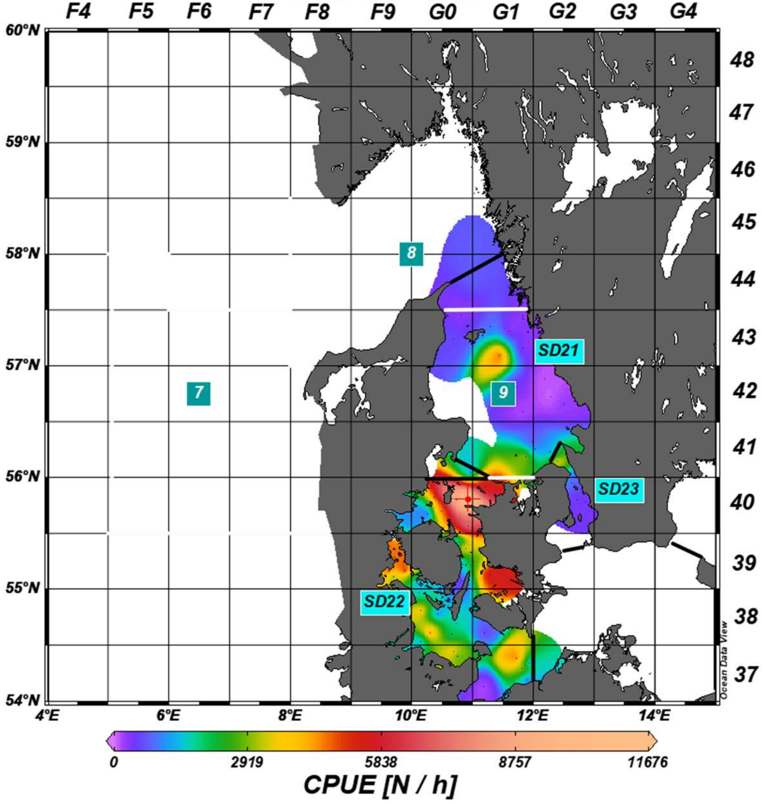


Dab Q4 2017

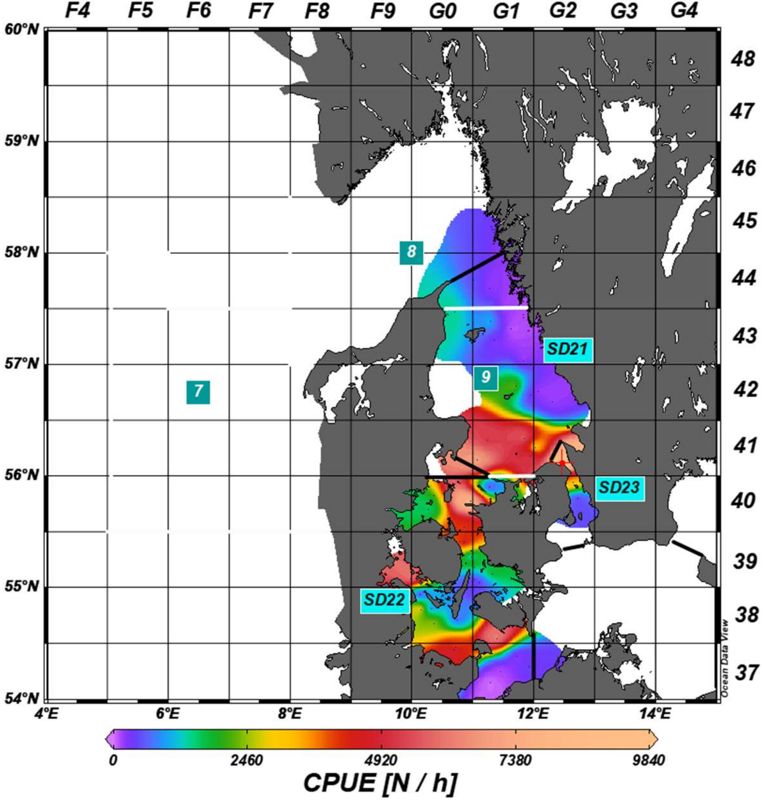


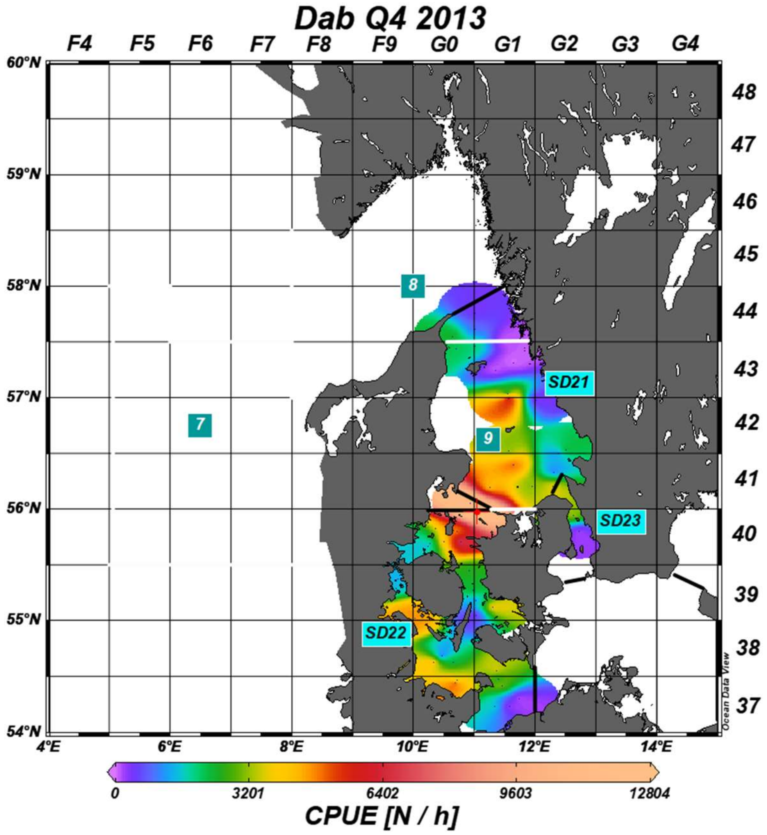
Dab Q4 2016

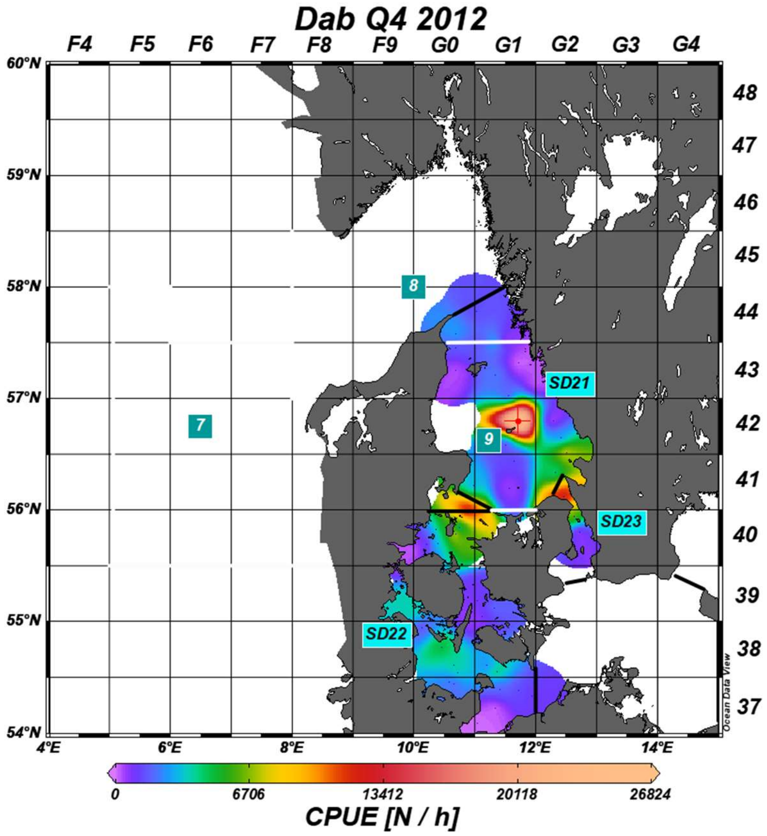
Dab Q4 2015

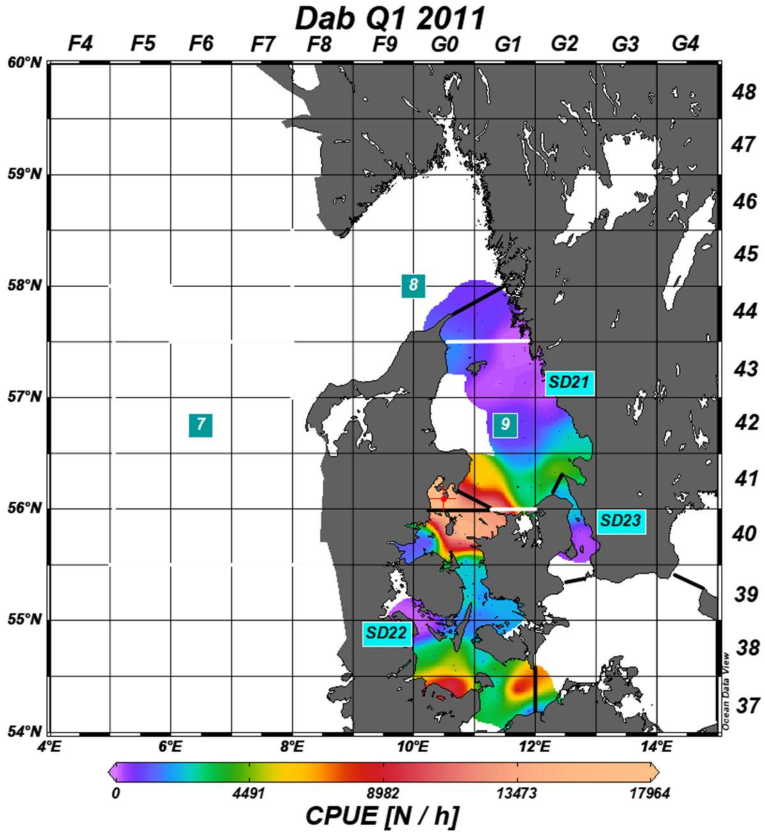


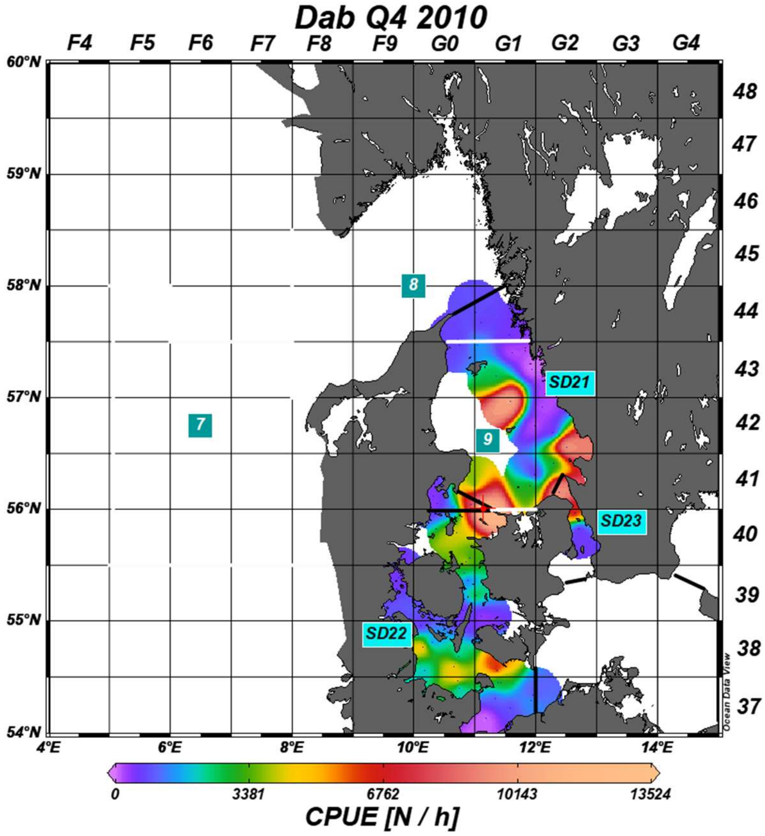
Dab Q4 2014

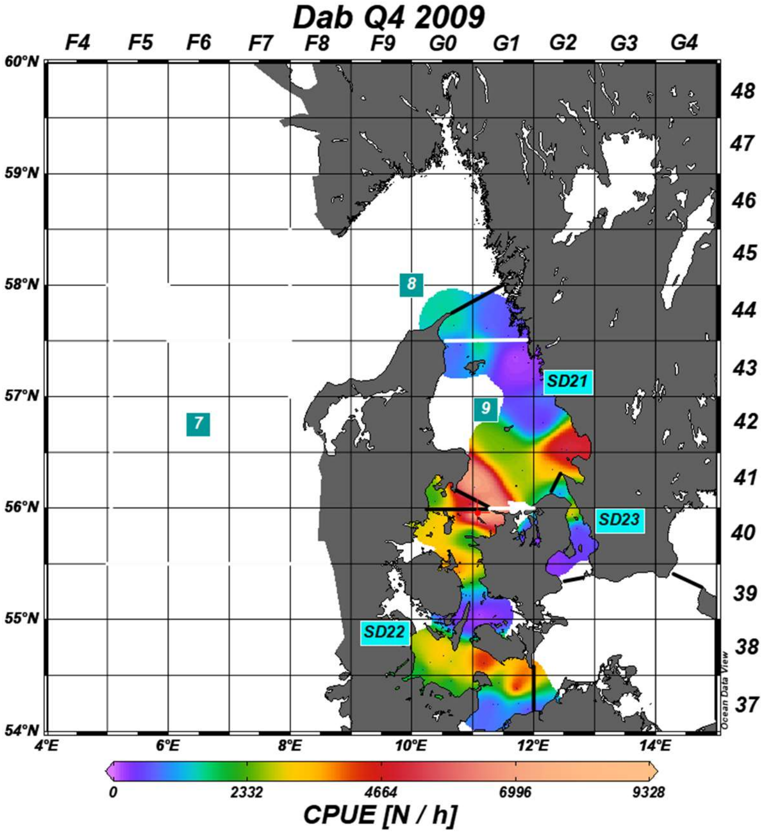


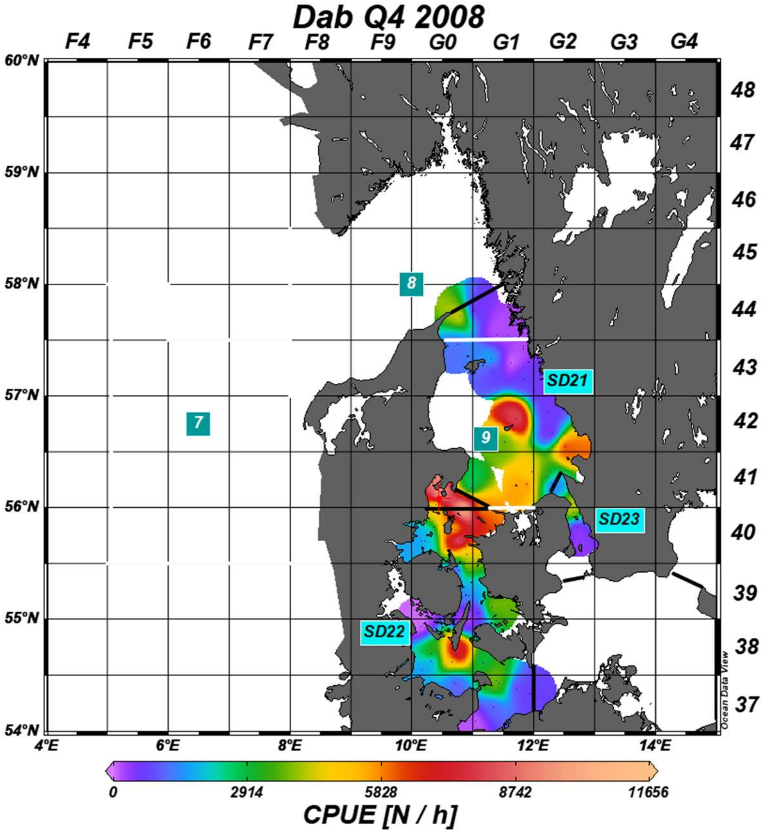

Dab Q4 2013

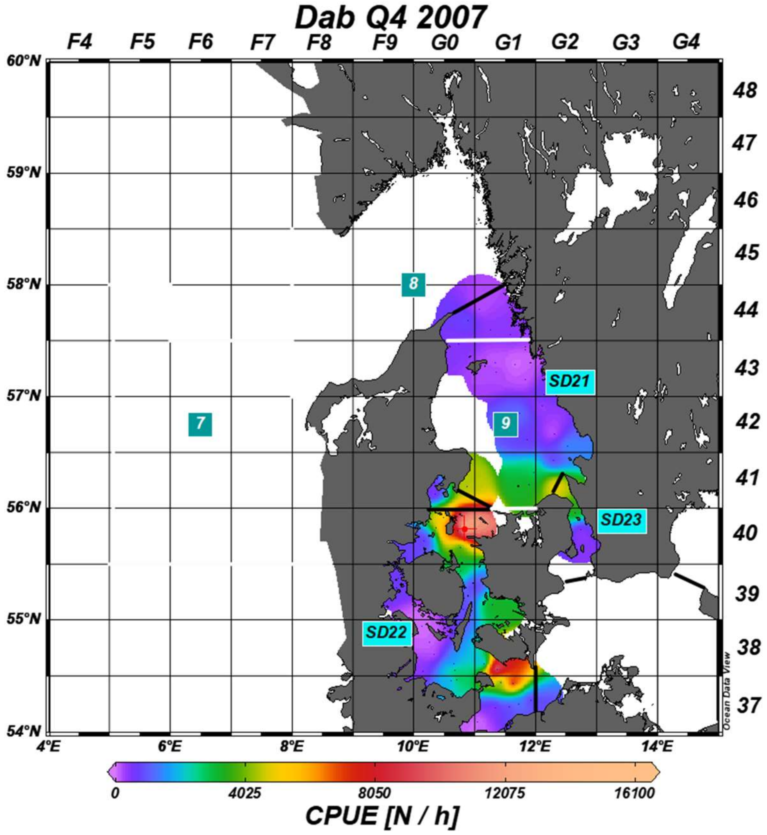

Dab Q4 2012

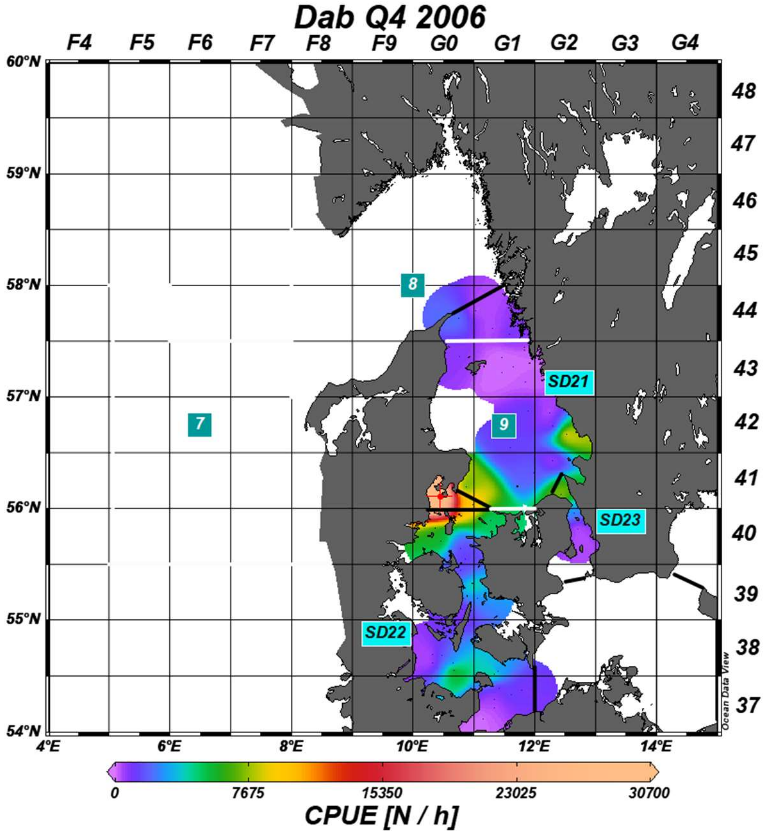

Dab Q1 2011
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
4491
8982
13473
17964
CPUE [N / h]

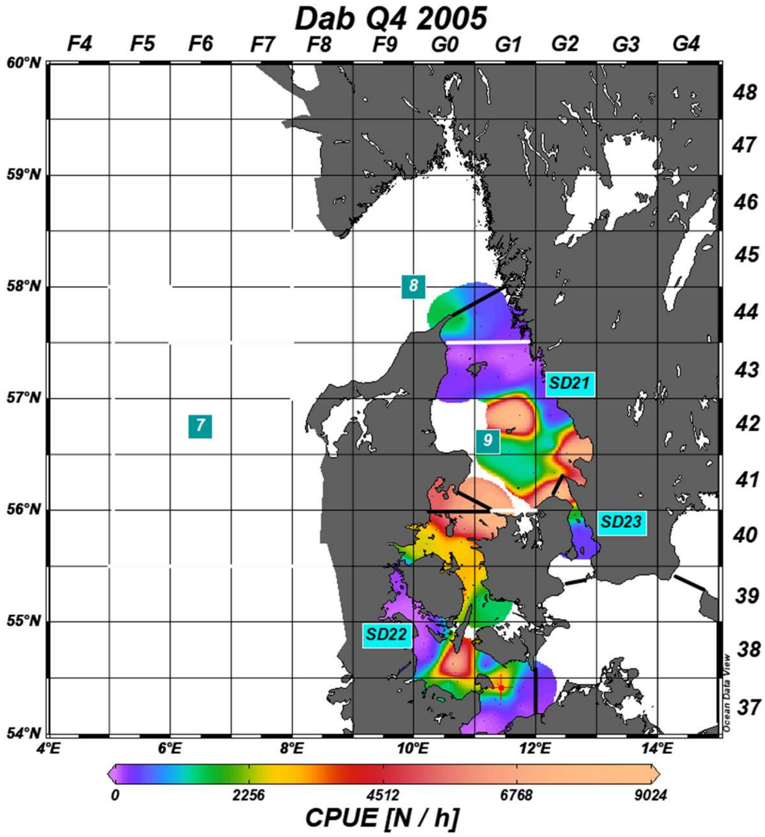

Dab Q4 2010
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
3381
6762
10143
13524
CPUE [N / h]

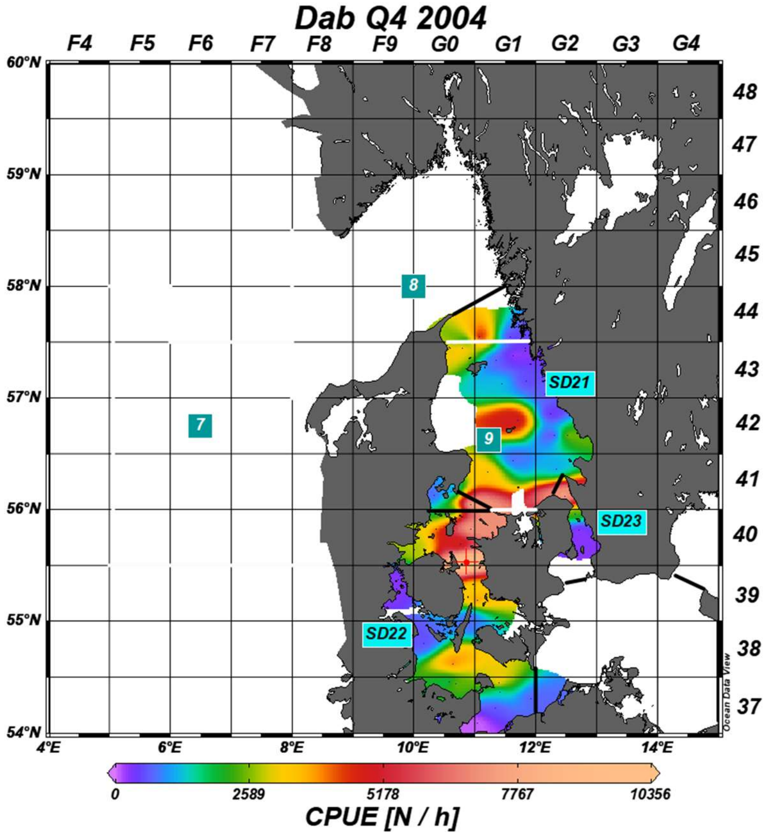

Dab Q4 2009
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
2332
4664
6996
9328
CPUE [N / h]

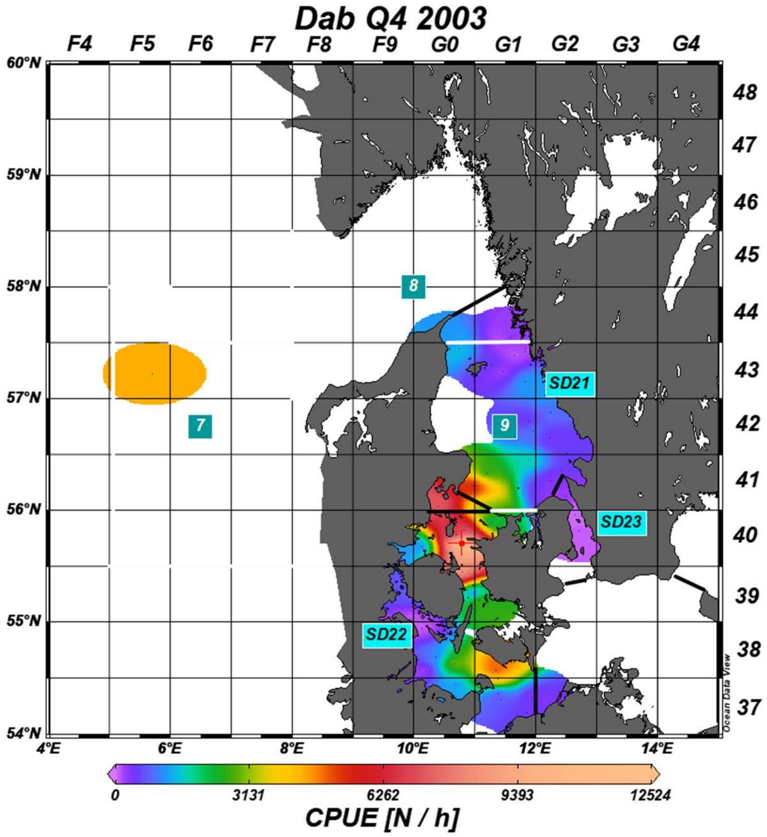

Dab Q4 2008
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
2914
5828
8742
11656
CPUE [N / h]

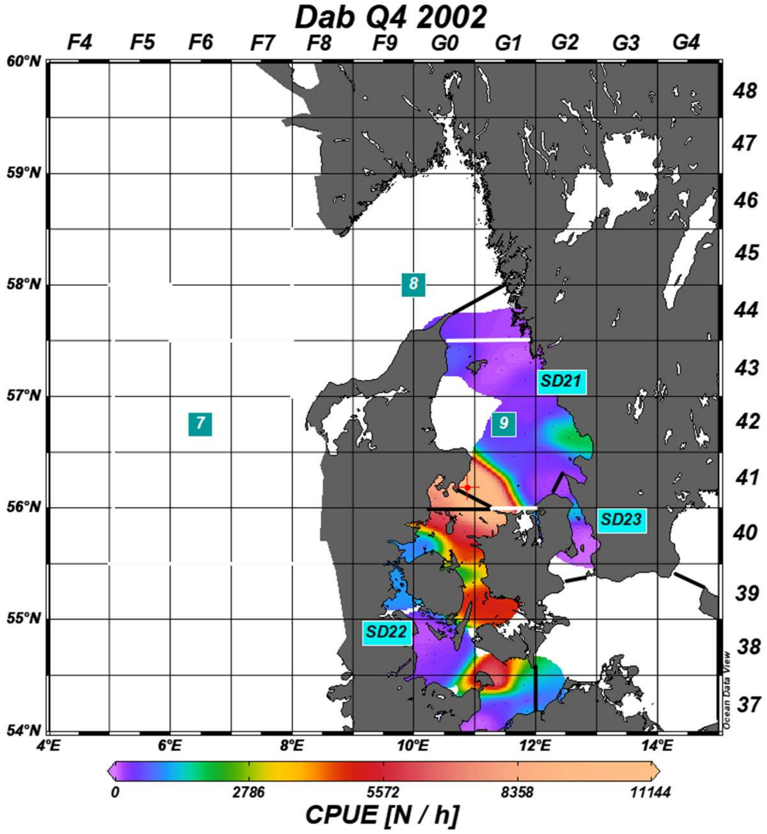

Dab Q4 2007
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
0
4025
8050
12075
16100
CPUE [N / h]
Ocean Data View

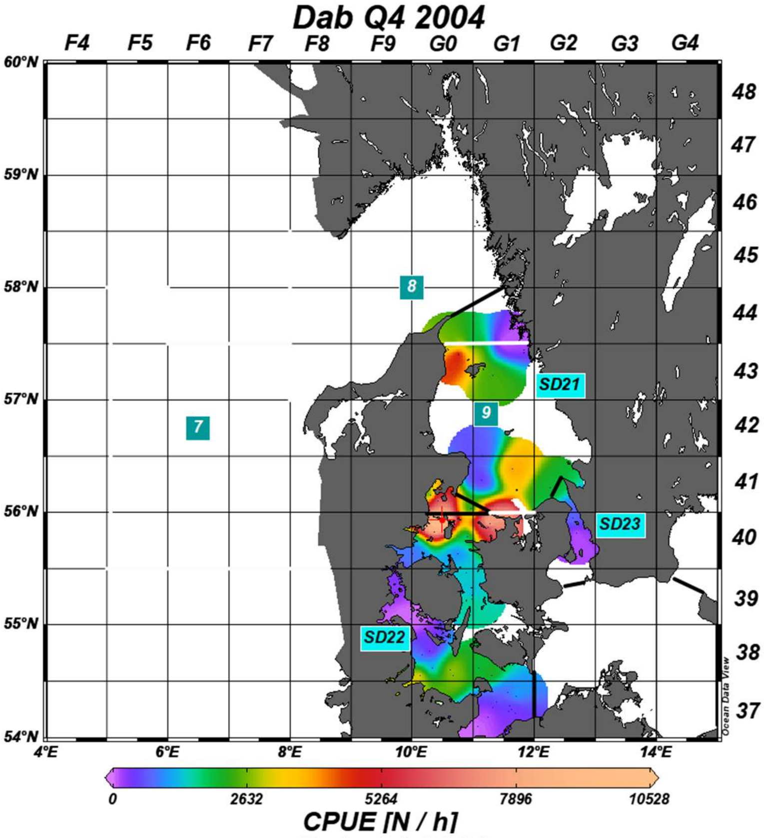

Dab Q4 2006
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
0
7675
15350
23025
30700
CPUE [N / h]
Ocean Data View


Dab Q4 2005
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
2256
4512
6768
9024
CPUE [N / h]

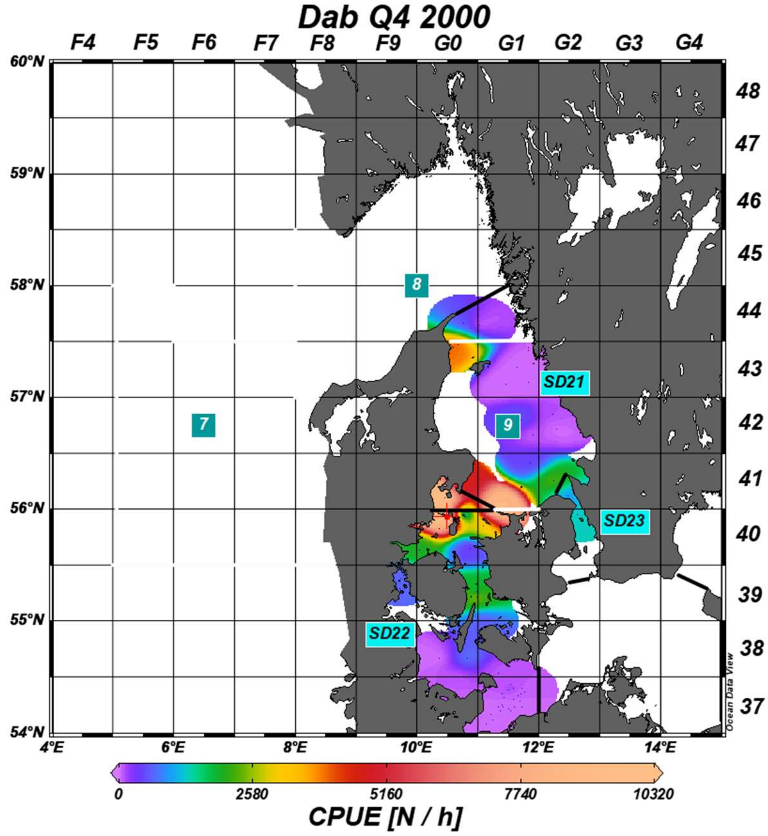

Dab Q4 2004
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
2589
5178
7767
10356
CPUE [N / h]


Dab Q4 2003
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
3131
6262
9393
12524
CPUE [N / h]

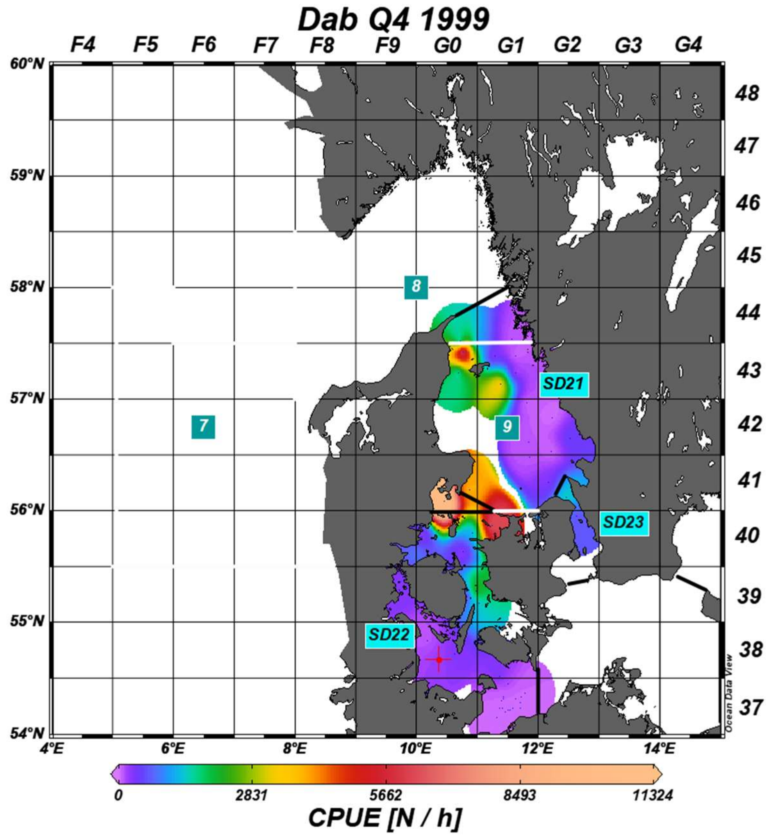

Dab Q4 2002
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
2786
5572
8358
11144
CPUE [N / h]

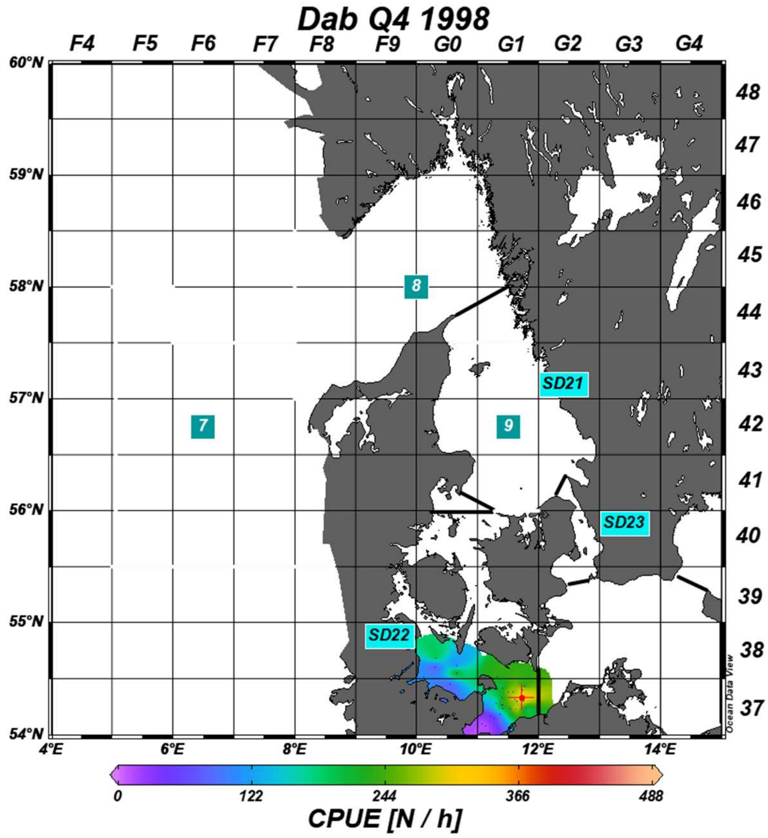


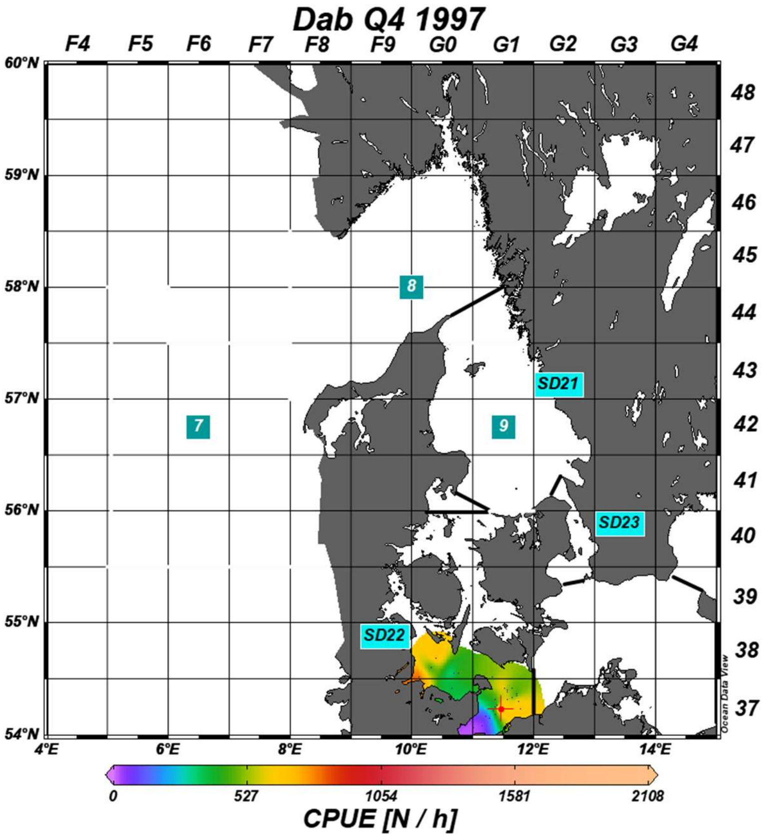
Dab Q4 2004

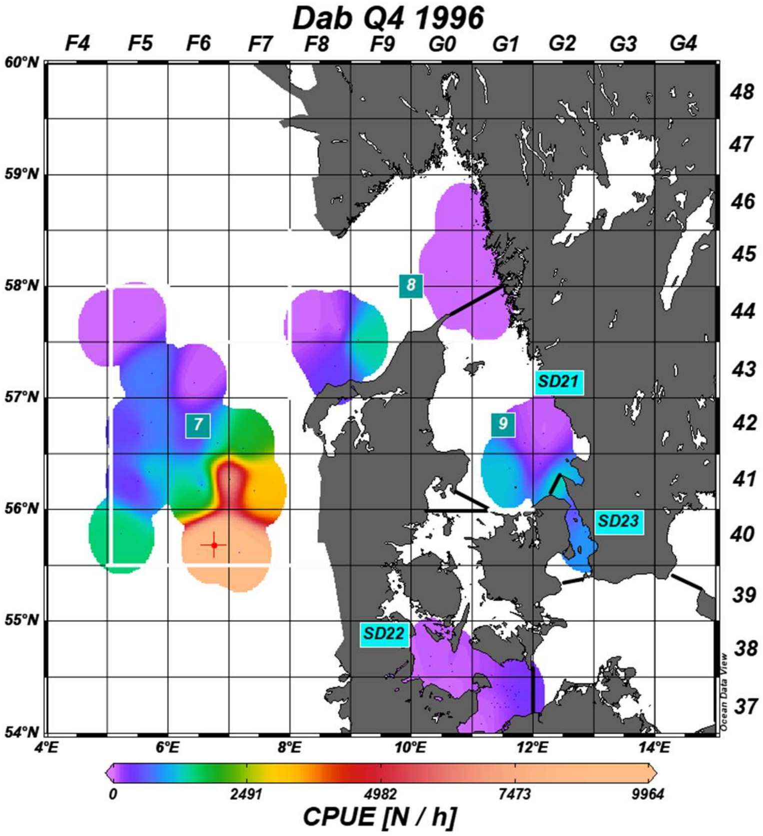


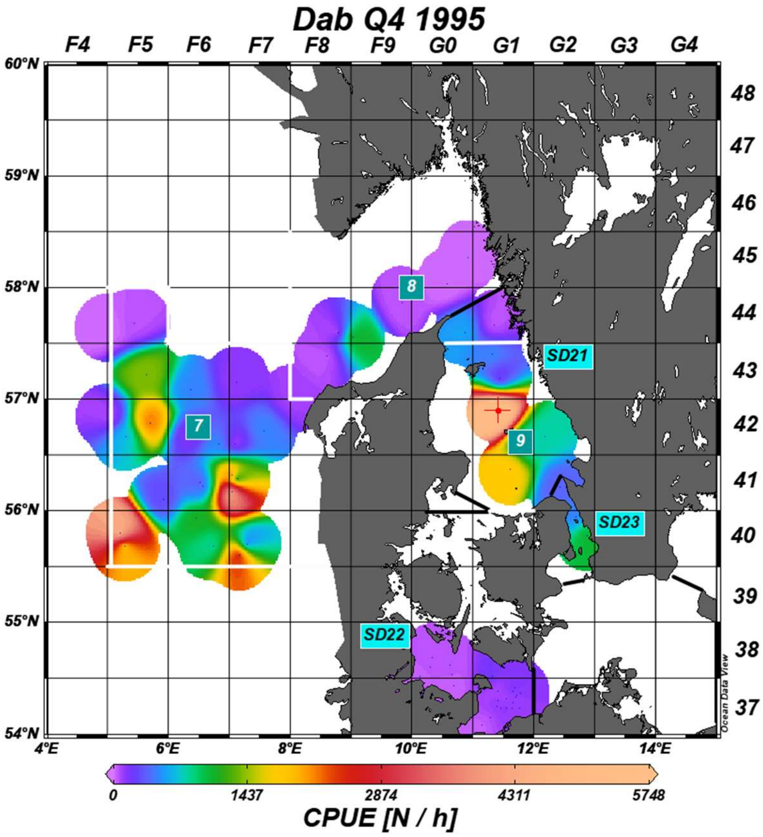
Dab Q4 2000

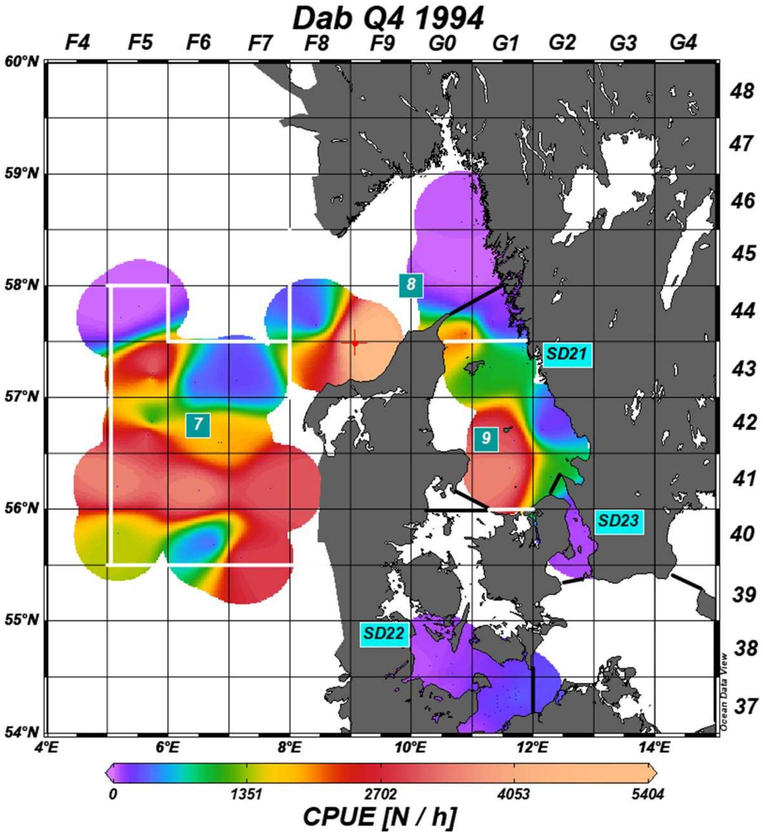

Dab Q4 1999
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
2831
5662
8493
11324
CPUE [N / h]


Dab Q4 1998
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
122
244
366
488
CPUE [N / h]


Dab Q4 1997


Dab Q4 1996


Dab Q4 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
1437
2874
4311
5748
CPUE [N / h]


Dab Q4 1994
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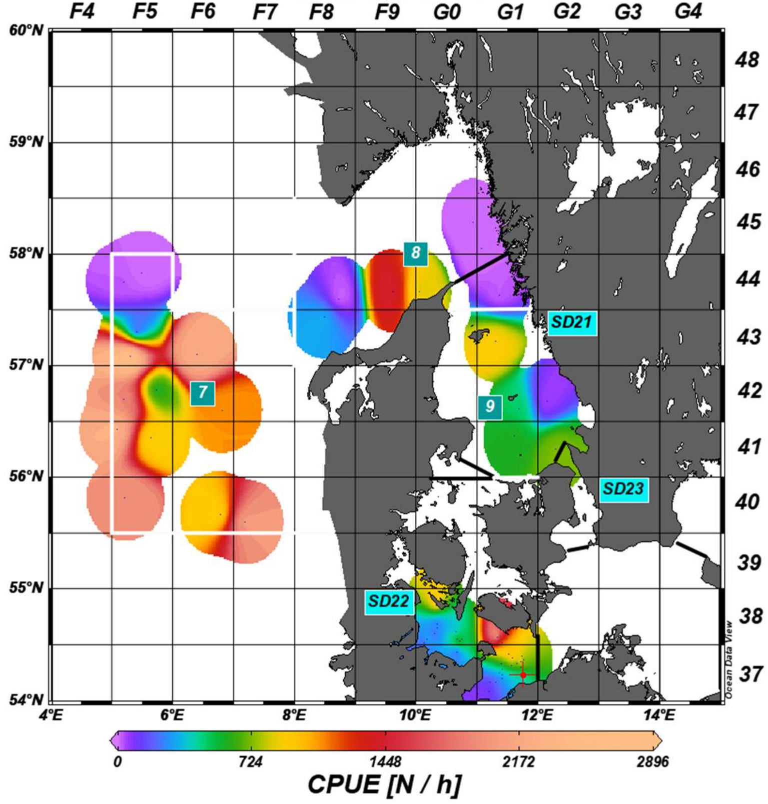

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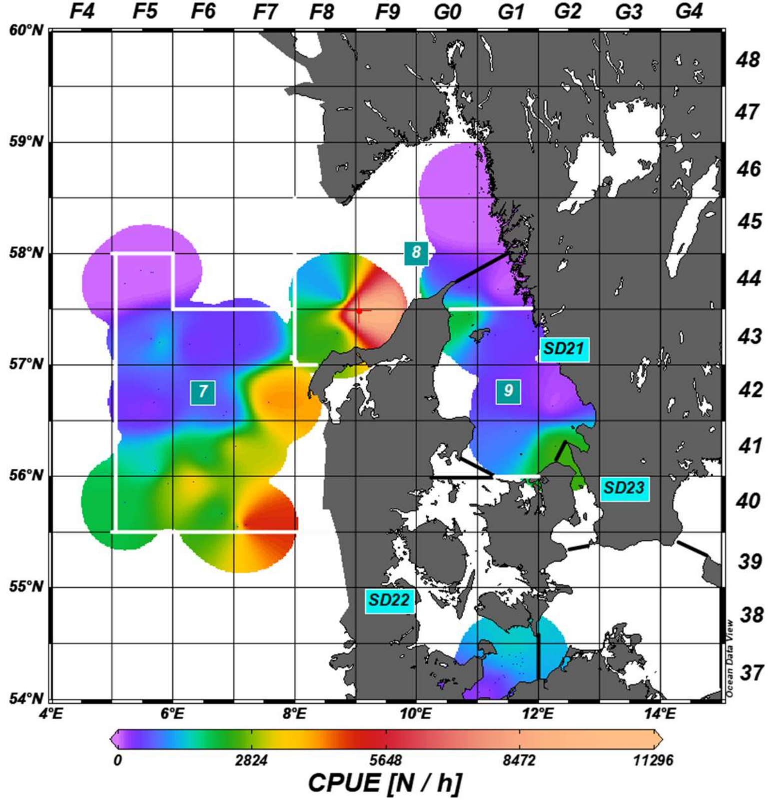

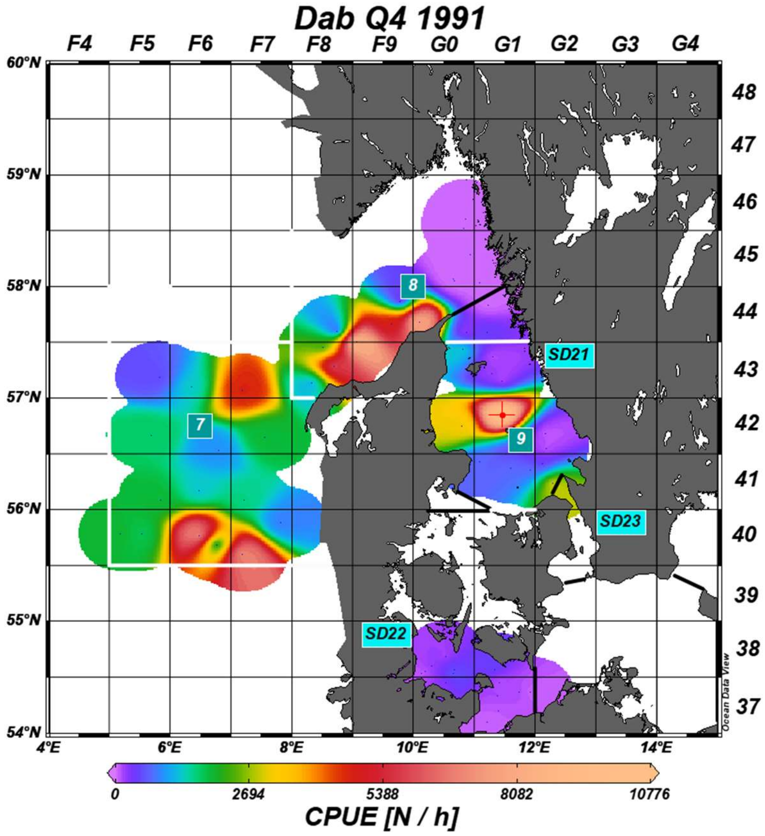
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Ocean Data View
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ANNEX 1.3

Annual landings of Dab in tons per ICES Subdivision and statistical rectangle

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b)

ICES. 2023b. Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Portal: https://www.rdb-fishframe.org/

ICES. 2023b. Data policy for the Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Guidelines. 7 pp. https://doi.org/10.17895/ices.pub.22188157

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.a.20	**590.095**	**376.283**	**425.817**	**417.406**		
43F7	0.095	0.024	0.203	0.051	0.093	0.02%
43F8	138.554	109.155	130.193	77.140	113.761	25.15%
43F9	114.922	87.528	70.113	56.228	82.198	18.17%
43G0	0.000	0.000	0.011	0.000	0.003	0.00%
43G1	0.000	0.003	0.004	0.000	0.002	0.00%
44F7	1.744	0.030	0.180	0.092	0.512	0.11%
44F8	57.612	37.211	35.616	25.892	39.083	8.64%
44F9	224.096	108.804	144.762	169.917	161.895	35.79%
44G0	50.367	29.823	42.105	84.585	51.720	11.43%
44G1	2.067	1.915	1.655	2.630	2.067	0.46%
45F9	0.040	0.050	0.083	0.026	0.050	0.01%
45G0	0.327	1.358	0.518	0.364	0.642	0.14%
45G1	0.232	0.363	0.228	0.480	0.326	0.07%
46G0	0.039	0.009	0.146	0.001	0.049	0.01%
46G1	0.000	0.010	0.000	0.000	0.003	0.00%

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.a.21	**22.688**	**17.887**	**25.553**	**32.087**		
40F7	0.000	0.000	0.064	0.000	0.016	0.07%
40G1	0.023	0.022	0.074	0.525	0.161	0.66%
40G2	0.009	0.022	0.000	0.017	0.012	0.05%
41G0	0.672	0.573	0.420	0.131	0.449	1.83%
41G1	2.612	2.166	8.156	8.781	5.429	22.11%
41G2	2.200	1.490	1.901	1.293	1.721	7.01%
42G0	0.749	0.118	0.692	0.385	0.486	1.98%
42G1	1.089	1.118	1.663	1.328	1.300	5.29%
42G2	1.652	0.752	1.009	1.062	1.119	4.56%

43F9	0.000	0.000	0.027	0.000	0.007	0.03%
43G0	3.863	3.229	2.329	5.933	3.839	15.63%
43G1	1.552	1.821	2.229	3.019	2.155	8.78%
43G2	0.067	0.023	0.016	0.002	0.027	0.11%
44F9	0.000	0.000	0.123	0.000	0.031	0.13%
44G0	6.073	4.292	5.870	7.669	5.976	24.34%
44G1	2.127	2.261	0.980	1.942	1.828	7.44%

Area	2019	2020	2021	2022	average	%
27.3.b.23	**16.072**	**13.002**	**8.131**	**7.320**		
39G2	0.059	0.030	0.003	0.006	0.025	0.22%
40G2	13.996	11.805	7.659	6.500	9.990	89.75%
40G3	0.000	0.079	0.055	0.020	0.039	0.35%
41G2	2.017	1.088	0.414	0.794	1.078	9.69%

Area	2019	2020	2021	2022	average	%
27.3.c.22	**955.6**	**854.0**	**654.5**	**211.9**		
37F0	0.0	0.0	0.0	0.0	0.005	0.00%
37F9	0.1	0.0	0.0	0.0	0.019	0.00%
37G0	53.1	62.0	93.5	34.0	60.663	9.07%
37G1	212.2	288.4	147.5	39.2	171.815	25.68%
37G2	0.0	0.0	0.2	0.0	0.044	0.01%
38F9	4.7	3.3	1.8	0.8	2.685	0.40%
38G0	611.2	424.2	302.2	126.7	366.097	54.72%
38G1	29.9	49.8	91.6	3.5	43.692	6.53%
38G2	0.0	0.3	0.0	0.0	0.066	0.01%
38H0	0.4	0.0	0.0	0.0	0.100	0.01%
39F9	1.1	2.2	1.3	0.9	1.398	0.21%
39G0	16.6	10.0	9.3	3.4	9.820	1.47%
39G1	21.3	12.3	5.7	1.8	10.277	1.54%
40G0	2.5	0.8	0.2	0.1	0.914	0.14%
40G1	2.0	0.6	1.0	1.4	1.252	0.19%
41G0	0.0	0.0	0.0	0.0	0.013	0.00%
41G1	0.4	0.0	0.1	0.0	0.137	0.02%

Area	2019	2020	2021	2022	average	%
27.4.b	**914.036**	**650.239**	**498.149**	**342.666**		
36F2	3.887	2.358	2.386	0.364	2.249	0.37%
36F3	4.645	4.476	3.366	0.46	3.237	0.54%
36F4	8.773	19.714	8.241	3.483	10.053	1.67%

36F5	1.079	4.798	10.877	1.218	4.493	0.74%
36F6	0.144	0.311	2.417		0.957	0.16%
36F7	0.353	1.287	0.282	0.076	0.500	0.08%
36F8	0.015		0.057	0.048	0.040	0.01%
37F0	1.625	1.527	0.053	0.822	1.007	0.17%
37F1	1.889	0.105	0.197	0.033	0.556	0.09%
37F2	4.777	2.561	1.25	0.199	2.197	0.36%
37F3	7.214	7.482	0.494	0.076	3.817	0.63%
37F4	4.781	3.856	3.491	2.849	3.744	0.62%
37F5	14.68	15.017	9.911	6.604	11.553	1.91%
37F6	6.004	10.174	7.865	1.18	6.306	1.04%
37F7	2.476	12.539	3.735	2.062	5.203	0.86%
37F8	0.478	3.949	0.247	0.106	1.195	0.20%
38F1	1.328	1.561	0.941	0.649	1.120	0.19%
38F2	0.154	0.452	0.01		0.205	0.03%
38F3	6.929	5.125	9.023	0.04	5.279	0.87%
38F4	6.24	19.29	12.718	2.954	10.301	1.71%
38F5	5.74	7.246	4.552	2.453	4.998	0.83%
38F6	5.19	8.728	6.185	6.721	6.706	1.11%
38F7	0.023		0.01		0.017	0.00%
38F8	0.003	0.275			0.139	0.02%
38F9		0.588			0.588	0.10%
39F0	0.154				0.154	0.03%
39F1	14.647	1.164	0.04		5.284	0.88%
39F2	0.58	0.273	0.051		0.301	0.05%
39F3	2.477	1.802	2.12	3.301	2.425	0.40%
39F4	8.091	5.309	3.763	0.63	4.448	0.74%
39F5	70.367	18.311	3.66	10.004	25.586	4.24%
39F6	31.103	5.045	12.946	11.605	15.175	2.51%
39F7	0.791	0.145	0.089		0.342	0.06%
39F8		0.138	0.037	0.633	0.269	0.04%
40F0	0.003			0.079	0.041	0.01%
40F1	2.464	0.004			1.234	0.20%
40F2	0.012	0.262			0.137	0.02%
40F3	0.374	0.141	0.714	0.17	0.350	0.06%
40F4	3.526	2.56	3.641	5.317	3.761	0.62%
40F5	155.894	82.815	8.774	19.519	66.751	11.06%
40F6	20.142	12.368	25.332	8.596	16.610	2.75%
40F7	7.634	2.758	2.799	2.545	3.934	0.65%
40F8	0.56	0.098	0.265	1.357	0.570	0.09%
41F0			0.002		0.002	0.00%
41F2	0.073	0.01			0.042	0.01%
41F3	1.049	1.191	0.538	0.091	0.717	0.12%
41F4	0.723	0.594	0.319	0.41	0.512	0.08%
41F5	66.086	24.616	13.037	9.87	28.402	4.71%
41F6	24.901	31.033	21.579	16.864	23.594	3.91%

41F7	39.481	37.942	40.743	30.816	37.246	6.17%
41F8	8.397	7.172	15.373	13.211	11.038	1.83%
42F2	0.185	0.117	0.056	0.039	0.099	0.02%
42F3	1.482	2.431	0.592	0.74	1.311	0.22%
42F4	6.767	5.078	2.61	1.089	3.886	0.64%
42F5	10.95	6.162	9.948	7.17	8.558	1.42%
42F6	37.526	30.162	30.585	15.366	28.410	4.71%
42F7	55.571	44.097	47.905	40.79	47.091	7.80%
42F8	10.004	11.879	16.123	6.029	11.009	1.82%
43F0	0.027		0.01		0.019	0.00%
43F2	0.166	0.516	0.047	0.051	0.195	0.03%
43F3	1.31	0.71	0.455	0.885	0.840	0.14%
43F4	10.943	9.98	4.045	3.223	7.048	1.17%
43F5	38.788	30.772	28.941	34.51	33.253	5.51%
43F6	53.589	21.377	23.541	13.498	28.001	4.64%
43F7	92.034	72.475	52.397	23.395	60.075	9.95%
43F8	28.076	25.385	33.523	27.594	28.645	4.75%
43F9			0.006		0.006	0.00%
44F3			0.017	0.006	0.012	0.00%
44F4		0.08	0.083	0.02	0.061	0.01%
44F6			0.081	0.009	0.045	0.01%
44F7			0.014		0.014	0.00%
(NA)	18.277	19.371	0.701	0.103	9.613	1.59%

Review and update of the stock definition of flounder in the Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)

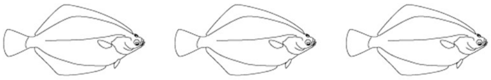

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Table of Content

Summary

European flounder is an estuarine flatfish species, migrating to higher salinity waters only during the spawning time. Presently, flounder in the Kattegat are considered as part of the North Sea stock. The adjacent flounder stock in the western part of the Baltic Sea covers the the Belt Sea and the Sound (SDs 22-23) and is one of four flounder stocks in the Baltic Sea.

We provide evidence that the management areas may require a change. Distribution maps from scientific surveys strongly suggest that there is no spatio-temporal separation between flounder in the Kattegat and the western Baltic (Belt Sea and the Sound) and that flounder in the Kattegat have negligible links to flounder in the North Sea. The Danish Straits are highly dynamic connecting channels between the southern Kattegat and Kiel and Mecklenburg Bight south of Denmark that make a stock separation between SDs 22-23 and SD 21 highly unlikely. No distinct differences were found in biological life history parameters (i.e. maturity and growth) between flounder from SD 21 and SDs 22-23. Additionally, genetic studies confirm that all flounder found in Kattegat and the western Baltic are in fact European flounder *Platichthys flesus*, whereas the Baltic flounder *P. solemdali* only occurs further east. Thus, a stock comprising flounder from the management areas SD 21-23 would realistically reflect the flounder population around the Danish archipelago.

Proposal

We propose to update the stock definition and boundaries of the flounder stocks in the North Sea and the Belt Sea and the Sound (western Baltic Sea) by removing Kattegat (Area 9, Subdivision SD 21) from the North Sea stock and adding it to the flounder stock of the Belt Sea and the Sound (SDs 22-23) to realistically reflect the flounder population around the Danish archipelago. Similar analyses already resulted in the inclusion of Kattegat to the western Baltic plaice stock (ple.27.21-23) and of Kattegat and Skagerrak to the Baltic sole stock (sol.27.20-24), making a similar scenario for other flatfishes very likely.

The updated flounder stocks *„fle.27.21-23"* (western Baltic Sea) and *„fle.27.3an4*" (North Sea) could be part of the benchmark "WKMSYSPICT3" by ICES in late 2023/early 2024 where the new stock ID and the respective changes in data can be implemented for stock assessment and stock status evaluation.

Current Status

North Sea

Flounder and dab in the North Sea have been assessed under a shared TAC until 2017. Since 2018 flounder in the North Sea is assessed as one stock (*fle.27.3a4*), covering Subarea 4 (North Sea) and Division 3.a. (Skagerrak and Kattegat) and is no longer subject to a TAC. Instead, a catch advice is given as long as dab and flounder remain largely bycatch species, with the main fleets catching dab and flounder continuing to fish the target species (plaice and sole) sustainably within the F_{MSY} ranges provided by ICES. If this situation changes, or flounder is no longer within safe biological limits, this advice would need to be reconsidered (ICES 2023a).

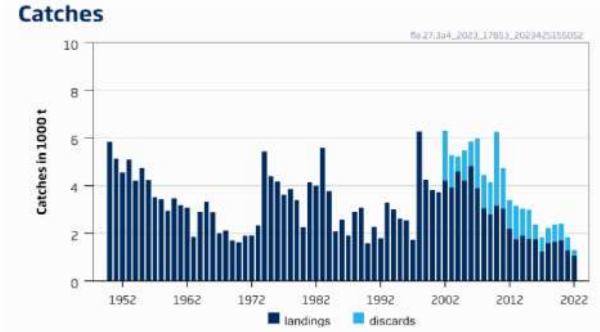


Figure 1: Official landings (1950–2001) and ICES estimates of landings and discards (2002–2021).

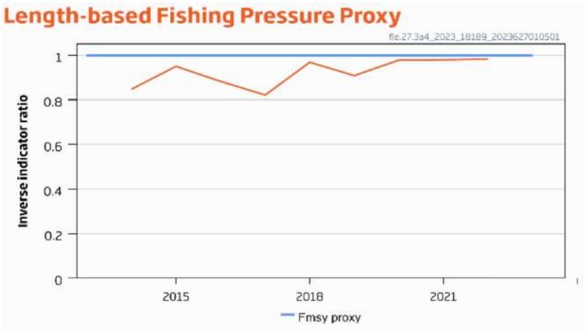


Figure 2: Index ratio L_{mean} /$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023b). The exploitation status is below the F_{MSY} proxy (dotted line) when the inverted index ratio value is lower than one.

Catch advice is given for two years and was last given in 2023 (for 2024 and 2025, ICES 2023a). Flounder is mainly a bycatch species in the mixed demersal fisheries targeting North Sea plaice and sole, with a variable medium discard rate (12-49% on average, included in the assessment since 2002). Flounder is of relatively little commercial importance in the North Sea and the Skagerrak/Kattegat. Therefore, there are uncertainties in the landings data with misreporting in previous years. Discard estimation are very uncertain due to the high variability between years and low priority in former catch sampling programs. Landings have decreased in the 2010s from around 3-4000t/year to around 1500t/year. Subarea 4 provides >90% of landings (ICES 2023a).

The stock is categorized as "data limited", following the ICES framework for category 3 stocks (ICES, 2023a). The most recent advice is based on the *chr* rule to provide MSY advice (ICES, 2023b). A survey combined biomass index is used as an indicator of stock development. An additional index ratio L_{mean}

/$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2023a) is used for the evaluation of the exploitation status.

Baltic Sea

Flounder is the most widely distributed among all flatfish species in the Baltic Sea, covering virtually the entire Baltic Sea. The flounder stocks in the Baltic were benchmarked in 2014. As a result, four different stocks of flounder were identified (WKBALFLAT, ICES 2014). Recently, a new flounder species was identified (Momigliano et al. 2018, Jokinen et al., 2019), characterised by demersal spawning, which is an adaptation to the low salinities in the north-eastern Baltic Sea. The two described flounder species (pelagic spawning European flounder *Platichthys flesus* and demersal spawning Baltic flounder *Platichthys solemdali*) are sympatric and are considered to mix in SDs 24-32 with an increasing share of *P. solemdali* east- and northwards (Kuciński et al., 2022, Table 2).

Currently these two Baltic flounder species can be separated only through genetic analysis, therefore at present there is no easy and inexpensive way to separate these species in commercial catches or in BITS survey trawls. Therefore, it is acknowledged that there are two different flounder species in the Baltic, and in all of management units, except for SDs 22 and 23 (Table 2), there is a mix of these two species, however, no separation between species is attempted during the assessment process.

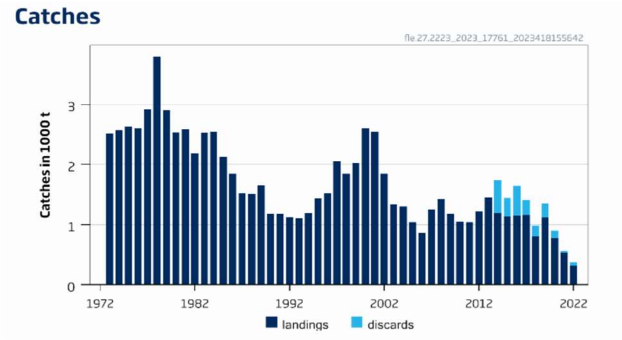


Figure 3: Official landings (1972–2001) and ICES estimates of landings and discards (2006–2022).

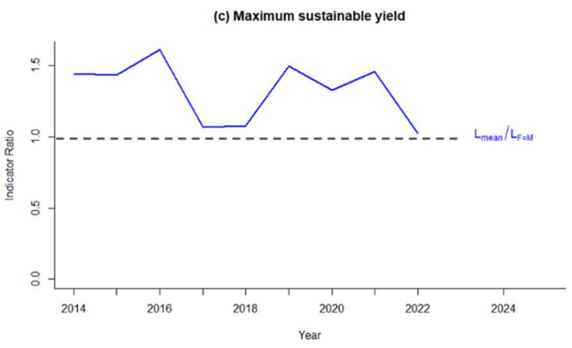


Figure 4: Index ratio L_{mean} /$L_{F=M}$ ratio from the length-based indicator method (LBI; ICES, 2023c). The exploitation status is below the F_{MSY} proxy (dotted line) when the index ratio value is higher than one.

The flounder stock in the Belt Sea and the Sound (SDs 22 and 23) consists only of European flounder (*P. flesus*) and even though there is no physical connection between SD 22 and SD 23, flounder in these areas are assumed to be connected through the western part of SD 24 (i.e., 12°-13°E of SD24, west of Darß sill and Hanö Bight). This connection and the presence of flounder from SDs 22 and 23 in the western part of SD 24 is however masked by the presence of the much larger flounder stock in SD 24-25. Additionally, survey data suggest a high connectivity with Kattegat, assuming it to be part of the flounder stock in the Belt Sea and the Sound (ICES 2023b). As the Darß sill in the Arkona Sea is the only physical barrier that would restrict flounder movements to SD 24, it is likely that a large part of flounder in area SD24.1 (i.e., the western part of the Arkona basin between 12° and 13°E) is also part of the stock fle.27.22-23. An inclusion of this area into the western Baltic flounder stock could be considered. A similar approach has been taken in the stock separation to account for the mixing between western Baltic cod and eastern Baltic cod in SD 24 (ICES 2015, 2019).

The largest and most productive flounder stock of Europe is found in the southern Baltic (SD 24-25). Fle.27.22-23 is the second largest flounder stock in the Baltic Sea. In this stock, flounder is mainly caught in the area of the Belt Sea (SD 22). The Sound (SD 23) is of minor importance for the contribution to the total landings. Commercial landings have been around 2000 tons/year since 1972. However, landings decreased to below 1000 tons in the early 1990s and again in the early 2000s and remained at around 1000 tons/year since then. Discards of flounder are recorded since 2014 and vary greatly with ratios around 20–50% of the total catch of vessels using active gears (e.g., otter trawls). Passive fishing gears have lower discards, varying between 10 to 20% of the total catch (ICES 2023d).

The flounder stock in SD 22–23 is categorized as a data-limited-stock (DLS). Especially sampling data from the beginning of the time-period (2000–2006) are considered poor with a low sampling coverage in time and space. More than half of the strata (landings and discards) from that period had to be filled with borrowed data (extrapolated length-distributions and mean weights per length-class). It is assumed that an analytical assessment using the data matrix prior to 2007 can only have the level of an exploratory assessment, but is recommended for a reasonable advice.

The update on the stock status is based on the data-limited approach of ICES. Catch advice is given since 2016. Recently, ICES is only requested to give stock status updates every three years. The last stock update was given in 2022 (for 2023 and 2024, ICES, 2022c). A survey combined biomass index is used as an indicator of stock development. An additional index ratio L_{mean} /$L_{F=M}$ from the length-based indicator method (LBI; ICES, 2022a) is used for the evaluation of the exploitation status.

Spatio-temporal distribution

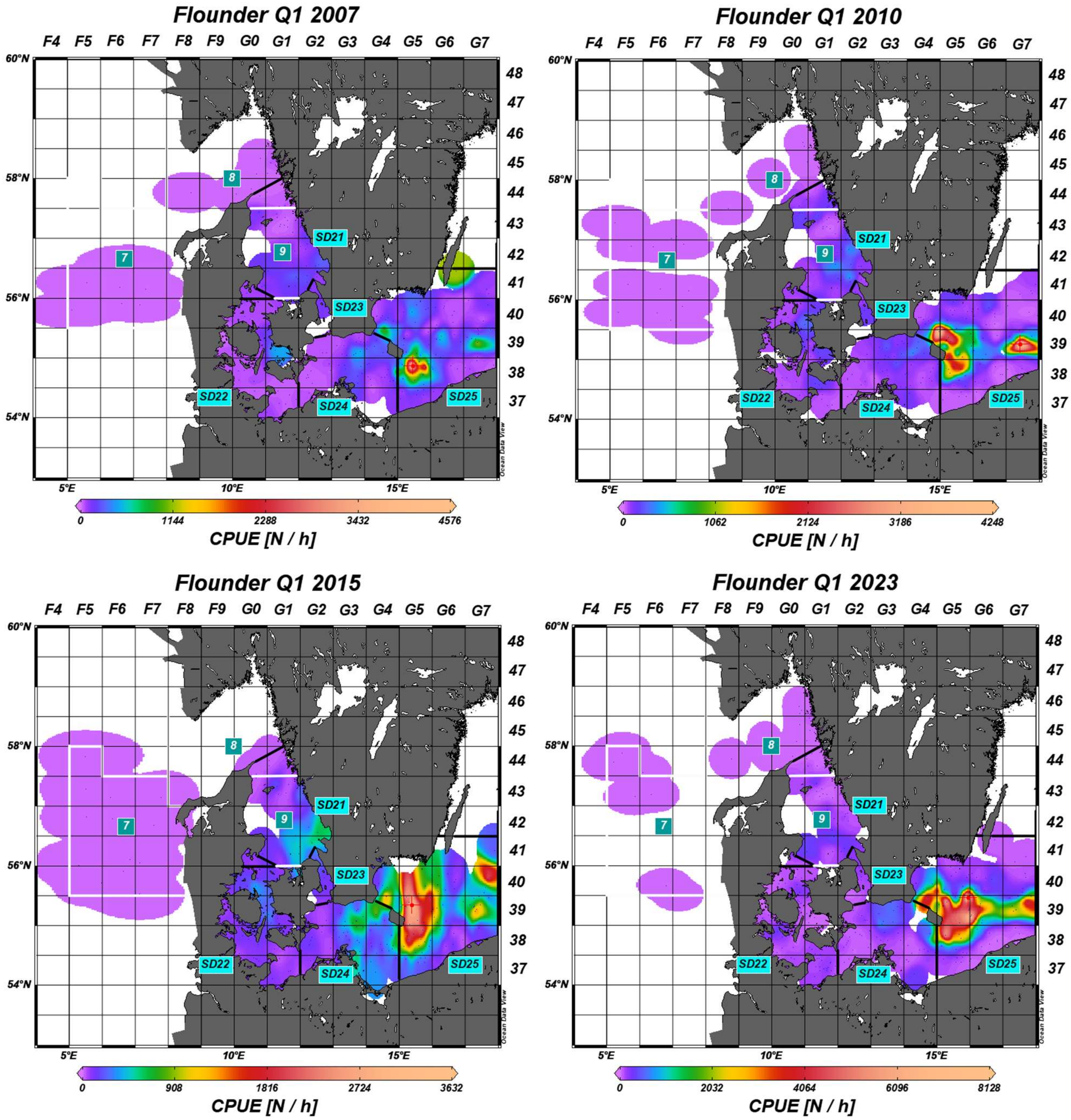
Surveys

The data of scientific trawl surveys were used to generate distribution maps and overviews for flounder in the north-eastern North Sea, Skagerrak and Kattegat, as well as the western Baltic Sea. The aim was to investigate spatio-temporal distribution patterns and changes since the start of the time series and between seasons.

The International Bottom Trawl Survey (IBTS) covers the North Sea (Subarea 4) and the Transition area (Division 3.a. including the Skagerrak 3.a.20 and Kattegat 3.a.21) and is conducted two times per year in Quarter 1 and 3 (Q1, Q3). The Baltic International Trawl Survey (BITS) covering the entire Baltic Sea and Kattegat (3.a.21) and is conducted also twice per year, in Q1 and Q4. Both surveys are conducted using the same sampling protocols and data are publicly available at the International Survey database DATRAS, hosted by ICES (https://datras.ices.dk). For the maps used in this document, the datasets of both surveys were merged and combined CPUE data were calculated using the respective method of the sampling manual of WGBIFS (ICES 2023d).

Combined survey indices of Q1 surveys from 1992-2023 in IBTS areas 7, 8, and 9 and the western Baltic Sea (SDs 22-25, Figure 5) showed that the highest densities of flounder occur in Division 3.a. and in the Baltic Sea around Bornholm Island and Arkona Sea. The latter reflects the major spawning aggregations of flounder in the southern Baltic (SD24-25) in Q1.

These high densities mask patterns in the Danish archipelago and therefore, data from SD 24-25 were omitted for the next overviews.


Flounder Q1 2007

Flounder Q1 2010

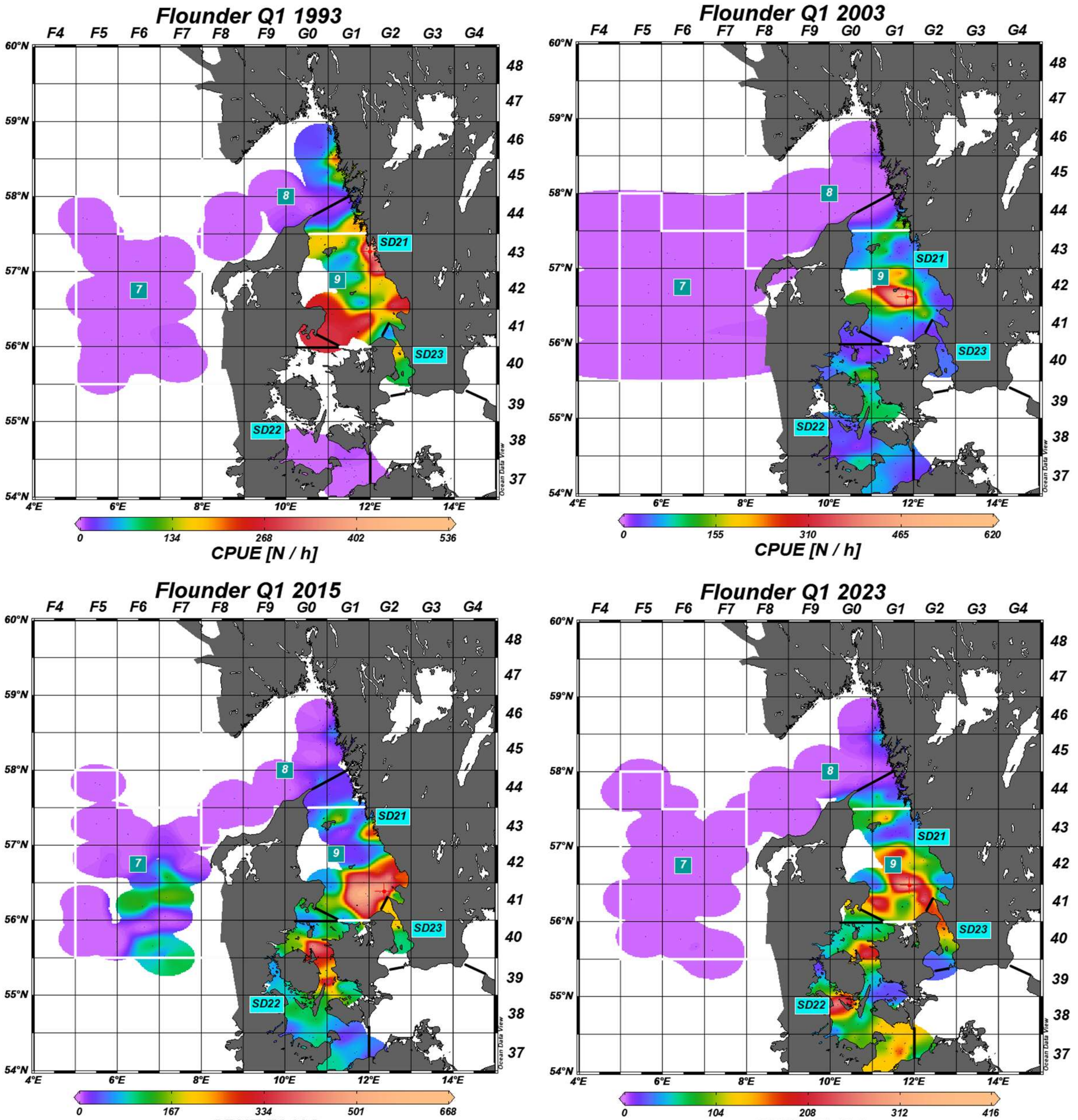
Flounder Q1 2015

Flounder Q1 2023

Figure 5: Survey-based CPUE distribution of flounder in the Baltic Sea (SDs 22-25, BITS) in Q1 surveys of selected years.

In the transition zone between North and the Baltic Sea the main distribution of flounder is located in the northern part of the Belt Sea and the southern Kattegat around Sjælland (Figure 6, Annex 1.1). In most years, a clear link with continuous higher densities in SDs 21, 22 and 23 is apparent, whereas flounder are rare in the Skagerrak and the North Sea with a CPUE of 0 in central Skagerrak.

The distribution shifts between years, moving from central to southern Kattegat in the mid 1990's and in the mid 2000's. Only very few flounder are found in the region between Skagerrak and Kattegat (Figure 6, Annex 1.1). Hence, while flounder densities are low in the North Sea and Skagerrak, higher densities characterize the Danish archipelago, ranging from the Kattegat to the southern Belt Sea.



Flounder Q1 1993

Flounder Q1 2003

Flounder Q1 2015

Flounder Q1 2023

Figure 6: Survey-based CPUE distribution of flounder in North Sea (Areas 7,8,9, IBTS) and western Baltic Sea (SDs 22-23, BITS) in Q1 surveys of selected years. Maps from all years are shown in Annex 1.1.

The Q4 BITS and IBTS surveys showed a similar distribution with high accumulations of flounder around Sjælland, connecting all three areas (SD21, 22 and 23) with each other (Figure 7, Annex 1.2). IBTS has only been conducted in Q4 until 1996, but also displayed similarly low abundances of flounder in Skagerrak as seen in Q1.

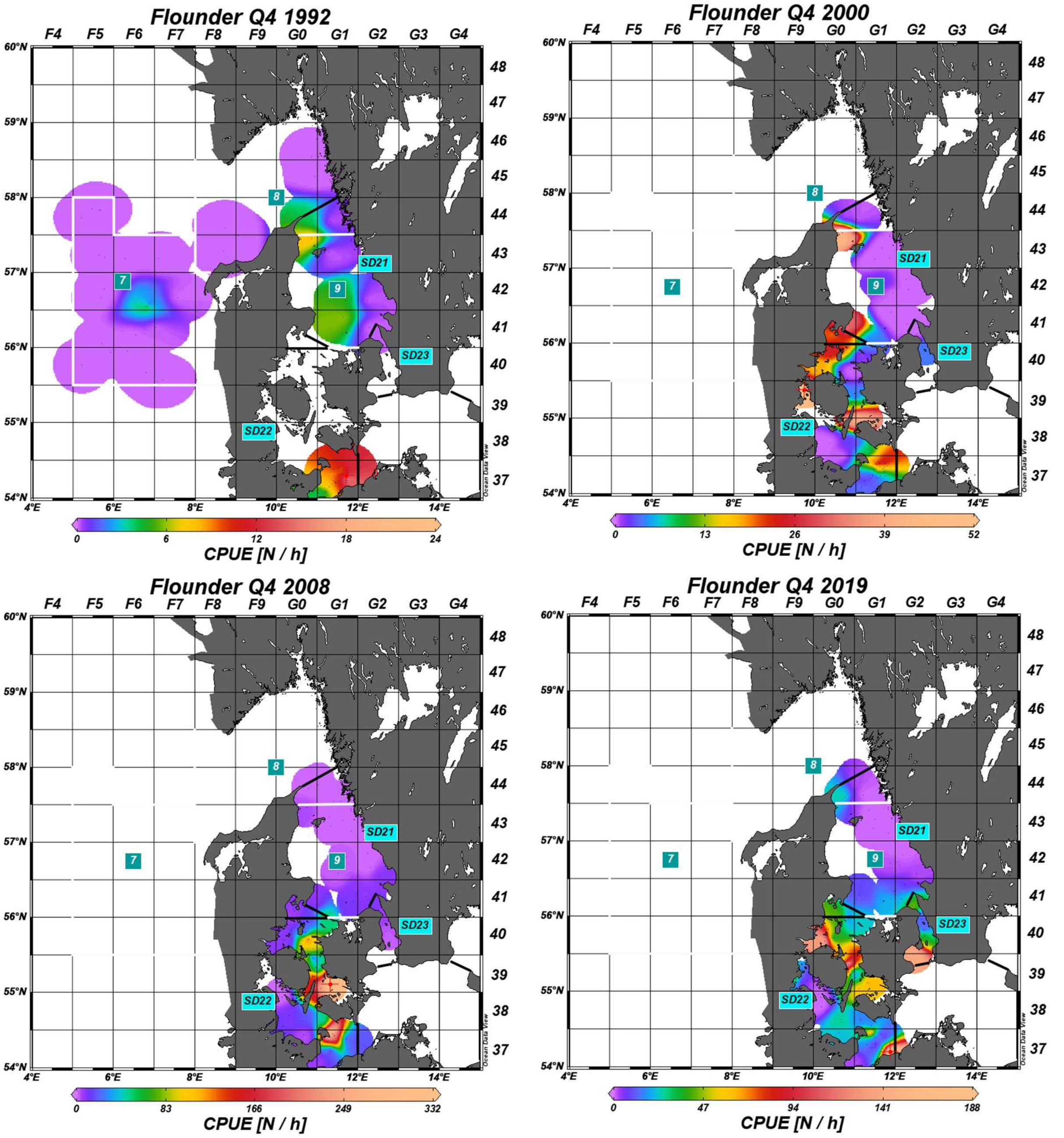
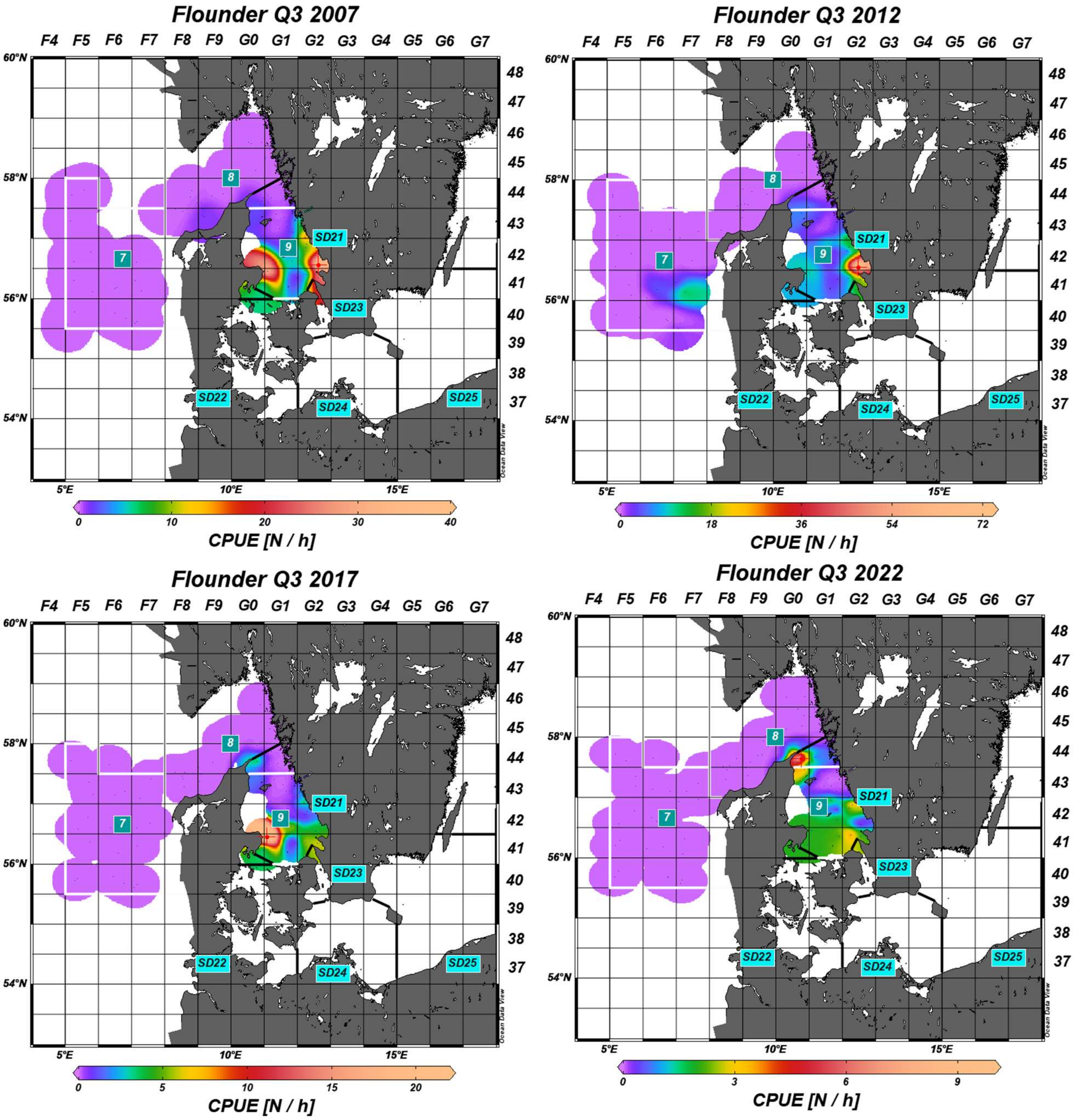


Figure 7: Survey-based CPUE distribution of flounder in North Sea (Areas 7,8,9, IBTS) and Baltic Sea (SDs 22-23, BITS) in Q4 surveys of selected years. Maps from all years are shown in Annex 1.2.

Likewise, the Q3 IBTS index of flounder displayed a similar distribution pattern (Figure 8) with high abundances of flounder in the southern Kattegat. The spatial connectivity between North Sea and Kattegat via the Skagerrak is as low as seen in the Q1 and Q4 surveys. Only a small aggregation of flounder was present along the northern Danish coast. This aggregation was fished and landed by commercial fisheries, whereas almost no landings (<1t/year per ICES statistical rectangle) were reported from the rest of the Skagerrak area.



Flounder Q3 2007

Flounder Q3 2012

Flounder Q3 2017

Flounder Q3 2022

Figure 8: Survey-based CPUE distribution of flounder in the North Sea (Areas 7,8,9) during the Q3 IBTS survey.

The lack of flounder between the North Sea and the Kattegat area derived from the IBTS data suggest that there is limited connectivity, and at least two separate stocks might exist (Jokinen et al., 2019, ICES 2023a). However, a robust understanding of the population structure in the North Sea, Skagerrak and Kattegat would require a thorough analysis of biological data and genetic analyses. WGNSSK stated that there is no information about stock identity and possible stock assessment areas in the North Sea, Skagerrak and Kattegat. Within the North Sea there may exist a number of sub-populations (ICES 2023a), given that flounder spend the feeding period mainly in or near estuaries and only migrate to more saline waters during the spawning period.

Additional analysis of the CPUE distribution of flounder in Q4 from surveys in the areas of Arkona Sea (SD 24) and Bornholm Sea (SD 25) displayed high densities of flounder in the coastal feeding grounds (Figure 9). The high CPUE of flounder from the southern Baltic stock in SD24-25 is masking possible connections between flounder from the Belt Sea and the Sound via SD24. Given that the Danish straits do not provide large physical barriers and hydrographical conditions are very dynamic, it is likely, that flounder from SDs 22 and 23 are also using the western parts of SD24. While several genetic studies

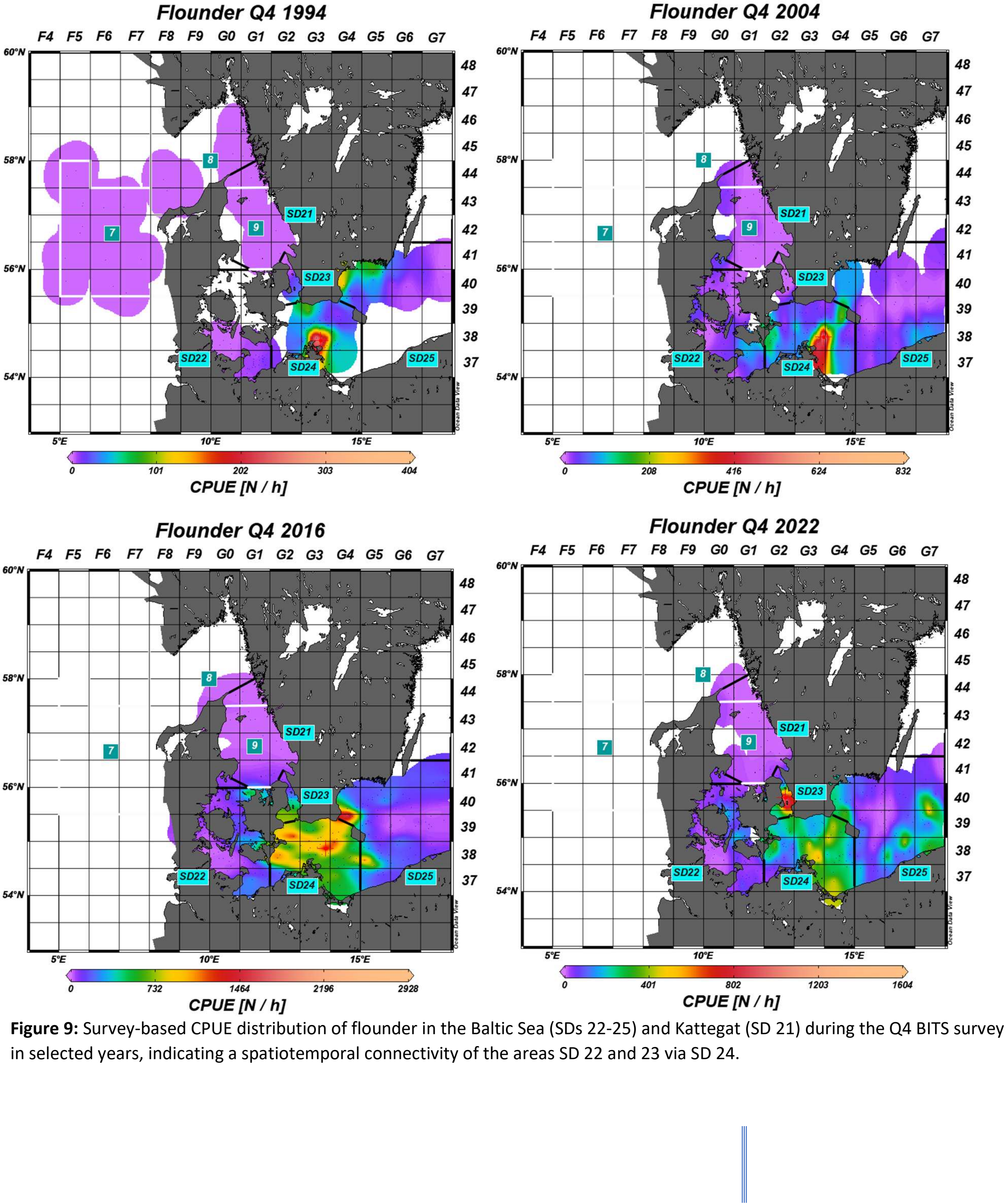


Figure 9: Survey-based CPUE distribution of flounder in the Baltic Sea (SDs 22-25) and Kattegat (SD 21) during the Q4 BITS survey in selected years, indicating a spatiotemporal connectivity of the areas SD 22 and 23 via SD 24.

confirmed that the major part of flounder in SD 24 is in fact European flounder (*P. flesus*, see chapter “Genetics”, e.g. Momigliano et al., 2018, 2019, Kuciński et al., 2023, Jokinen et al., 2019), so far no attempts have been undertaken to genetically assess the detailed population structure of flounder from the North Sea into the Baltic Sea.

Fishery

The fishing pattern in Division 3.a. (i.e. SDs 20 and 21) basically reflects the distribution of flounder from the survey indices, with the major parts of flounder landings originating from southern Kattegat and western Skagerrak close to the two major harbours in northern Denmark, Hirtshals and Skagen.

Only occasional and very low (<1t/year) landings were registered from other areas of Skagerrak and Kattegat, confirming the low abundance of flounder in this area (Figure 10, Annex 1.3).

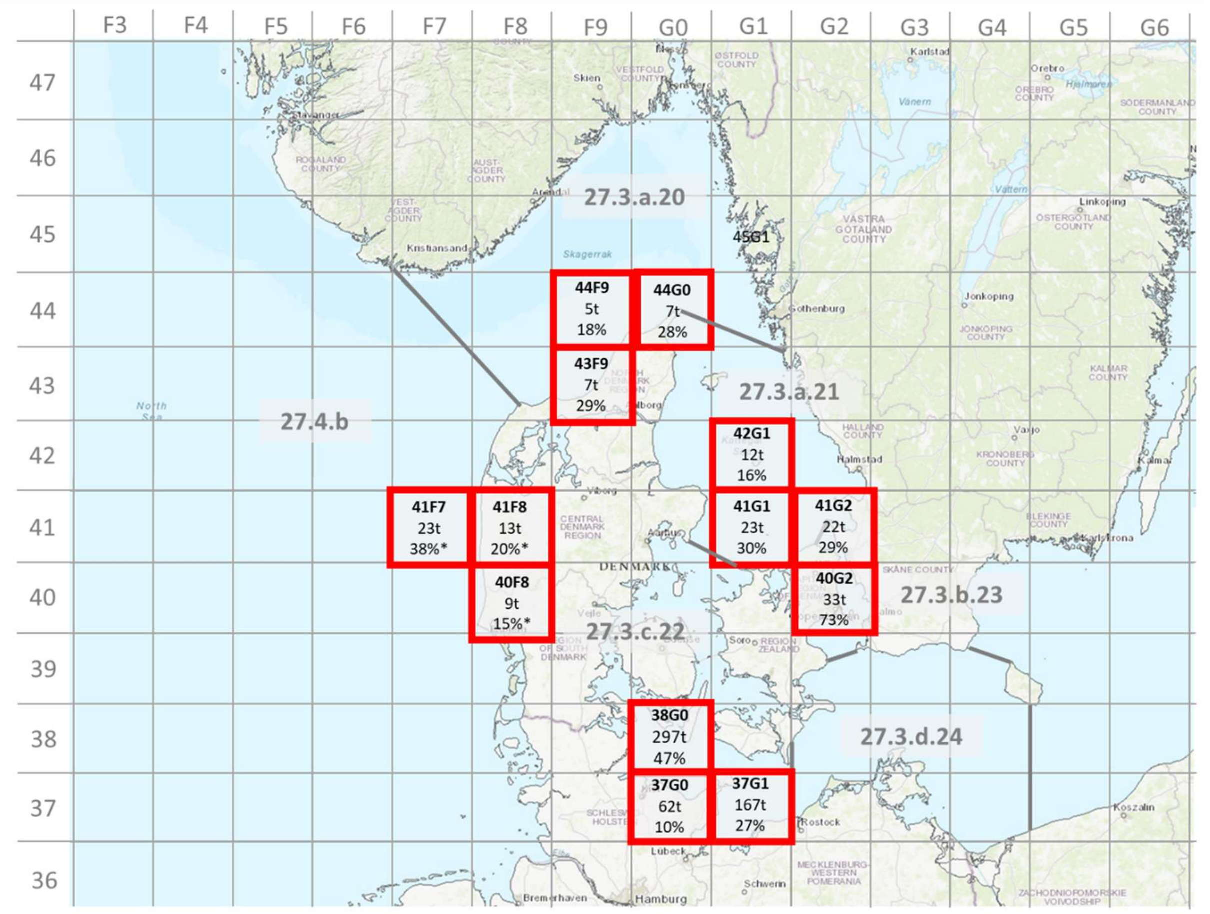


Figure 10: Landings of flounder in the North Sea (27.4.b), transition area (27.3.a) and the western Baltic Sea. Averaged (2019-2022) contribution of ICES statistical rectangles that provide >75% of landings per Subdivision.

* 60% (~100t) of flounder landings in the North Sea are not allocated to a statistical rectangle and were not used for the calculation

The Kattegat (SD21) had relatively low landings of flounder (around 80t/year), where the species is mainly caught as bycatch in *Nephrops*-directed fisheries and thus usually discarded. The major part (>60%) of the landings is taken in the southern area (ICES statistical rectangles 41G1 and 41G2) at the border to SD 22 and SD 23.

Landings in Skagerrak (SD20) were usually low at around 20t/year and were taken mostly along the northern Danish coastline of western Skagerrak, with 43F9, 44F9 and 44G0 contributing most (>75%)

of the landings. Discards were estimated for Kattegat and Skagerrak together (as Division 3.a) and range from 27% to 87% of the total flounder catch and were usually higher than in the North Sea or western Baltic Sea (ICES 2023a, 2023b).

The fishery on flounder in the western Baltic Sea was concentrated in the Belt Sea. On average, >95% of the annual landings originated from the Belt Sea, mainly by Germany and Denmark. Average landings have been >1000t/year, decreasing to around 700t/year in 2020/2021. A strong decline in fishing activity (caused by low TACs on western Baltic cod and decreased fishing opportunities) in 2022 also decreased landings of flounder to around 320t (Figure 3). Discards have been stable in the last few years at around 18% of the total catch (ICES 2023d).

Life history parameters

Different life history parameters were obtained from Q1 surveys (IBTS for the North Sea) and from BITS, covering Kattegat and the western Baltic Sea. Maturation and growth in North Sea, Kattegat and western Baltic Sea were very similar (Figure 11, Table 1), with an average maturation at around 20cm total length and similar growth patterns in the current data year. Flounder in Kattegat was only occasionally sampled for detailed biological data so that life history parameters for the comparison could only be obtained for 2010.

Flounder in the North Sea displayed a growth pattern very similar to flounder caught in the Kattegat and the western Baltic and length-weight relationships were also very similar.

Table 1: Life history parameter of flounder caught in Q1 Surveys in 2022 in the North Sea (IBTS), Kattegat (BITS) and Baltic Sea (BITS)

	North Sea*	**Kattegat**	**Baltic Sea**
Maturity-at-length	21cm	20cm**	20.5cm
Growth intercept	0.004	0.0122**	0.0166
slope	3.262	2.948*	2.872
L_{inf}	41.3cm	-***	44.3cm
N	318	78	362

* Flounder is only sampled occasionally during IBTS, data are averaged from 2012, 2013 and 2022 Q1 surveys

**only Q1 2010 data available, only few individuals measured

***no age reading conducted in SD21

Figure 11: length-weight correlation of flounder in the North Sea (blue line), Kattegat (red line) and western Baltic Sea (green line). Data obtained from Q1 surveys (IBTS and BITS).

Genetics

It has been long acknowledged that in the European flounder in the Baltic Sea has two distinctively different ecotypes (sometimes also considered as two sympatric flounder populations): the pelagic and demersal spawning flounder. In 2018 Momigliano et al. revealed that these two ecotypes are in fact two different species - European flounder *Platichthys flesus* (pelagic spawners) and Baltic flounder *Platichthys solemdali* (demersal spawners).

Despite having a parapatric distribution, *P. flesus* and *P. solemdali* in the Baltic Sea show strongly bimodal genotypic clustering based on genome-wide single nucleotide polymorphism (SNP) markers and strong reproductive isolation (Momigliano et al., 2017). Genetic studies carried out over the past decade demonstrated that these morphological, physiological, and life-history differences are linked to stable and distinct genetic populations. Hemmer-Hansen et al. (2007) and Florin and Höglund (2008) investigated *P. flesus* population genetics using microsatellite markers, and discovered significant (albeit very weak, F_{ST} 0.01–0.03) genetic differentiation associated with spawning behaviour. Using a combination of genome-wide SNP genotyping and approximate Bayesian computation modelling, Momigliano et al., 2017 demonstrated that the two flounder types originated via two distinct colonisations of the Baltic Sea from the same ancestral population.

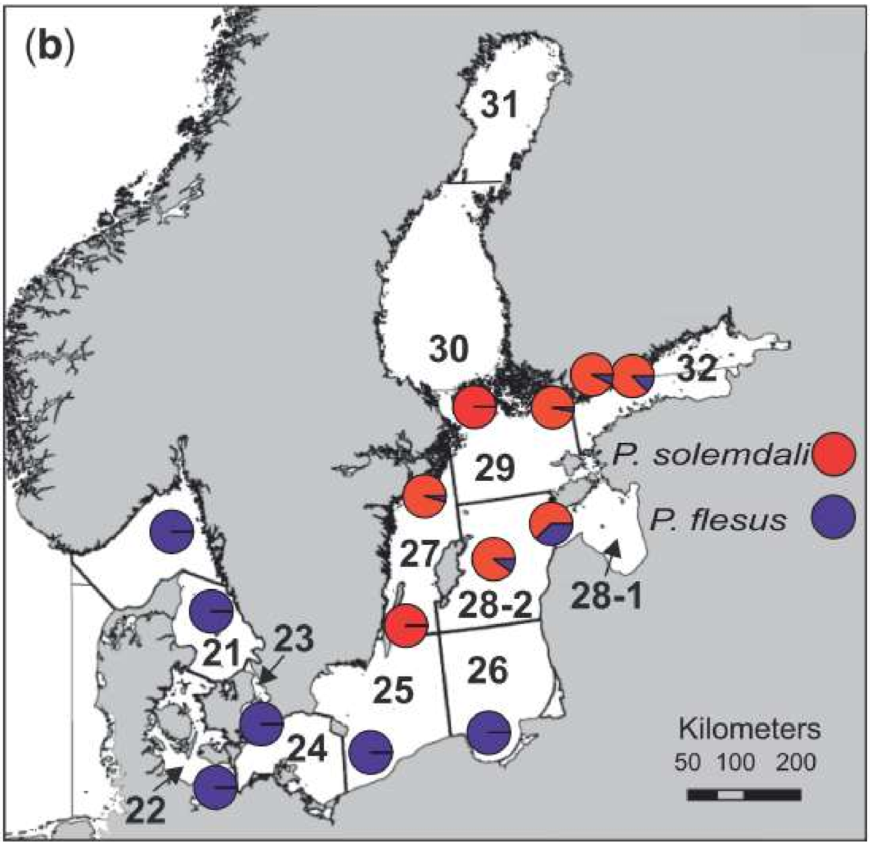


Figure 12: Contemporary proportion of the two main flounder lineages (European *P. flesus*, Baltic Sea *P. solemdali*) in different localities and across ICES subdivisions of the Baltic Sea (SD 21–32), based on previously published data (Momigliano et al., 2017, 2018, 2019).

It should be noted that these do not represent accurate and stable proportions in each of the localities, as they are likely affected by sampling strategy (both within and between years, and water depths), but they do provide evidence of mixed stocks in several locations (Jokinen et al. 2019)

However, none of these studies could find differences in genetic population structure between the areas SD 21 (Kattegat) and SD 22 (Belt Sea), where all sampled species were identified as European flounder *P. flesus* (Figure 12). Additionally, about 97% of the sampled individuals in SD 24 (Arkona Sea) were identified as European flounder (Jokinen et al. 2019, Figure 12, Table 2). A recent study investigated flounder sampled along the Polish coast of SD 24 concluded that European flounder (P. *flesus*) from the southern Baltic Sea represent a single and homogenous genetic cluster (Kucinski et al. 2022).

Table 2. Proportion of flounder with pelagic eggs (European flounder) per SD in the Baltic Sea (from: Momigliano et al., 2018).

ICES Subdivision	Proportion
32	8%
28	24%
26	98%
25	76%
24	97%

Linking these genetic findings with the distribution from the two scientific surveys suggests that the flounder population in Kattegat (SD 21) is rather part of the larger population of European flounder in the western Baltic Sea. European flounder seems to have three areas of occurrence with distinct density levels: Low levels are found in the North Sea and Skagerrak, medium densities around the Danish archipelago involving the Kattegat, Belt Sea and the Sound (SDs 21-23); and highest densities of European flounder in the southern Baltic Sea, populated by the highly productive flounder stock of SD 24-25.

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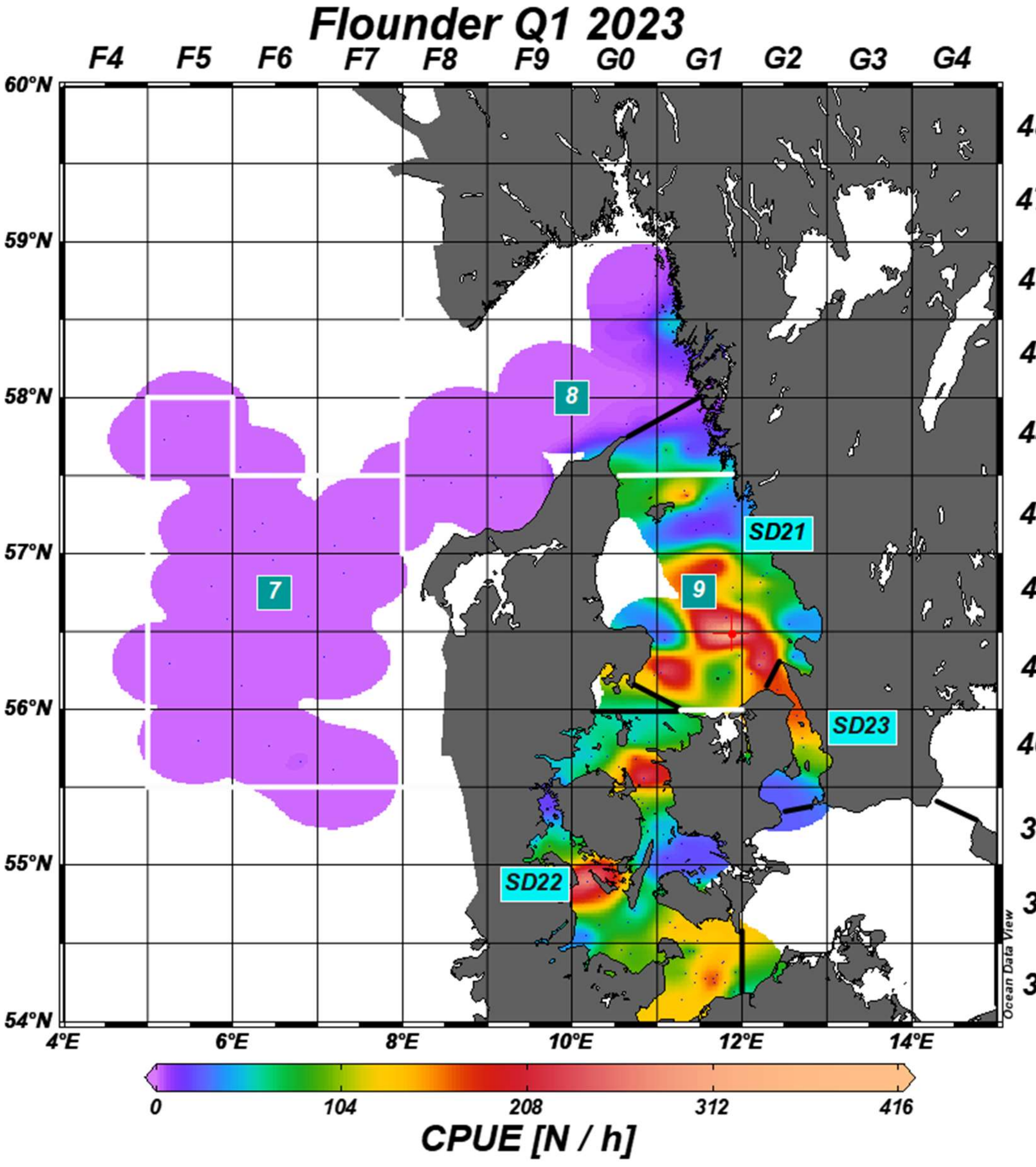
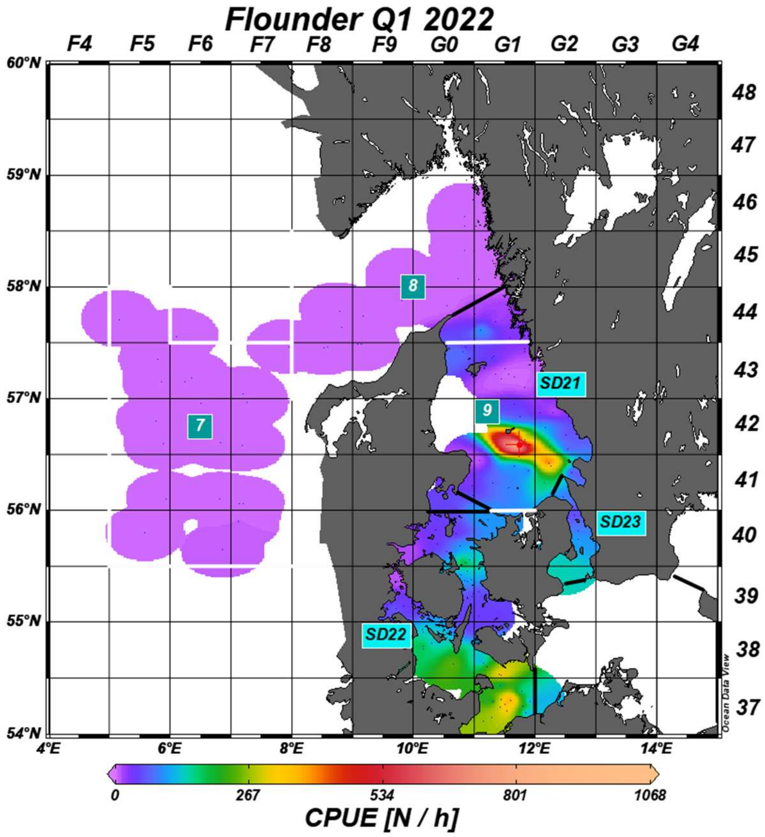
ANNEX 1.1

Combined **Quarter 1 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.




Flounder Q1 2022
F4
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G0
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G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
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42
41
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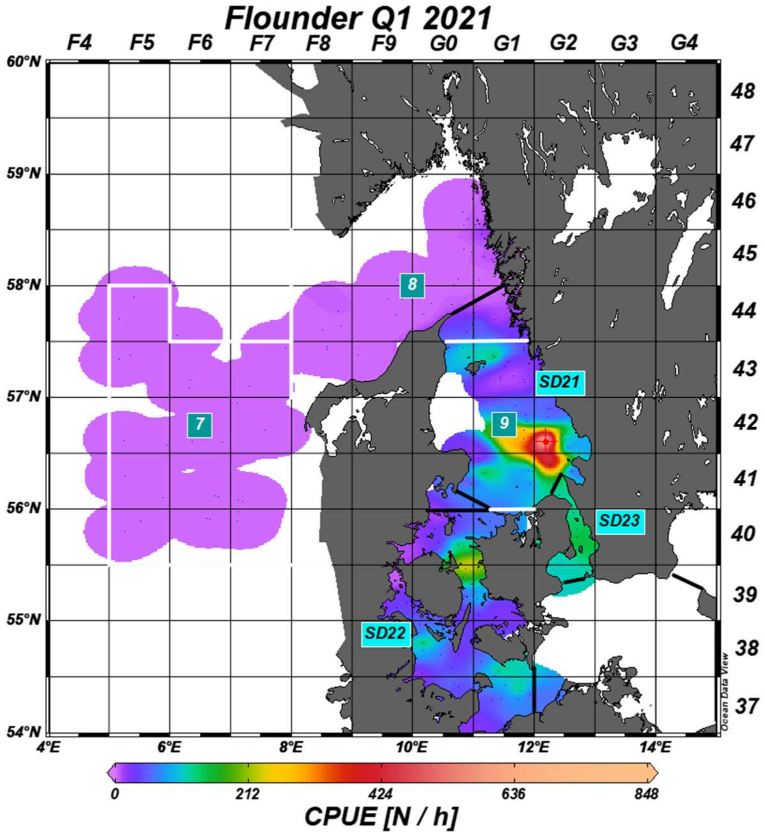
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
4°E
6°E
8°E
10°E
12°E
14°E
0
267
534
801
1068
CPUE [N / h]


Flounder Q1 2021
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SD21
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SD22
Ocean Data View
4°E
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424
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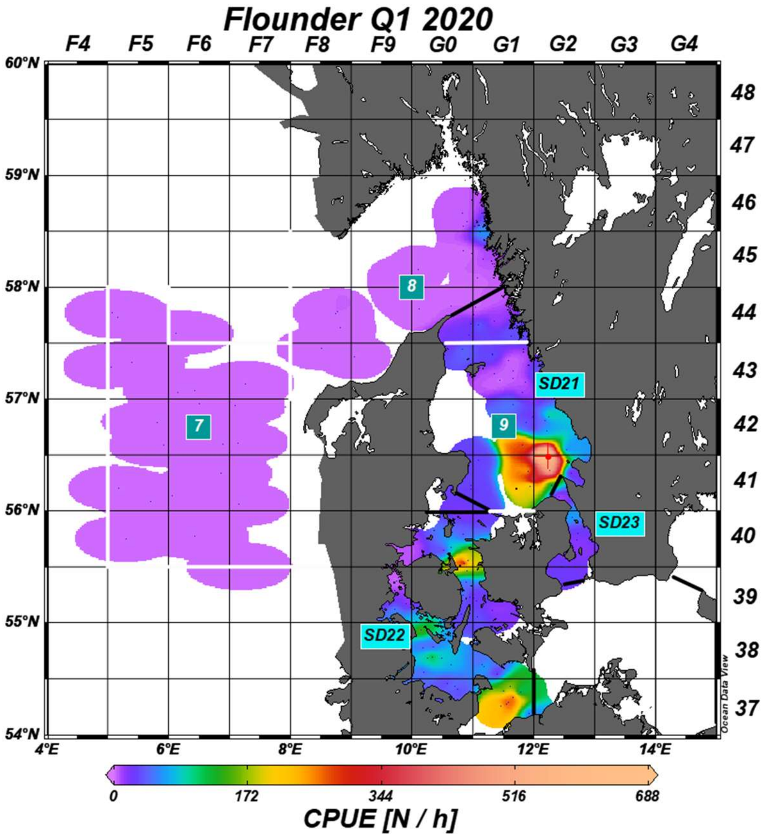
CPUE [N / h]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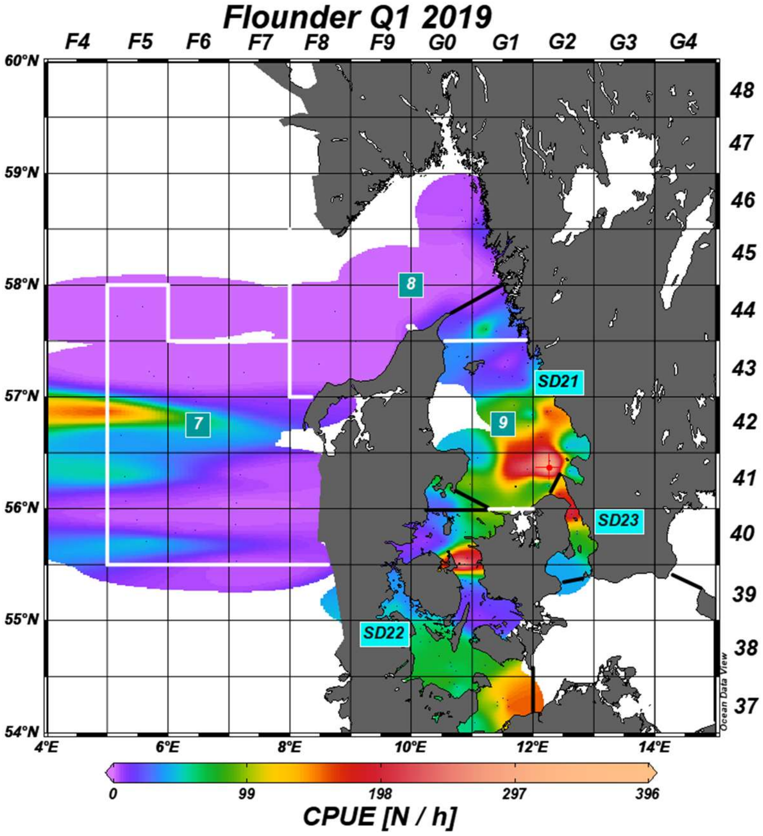
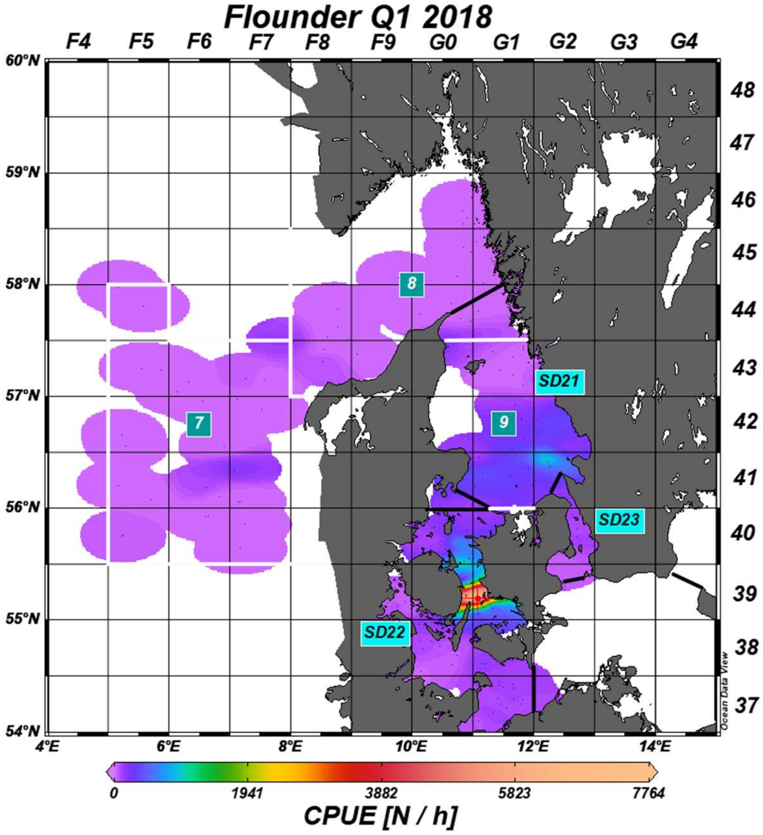

Flounder Q1 2019


Flounder Q1 2018
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
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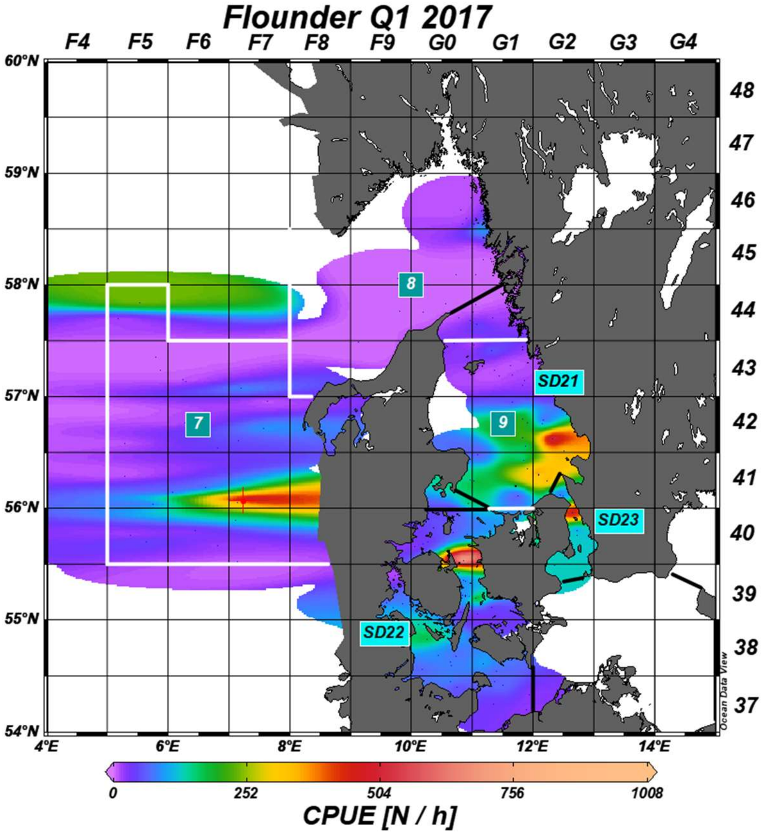
CPUE [N / h]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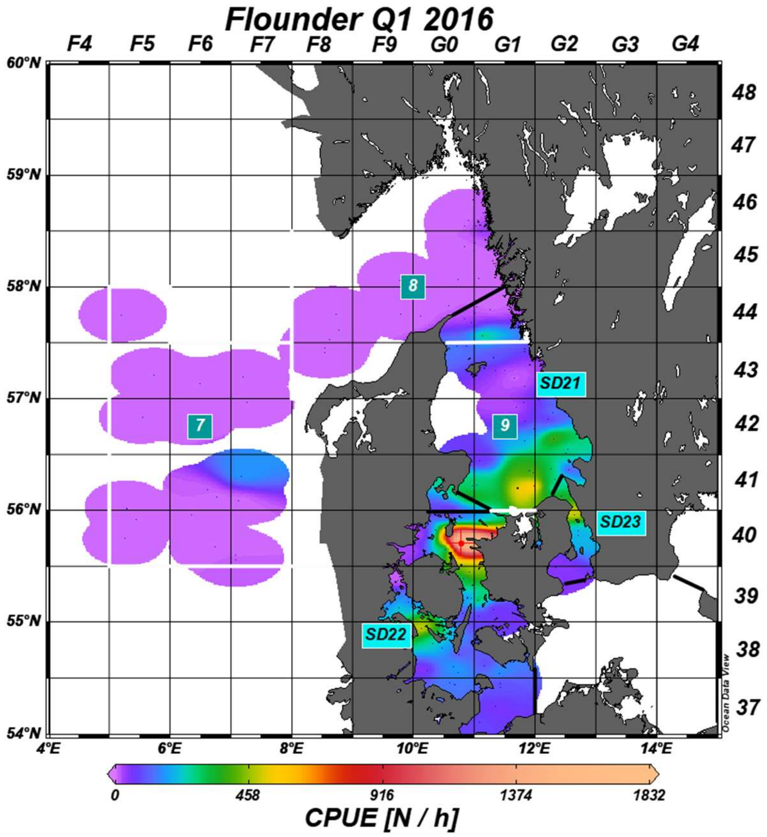
Ocean Data View
0 252 504 756 1008
CPUE [N / h]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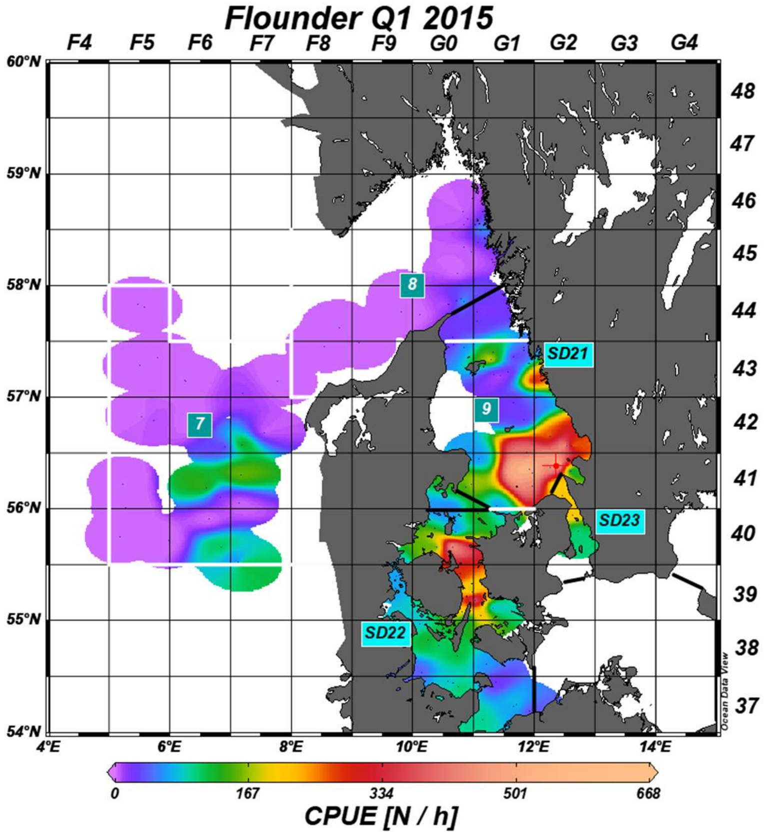
CPUE [N / h]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SD21
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Ocean Data View
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167
334
501
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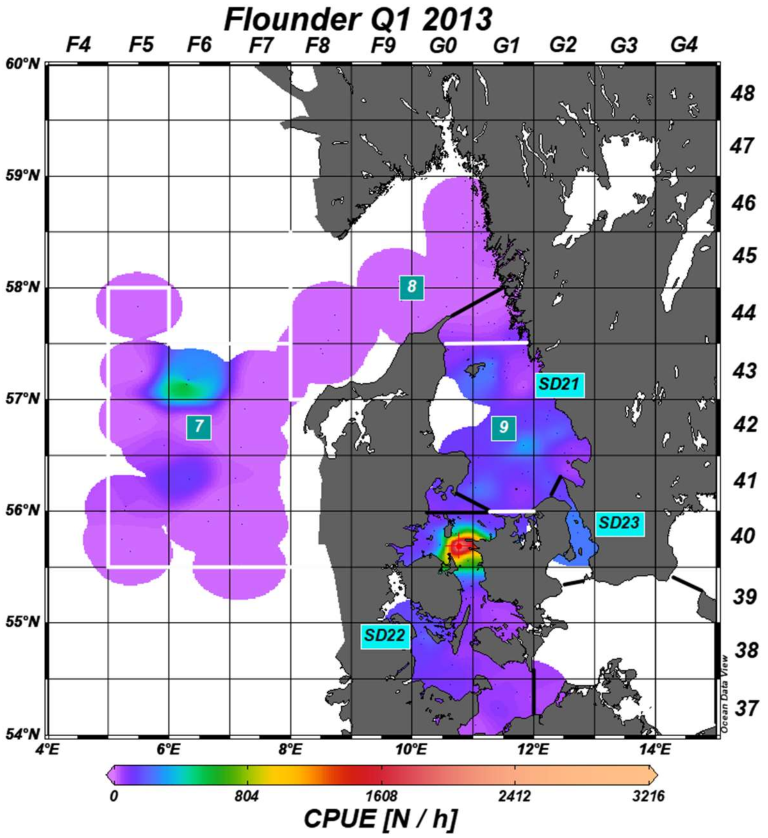
CPUE [N / h]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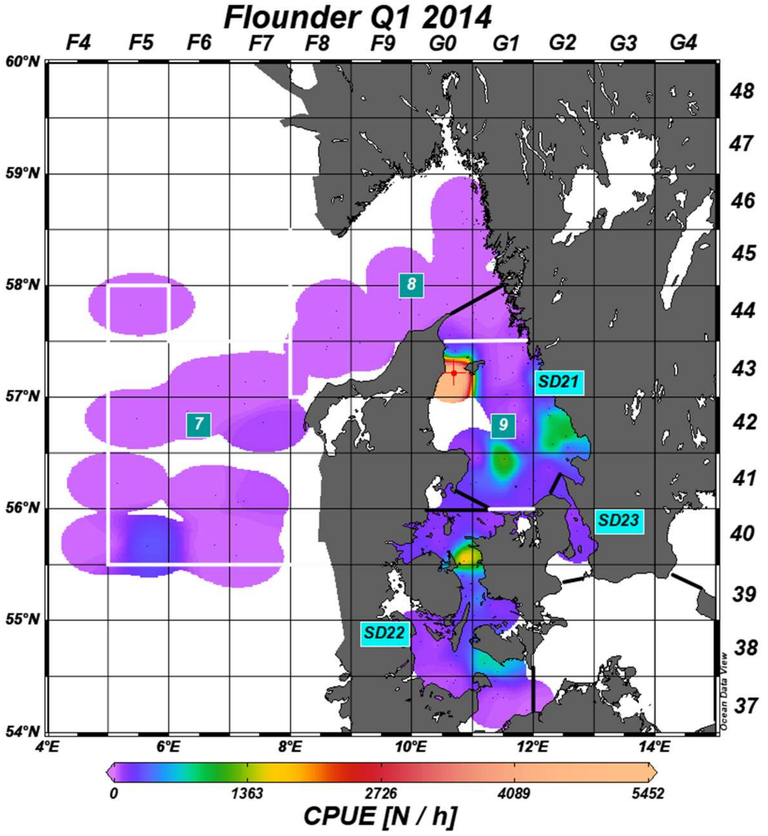
CPUE [N / h]


Flounder Q1 2014
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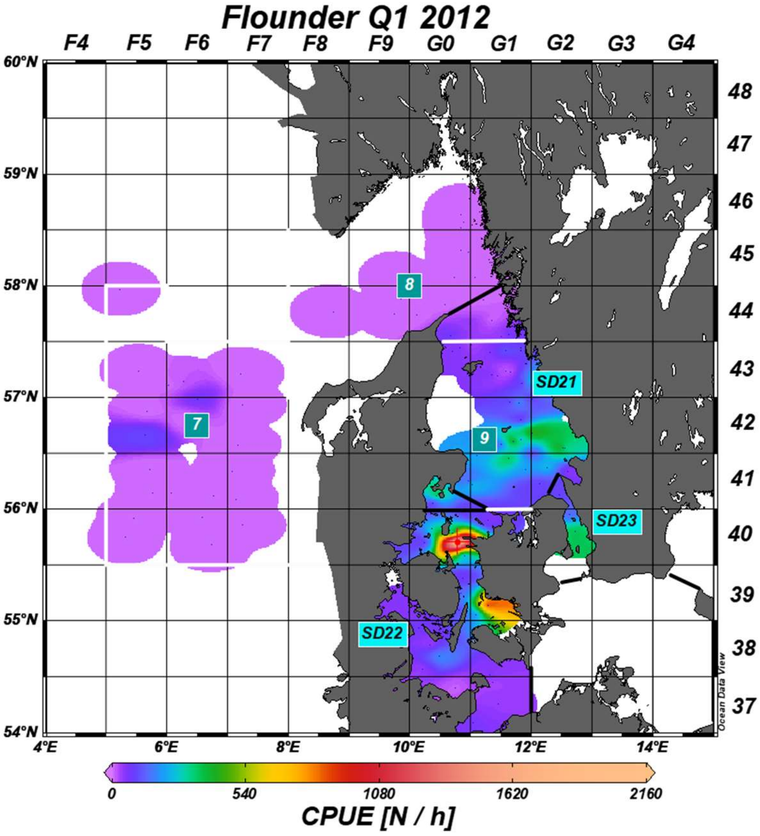
CPUE [N / h]


Flounder Q1 2012
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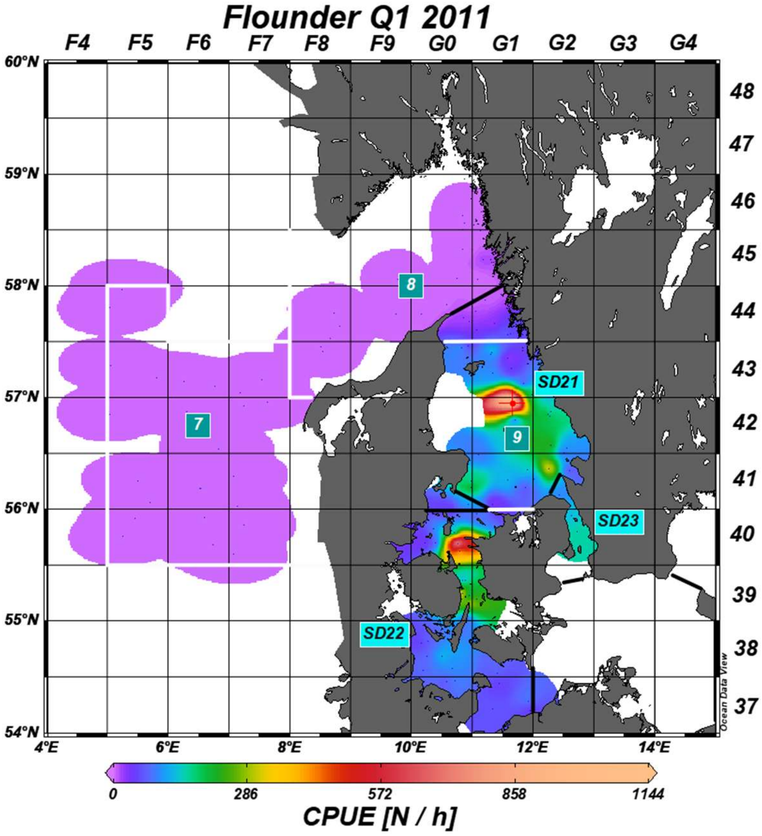
CPUE [N / h]


Flounder Q1 2011
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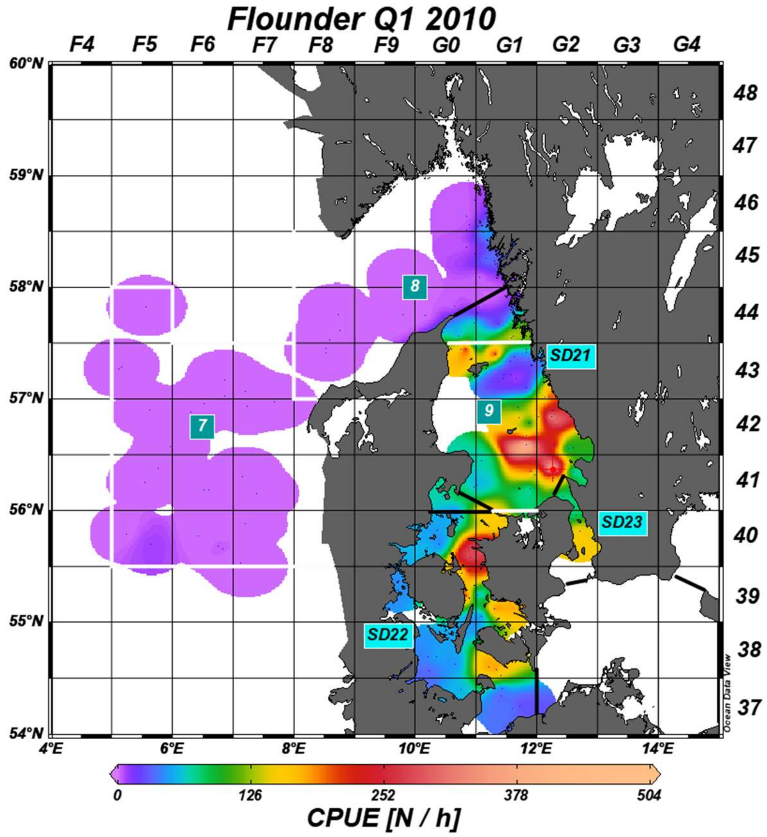
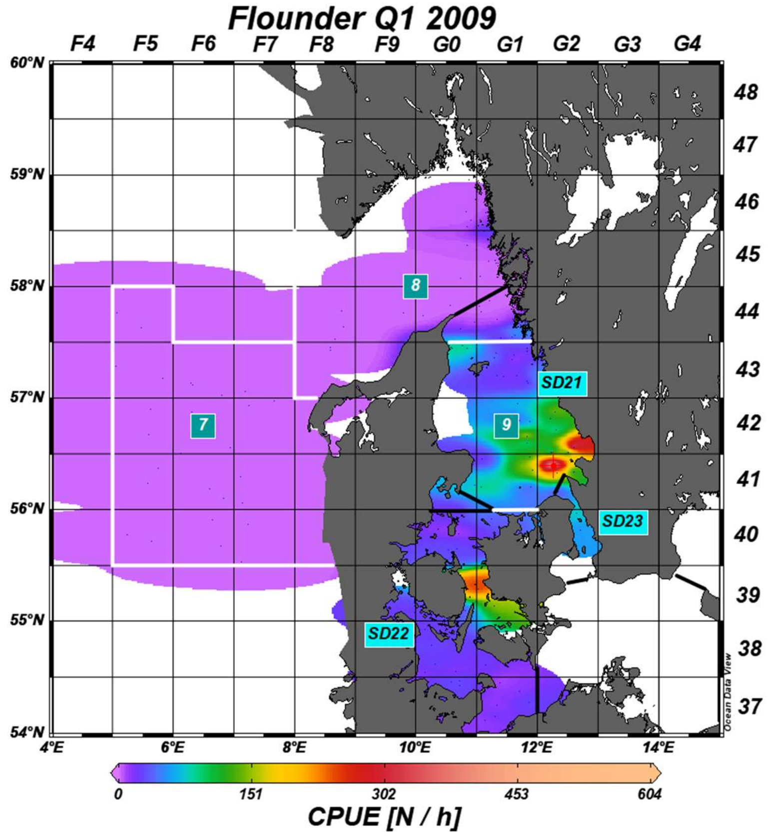
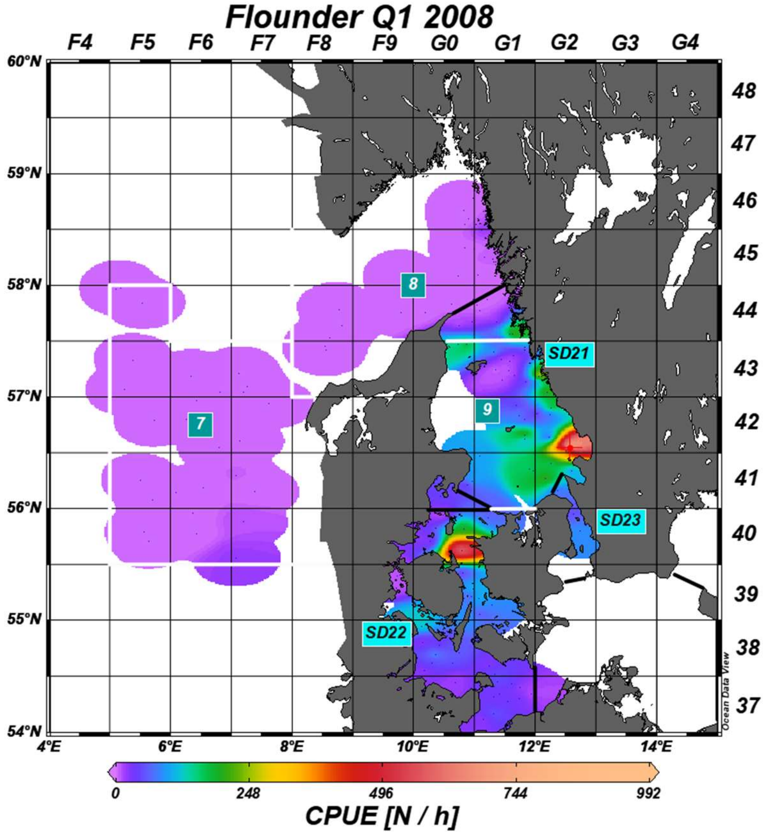
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
286
572
858
1144
CPUE [N / h]

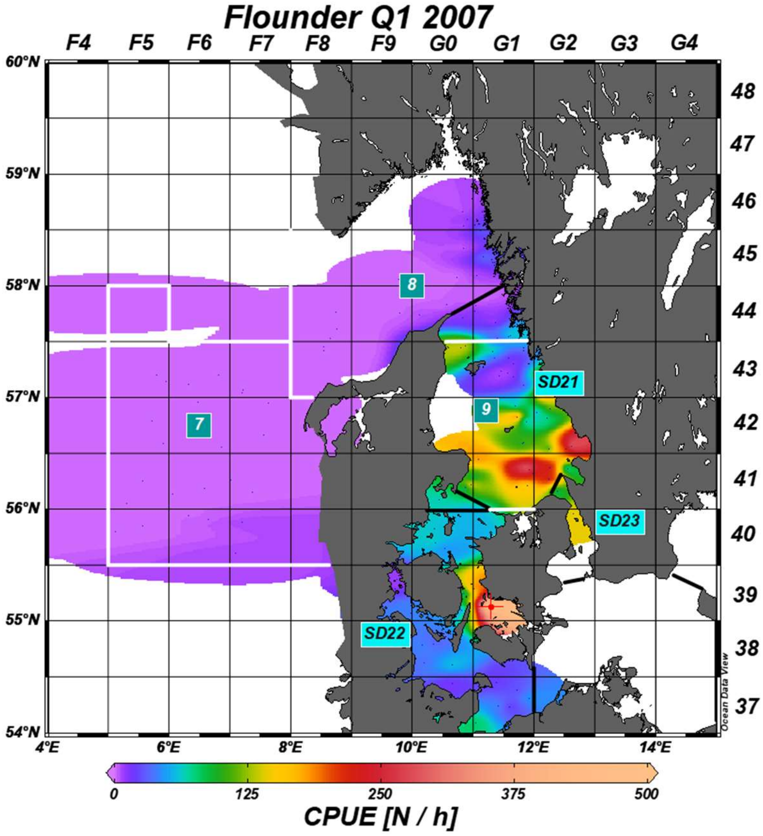


Flounder Q1 2010

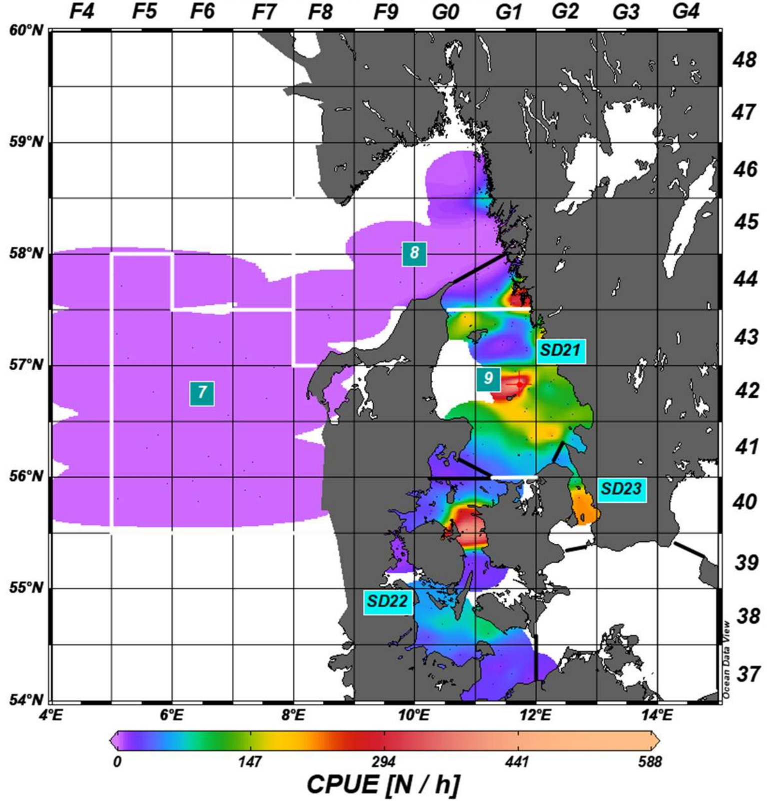


Flounder Q1 2009

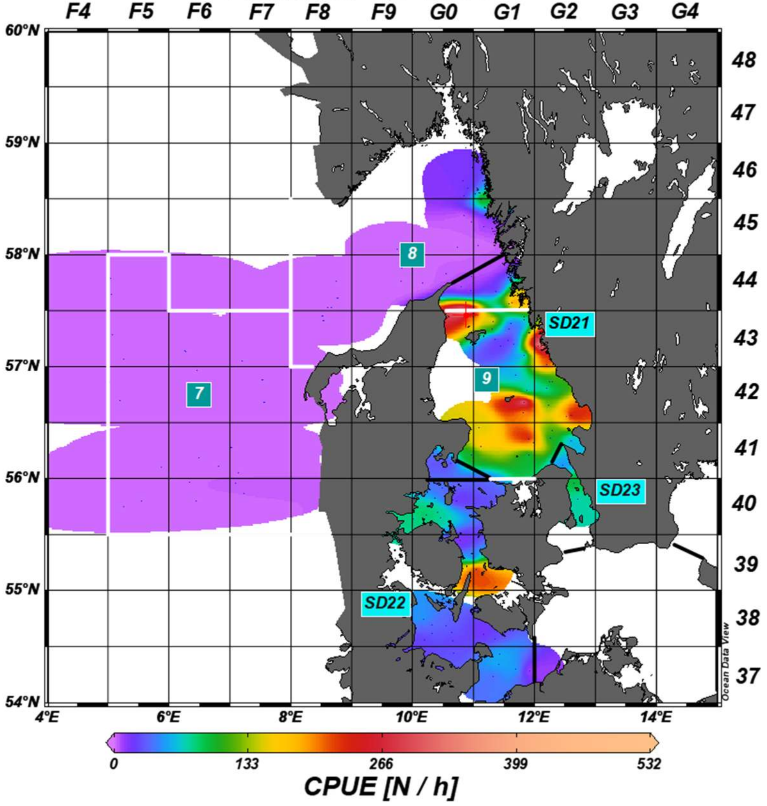

Flounder Q1 2008
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
248
496
744
992
CPUE [N / h]

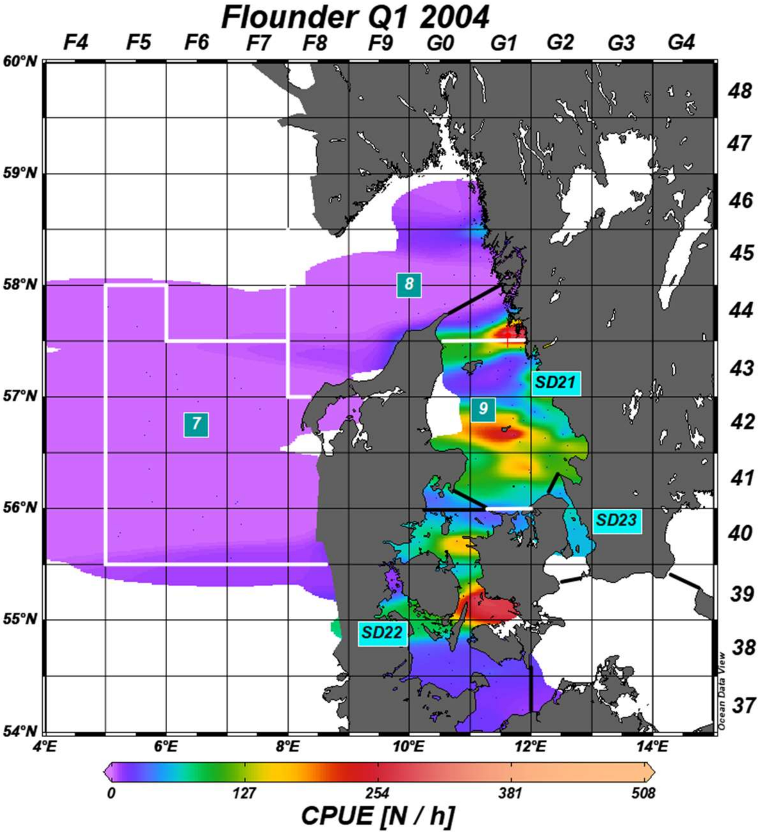

Flounder Q1 2007
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
125
250
375
500
CPUE [N / h]

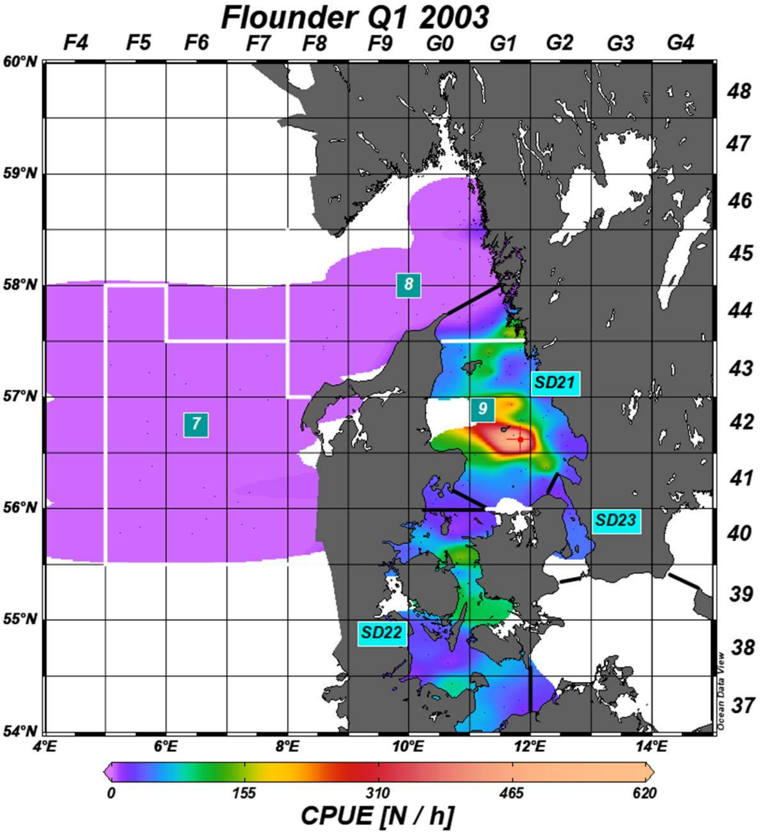
Flounder Q1 2006

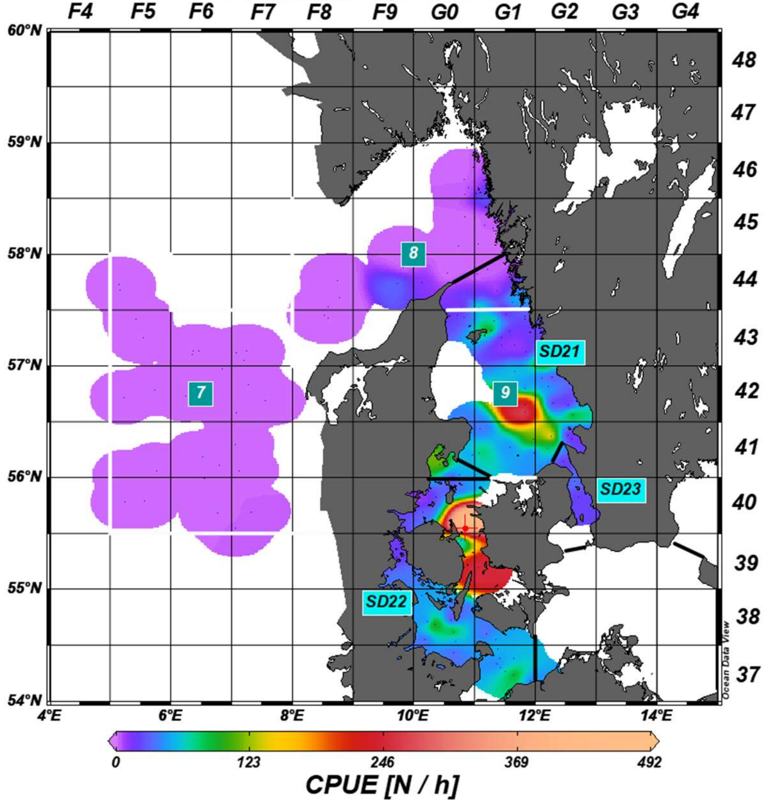


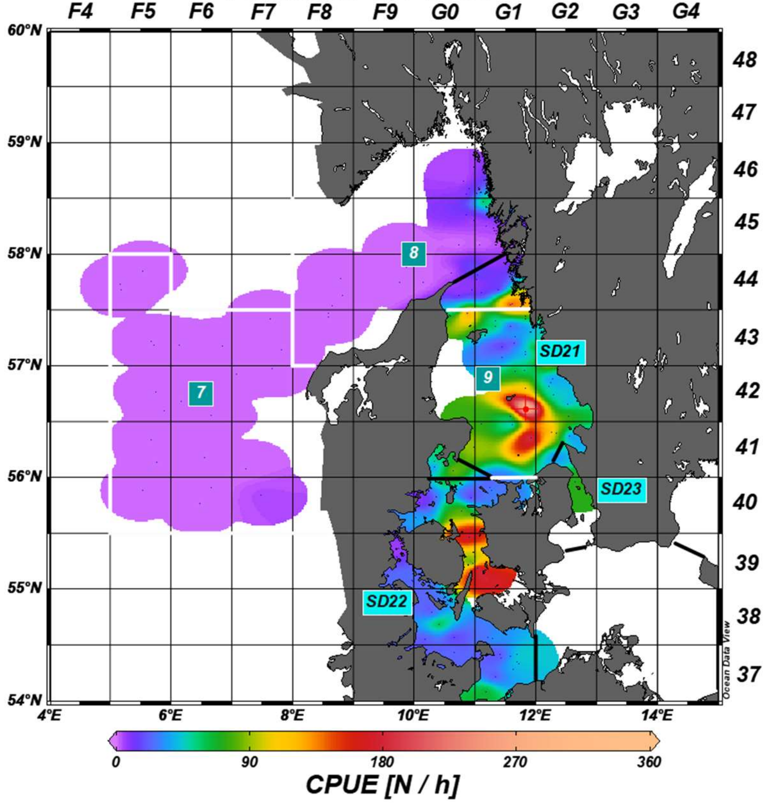
Flounder Q1 2005

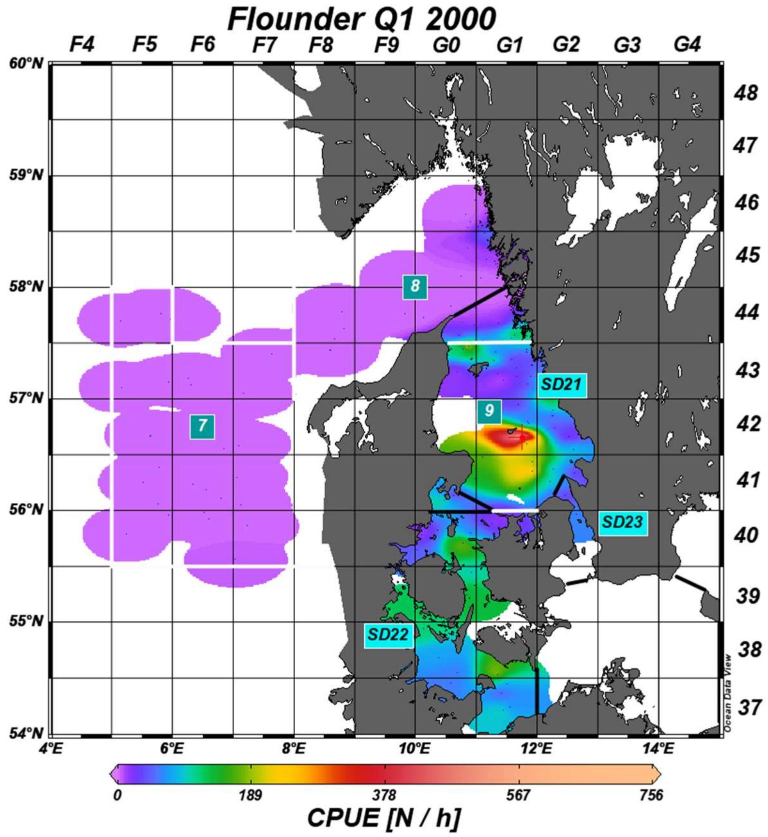



Flounder Q1 2004
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
127
254
381
508
CPUE [N / h]

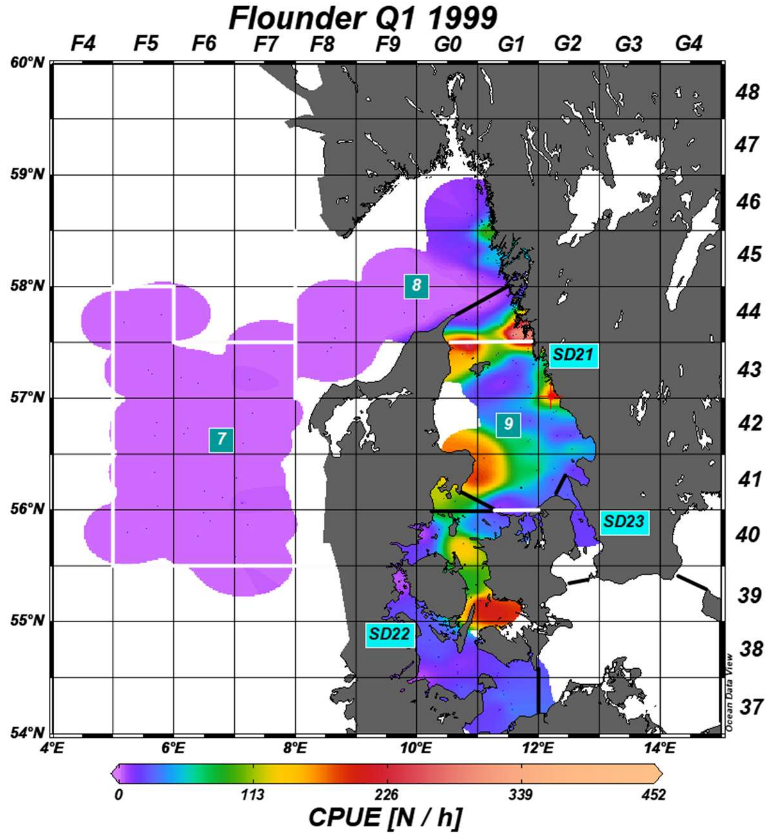

Flounder Q1 2003
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
155
310
465
620
CPUE [N / h]


Flounder Q1 2002

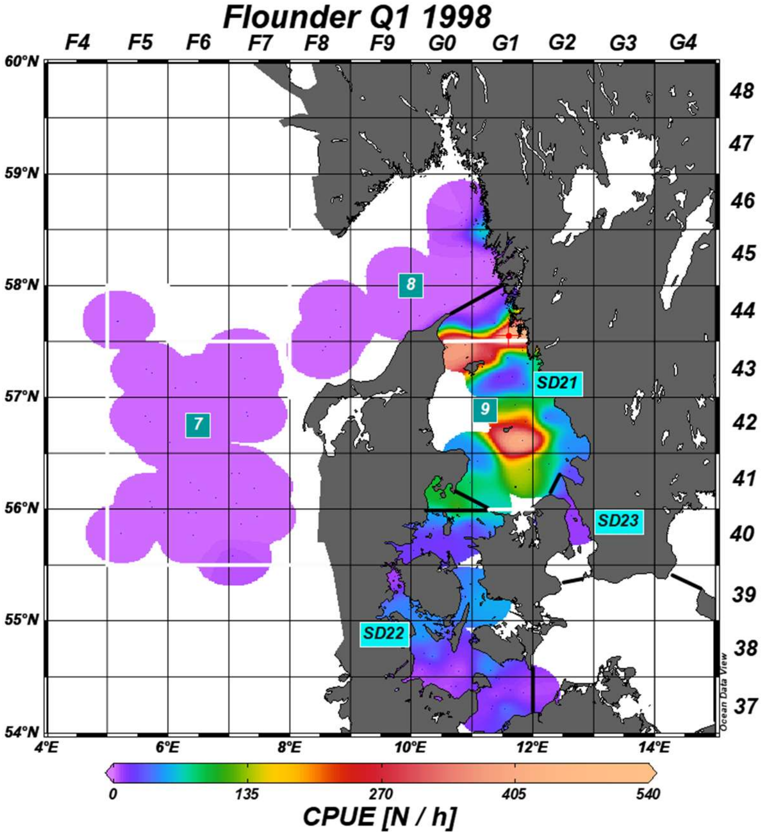

Flounder Q1 2001

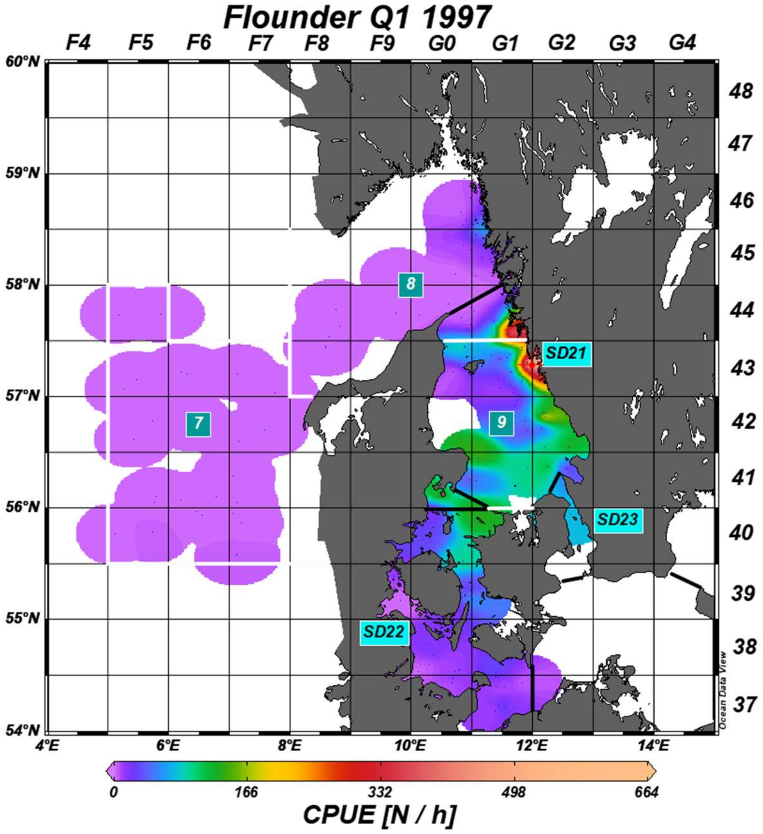


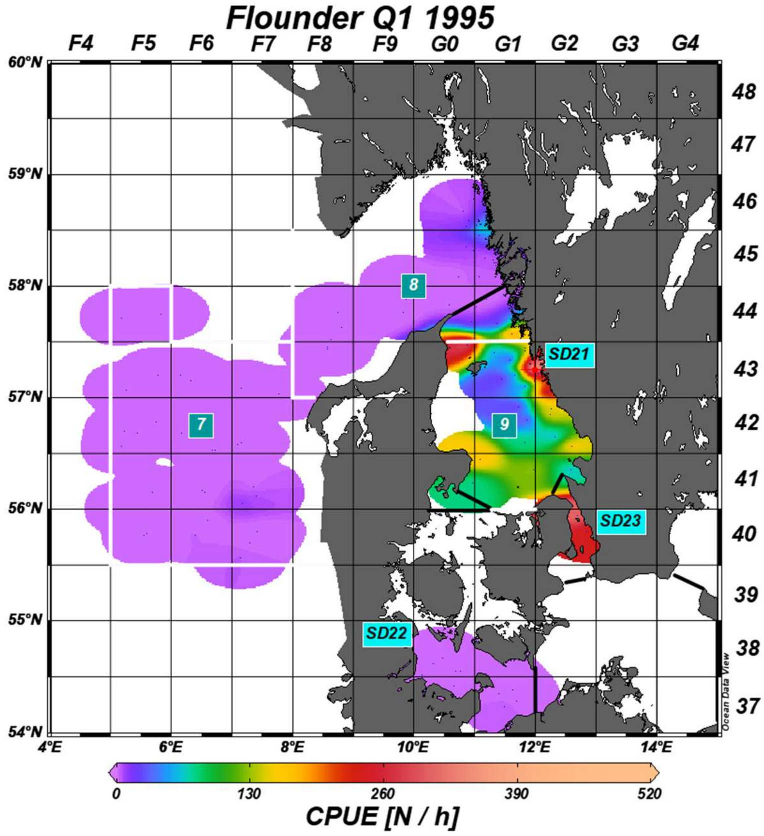
Flounder Q1 2000

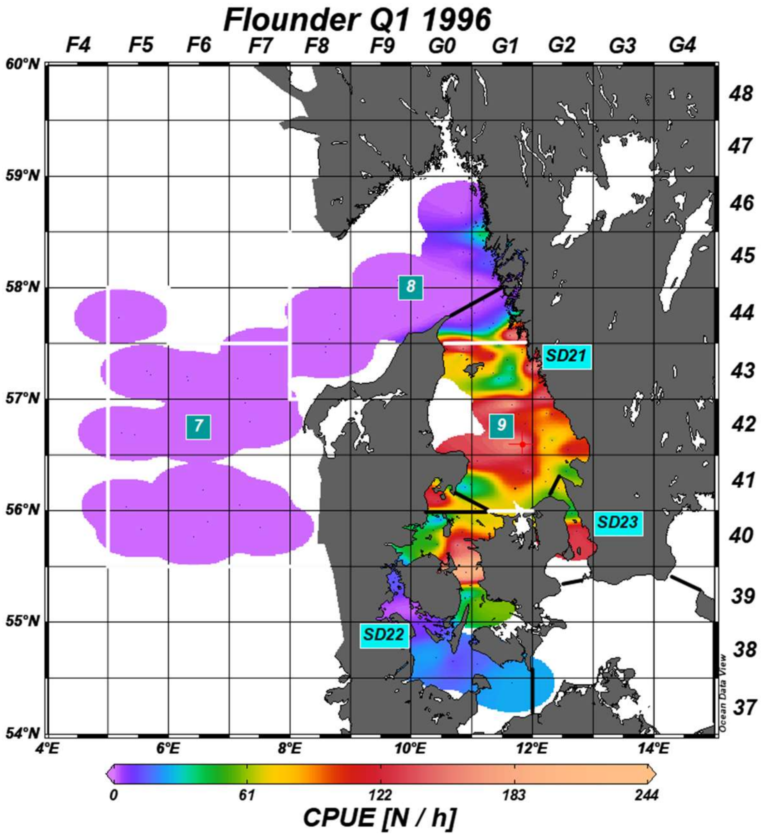


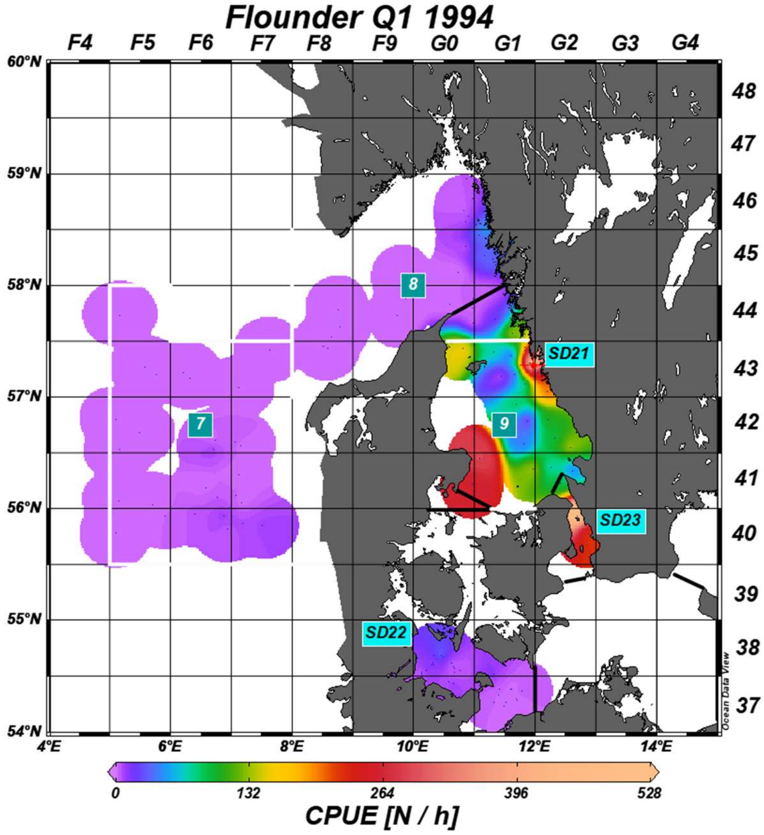
Flounder Q1 1999

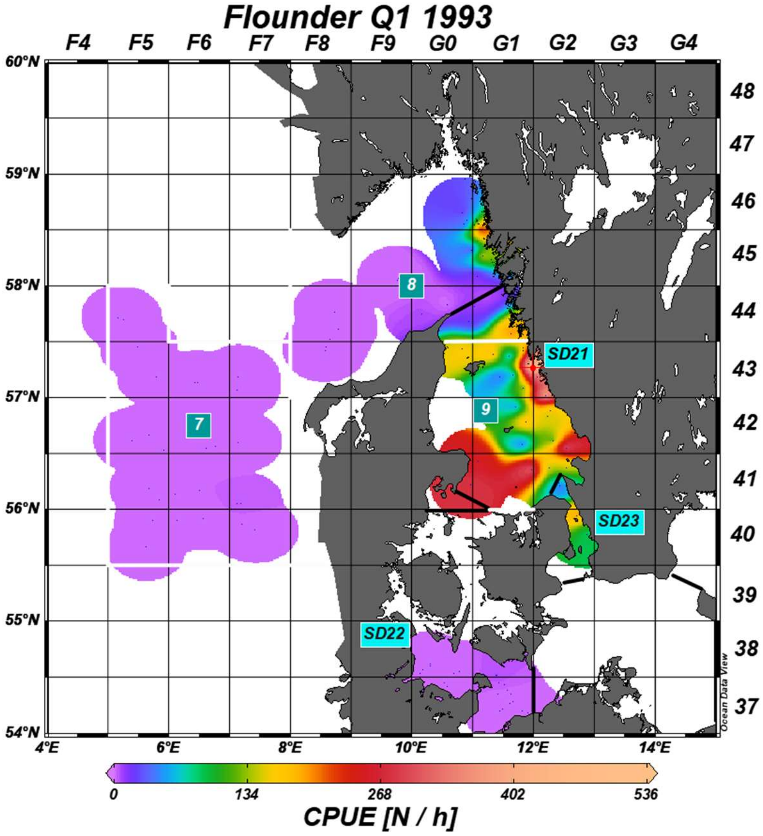

Flounder Q1 1998
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
135
270
405
540
CPUE [N / h]

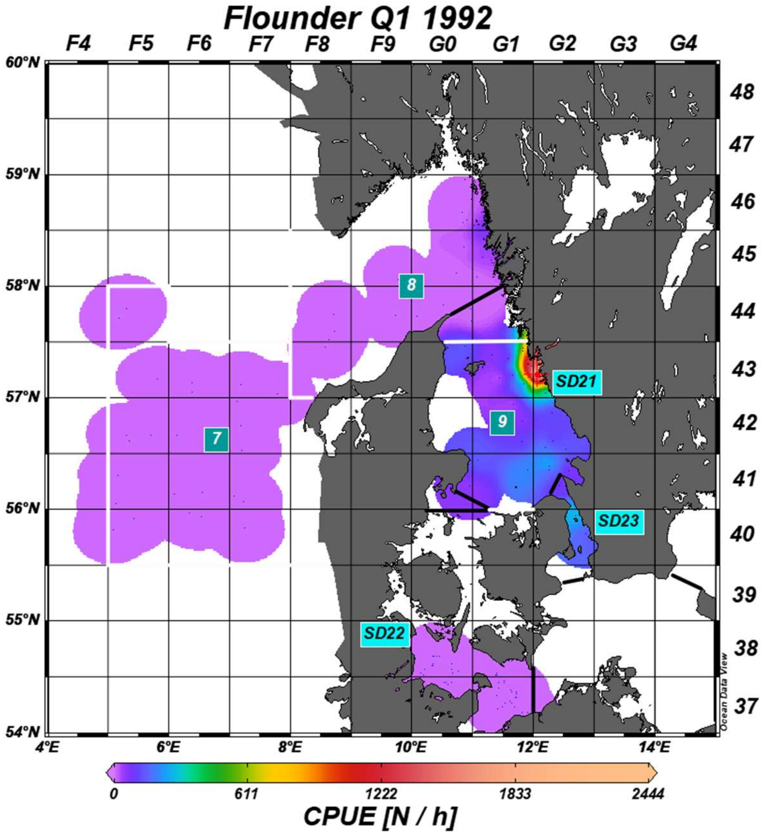

Flounder Q1 1997
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
166
332
498
664
CPUE [N / h]

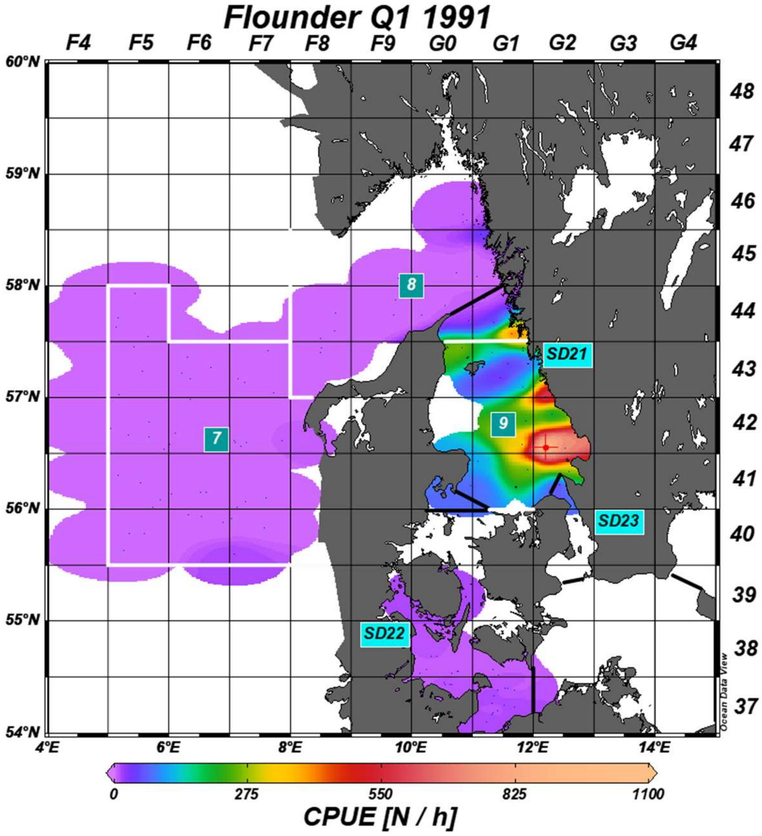

Flounder Q1 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
130
260
390
520
CPUE [N / h]


Flounder Q1 1996
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
Ocean Data View
0
61
122
183
244
CPUE [N / h]


Flounder Q1 1994
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
132
264
396
528
CPUE [N / h]


Flounder Q1 1993
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
134
268
402
536
CPUE [N / h]

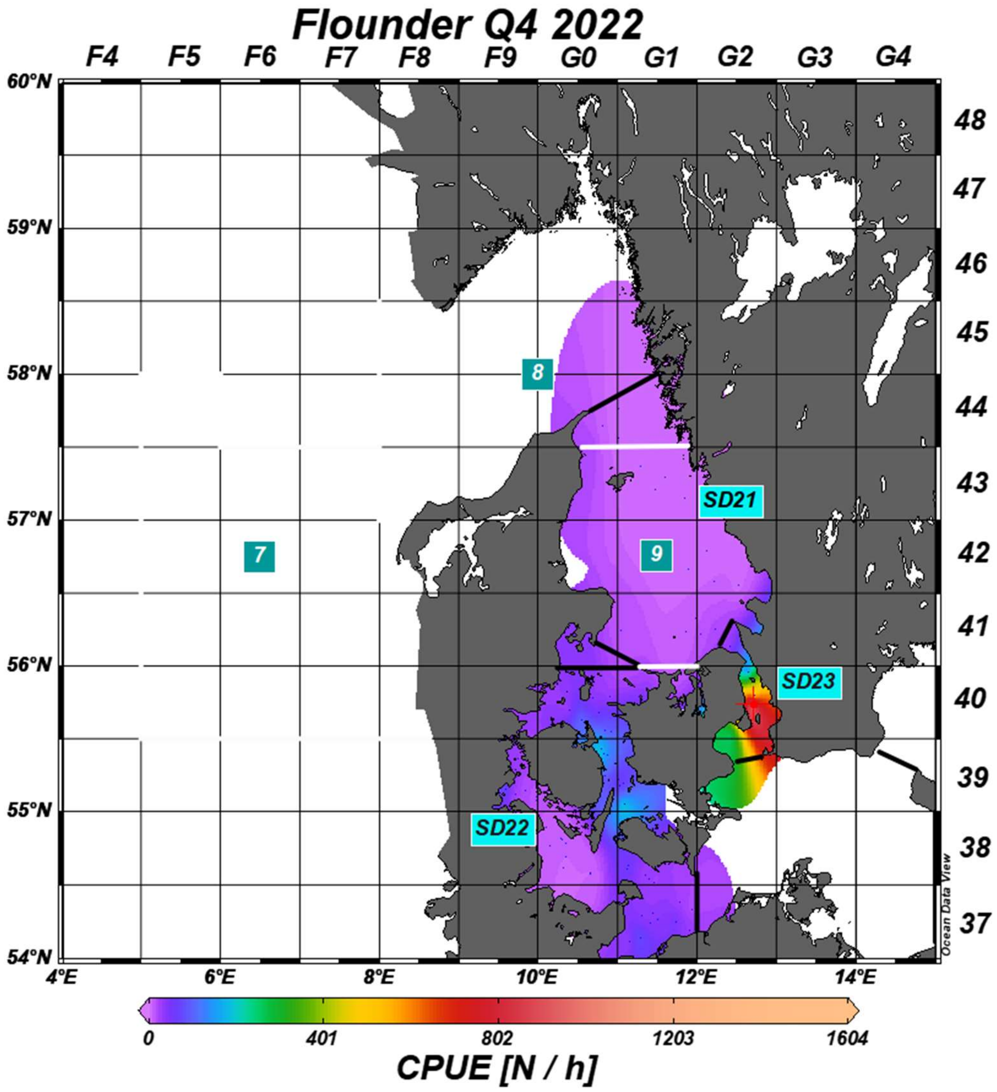

Flounder Q1 1992

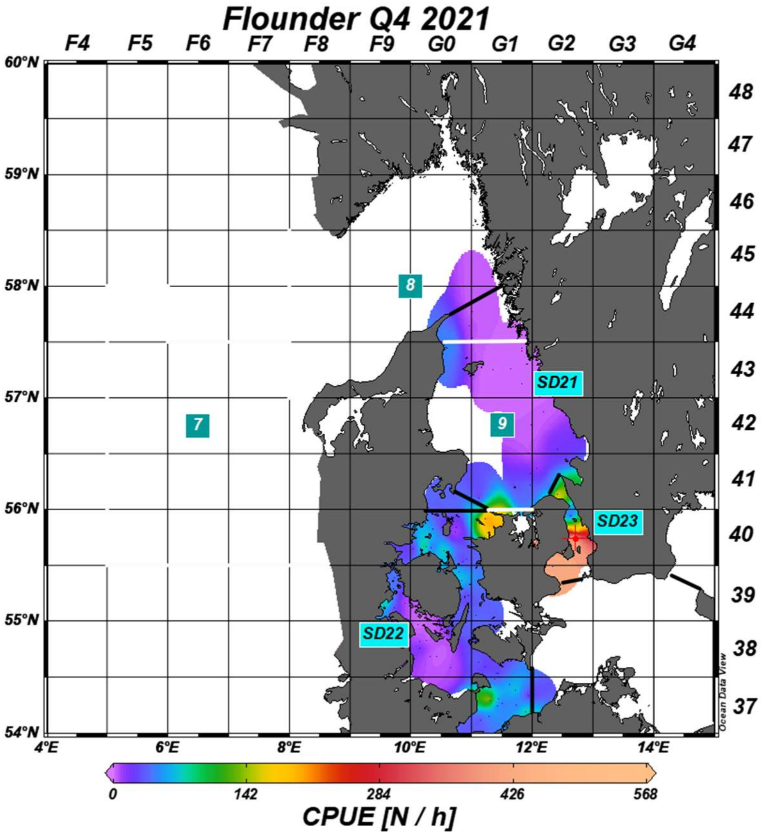

Flounder Q1 1991

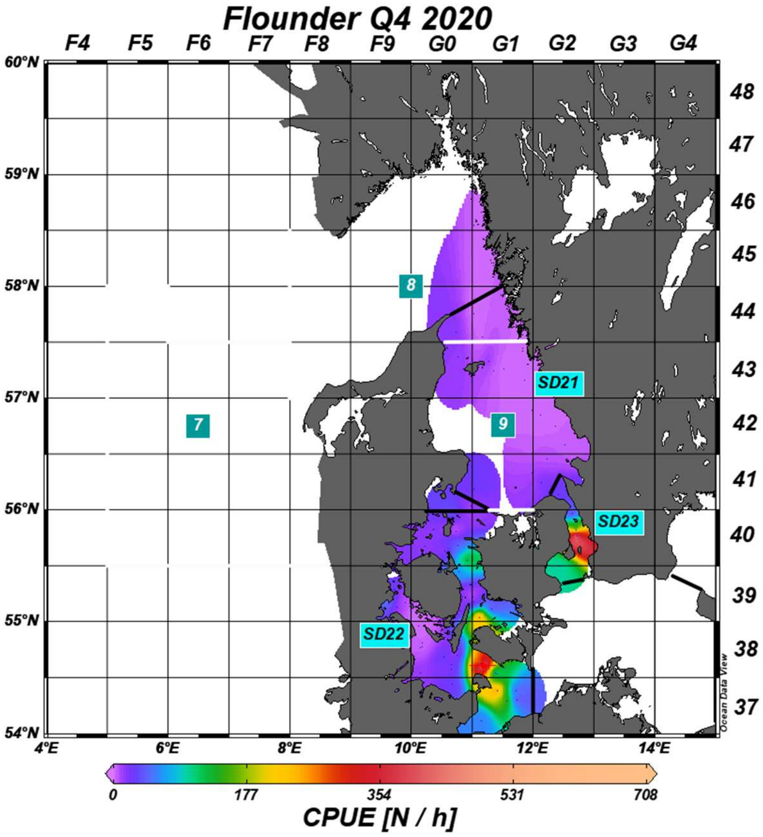
ANNEX 1.2

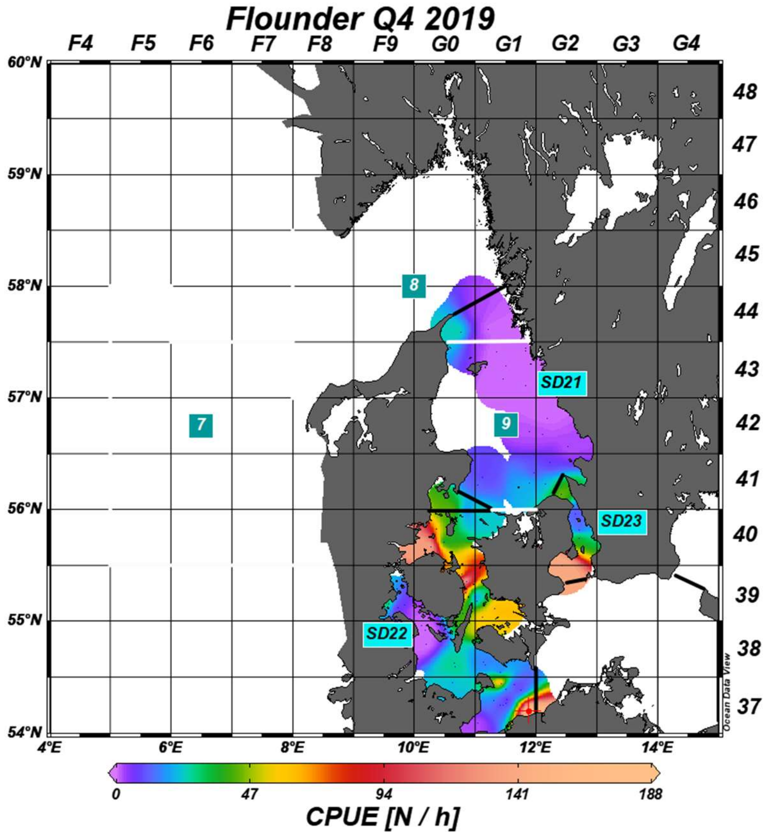
Combined **Quarter 4 Survey Index** CPUE (no/hour) of IBTS, covering Areas 7, 8 and 9 and BITS, covering Areas SD21, 22 and 23. IBTS has not been conducted in Q4 since 1996.

The colour scheme is adjusted to the maximum value of each year to make maps easier to read.

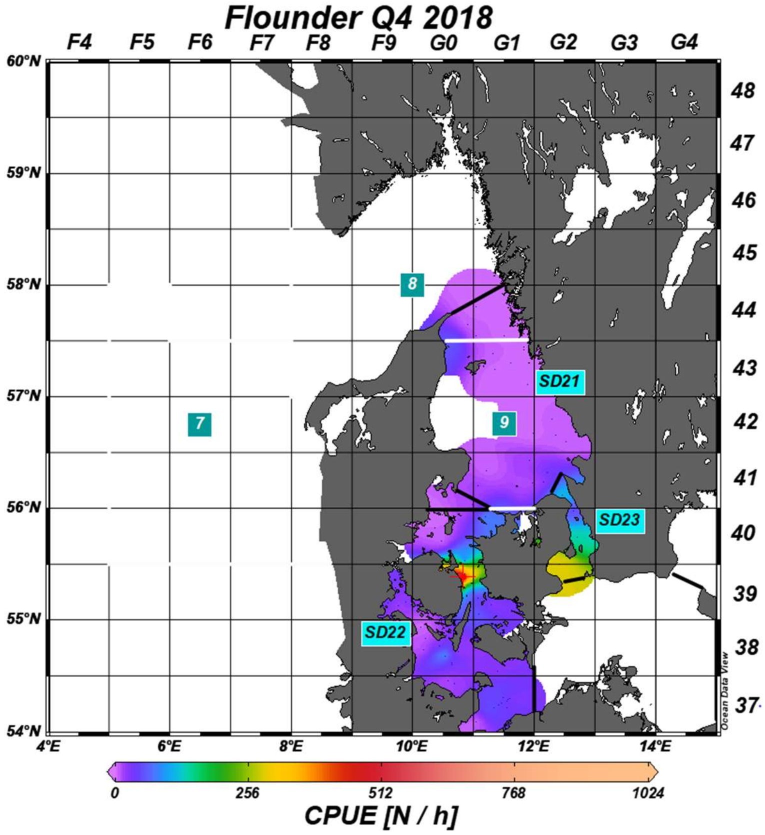



Flounder Q4 2021
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
142
284
426
568
CPUE [N / h]

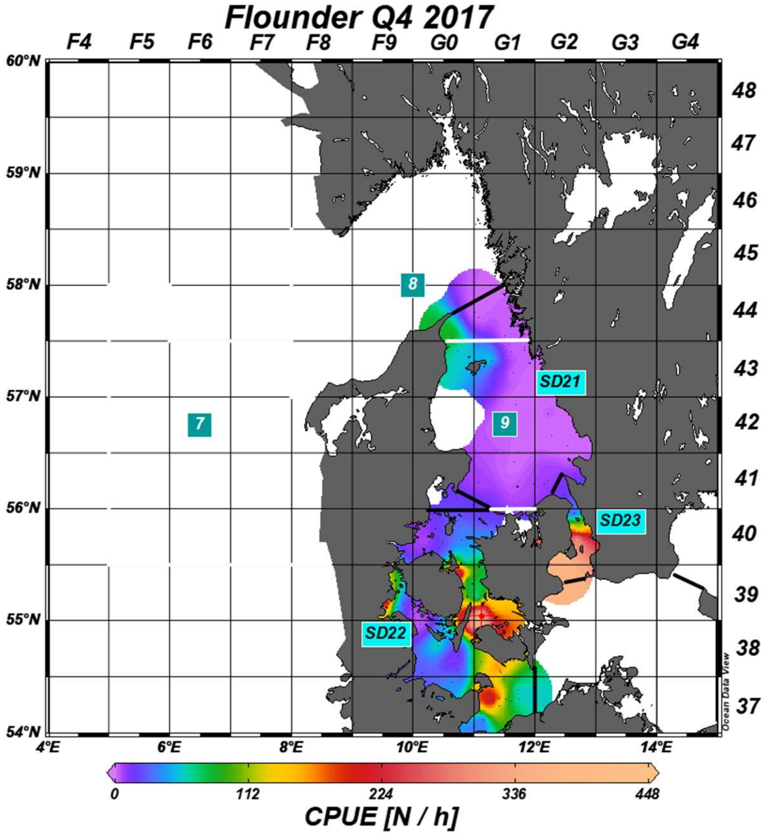

Flounder Q4 2020
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
177
354
531
708
CPUE [N / h]

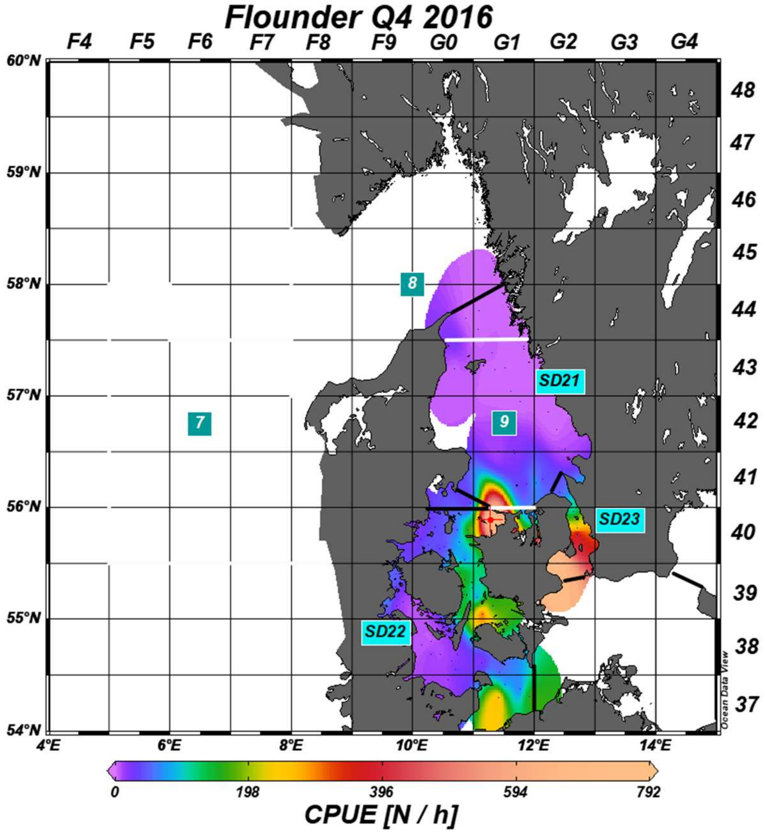


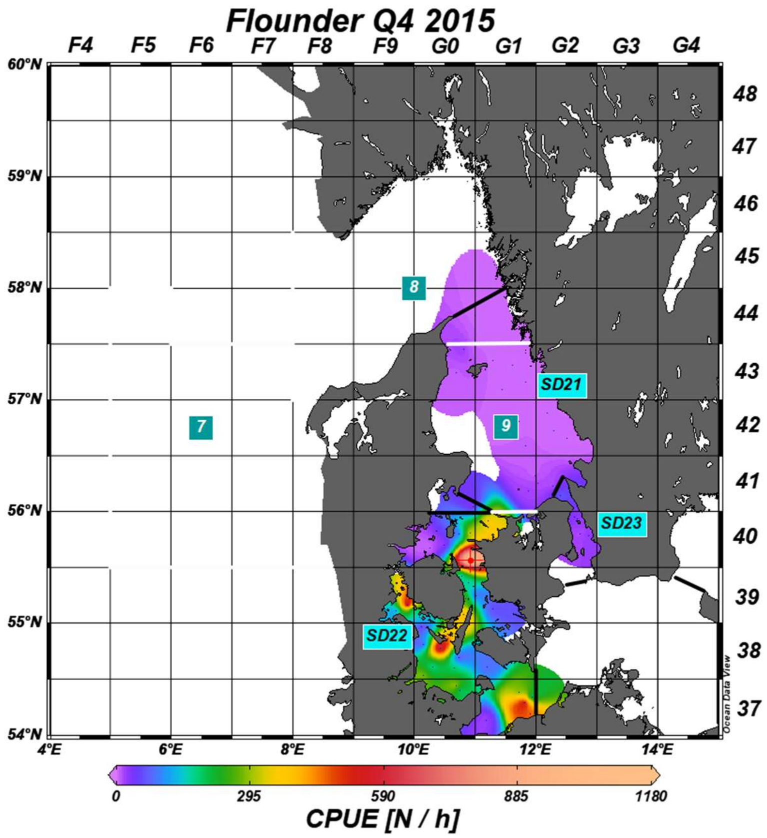
Flounder Q4 2019

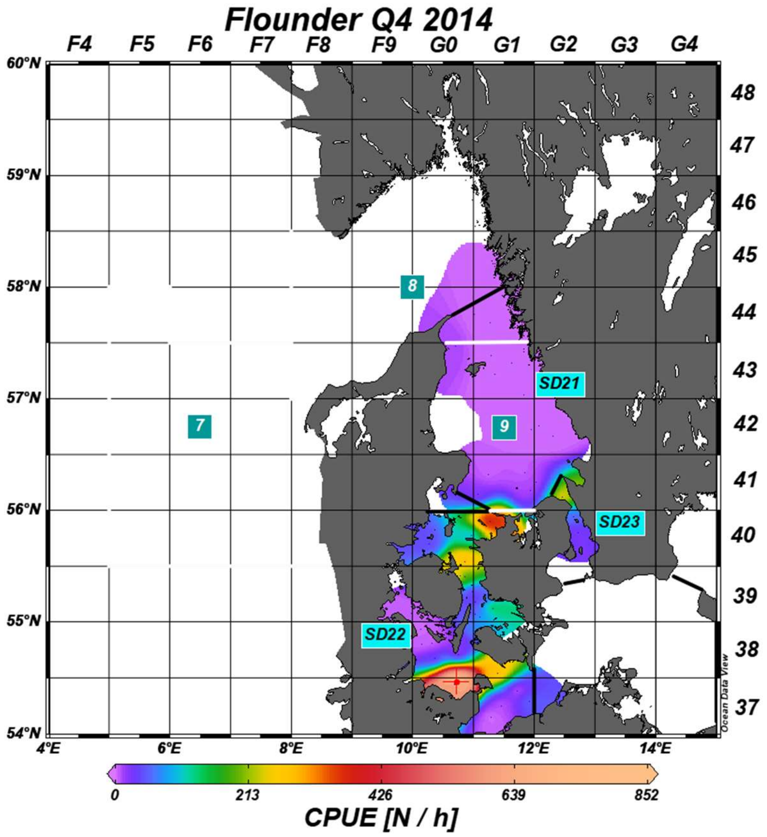


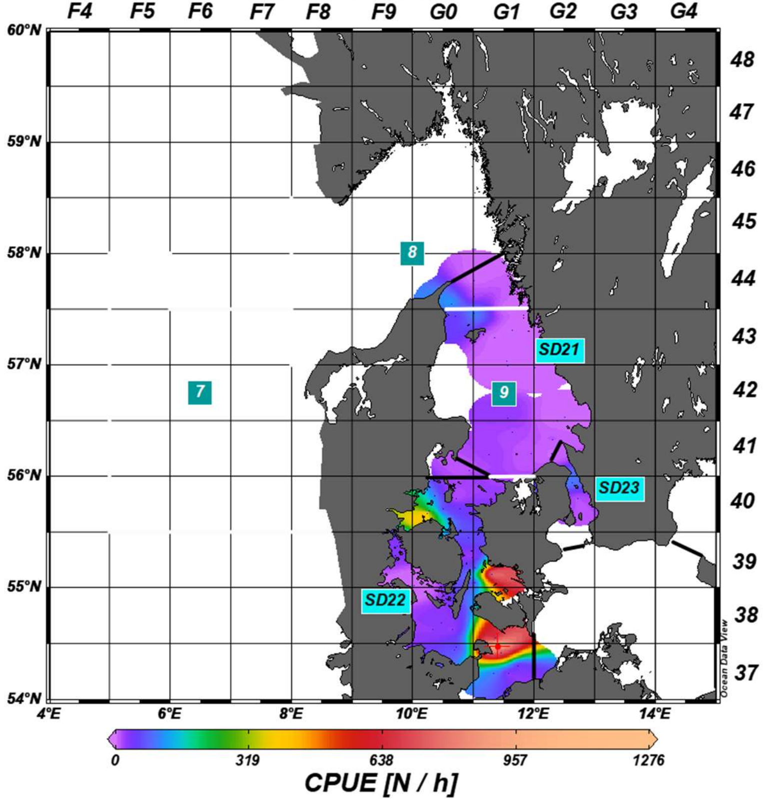
Flounder Q4 2018

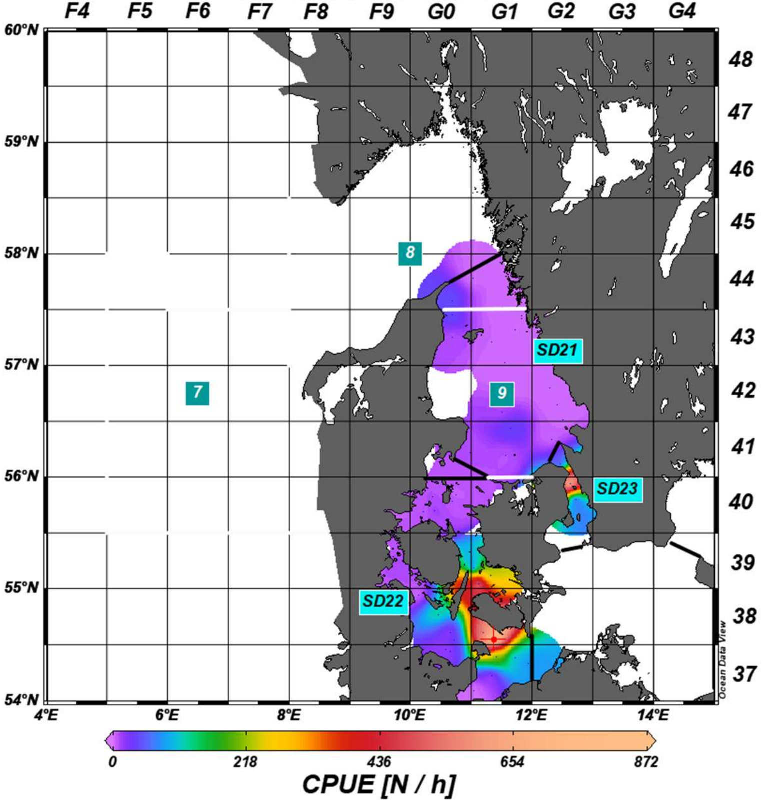

Flounder Q4 2017
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
112
224
336
448
CPUE [N / h]

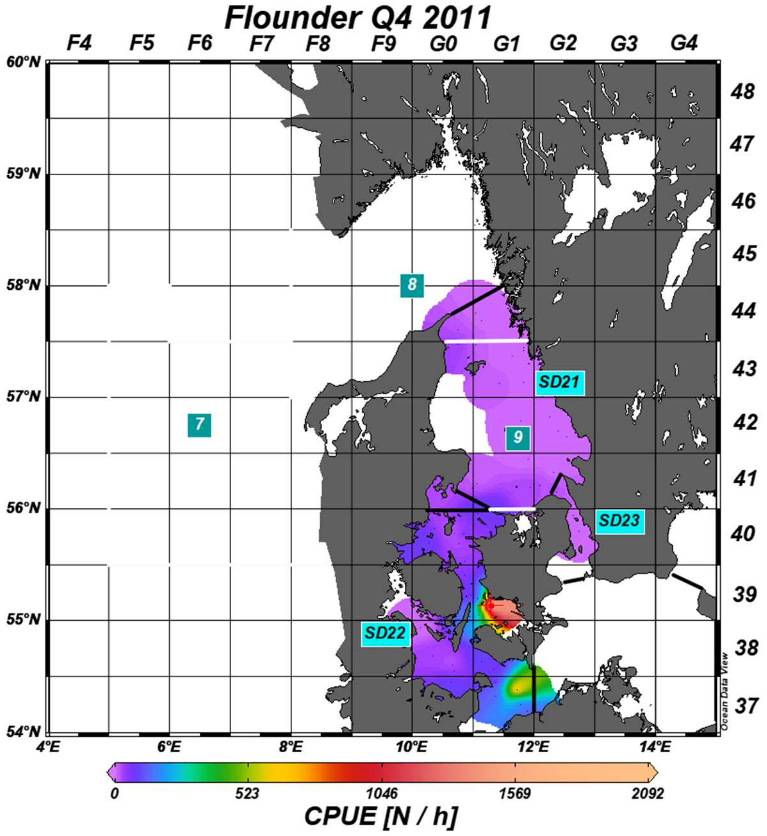

Flounder Q4 2016
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD22
SD23
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
198
396
594
792
CPUE [N / h]

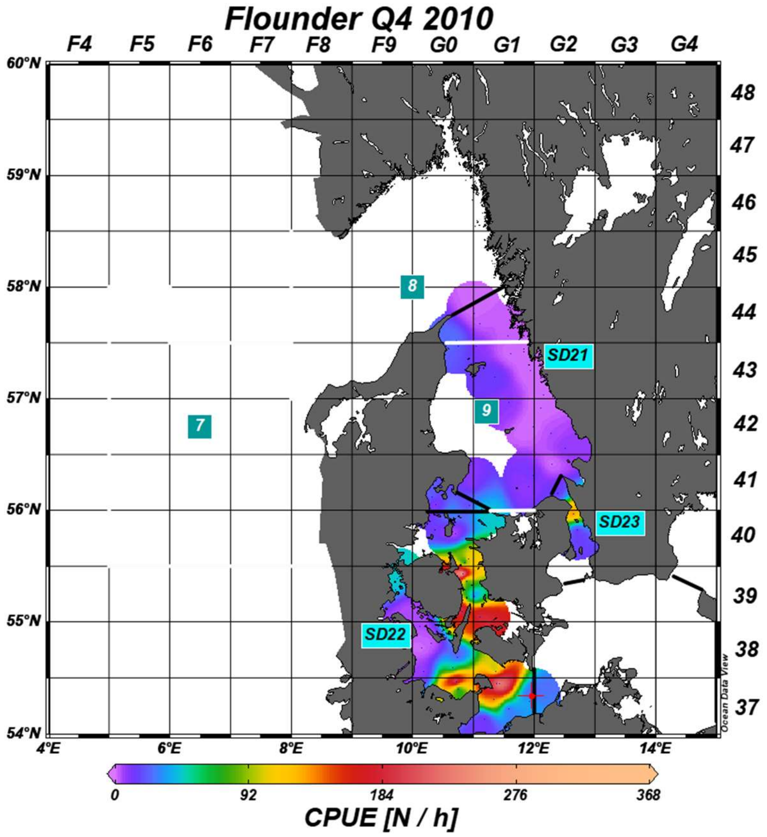

Flounder Q4 2015
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
295
590
885
1180
CPUE [N / h]

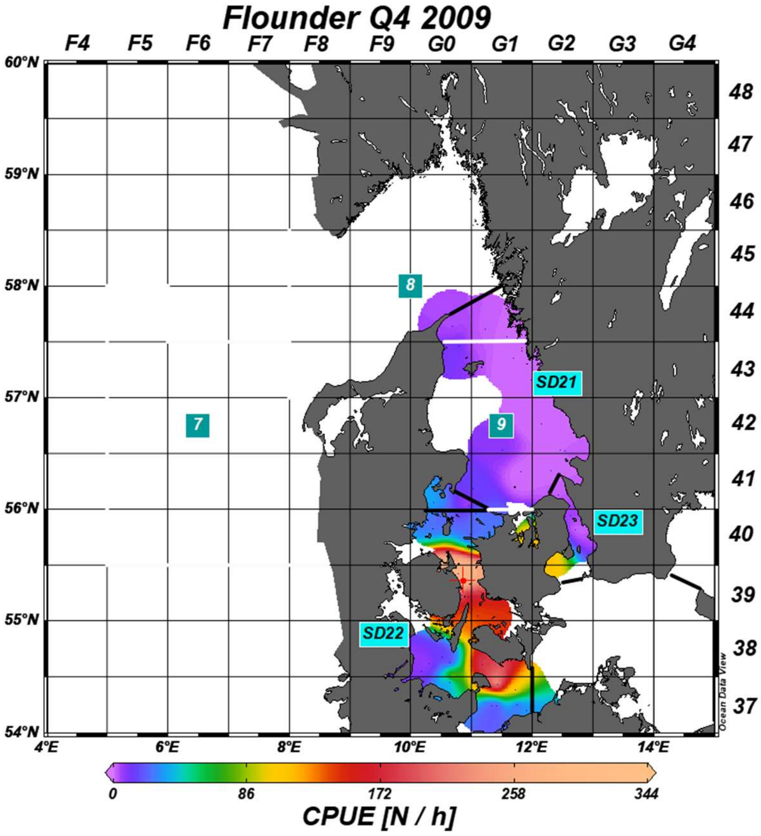

Flounder Q4 2014
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
213
426
639
852
CPUE [N / h]


Flounder Q4 2013

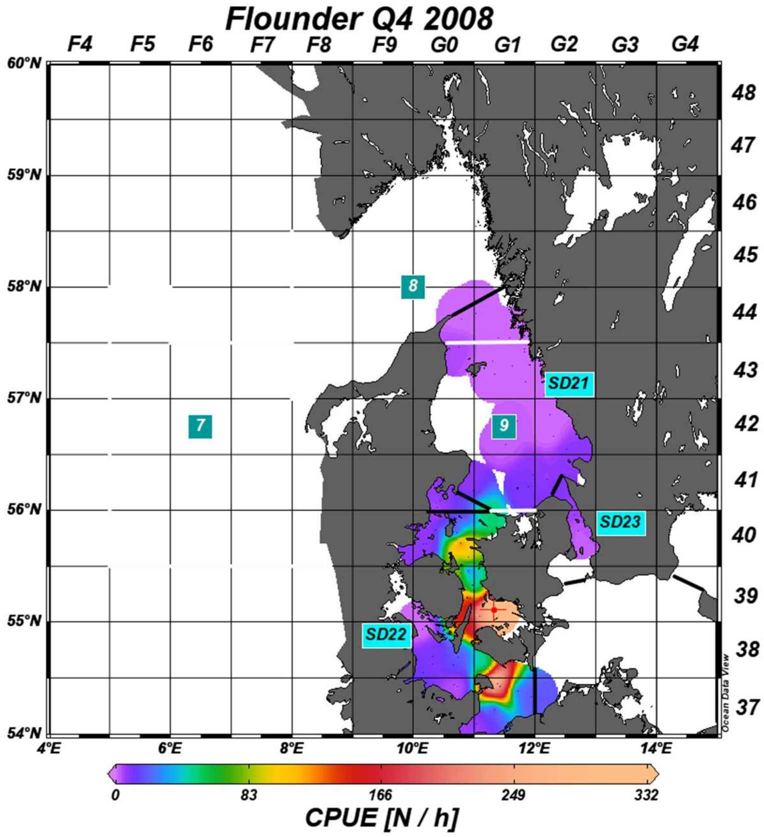

Flounder Q4 2012


Flounder Q4 2011
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
523
1046
1569
2092
CPUE [N / h]

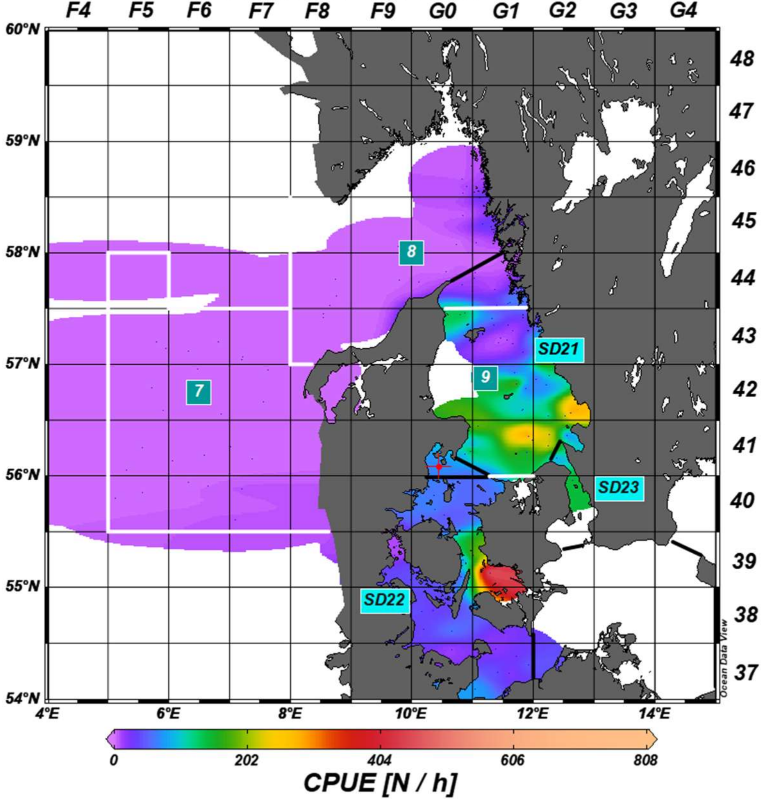

Flounder Q4 2010
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
8
7
9
SD21
SD23
SD22
Ocean Data View
0
92
184
276
368
CPUE [N / h]



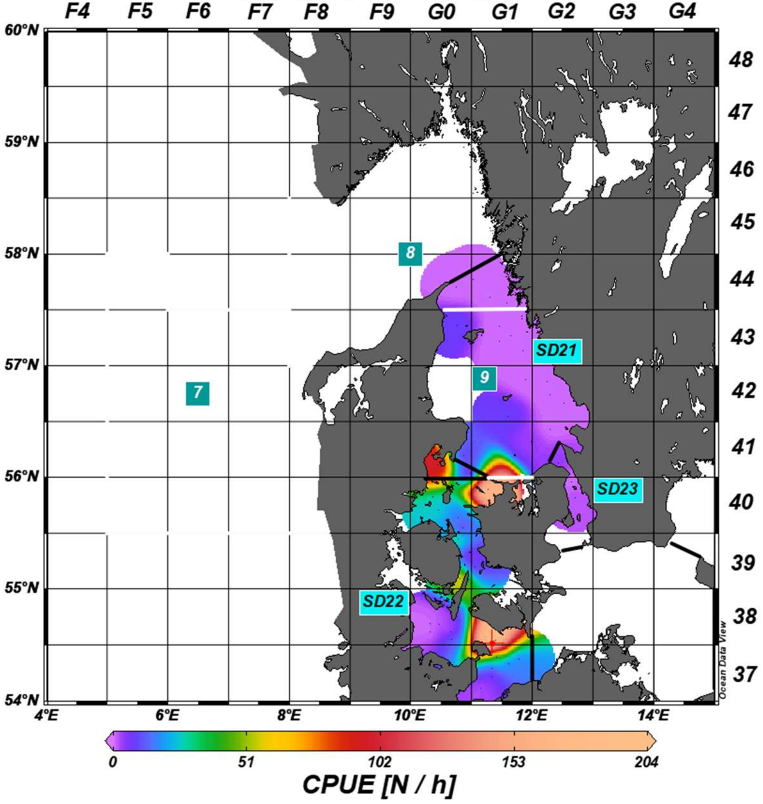
Flounder Q4 2009



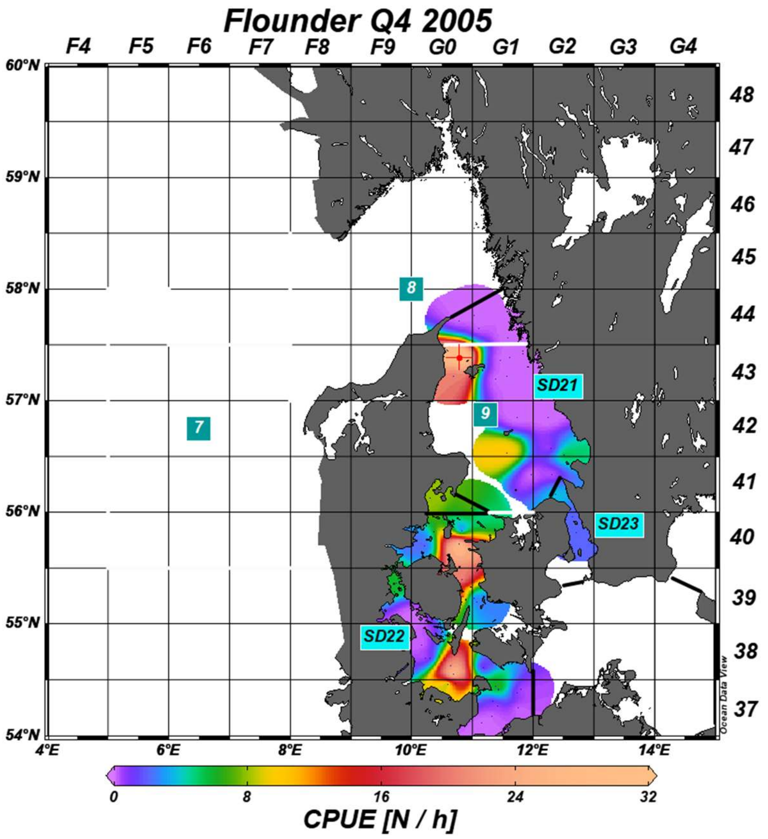
Flounder Q4 2008

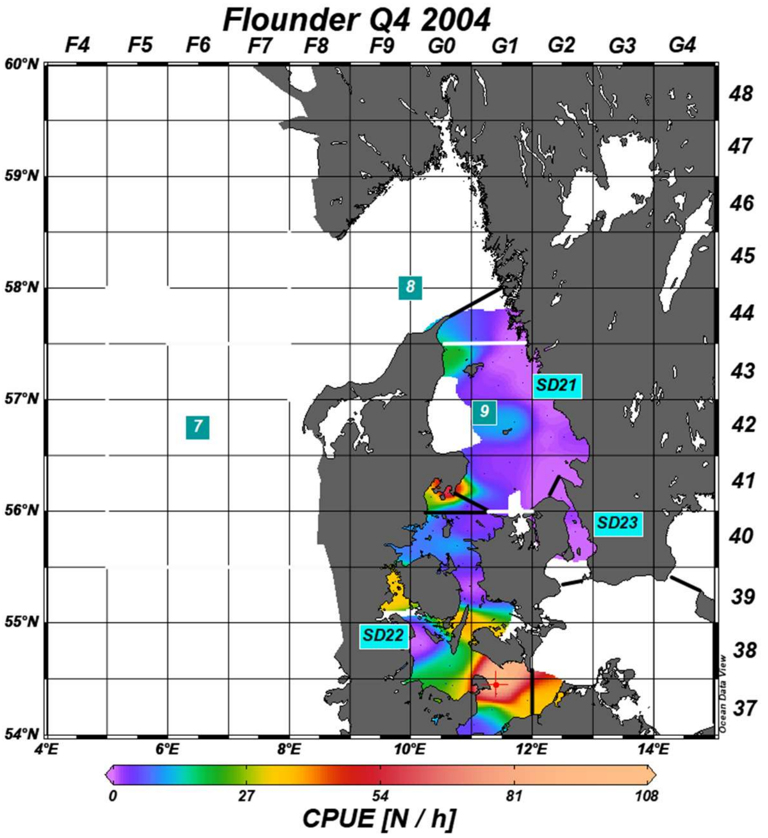


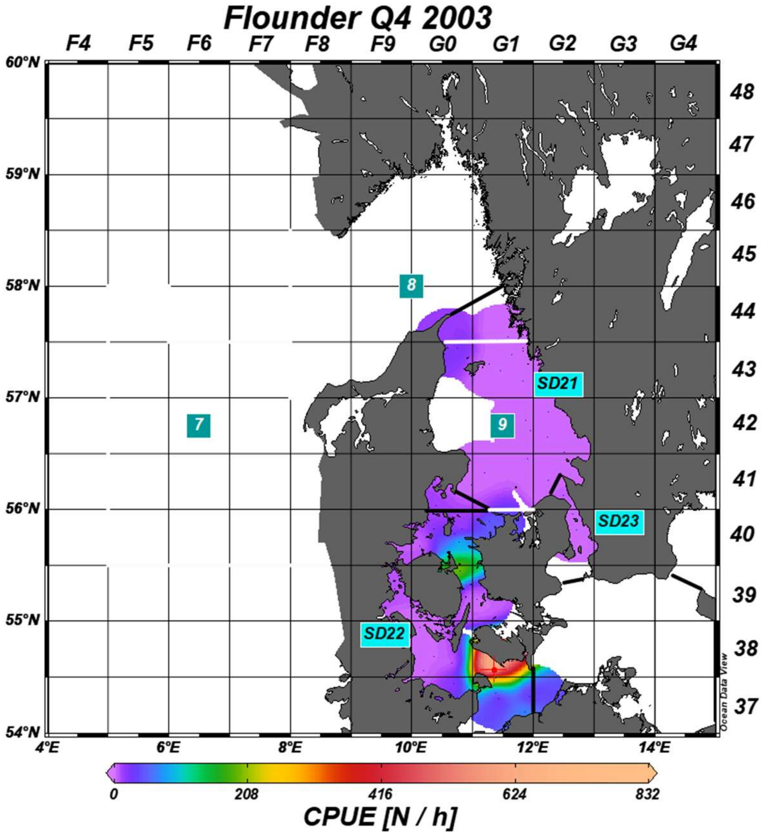
Flounder Q4 2007



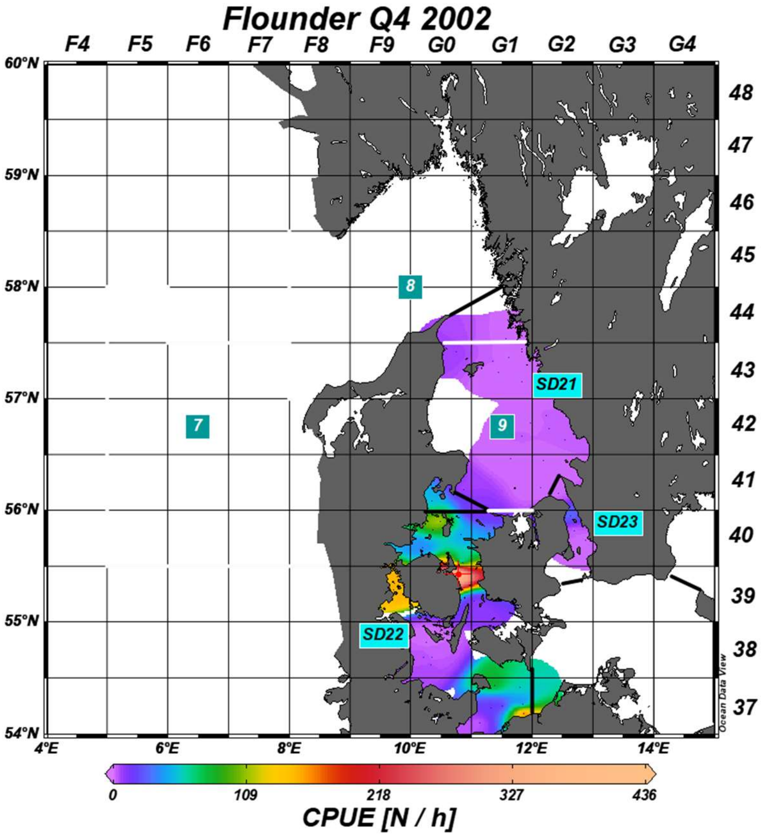
Flounder Q4 2006


Flounder Q4 2005

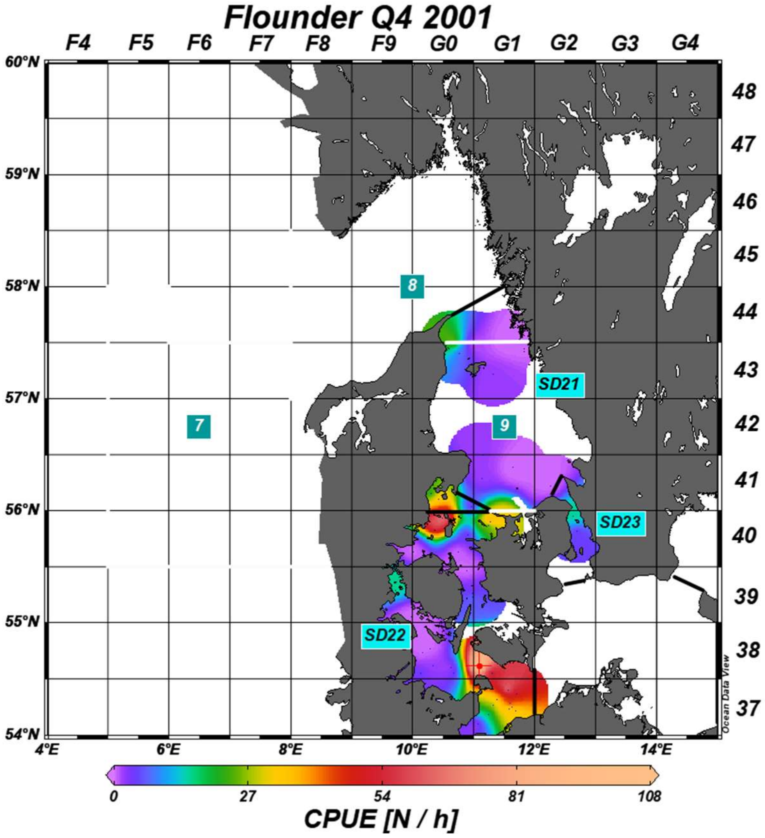

Flounder Q4 2004

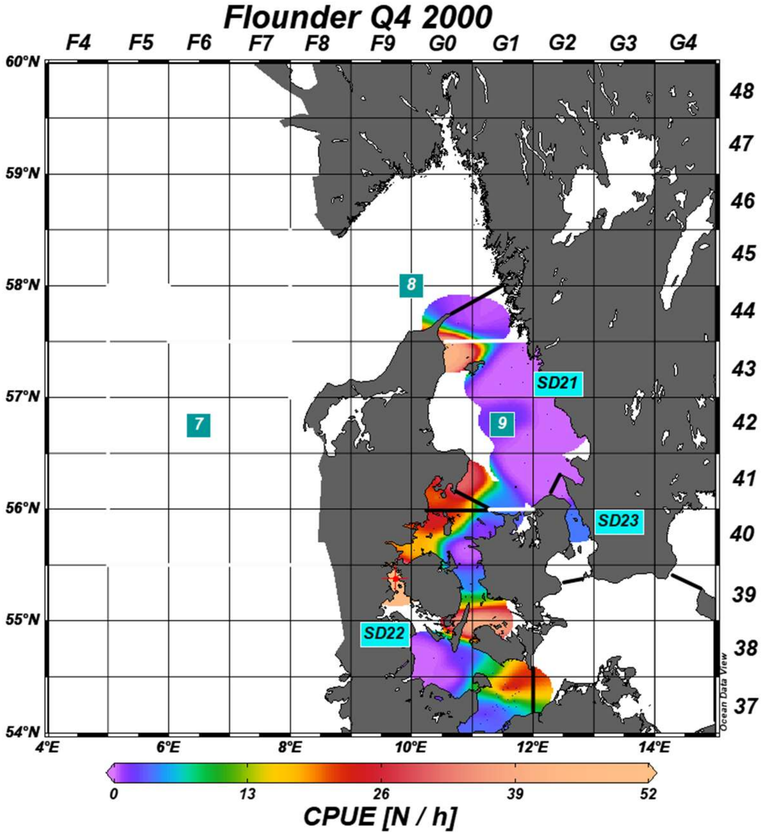


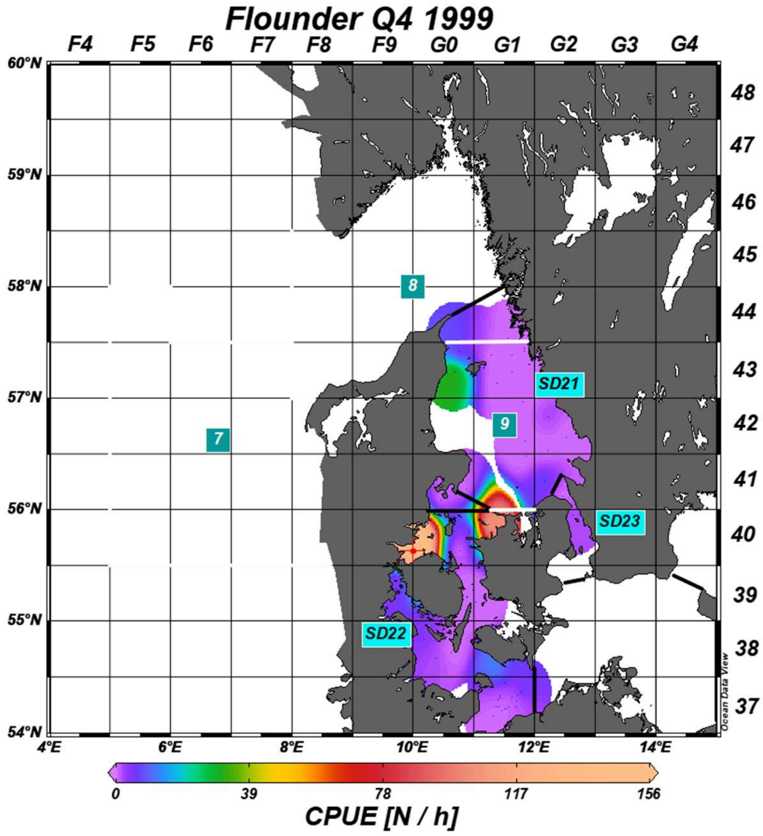
Flounder Q4 2003

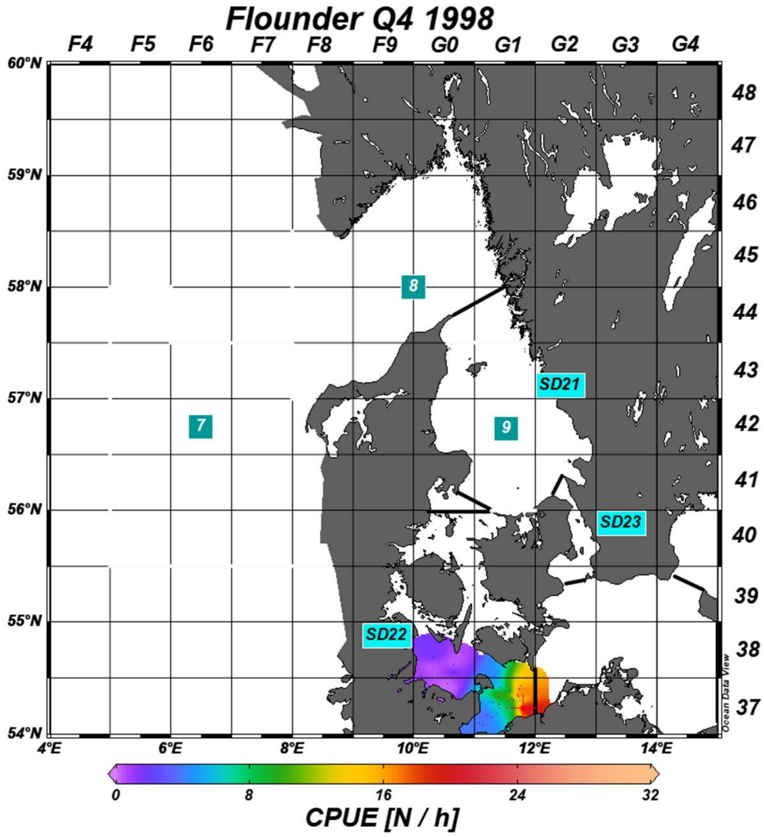


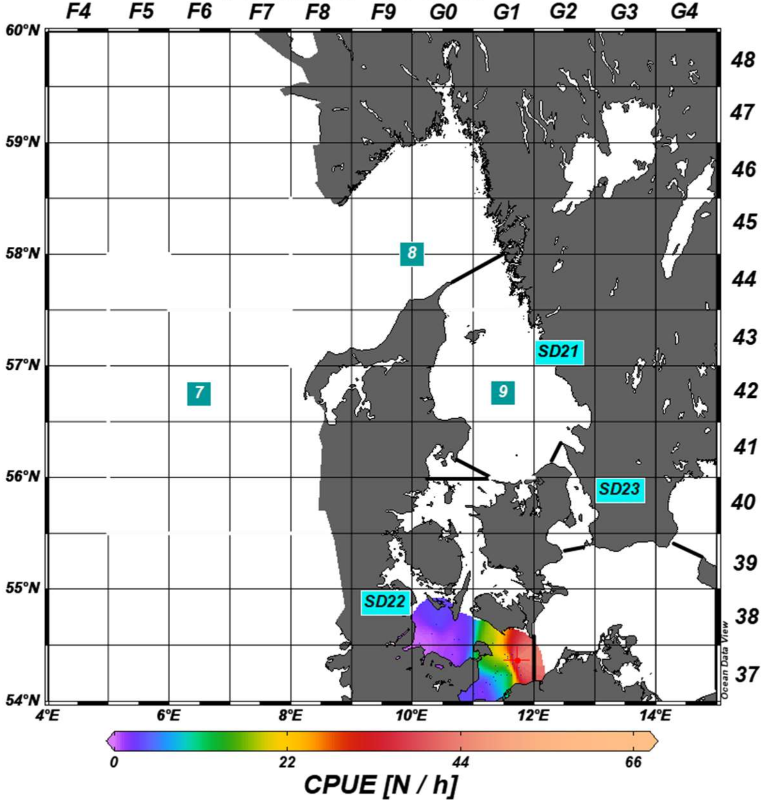
Flounder Q4 2002


Flounder Q4 2001
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
27
54
81
108
CPUE [N / h]

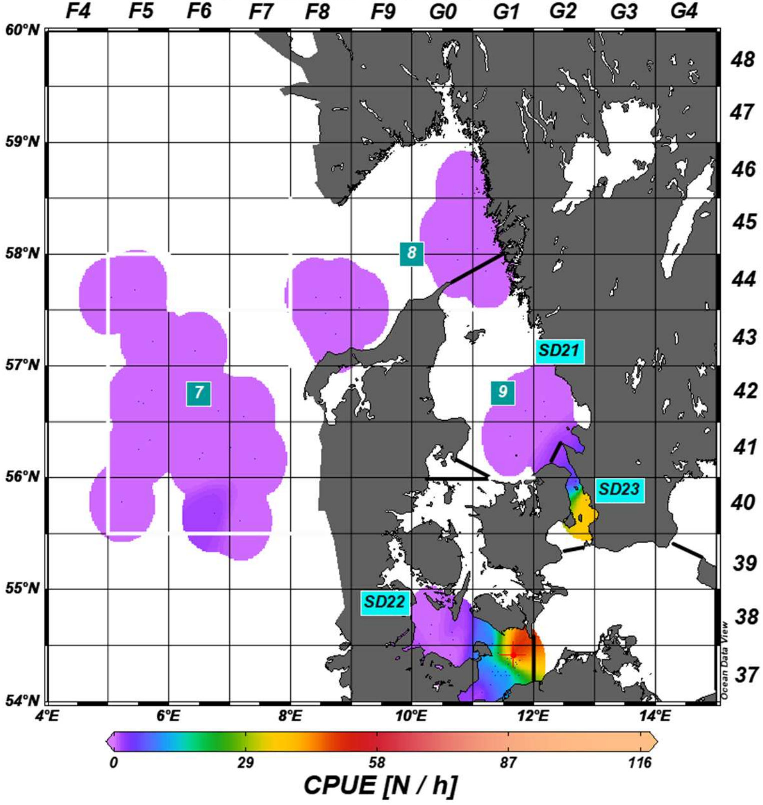

Flounder Q4 2000
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
Ocean Data View
0
13
26
39
52
CPUE [N / h]


Flounder Q4 1999
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
4°E 6°E 8°E 10°E 12°E 14°E
0 39 78 117 156
CPUE [N / h]
Ocean Data View

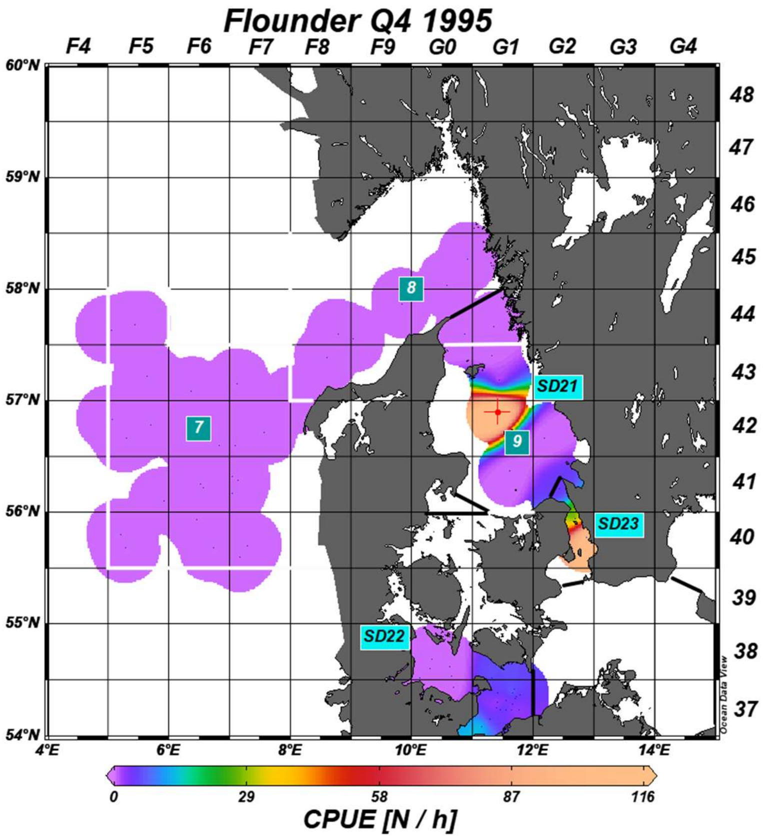

Flounder Q4 1998
F4 F5 F6 F7 F8 F9 G0 G1 G2 G3 G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48 47 46 45 44 43 42 41 40 39 38 37
8
7
9
SD21
SD22
SD23
4°E 6°E 8°E 10°E 12°E 14°E
0 8 16 24 32
CPUE [N / h]
Ocean Data View

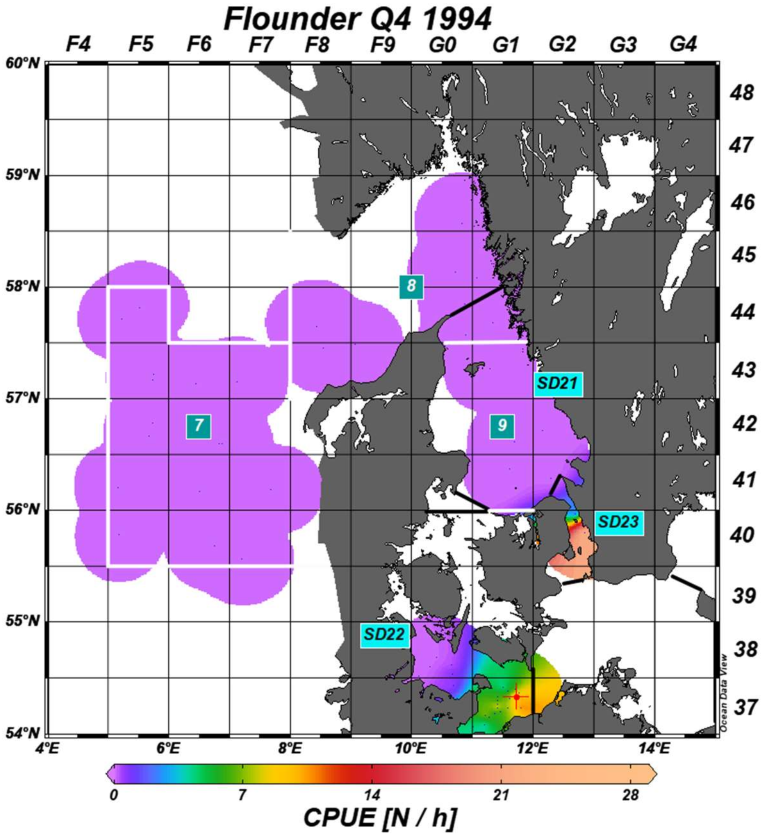


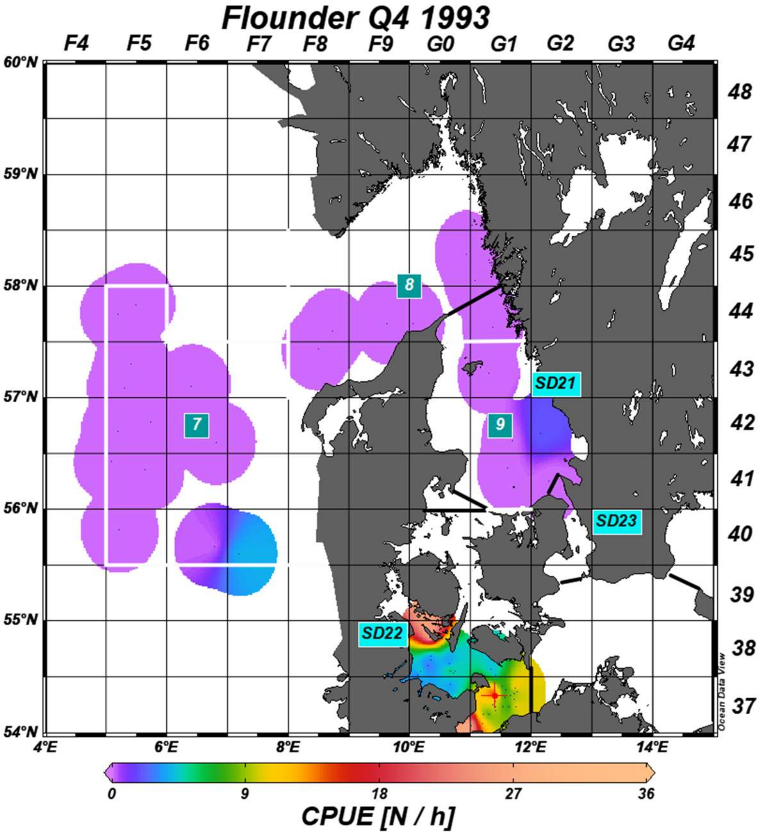
Flounder Q4 1997

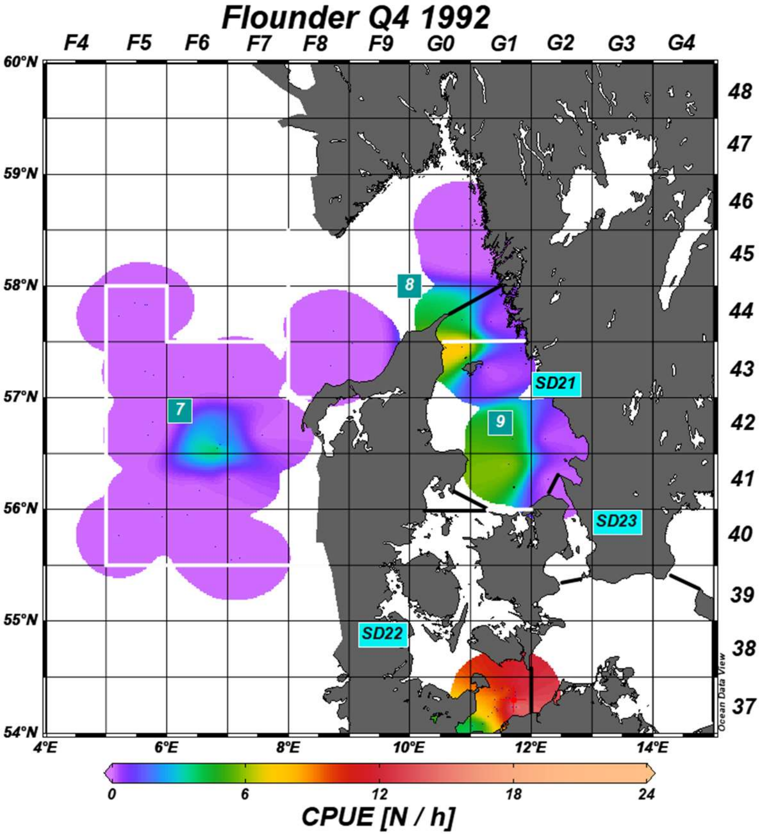


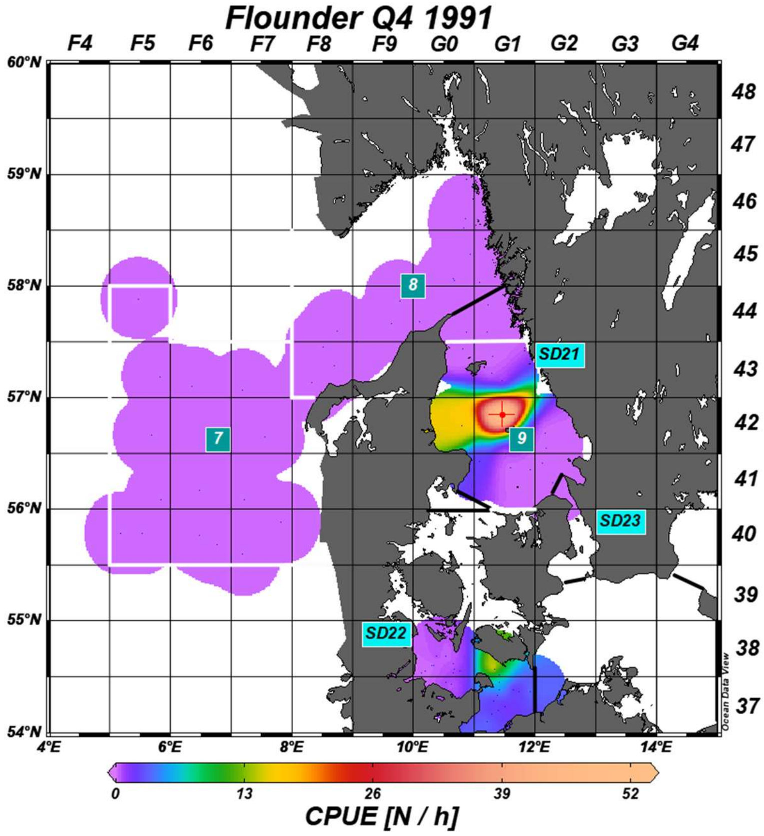
Flounder Q4 1996


Flounder Q4 1995
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
29
58
87
116
CPUE [N / h]


Flounder Q4 1994
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
4°E
6°E
8°E
10°E
12°E
14°E
7
8
9
SD21
SD22
SD23
Ocean Data View
0
7
14
21
28
CPUE [N / h]


Flounder Q4 1993
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
7
8
9
SD21
SD22
SD23
Ocean Data View
0
9
18
27
36
CPUE [N / h]


Flounder Q4 1992
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
4°E
6°E
8°E
10°E
12°E
14°E
48
47
46
45
44
43
42
41
40
39
38
37
7
8
9
SD21
SD22
SD23
Ocean Data View
0
6
12
18
24
CPUE [N / h]


Flounder Q4 1991
F4
F5
F6
F7
F8
F9
G0
G1
G2
G3
G4
60°N
59°N
58°N
57°N
56°N
55°N
54°N
48
47
46
45
44
43
42
41
40
39
38
37
8
7
9
SD21
SD23
SD22
4°E
6°E
8°E
10°E
12°E
14°E
Ocean Data View
0
13
26
39
52
CPUE [N / h]

ANNEX 1.3

Annual landings of flounder in tons per ICES Subdivision and statistical rectangle

All data are taken from the Regional Database (RDB) hosted by ICES (ICES 2023a). Aggregation of data is following the ICES Data Guidelines (ICES 2023b)

ICES. 2023a. Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Portal: https://www.rdb-fishframe.org/

ICES. 2023b. Data policy for the Regional Database (RDB) and Regional Database and Estimation System (RDBES). ICES Data Guidelines. 7 pp. https://doi.org/10.17895/ices.pub.22188157

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.a.20	**42.37**	**17.015**	**24.958**	**18.913**		
43F8	8.084	2.316	4.057	3.182	4.410	**17.1%**
43F9	10.383	3.679	9.572	6.077	7.428	**28.7%**
43G0			0.002		0.002	**0.0%**
43G1			0.033		0.033	**0.1%**
44F7	0.037		0.01	0.003	0.017	**0.1%**
44F8	0.076	0.197	0.033	0.02	0.082	**0.3%**
44F9	7.945	1.851	6.358	2.524	4.670	**18.1%**
44G0	15.069	3.757	3.868	5.878	7.143	**27.6%**
44G1	0.736	4.992	0.937	1.079	1.936	**7.5%**
45F9	0.003	0.007		0.002	0.004	**0.0%**
45G0	0.013	0.027	0.028	0.071	0.035	**0.1%**
45G1	0.015	0.181	0.04	0.048	0.071	**0.3%**
46G0	0.009	0.008	0.02	0.008	0.011	**0.0%**
46G1				0.015	0.015	**0.1%**
47G0				0.006	0.006	**0.0%**

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.a.21	**78.182**	**78.447**	**66.333**	**78.887**		
40F7			0.229		0.229	0.30%
40G1	0.615	0.35	0.612	2.809	1.097	1.45%
40G2	0.591	0.017	0.36	0.77	0.435	0.57%
41G0	0.63	1.189	0.793	0.6	0.803	1.06%
41G1	21.717	28.194	15.147	26.112	22.793	30.12%
41G2	31.091	18.456	17.032	21.471	22.013	29.09%
42G0	0.014	0.001	0.581	1.075	0.418	0.55%
42G1	9.552	12.953	13.93	12.611	12.262	16.20%
42G2	7.386	2.415	6.03	4.587	5.105	6.74%

43G0	1.59	2.89	1.549	1.793	1.956	2.58%
43G1	1.182	2.751	2.59	1.422	1.986	2.62%
43G2	0.003	0.226	0.085	0.046	0.090	0.12%
44F9			0.06		0.060	0.08%
44G0	2.88	4.666	6.176	4.214	4.484	5.93%
44G1	0.931	4.339	1.159	1.377	1.952	2.58%

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.b.23	**64.449**	**43.687**	**45.44**	**30.248**		
39G2	5.968	3.552	4.239	2.36	4.030	8.77%
40G2	47.593	29.26	35.082	19.387	32.831	71.44%
40G3	1.293	1.633	2.177	3.61	2.178	4.74%
41G2	9.595	9.242	3.942	4.891	6.918	15.05%

Area	**2019**	**2020**	**2021**	**2022**	**average**	**%**
27.3.c.22	**1055.812**	**697.052**	**480.367**	**291.322**		
36G0				0.008	0.008	0.00%
37F0		0.081	0.046	0.032	0.053	0.01%
37F9	1.377	2.489	2.181	3.311	2.340	0.37%
37G0	66.428	73.938	57.232	50.079	61.919	9.80%
37G1	254.742	212.689	128.976	79.146	168.888	26.73%
37G2				0.297	0.297	0.05%
38F9	11.568	13.395	14.571	16.04	13.894	2.20%
38G0	542.282	310.115	219.864	111.809	296.018	46.85%
38G1	19.791	25.52	15.932	1.55	15.698	2.48%
38G2		0.327	0.005		0.166	0.03%
38H0	0.25				0.250	0.04%
39F9	6.709	3.867	9.548	7.379	6.876	1.09%
39G0	71.185	38.742	16.832	11.967	34.682	5.49%
39G1	67.183	12.444	9.222	2.721	22.893	3.62%
40F9				0.062	0.062	0.01%
40G0	8.377	2.657	1.024	0.963	3.255	0.52%
40G1	4.798	0.788	4.592	5.64	3.955	0.63%
41G0	0.004		0.187	0.303	0.165	0.03%
41G1	1.118		0.155	0.015	0.429	0.07%

Area	2019	2020	2021	2022	average	%
27.4.b	**136.453**	**127.172**	**102.883**	**35.833**		
36F2	0.013	0.012	0.005	0.02	0.013	0.02%
36F3	0.046	0.012	0.059		0.039	0.06%
36F4	0.497	0.507	2.696	0.259	0.990	1.62%
36F5	0.003	0.138	3.753	0.01	0.976	1.59%
36F6		0.024			0.024	0.04%
36F7	0.132	0.004	0.02	0.015	0.043	0.07%
36F8	0.081		0.03		0.056	0.09%
36F9	0.064	0.066	0.031		0.054	0.09%
37F3		0.012			0.012	0.02%
37F4	0.014	0.002	0.126	0.001	0.036	0.06%
37F5	0.102	0.33	1.898	0.171	0.625	1.02%
37F6	0.042	0.28	0.782	0.005	0.277	0.45%
37F7	0.36	0.178	0.087		0.208	0.34%
37F8	0.204	0.034	0.01		0.083	0.13%
37F9		2.489			2.489	4.06%
38F1		0.033			0.033	0.05%
38F2		0.054			0.054	0.09%
38F5	0.026	0.001	0.002		0.010	0.02%
38F6	0.028	0.032	0.13		0.063	0.10%
38F7	0.03		0.01		0.020	0.03%
38F8		0.054	0.003	0.001	0.019	0.03%
38F9		6.81			6.810	11.11%
39F1		0.031			0.031	0.05%
39F5	0.002	0.05			0.026	0.04%
39F6	0.001		0.055	0.002	0.019	0.03%
39F7	0.045	0.006			0.026	0.04%
40F5	0.002			0.084	0.043	0.07%
40F6	0.151		0.777	0.024	0.317	0.52%
40F7	2.966	0.513	0.308	0.291	1.020	1.66%
40F8	3.388	4.211	24.396	5.843	9.460	15.44%
41F4		0.066			0.066	0.11%
41F5	0.011	0.101	0.005	0.008	0.031	0.05%
41F6	0.041	0.008	0.059	0.019	0.032	0.05%
41F7	24.315	8.94	39.016	20.41	23.170	37.81%
41F8	8.137	6.822	27.24	7.815	12.504	20.41%
42F5	0.005				0.005	0.01%
42F6	0.022		0.007		0.015	0.02%
42F7	0.584	0.749	0.237	0.291	0.465	0.76%
42F8	0.305	0.063	0.533	0.373	0.319	0.52%
43F0			0.03		0.030	0.05%
43F5		0.001			0.001	0.00%
43F6	0.008	0.005	0.14	0.002	0.039	0.06%
43F7		0.332	0.004	0.008	0.115	0.19%

43F8	1.408	0.455	0.389	0.181	0.608	0.99%
(NA)	93.42	93.747			93.584	60.43%