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METACOD

The role of sub-stock structure in the maintenance of cod metapopulations

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ÁGRIP

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Stærð þorskstofna í Norður Atlantshafi hefur farið ört minnkandi á undaförnum áratugum. Talið er að helstu orsakanna sé að leita í of mikilli sókn og er nú svo komið að flestir stofnarnir eru taldir vera í sögulegri lægð. Minnkun stofna vegna of mikillar sóknar hefur margs konar afleiðingar sem koma m.a. fram í mun takmarkaðri útbreiðslu stofna og hugsanlegu tapi á erfðabreytileika m.a. vegna hruns undirstofna. Talið er að forsendan fyrir góðri afkomu þorsksins felst í fjölbreytileika undirstofna hans. Þessar niðurstöður hafa ekki verið nýttar við útfærslu á fiskveiðiráðgjöf. Almennt er skortur á upplýsingum um samsetningu nytjastofna sérstaklega hvað varðar fjölda og gerð aðgreinanlegra stofneininga eða undirstofna. Megin markmið þessa verkefnis er því að þróa "theoretískann", stærðfræðilegan, grunn sem mun nýtast við ráðgjöf um veiðar í þeim tilgangi að byggja upp ekki eingöngu stærð stofnanna heldur einnig fjölbreytileika. Verkefnið skiptist í 5 verkefnaflokka. Í fyrsta flokknum er stefnt að því að taka saman allar fáanlegar upplýsingar um staðsetningu hrygningarsvæða og stærð, aldur og fjölda þorska er ganga til hrygningar á hverju svæði. Í öðrum flokki er unnið að því að greina undirstofnana í sundur með notkun erfða- og líffræðilegra aðferða. Í flokki þrjú er unnið að því að skoða útbreiðslu ungviðis frá hinum mismunandi svæðum og reyna að meta áhrif strauma á flutning eggja og lirfa frá hrygningarsvæðunum með líkönum sem líkja eftir flæði og flutningi sjávar. Í flokki fjögur er reynt að meta dánartíðni eggja, lirfa og seiða í tengslum við þá umhverfisþætti sem hafa áhrif á ungviðið á hinum mismunandi svæðum. Í síðasta flokkinum verður reynt að meta framlag mismunandi hrygningarsvæða til veiðstofnsins hverju sinni um leið og þróaðar verða aðferðir til að meta stofnstærð, nýliðun og stofnstærðarbreytingar sem byggja á upplýsingum um fjölda og stærð undirstofna þorsks við Ísland og Skotland.

ABSTRACT

Marteinsdottir, G, P. Wright, E. Nielsen, I. Harms, A.K. Danielsdóttir, M. Heath, A. Gallego, V. Thorsteinsson, D. Ruzzante, C. Pampouli, J. O. Backhaus, G. Begg, H. Valdimarsson, B. Gunnarsson, F. Gibb, D. Brickman, S. Campana. 2003. METACOD: The role of sub-stock structure in the maintenance of cod metapopulations. Marine Research Institute. Technical Report no. 93

North Atlantic cod stocks appear to be overexploited and in a depleted state. A recurrent feature of the declines in abundance, has been collapse of the spatial distributions of fish and loss of the distinct sub-stocks. There is evidence that a diverse sub-stock structure is necessary to ensure the long term health and productivity of fish stocks, but maintaining this is not recognised as an objective of current fisheries management. The overall objective of this project is to develop the conceptual and mathematical basis for advising on how fisheries management measures might be framed to conserve or restore not only stock biomass, but also sub-stock diversity. The project is constructed around 5 topics. The aim of the first topic is to establish the location of the spawning grounds and how they have changed through the decades. The aim of the second topic is to determine how distinct the spawning groups are. This will be done by establishing the genetic, behavioural and oceanographic basis for the richness of the cod stocks, and the variations in productivity between sub-stocks. The aim of the third topic is to explore how oceanographic processes segregate juveniles from different spawning groups. This will be done by developing a fine scale hydrodynamic models of the spawning as well as to conduct particle tracking simulations of the dispersal of eggs and larvae. The aim of the fourth topic is to establish the differences in recruitment performance of the various spawning groups and the aim of the fifth and final topic is to compile all the strands of evidence for sub-stock diversity into a conceptual and mathematical model of the overall population dynamics incorporating sub-stock dynamics and use this model to generate advice on how to conserve or restore stock biomass and sub-stock diveristy.

Project Progress Summary

Objective: North Atlantic cod stocks appear to be overexploited and in a depleted state. A recurrent feature of the declines in abundance, has been collapse of the spatial distributions of fish and loss of the distinct sub-stocks. There is evidence that a diverse sub-stock structure is necessary to ensure the long term health and productivity of fish stocks, but maintaining this is not recognised as an objective of current fisheries management. The overall objective of this project is to develop the conceptual and mathematical basis for advising on how fisheries management measures might be framed to conserve or restore not only stock biomass, but also sub-stock diversity.

Results and Milestones: The project is constructed around 5 topics constituting 12 work packages.

The aim of the first topic (WP1- 2) is to establish where the spawning grounds are located and how they have changed through the last 30-40 years. Work within this theme involves the assemblage of all possible data that contains information on spawning cod, distribution of eggs and larvae as well as oceanographic features of the spawning sites. This work has started and the second milestone (Assessment of initial findings from WP1 on the locations of spawning sites) has been met.

The aim of the second topic (WP3-6) is to determine how distinct the spawning groups are. This will be done by establishing the genetic, behavioural and oceanographic basis for the richness of the cod stocks, and the variations in productivity between sub-stocks. This topic is at the heart of the project and the greatest amount of effort has been spent on it so far. Sampling for genetic and otolith mircrochemistry analysis has been performed at all major spawning sites and several smaller less recognised sites in Icelandic and Scottish waters. Sampling has been without problems in the Icelandic waters but due to particularly low abundance of cod in the Scottish waters fewer cod, especially spawning cod, were captured in these regions. Calibration and extraction of DNA has started in both labs (Iceland and Denmark) and a meeting for calibration of methods between the two labs was conducted in Denmark in the fall of 2002. Otoliths for shape and mircrochemistry analysis have been scanned and prepared for the determination of the elemental fingerprints. Several tagging experiments have been conducted both on juvenile and adult spawning fish. Results from these tagging experiments as well as older tagging data will give valuable information on migration and behaviour of both adult and juvenile cod. No deliverables are required for this theme during this reporting period.

The aim of the third topic (WP7-8) is to explore how oceanographic processes segregate juveniles from different spawning groups. This will be done by developing a fine scale hydrodynamic models of the spawning regions around southern Iceland, west of Scotland and the north-western North Sea as well as to conduct particle tracking simulations of the dispersal of eggs and larvae in order to establish the extent of mixing between offsprings from different spawning locations. Finally, the results form these exercises will be compared with the classification of juvenile cod throughout their distributional range, based on stock identification tools developed in the work packages of second topic. The work on the hydrodynamic model has started. A model system that

consists of a North Atlantic Model domain has been set up, in which two high resolved areas (Icelandic and Scottish waters) are embedded. Samples of 0-group cod were sampled at all major locations within the nursery sites in Icelandic waters, however, sampling in Scottish waters was unsuccessful due to low abundance of cod.

The aim of the fourth topic (WP9) is to establish the differences in recruitment performance of the various spawning groups. A bio-physical model of the dispersal, growth and survival of cod will be modified to incorporate fine-resolution flow and environmental fields developed in WP7 for Icelandic and west/north of Scotland waters. Although the deliverable (bio-physical model implementation) is not due until the end of the second reporting period, preparatory work is already underway. This also includes frequent communication with other partners involved in modelling activities.

The aim of the fifth and final topic (WP10-12) is to compile all the strands of evidence for sub-stock diversity into a conceptual and mathematical model of the overall population dynamics incorporating sub-stock dynamics and use this model to generate advice on how to conserve or restore stock biomass and sub-stock diversity. Within this topic is one milestone (First draft of conceptual mathematical and probabilistic simulation model) and two deliverables ("Documented, reasoned argument for a point-of-departure conceptual model of the dynamics of sub-stock structure in Icelandic and west of Scotland cod, mathematical implementation and analysis" and "initial version of bootstrap simulations and first-draft advice, based on the point-of-departure models produced by WP11"). These milestones and deliverables have been met. A first draft of a conceptual model (METAFOR) has been assembled and tested.

Future Actions:

The main problems encountered in 2003 had to do with low abundance of cod in the Scottish waters. Initially, sampling was planned for 2002 and 2003 in the Icelandic waters but only for 2002 in the Scottish waters. Due to the problems encountered in obtaining adequate numbers of spawning and juvenile cod in the Scottish waters, a special effort will be made to obtain more samples in 2003.

Otherwise, work on all work packages will continue as planned.

Contents

1. OBJECTIVES AND EXPECTED ACHIEVEMENTS

North Atlantic cod stocks appear to be overexploited and in a depleted state. A recurrent feature of the declines in abundance, has been collapse of the spatial distributions of fish and loss of the distinct sub-stocks. There is evidence that a diverse sub-stock structure is necessary to ensure the long term health and productivity of fish stocks, but maintaining this is not recognized as an objective of current fisheries management. The overall objective of this project is to develop the conceptual and mathematical basis for advising on how fisheries management measures might be framed to conserve or restore not only stock biomass, but also sub-stock diversity. We shall accomplish this by studying, and developing models based on, the cod stocks off Iceland and the west and north of Scotland. The aim will be to establish the extent of genetic sub-structure in these stocks, how it is maintained, and the extent to which overall population dynamics are dependent on the sub-stocks.

At a more detailed level, the objectives of this project are to:

- Establish the current state of, and where possible the trends over the last 40 years in, stock-richness of cod around Iceland and to the west and north-west of Scotland, and relate these to changes in stock biomass.
- Establish the genetic, behavioural and oceanographic basis for the richness of the cod stocks, and the variations in productivity between sub-stocks.
- Compile all the strands of evidence for sub-stock diversity in these cod stocks into a conceptual and mathematical model of the overall population dynamics incorporating sub-stock dynamics.
- Use the models to generate advice on how the dual aims of conserving or restoring stock biomass and sub-stock diversity might be achieved.

To achieve these objectives, the following specific tasks will be undertaken:

- Document, from historical trawl survey, egg survey, and fishery data, and the indigenous knowledge of fishermen, the past and present day spawning locations of cod around Iceland, to the west of Scotland and in the north-western North Sea.

- Relate trends in the distribution of spawning locations to changes in overall stock biomass.

- Analyse historical tagging data, and undertake new tagging experiments, to determine the spawning site fidelity of cod, and the annual migration scales of cod from different spawning locations.

- Analyse microsatellite DNA and *Syp* I from samples of cod from different spawning locations, to establish the extent of genetic differentiation of spawning groups and their stability through time. Examine temporal stability by analysing the genetic composition of historical samples of cod (obtained from archived otolith collections) and correlate genetic structures with known changes in population size.

- Characterise each of the spawning groups in terms of their otolith elemental fingerprint and otolith shape, for use as a natural tag or marker in tracking subsequent movements.

- Assemble and collect information on biological parameters influencing reproductive outputs and estimate total egg production by each spawning component. Construct a population abundance index that can be used to partition the total stock into spawning components.

- Develop fine scale hydrodynamic models of the spawning regions around southern Iceland, west of Scotland, and the north-western North Sea. Then, conduct particle tracking simulations of the dispersal of eggs and larvae, in order to establish the extent of mixing between offspring from different spawning locations.

- Conduct sampling of juvenile cod populations which the tracking models indicate should comprise fish from a mixture of spawning groups, estimate their actual composition from analysis of microsatellite DNA and *Syp* I genetic markers, otolith elemental composition and growth rates from analysis of otolith microstructure.

- Estimate the survival to juvenile stage from different spawning groups using an existing bio-physical model of dispersal, growth and mortality, calibrated using the genetic and otolith data collected from mixed juvenile populations.

- Examine the composition of mixed feeding aggregations generally targeted by fisheries, by quantifying the proportions of fish from the various regional spawning components using discrimination techniques developed in workpackages 4 and 5.

- Conduct an assessment of the sub-stock structure of the Icelandic, west of Scotland and north-western North Sea cod stocks, to include estimates of the yield per recruit, and stock-recruitment relationships of the main sub-stocks.

- Develop advice on how catch and/or effort control measures might be structured in space and time to both manage the population abundance at the scale of whole stock, and conserve or hasten the rebuilding of sub-stock structure.

2 PROJECT WORKPLAN

2.1 Introduction

The project will be organised into 5 main topics (Fig. 1), each containing a number of work packages. The topics represent a progression, beginning with the gathering of basic information on where and when cod spawn in the regions of interest, through state-of-the-art molecular analysis, oceanographic and bio-physical modelling, and culminating in the development of proposals as to how fish stock might be managed to conserve or restore both stock biomass and stock richness.

2.2 Project structure, planning and timetable

The topics and work packages are listed in table 1 and figure 1, and described in detail in sections 2.3. The connections between workpackages and the project timetable are shown in Figure. 1. The timetable is shown in figure 2 and table 2 and milstones and deliverables are listed in tables 3 and 4.

Figure 1. *Diagram showing the organisation of the Workpackages into topics partners involved, and the information flow between topics.*

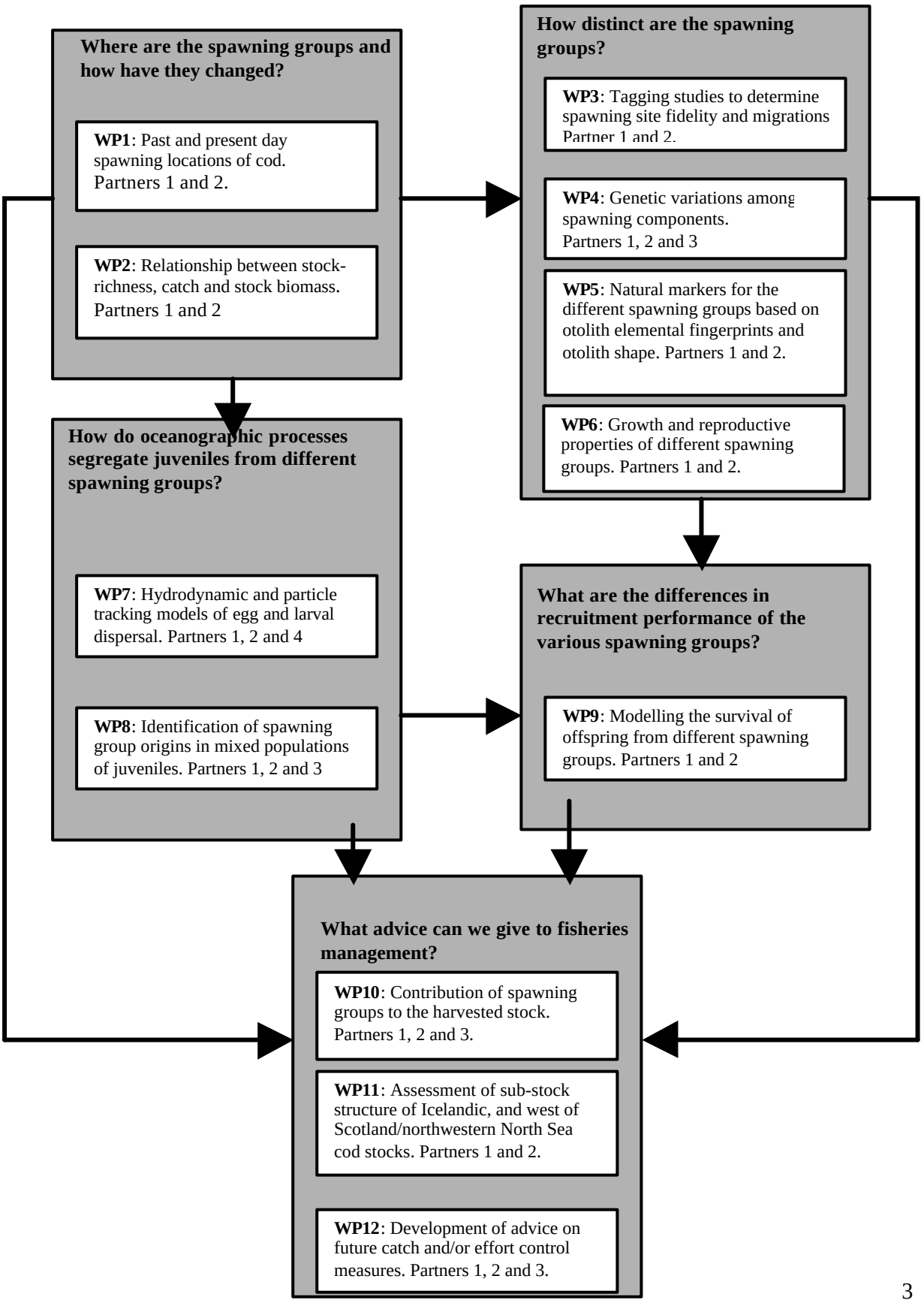

Table 1. *List of workpackages*

Work-package No	Workpackage title	Lead contractor No	Person-months	Start month	End month	Deliverable No
1	Past and present day spawning locations of cod.	1	18	0	48	20, 21, 53
2	Relationship between stock-richness, catch and stock biomass.	2	9.5	0	36	25
3	Tagging studies to determine spawning site fidelity and migrations	1	14	0	42	7, 26, 42
4	Genetic variations among spawning components	3	73	3	48	8, 27, 43, 44
5	Natural markers for the different spawning groups based on otolith elemental fingerprints and otolith shape	1	27	3	48	9, 28, 29
6	Growth and reproductive properties of different spawning groups.	2	19	3	48	10, 30, 31
7	Hydrodynamic and particle tracking models of egg and larval dispersal.	4	60	0	48	3, 6, 11, 12, 13, 18, 19, 22, 32, 33, 45, 46
8	Identification of spawning group origins in mixed populations of juveniles.	1	38	8	48	23, 34
9	Modeling the survival of offspring from different spawning groups.	2	20	4	48	14, 24, 35, 36, 39, 47
10	Contribution of spawning groups to the harvested stock.	1	75	12	48	15, 37, 38
11	Assessment of sub-stock structure of Icelandic, and west of Scotland/north-western North Sea cod stocks.	2	10.5	0	48	1, 4, 16, 40, 48
12	Development of advice on future catch and/or effort control measures.	2	12.4	0	48	2, 5, 17, 41, 49, 50, 51, 52
	TOTAL		376.4			

Figure 2. *Timetable showing the duration and timing of effort by each partner on each Workpackage, together with the approximate distribution across calendar years.*

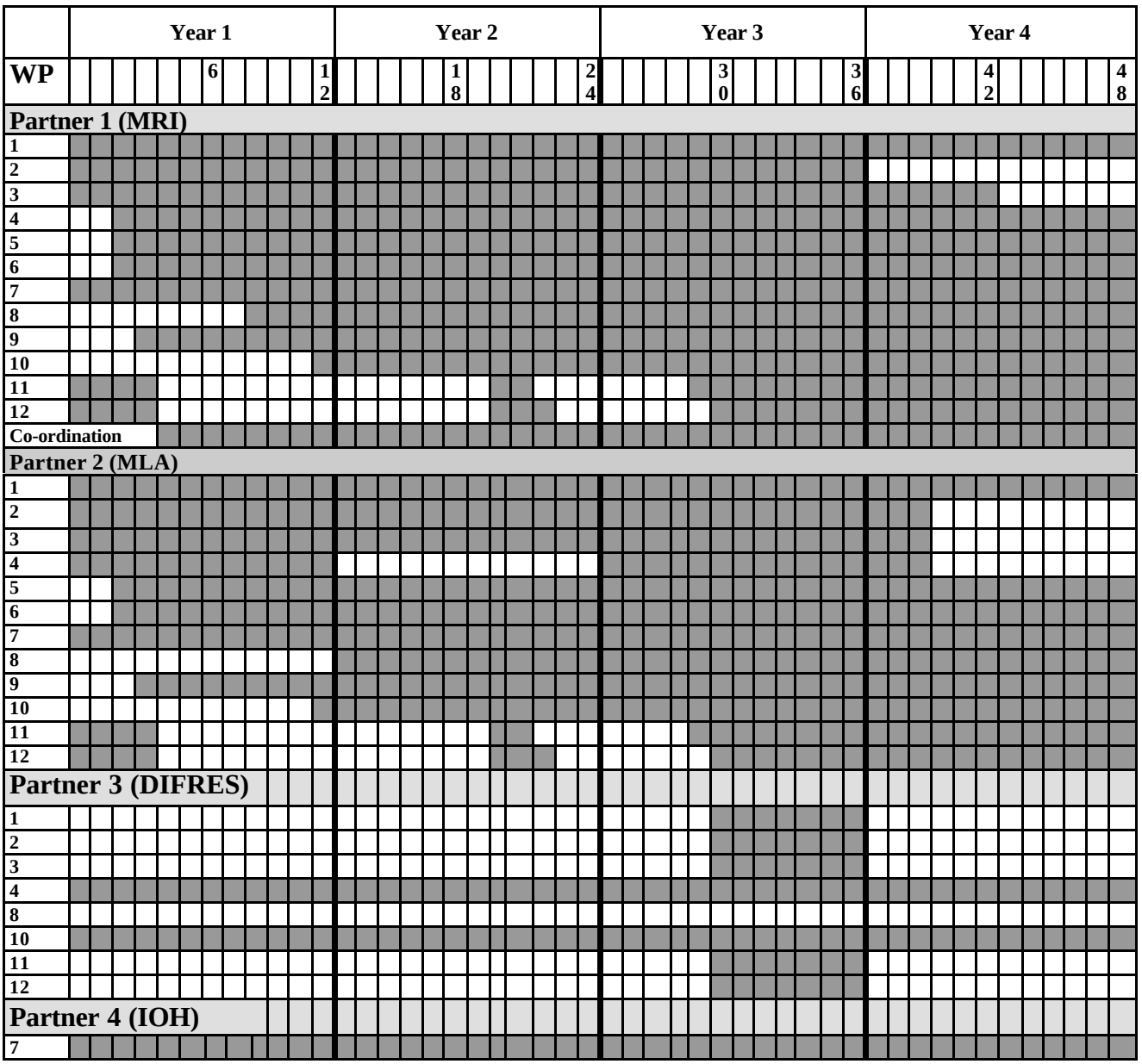

Table 2. *Timetable showing the duration and timing of each workpackage, time of meetings and deliverance of reports*

WP	Year 1	Year 2	Year 3	Year 4	Partners
1	Past and present day spawning locations of cod				1, 2
2	Relationship between stock-richness, catch and stock biomass				1, 2, 3
3	Tagging studies to determine spawning fidelity				1, 2, 3
4	Genetic variations among spawning components				1, 2, 3
5	Natural markers for the different spawning groups based on otolith elemental fingerprints				1, 2
6	Growth and reproductive properties of different spawning groups				1, 2
7	Hydrodynamic and particle tracking models of egg and larval dispersal				1, 2, 4
8	Identification of spawning group origins in mixed populations of juveniles				1, 2, 3
9	Modelling the survival of offspring from different spawning groups				1, 2
10	Contribution of spawning groups to the harvested stock				1, 2, 3
11			Assessment of sub-stock structure		1, 2, 3
12			Development of advice on future catch		1, 2, 3
	1 2 3	4	5, 6, 7 8	9 10 11 12 13 14	Milestones
Project Management Meetings and Reports					
	x x	x	x		Meetings
	Reports	Reports	Reports	Reports	Annual and Final reports

Table 3. *List of milestones. Status: C = completed, P = in progress, N = not started; D = delayed.*

Milestone Number	Milestone Month	Status	Milestone description	Relationship to workpackages
1	4	C	First draft of conceptual, mathematical and probabilistic simulation models from WP11 and 12, synthesising the current state of understanding, and acting as a point of departure from the project.	This will be a defining moment because it represents the point of departure for the sampling, interpretation and analysis in rest of the programme.
2	6	C	Assessment of initial findings from WP1 on the locations of spawning sites.	The initial findings on spawning site locations will be important for configuring the seagoing surveys to follow, during which the biological samples for WP4, 5, and 6 will be collected
3	12	C	Completion of field sampling in 2002	At this point, all of the biological samples from the first field season will have been collected and WP4, 5, 6, 8 and 10 will have their first year material to analyse
4	15	P	First annual update of conceptual, mathematical and probabilistic simulation models from WP11 and 12.	This will be the first iteration of the synthesis of results from all the WP's and revision of the initial concepts and models.
5	27	N	Completion of field sampling in 2003	This stage will represent the completion of all biological sampling in the project. All sample analysis WP's will have their full range of material at this point.
6	27	P	Delivery of fine resolution flowfields for SW Iceland from WP7	Access to the fine resolution flow-fields will enable the particle tracking in WP7 and the biophysical modelling in WP9 to get underway.
7	27	N	Second annual update of conceptual, mathematical and probabilistic simulation models.	This will be the second iteration of the synthesis of results from all the WP's and revision of the initial concepts and models.
8	30	P	Delivery of fine resolution flowfields for west and north of Scotland.	Access to the fine resolution flow-fields for Scottish waters will enable the particle tracking in WP7 and the biophysical modelling in WP9 to begin simulating scenarios for this region.
9	38	P	Completion of genetic, otolith shape and fingerprint, and reproductive sample analysis from WP4, 5 and 6, 8 and 10, and initial interpretation of results.	At this point the basic analysis of all biological material will be completed and definitive interpretation of the results can begin.
10	39	N	Third annual update of conceptual, mathematical and probabilistic simulation models from WP11 and 12	This will be the third iteration of the synthesis of results from all the WP's and revision of the initial concepts and models.
11	40	N	Completion of particle tracking and bio-physical modelling from WP7 and 9	At this point the definitive interpretation of stock-recruitment dynamics can be finalised.
12	46	N	Finalised versions of the conceptual and mathematical models of sub-stock interactions and contribution to metapopulation dynamics from WP11.	At this point the details of the interacting stock-recruit models will be fixed and agreed, as the basis for the final advice generation in WP12.
13	47	N	Agreement between partners on the content of the final advice from WP12 on fisheries management measures to be delivered by the project.	This will be the defining moment in the project where all the preceding WPS come together to deliver the definitive advice deliverables.
14	48		Completion of the project.	

Table 4. *List of deliverables.*

Deliverable No[1]	WP Deliverable number and Deliverable title	Partners	Delivery date[2]	Status
1	11.1: Documented, reasoned argument for a point-of-departure conceptual model of the dynamics of sub-stock structure in Icelandic and west of Scotland cod, mathematical implementation and analysis.	1, 2	3	C
2	12.1: Initial version of probabilistic simulations and first-draft advice, based on the point-of-departure models produced by WP11 (deliverable 11.1).	1, 2	4	C
	First year progress report	1, 2, 3, 4	12	C
3	7.1: Gridded configuration, initial, boundary and driving data for the south-west Iceland fine-resolution model region.	1	18	P
4	11.2: At the beginning of year 2, documented and justified revision of point-of-departure models from 11.1.	1, 2	14	P
5	12.2: First update of simulations and draft advice at start of year 2.	1, 2	15	P
6	7.2: Gridded configuration, initial, boundary and driving data for the west of Scotland/north-western North Sea fine-resolution model region.	2	18	P
7	3.1: Database of release and recovery information for cod.	1, 2	24	P
8	4.1: Collections of cod gill filaments from spawning surveys in 2002 and 2003.	1, 2	24	P
9	5.1: Collections of cod otoliths from spawning and juvenile surveys in 2002 and 2003.	1, 2	24	P
10	6.1: Collections of gonad material, otoliths and population abundance data from spawning surveys in 2002 and 2003.	1, 2	24	P
11	7.3: Database of time and space dependent velocity observations derived from RCM and drift buoy records from Iceland and west/north of Scotland.	1, 2	24	N
12	7.4: Detailed comparison of observed velocity data with results from climatological simulations using the fine-resolution model at Iceland.	1, 2, 4	24	N
13	7.5: Fine-resolution model simulation of velocity, temperature and salinity fields for a selected period corresponding to the field sampling of cod juveniles at Iceland in 2002.	4	24	N
14	9.1: Biophysical model implemented with fine-resolution flow and environmental fields.	1, 2	24	N
	Second year progress report	1,2, 3, 4	24	N

[1] Deliverable numbers in order of delivery dates: D1 – Dn P

[2] Month in which the deliverables will be available. Month P 0 marking the start of the project, and all delivery dates being relative to this start date.

[3] Status: C = completed; P = still in progress; N = not started; D = delayed.

15	10.1: Samples of adult cod from summer/autumn feeding grounds in 2002 and 2003.	1, 2	27	P
16	11.3: At the beginning of year 3, documented and justified revision of models from 11.2.	1, 2	27	N
17	12.3: Second update of simulations and draft advice at start of year 3	1, 2	27	N
18	7.6: Mixing indices for eggs and larvae from spawning sites off south-west Iceland, derived from particle tracking results using the climatological and 2002 flowfields.	1	36	N
19	7.7: Detailed comparison of observed velocity data with results from climatological simulations using the fine-resolution model of the west of Scotland/north-western North Sea.	2	30	N
20	1.1: Data base on oceanographic data of the spawning sites	1, 2	30	N
21	1.2: Analysis of trends in stock-richness for each stock.	1, 2	30	P
22	7.8: Fine-resolution model simulation of velocity, temperature and salinity fields for a selected period corresponding to the field sampling of cod juveniles of western Scotland/north-western North Sea in 2002.	2	30	N
23	8.1: Assignment of juveniles to spawning origin based on genetic and otolith information.	1, 2	36	N
24	9.2: Climatological simulations of survival from different spawning groups.	1, 2	36	N
25	2.1: Comparative analysis of trends in stock richness, catch and the overall state for each of the stocks.	1, 2	36	P
26	3.2: Analysis of homing and dispersal of adult cod.	1, 2	36	P
27	4.2: Database of genotypes for all spawning cod sampled in 2002 and 2003, and archived otolith material.	1, 2, 3	36	P
28	5.2: Otolith elemental fingerprints and otolith shapes for each spawning group.	1, 2	36	P
29	5.3: Otolith elemental fingerprints corresponding to the larval/juvenile stage for specific year-classes in the spawning groups.	1, 2	36	N
30	6.2: Data base on population parameters for the regional spawning components.	1, 2	36	P
31	6.3: Reproductive outputs of spawning components.	1, 2	36	N
32	7.9: Mixing indices for eggs and larvae from spawning sites off west and north of Scotland, derived from particle tracking results using the climatological and 2002 flowfields.	2	36	N
33	7.10: Fine scale model simulations of velocity, temperature and salinity fields for 2-3 selected periods for each region, including the field sampling period in 2003.	1, 2, 4	36	N
	Third year progress report	1, 2, 3, 4	36	N

34	8.2: Estimates of the juvenile source of spawners sampled in 2002 and 2003.	1, 2	38	N
35	9.3: Strategic analysis of simulated stock-recruit relationships for Iceland and Scottish regions.	1, 2	38	N
36	9.5: Estimates of spatial and temporal patterns in cod early-life stage survival from juvenile sampling at Iceland and off Scotland in 2002 and 2003.	1, 2	38	N
37	10.2: Analysis of genetic and otolith chemistry and shape properties for sampled cod.	1, 2, 3	38	P
38	10.3: Analysis of genetic and otolith data, using the equivalent properties measured in fish sampled at spawning grounds, to apportion the summer feeding samples between the various spawning groups.	1, 2, 3	38	P
39	9.4: Simulations of spatial and temporal patterns in cod early-life stage survival at Iceland and off Scotland in 2002 and 2003.	1, 2	38	N
40	11.4: At the beginning of year 4, documented and justified revision of models from 11.3.	1, 2	38	N
41	12.4: Third update of simulations and draft advice at start of year 4.	1, 2	39	N
42	3.3: Analysis of dispersal and migration patterns of juvenile cod.	1, 2	40	P
43	4.3: Analysis of genetic differentiation within the sampled cod.	1, 2, 3	40	N
44	4.4: Comparison of modern and historical genetic compositions of cod.	1, 2, 3	40	N
45	7.11: Particle tracking model analysis of stock mixing in 2003 for each region.	1, 2	40	N
46	7.12: Particle tracking analysis of interannual variability in stock mixing indices, based on additional flowfields from each region, and comparison with North Atlantic Oscillation and other meteorological and hydrographic indices.	1, 2	40	N
47	9.6 Comparisons of 2002 and 2003 field estimates of survival patterns (9.5) with simulated results from deliverable 9.4.	1, 2	40	N
48	11.5: Final, documented and justified versions of conceptual and mathematical models. Yield per recruit relationships for the individual sub-groups making up the metapopulations at Iceland and Scotland. Estimated relationships between metapopulation productivity and stock richness.	1, 2	46	N
49	12.5: Comparison of the probability of stock collapse for a given harvesting strategy, assuming either a homogeneous population or a structured metapopulation – final version	1, 2	47	N
50	12.6: Estimates of the harvesting strategies which result in equal probability of collapse for both the homogeneous and structured populations – final version.	1, 2	47	N
51	12.7: Estimates of the relationship between the magnitude and configuration of catch that optimise the probabilities of conserving stock richness and biomass, and initial guidelines as to how the system could be managed by constraining the spatial distribution of fishing effort – final version.	1, 2	47	P
52	12.8: Estimates of the probability of restoring stock-richness under scenarios of limited harvesting on a collapsed stock – final version.	1, 2	47	P
53	1.3: Atlas of cod spawning sites and description of characteristics.	1, 2	48	P
	Final progress report/Final report	1, 2, 3, 4	48	P

2.2.1 Progress during the first reporting period

WP1 - The main objective of this workpackage is to document the past and present day spawning locations of cod in the Icelandic and Scottish waters. Therefore, one of the main tasks of this workpackage is the retrieval of data from miscellaneous sources, including archived data at the Institute, data that have not been entered into the data bases as well as the ingenious knowledge from local fishermen. This work is continuing both in Iceland and Scotland. First results based on archived data have been used for guidance in the selection of spawning sites to be sampled in WP4-5 (milestone 2). No deliverables are required for this reporting period.

WP2 - The major task for this WP is to examine changes that have occurred in the distribution of spawning cod in relation to catch and stock biomass. Assembling of data have started in both areas. No deliverables are required for this reporting period

WP3 - Large amounts of tag-recapture data exist in the data storage of various fisheries institutes. Some of this data has been reported, while the majority still remains to be analysed. Available tagging data, particularly on mature and spawning fish, are currently being archived and incorporated into appropriate databases for cod in waters off Iceland and Scotland, respectively. Additional tagging of both adult spawning cod and juveniles were performed during last year both in the Icelandic waters and the North Sea. No deliverables are required for this reporting period.

WP4 - Sampling of archived otoliths for historical genetic analysis has been completed in Iceland and Scotland. Genetical analysis of these samples has not started. Sampling of spawning cod was performed at several location in Icelandic waters and the North Sea. In Iceland, 100 spawning cod were obtained from each location. However, due to low abundance of cod in the Scottish waters, fewer cod, especially spawning cod, were obtained at each site. Calibration and extraction of DNA has started and twelve mircorsatellite loci have been screened. A calibration meeting between the two labs conducting the genetic analysis (e.g. the Icelandic and the Danish lab) was held in December 2002 in Silkeborg, Denmark. The aim of the meeting was to standardise the procedure for genetic analysis and to calibrate the scoring of the microsatellite loci between DIFRES and MRI. First results from the screening of 46 standard individuals from three areas: Iceland, Faroe Islands and the North Sea, respectively, have shown significant genetic differentiation among all areas. No deliverables are required for this reporting period.

WP5 - Otoliths for shape analysis and detection of elemental fingerprints were sampled from all cod collected in WP 4. In Iceland, all otoliths have been scanned for shape analysis and half of the otoliths have been decontaminated for elemental analysis. All methods were set up under the guidance of Steven Campana, but Steven visited the Icelandic lab in May 2002 and consulted on methods and technical set up at MRI and ITI (Institute of Technology) who have been sub-contracted to run the elemental analysis. As planned, no work has been carried out on otoliths from the Scottish waters. No deliverables are required for this reporting period.

WP6 - Work on this work package has begun from sampling in spring and autumn 2002 and databases are being established. However, no deliverables is required for this reporting period.

WP7 - The objective of WP7 is to develop fine scale hydrodynamic models of the spawning regions around southern Iceland, west of Scotland, and the north-western North Sea and to conduct particle tracking simulations of the dispersal of eggs and larvae, in order to establish the extent of mixing between offspring from different spawning locations. The work in WP 7 concentrated in the first year on the development of the hydrodynamic models and the collection and preparation of relevant initial and forcing data. A model system was set up that consists of a North Atlantic Model domain in which two high resolved areas (Icelandic and

Scottish waters) are embedded. Initial data and forcing data was collected from institutional records and other sources. These data encompass topographic data, meteorological data and climatological temperature and salinity data. All data sets were gridded and interpolated on the 3-D model grid. No deliverables are required for this reporting period.

WP8 - The objective of this workpackage is to classify and assign the surviving population of juveniles to their spawning group origin. In 2002, 0-group cod were sampled in 6 major areas west, north and east of Iceland. Otoliths have been extracted and ageing and preparation of these otoliths for elemental fingerprint analysis have begun. Similarly, genetic samples were obtained from all juveniles and preserved in alcohol. As planned, genetic analysis of these samples has not started. Preparation for the classification of juveniles in relation to their future spawning groups have also begun. Juveniles from 1995, 1998 and 1999 have been selected in order to represent years of different drift patterns. Otoliths from these samples are ready for coring, however, as planned, no coring of either juveniles or adults has started. Sampling of 0-group cod in Scottish waters was less successful. Due to extremely low abundance of juvenile cod, 100 specimens were obtained despite a great sampling effort. No deliverables are required for this reporting period.

WP9 - The objective of this workpackage is to estimate the survival to juvenile stage from different spawning groups. An existing bio-physical model of the dispersal, growth and survival of cod will be modified to incorporate fine-resolution flow and environmental fields developed in WP7 for Icelandic and west/north of Scotland waters. Although the deliverable (bio-physical model implementation) is not due until the end of the second reporting period, preparatory work is already underway. This also includes frequent communication with other partners involved in modelling activities.

WP10 - The main objective of this workpackage is to examine the composition of mixed feeding aggregations generally targeted by fisheries by quantifying the proportions of fish from the various regional spawning components. In 2002, cod were sampled on the main fishing grounds East and West of Iceland and at several locations in Scottish waters. Otoliths have been removed from all cod and scanned and measured for otolith shape analysis. As planned, further analysis, including genetic analysis has not started. All field sampling in 2003, including sampling of spawning cod, juvenile cod and cod on the fishing grounds, have therefore been completed and milestone 3 has been achieved. No deliverables are required for this reporting period.

WP11 - The main objective of this workpackage is to conduct an assessment of the sub-stock structure of the Icelandic, west of Scotland and north-western North Sea cod stocks. A first draft of a conceptual model (METAFOR) has been assembled and the first milestone and deliverable have been met. In the model, the stocks are reviewed as metapopulation composed of a number of subpopulations where each subpopulation has its own stock-recruitment relationship and the sustainability of each subpopulation will depend on the balance between its particular mortality and recruitment rates.

WP12 - The initial version of a probabilistic simulations based on the conceptual model METAFOR developed in WP11 has been tested (the first milestone and deliverable). The first task was to explore the dynamics of the model under the simplest possible test conditions using 3 natal sub-populations based on numbers at age from STEREO reanalysis of ICES assessment working group outputs for North Sea and west of Scotland cod stocks. The first run of the model have provided useful information and have illustrated several important points that need special attention (see appendix 4) including: 1) need for greater understanding of stock-recruit relationships at the sub-stock level and how they relate to S/R relationships at the whole population level; 2) greater understanding of environmental conditions of the natal spawning grounds and how they may influence attraction of fish and possibly override natal instincts; 3) importance of good subpopulation data including those parameters that influence egg production; 4) greater understanding of straying and those factors that override the eroding effects of straying in the model.

2.2.2 Discussion

WP1 - Although, the location of the main spawning sites of cod in the North Atlantic are generally well known, more detailed description of spawning sites on a finer geographical scale are often lacking. The results from this workpackage will be used to create an atlas of cod spawning sites in Icelandic waters and North Sea. Presently, such an atlas does not exist.

WP2 The data sources available for this work package are being reviewed. The ability to obtain sufficient data at the population level will depend on the geographic scale of structuring evident from WP 4 and others.

WP3- Dispersal and migration of cod from the spawning areas from and to the feeding grounds are often not well known. At the same time, only scarce data exit on juvenile dispersal and information regarding their fidelity to their spawning sites as well as integration into the fishing stock are limited. The results of this WP will provide a valuable assessment of migration and homing of cod to and from spawning areas as well as between different spawning or feeding areas.

WP4 - Heavily exploited marine fish tend to exhibit wide variations in population size through time often culminating in population crashes and commercial extinction. Drastic decreases in population size typically result in the loss of genetic variation and evolutionary potential through the random loss of rare alleles. A decrease in genetic diversity can occur even when the final size of populations is still large as is the case for most exploited marine fish populations. Dispersal (migration with gene flow) among components in a (meta)-population complex can also increase with increased variation in size of the local populations, and this process can also lead to decreased genetic differentiation among population components. Finally, genetic diversity can also be lost when demographically and genetically diverse complexes of migratory marine fish that intermingle seasonally are misidentified and managed spatially and temporally as a single panmictic unit. This WP is the heart of the project and will deliver the most valuable and comprehensive assessment of genetic structure of cod stocks in the eastern Atlantic to date.

WP5 - The aim of this workpackage is to use the otolith elemental composition and shape specific to each spawning group to identify and track these fish as they later disperse to the feeding grounds and fishery locations. Some of the trace elements incorporated into the growing surface of fish otoliths have been shown to reflect the physical and chemical characteristics of the ambient water (Begg et al., 1998; Campana, 1998; Campana et al., 2000). To the extent that groups of fish inhabit different environments, the otolith elemental composition (the "otolith elemental fingerprint") then becomes a natural marker or tag of those groups. Use of an elemental fingerprint as a natural tag takes advantage of the fact that otoliths are metabolically inert, and cannot change appreciably in size or composition over a brief time period. Once the elemental fingerprint of all potential source (e.g.- spawning) groups has been determined, fish remain identifiable as to their spawning group, despite any mixing with other groups, until later otolith growth substantially alters overall elemental composition. An appealing feature of this application is that the elemental fingerprint need not be linked to potential sources or locations in the environment. Rather, the fingerprints are used as natural, short-term tags of pre-defined groups of fish. It is important to note that the elemental fingerprints are not stock discriminators, since genetic differences are not implied. However when differences in the fingerprints among spawning groups exist, the fingerprint becomes a powerful discriminator of those groups. This WP will, in combination with WP4, provide valuable assessment of the population structure of cod in the Icelandic and the Scottish waters.

WP6 - Stock structure information provides a basis for understanding the dynamics of fish populations. Each stock may have unique demographic properties displayed by different growth, morphology and reproductive characteristics. Great differences exist in growth, size, age and condition of spawning cod among different spawning areas and estimated total egg production has been shown to vary dramatically based on abundance and mean size of spawners (Marteinsdottir et al., 2000). Regional differences in size at age and age at maturity have also been reported in the North Sea although it is not clear how these relate to different spawning components (Daan, 1978; ICES, 1994). the results of this workpackage will therefore play an important role in defining the spatial the variation in population parameters among the different spawning groups including size, age, condition, growth, age at maturity and sex ratios. Attempt to estimate the relative size of each spawning component and to use the information to estimate potential production in each area by using an egg production model will be based on these information as well as existing relationships between size and condition of female cod and egg production.

WP7- The extent to which the various sub-stocks remain segregated during their life cycle is an important aspect of both the assessment of sub-stock structure and the development of advice on how to conserve the structure. The aim of this Workpackage is to simulate the passive mixing of early life stages from different spawning groups, due to oceanographic processes. Particle tracking models are widely used to simulate the dispersal of materials and biota in the marine environment, and have been extensively used to investigate the transport of fish eggs and larvae. Briefly, such systems require output from a hydrodynamic model (HDM) (time resolved velocities at a 3-dimensional network of geographical locations), to drive the trajectories through space and time of simulated particles in the tracking model. The horizontal advective component of velocity at each instantaneous particle location is interpolated directly from the HDM data, and to this is added a stochastic component to represent diffusion which is usually parameterised from the velocity shear. HDM data for the north-east Atlantic, in particular the Greenland-Scotland Ridge area which is the particular focus of this project, already exist in the public domain Heinbucher and Backhouse, 1999, Harms et al., 2000). However, the spatial resolution of these data (1/8 degree latitude x 1/4 degree longitude; approximately 14km), whilst adequate for simulating the broad scale dispersal of cod eggs and larvae, is not adequate for investigating the oceanographic basis for segregation of offspring from different spawning grounds. This is because the eddies generated by bathymetry, haline, and temperature discontinuities which most likely dictate the segregation, cannot be resolved at 14km resolution. Consequently, for this project, we will need to develop a nested system of hydrodynamic models by embedding a fine resolution, eddy resolving model of the key areas of interest, within the 14km resolution Atlantic model.

WP8- O-group indices that are usually assembled for large geographical areas, ignoring the fact that that the surviving populations of juveniles may have originated from different spawning sites, each characterised by diverse stock-environmental interactions, are not likely to give an accurate estimate of year-class strength. Discrimination of juveniles from different spawning sites will provide new insight into how multiple spawning aggregations maintain balanced recruitment levels in the cod stocks. The stock identity of juvenile aggregations can be interpreted in either a backward- or forward-facing perspective; traditional backward-facing analyses determine the spawning group which produced the juveniles, while forward-facing analyses determine the spawning group to which the juveniles later recruit. On average, one would expect the juvenile progeny of a particular spawning group to later recruit to that same spawning group. However, in a variable environment, and particularly where year-to-year variations in current flow and direction result in variable distributions of juveniles, a substantial portion of the juveniles may recruit to other spawning locations. Discrimination between the two possible measures of stock identity requires different approaches. DNA markers are most suited to determining the spawning source of the juveniles, but cannot be used to determine their subsequent spawning location as adults. In contrast, otolith elemental fingerprints cannot be used to determine the source of the juveniles, but are well suited to determining their eventual fate (through comparison with the elemental fingerprint of the otolith core, corresponding to the juvenile phase, of the juvenile

year-class once it begins spawning). The aim of this workpackage is to validate the predicted dispersal of juveniles based on results from the particle tracking model (WP7). The predicted distribution of the juveniles will be compared with those actually observed in the 0-group surveys. The genetic origin of major aggregations of juveniles will be determined through comparison with the DNA results of WP 4. The subsequent fate of the juveniles as adult spawners will be determined through comparison of the juvenile elemental fingerprints with those characteristic of the adult spawner otolith cores from the same year-class later on (WP 5).

WP9 - In order to assess the impact of eroding of stock-richness on overall stock-recruitment relationships, we will need to determine the survivorship of eggs, larvae and juveniles from the various spawning groups. We can expect these to be different by virtue of 1) the differences in environmental conditions which offspring spawned at different times and locations will experience during their early life, and 2) the different habitats to which juveniles are carried from different spawning sites. In this project we will assess the spatial and temporal structure of survivorship by means of a combination of modelling and analysis of field sampled material.

WP10 - Distribution of the fishing stocks is generally well recorded both in annual surveys and in fishermen's log-books. However, no information exists with respect to their origins. Annual fluctuations in abundance within different areas of the main fishing grounds may by influenced by a diverse array of factors (fishing, environment, changes in distribution, migration and variable cohort structure), that operate in a complex, multiplicative fashion. Distinguishing the effects of these factors is a necessary process in understanding stock and recruitment processes, but are rarely known. Furthermore, in order to successfully explore the dynamic behaviour of fishing populations the first prerequisite calls for a sufficient knowledge of the populations structure. The results of this WP will give valuable information regarding the exploitation of the different spawning groups during the time of the year when the fish from different sub-stocks are mixed.

WP11 - The aim of this Workpackage is to produce a synthesis of the dependence of each of the cod metapopulations in the study on their underlying sub-stock structure. Our first requirement is to develop the conceptual model that describes how the sub-stocks interact and contribute to the overall population dynamics of the metapopulation. Our points of departure in developing the conceptual model are:

- Density independent (environmentally determined) factors governing rates of early life survival are specific to each sub-stock, whilst density dependent process act indiscriminately across sub-stocks due to passive mixing.
- Recruitment to each sub-stock is a function of both pre-recruit survival and the extent of natal fidelity.
- Natal fidelity may vary between sub-stocks depending on oceanographic segregation, and with spawning stock abundance.

All of this work depends on the work done in the other workpackages where information on abundance, population parameters and local environmental factors are being assembled.

WP12 - Our first aim in this final workpackage will be to indicate how the advice on whole-stock safe biological limits might differ from that given at present, if it was to take into account the need to conserve sub-stock diversity as well as overall stock biomass. We hope to accomplish this by running a simulation of the temporal dynamics of a metapopulation in which the underlying stock-recruitment relationship is provided by the interacting sub-stock models developed in WP11, and comparing this with equivalent results obtained with a single homogeneous stock-recruitment relationship. The principle of the method is to run the model many times for a given whole-stock harvesting strategy (defined in terms of either integrated catch or fishing mortality), with selected parameter values assigned for each run from underlying statistical distributions designed to simulate uncertainty or variability in the actual values. The resulting family of simulated time-series is then used to calculate the time varying

probability distribution around various quantities, for example stock biomass. By this technique, we shall compare the probability of stock collapse for a given harvesting strategy, assuming either a homogeneous population or a structured metapopulation. Finally, we shall determine the harvesting strategies which result in equal probability of collapse for both the homogeneous and structured populations.

2.2.3 Future action

WP1 - Work on this workpackage is continuing as planned.

WP2 - Work on this workpackage is continuing as planned.

WP3 - Additional tagging experiments, especially on mature and spawning cod, will be performed in Icelandic waters and the North Sea next year. Following completion of the archived databases analysis of homing and dispersal patterns of adult and juvenile cod will occur.

WP4- As planned, sampling of spawning cod will be preformed at 8-12 sites in the Icelandic waters in the year 2003. Some of these sites (4-5) will be repeated from last year, but most of them will be an addition to the 2002 sampling. Given the low numbers obtained in the Scottish waters, additional sampling is also planned for 2003. The sampling strategy will be revised in the light of the findings in 2002 where sampling will be focussed on fewer discrete areas.

WP5 - As planned, sampling of spawning cod will continue in 2003 in Icelandic waters (see WP4). Due to low sample sizes in Scottish waters, sampling will also be repeated in that area in 2003. Following the decontamination of all otoliths, analysis of elemental fingerprints will proceed.

WP6 - Due to the problems encountered in obtaining adequate numbers of spawning cod in 2002, additional sampling is planned in the Scottish waters for 2003. This will include sampling from the 1st quarter ICES IBTS in February and VIa groundfish Scottish survey in March 2003. Where possible, commercial samples will be obtained from relevant sample areas, although this may depend on plans currently being discussed for cod management.

WP7-Next years actions for this workpackage will still concentrate on data collation and incorporation for model forcing, comparison and validation. Model validation and improvement will be the most important task in WP7 for the second year in METACOD. The second project meeting will give the opportunity to exchange first results in order to test particle tracking with the simulated flow fields.

WP8 - As planned, 0-group cod will be sampled again in Icelandic waters in 2003. Genetic and elemental analysis will also start in 2003. In Scotland, sampling will be also be repeated, e.g. due to low sample sizes in 2002.

WP9 - Work on this workpackage is continuing as planned.

WP10 - Work on this workpackage is continuing as planned. Sampling will be repeated on the feeding grounds in Icelandic and Scottish waters in the fall 2004. In Iceland, attempts will be made to sample cod from a greater area around the country including more shallow waters.

WP11 & WP12 - Having established the basic principle of the METAFOR model, the next phase will be to thoroughly discuss the concepts amongst the project partners. This will lead to a second iteration of the model which will probably be recorded in FORTRAN. At this stage, we shall incorporate stochastic properties in order to take account of uncertainty in the

parameters of the system. Attempts will also be made to compare the results from METAFOR, by modelling the dynamics of the metapopulations with another tool, GADGET (Globally Applicable Area-Desegregated General Ecosystem Toolbox), that is being developed in another EU project "Development of structurally detailed statistically testable models of marine populations (dst^2). A special attention will be given to the points that were shown to be important resulting from the first run of the model (see WP12 in chapter 2.2.2 and appendix 2) This work will start in 2003.

2.3 Description of workpackages

Workpackage 1: Past and present day spawning locations of cod.

Start date: January 2002

Completion date: December 2005

N° of the partner responsible: 1

N° of other partners involved: 1, 2, 3

Table 1.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	2.5	0.9	0	0
Total to date	2.5	0.9	0	0
Total planned	10	7	1	0

Objectives and input to workpackage

Document, from historical trawl survey, egg survey, fishery data, log-books, and the indigenous knowledge of fishermen, the past and present day spawning locations of cod around Iceland, to the west of Scotland and in the north-western North Sea.

Methodology and study material

1) All data containing records of spawning cod will be extracted from archived trawl survey data, tagging data bases, individual cruises and landed catch collections made in the Icelandic waters, west of Scotland and the north-western North Sea. Where possible, data extending back to the beginning of the 20th century, will be analyzed for the incidence of spawning female cod.
2) Both old (back to the beginning of the 20th century) and more recent plankton survey data for which fish eggs have been analyzed, will be examined for the incidence of early stage cod eggs.
3) Fishing vessel log-book data and commercial catch records will be analyzed to identify the incidence and location of spawning cod.
4) Current programs of surveying the indigenous knowledge of Icelandic and UK fishermen will be adapted to seek information on the historical and modern day locations of cod spawning sites.
5) All available historic data on time and duration of spawning at the different spawning sites will be collected and assembled from trawl and gill net surveys including results from EU-project[23]. Samples and data on spawning cod from Scottish waters collected in 2002 will also be made available to the project from a nationally funded project.
6) All available oceanographic data will be assembled for each of the spawning sites.

Assessments of the trends in stock-richness will be produced for each of the stock regions.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table1.1 and the deliverables within the workpackage are listed in table 1.2.

MRI:

The main spawning grounds of cod in Icelandic waters are located along the south coast (Sæmundsson, 1924). Additional spawning was also shown to occur within fjords of the West and North coast although it was considered to be on a much smaller scale than the spawning at the South coast (Sæmundsson, 1924). Distribution of eggs and larvae in 1976-1981 confirmed this general pattern (Fridgeirsson, 1982). It was shown that the greatest abundance of eggs were generally obtained in the coastal areas at the South and Southwest coast (Fig. 1.1 from Fridgeirsson, 1982).

Fridgeirsson did also find newly hatched gadoid eggs at locations within fjords West, North and East of the country. He was, however, not able to discriminate between the cod and haddock eggs. More recent studies have confirmed the existence of eggs and larvae within these local fjords (Gunnars et al., unpublished). These studies have also demonstrated that pelagic juvenile cod originate from spawning locations all around the island (Marteinsdottir et al., 2000) and that the production of the smaller infjord spawning components may in some years contribute significantly towards the surviving population 0-group cod (Begg and Marteinsdottir, 2000, 2002).

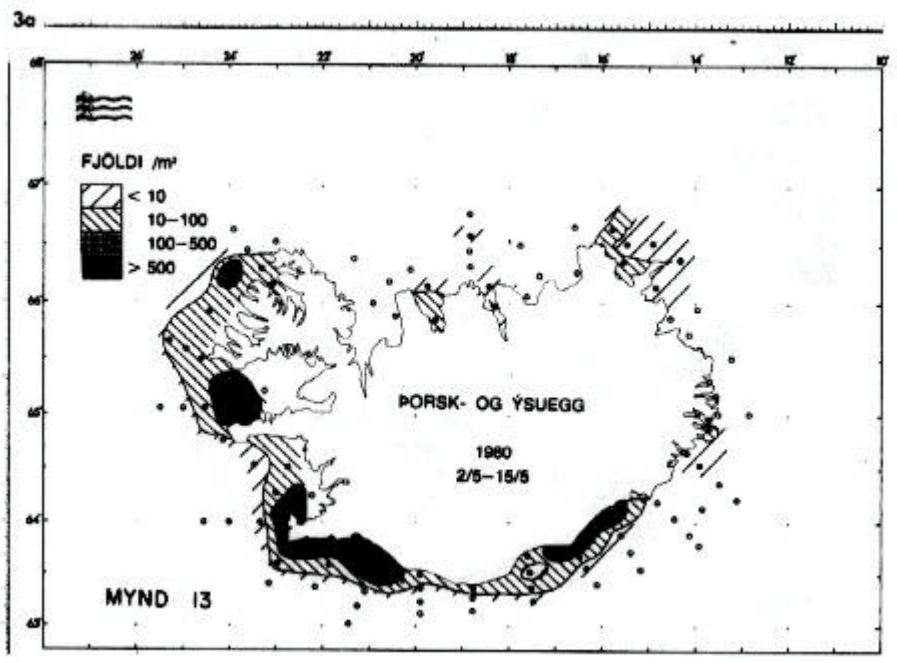

Figure 1.1. *Distribution of one day old gadoid eggs in 1976-1981 (from Fridgeirsson, 1982).*

One of the major tasks of this workpackage is to identify all areas where spawning is likely to occur. Data on spawning cod (cod in stage III characterised by fluid running sperm or fully mature translucent eggs in the gonads) have been subtracted from the MRI data base. The data base contains a total of 38296 spawning cod during the time period 1979-2002. A preliminary graph showing the distribution of spawning cod based on this data indicate the presence of spawners on the main spawning grounds but also in offshore areas both south, west and north of the country. These data are presently being updated for time periods prior to this. Data from egg surveys both recent ones, the ones from 1979-1981 as well as older ones dating back to the beginning of last century are also being assembled.

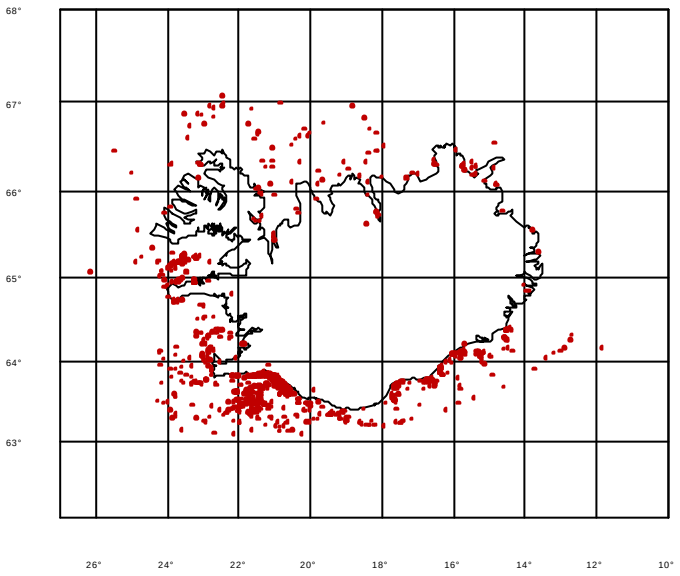

Figure 1.2. *Distribution of spawning female cod collected in March - May (stage III = fully mature with transparent running eggs): The figure represents all females at stage III (8754 females) present in the MRI data base since 1979. No effort has been done to correct for effort or typographical error.*

MLA:

There has been no previous intensive investigation into cod spawning sites in Scotland, and most of the information has been derived from historic egg surveys and research vessel surveys. The Butt of Lewis and the Moray Firth have been identified in the literature as sites with high concentrations of cod eggs, but their relative importance as spawning sites has not been investigated. For this workpackage, archival data on the locations of spawning cod have been located from various sources, primarily from FRS's Research Vessel Programs Database (RVR). Although no commercial log book data have been analysed, advice from local fishermen has been sought and a few possible areas around Shetland identified. Further contact with fishermen is planned for early 2003.

The Research Vessel Programs Database (RVR) contains survey data collected by the Marine Laboratory's research vessels Mara, Explorer, Scotia and Clupea. The database starts in 1925 and is continuously updated after each cruise. There are over 16,000 separate hauls contained within these files, including data such as gear, date, ICES statistical rectangle, time shot, time hauled, depth and start and stop longitude and latitudes. It is believed that some vessel data has not electronically recorded on the database, such as charter, tagging and vessel

comparison cruises. A full search through the original written summaries is being conducted at present to determine which data are missing.

A database for cod catches by available research cruise records from 1925-2002 has been created, and will be updated as and when additional cruise data becomes available. Length frequency data (LFD files) is available for cod from every haul from 1925. Files on age (ALK's) and maturity (SMALK's) at length for cod are available from the 1975 and 1984 respectively. The RVR database samples one cod per 1cm length class and therefore it is not possible to investigate trends in spawning cod abundance over a temporal scale, although it does give an indication of annual changes in the spatial extent of spawning cod.

Cod spawning locations were defined by extracting cod records for fish over 25cm in length during Quarter One (January- April) for each decade. From these data we selected areas of high cod density as suitable areas to conduct sample collection during the spawning season cruises in 2002. A total of 8 inshore sites (Moray Firth, Orkney, Shetland, North Minch, South Minch, Clyde and Buchan) and 6 offshore sites (Central, Forties, Butt of Lewis, Papa Bank, Outer Hebrides and North Ireland) were identified. Viking Bank and Faroe were selected as outlier areas for the genetic analyses (WP 4).

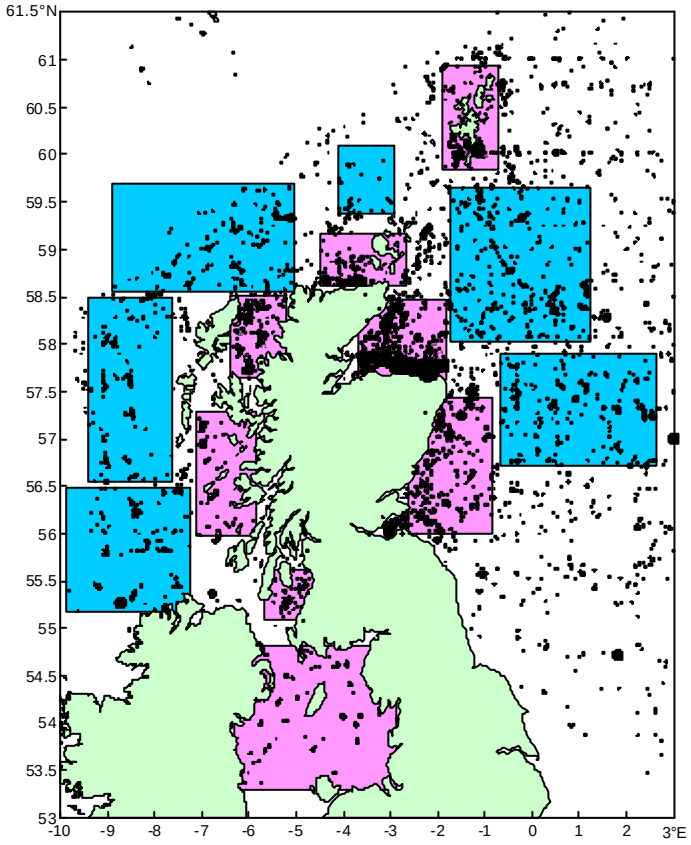

Figure 1.3. *Cod (over 25 cm in length) catches per hour during Quarter One from 1925-2002. The colored boxes define areas of high cod densities selected as FRS's sampling sites for 2002. Inshore (pink) and Offshore (Blue).*

Table 1.2. *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D20	1.1 Data base on oceanographic data of the spawning sites	30	N
D21	1.2 Analysis of trends in stock-richness for each stock	30	P
D53	1.3 Atlas of cod spawning sites and description of characteristics	48	P

Expected results and relevant corresponding milestones

This WP is expected to result in an atlas of cod spawning sites for Icelandic and Scottish waters, which will be produced as a stand-alone atlas. The WP will also provide material for milestone 2 which will define the survey plans for the filed sampling programme.

Workpackage 2: Relationship between stock-richness, catch and stock biomass.

Start date: January 2002

End date: December 2004

N° of the partner responsible: 2

N° of other partners involved: 1, 2, 3

Table 2.1 *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	1	1.17	0	0
Total to date	1	1.17	0	0
Total planned	6	2.5	1	0

Objectives and input to workpackage

Relate trends in the distribution of spawning locations to changes in catch and stock biomass.

Methodology and study material

1) Assemble assessment data (catch, effort) for the Icelandic, west of Scotland and northwestern North Sea cod, extending as far back in time as possible.
2) For years prior to modern assessments, reconstruct stock biomass for catch, effort and other such data as are available.
3) Compare trends in stock richness with catch and stock biomass data.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table2.1 and the deliverables within the workpackage are listed in table 2.2.

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The major goal for this workpackage is to examine changes that have occured in the distribution of spawning cod in relation to catch and stock sizes.

In Iceland, data on spatial distribution and abundance of mature and spawning cod sampled in the spring survey (conducted in March at the beginning of the spawning season) have been subtracted from the MRI database for the years 1990-1999. These data are presently being updated for the years 2000-2002. Additional data will be obtained from the gill net survey conducted at peak spawning along the south and southwest coast (1996-2002) as well as from all commercial catch samples collected during the spawning periods either at sea or from landed catch during the second half of last century. Data collected previous to 1979 are presently being entered into the database. These data will be used to form a base for METACOD containing information on the presense/absense of mature and spawning cod as well as catch and effort (where available) for individual areas (Fig. 2.1).

In the North Sea, catch and effort data were collated by Pope and Macer (1996), and used in a VPA to estimate abundance of these stocks from 1920 onwards. However, they used exclusively English data series, pertaining mostly to the southern North Sea. Data on Scottish, Norwegian and other relevant fisheries will need to be collated for a similar exercise to be carried out in the areas of relevance to METACOD. The methodology used by Pope and Macer forms a good starting point for generating catch and effort estimates, once data are available.

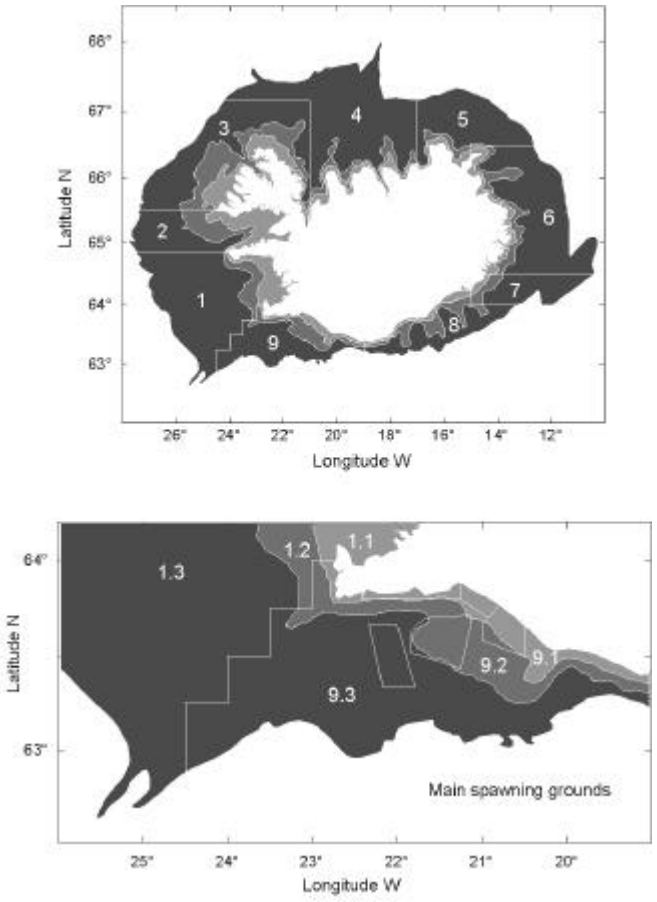

Figure 2.1. *Division of areas for the estimation of abundance and distribution of spawning cod in Icelandic waters. Each Area (1-9) will be divided into three areas based on depth (< 100 m, 100-150 m and > 150 m). Where possible, smaller areas (especially within the shallow zones) will be established. As such, area 9 does already contain 4 subareas within 9.1 and two subareas within 9.2. Similar subareas have been identified within area 8, 1 and 2. These areas will be identified as 9.1.1-9.1.4, etc., respectively.*

Table 2.2. *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D25	2.1 Comparative analysis of trends in stock richness, catch and the overall state for each of the stocks	36	P

Expected results and relevant corresponding milestones

The WP will result in a historical analysis of the decadal scale temporal changes in cod stock abundance and stock-richness. The outcomes will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13).

Workpackage 3: Tagging studies to determine spawning site fidelity and migrations of adult and juvenile fish.

Start date: January 2002

End date: July 2005

N° of the partner responsible: 1

N° of other partners involved: 1, 2, 3

Table 3.1 *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	2.5	2.75	1	0
Total to date	2.5	2.75	1	0
Total planned	8	5	1	0

Objectives and input to workpackage

Analyse historical tagging data, and undertake new tagging experiments, to determine the spawning site fidelity of cod, and the annual migration scales of cod from different spawning locations

Methodology and study material

1) Archive available tagging data and construct a database with tag/recapture information on mature and spawning fish
2) Explore homing pattern of adult fish including movements from and to the spawning sites and the major feeding grounds.
3) Conduct new tagging experiments at spawning locations that do not have any tagging data (mainly at the north and north-west coast of Iceland, and some parts of the north and west of Scotland).
4) Tag juveniles (1+) within local fjords in the proximity of the spawning sites and explore dispersal from the spawning sites to the major feeding grounds.
5) Assemble and analyse temporal and spatial variation in dispersal of 1-3 year old cod based on survey data.

6) All tagged fish will be sampled for genetics at the time of tagging and all recaptured fish will be analysed with respect to genetics, elemental fingerprints and otolith shape, growth and age, when possible. All tagged fish will be weighed and measured at tagging and re-measured at recapture if possible.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table3.1 and the deliverables within the workpackage are listed in table 3.6.

MRI:
Progress of work to determine spawning site fidelity and migrations of adult and juvenile cod using tag-recapture data is proceeding according to the timetable specified for the workpackage deliverables (Table 3.2).

Available tagging data, particularly on mature and spawning fish, are currently being archived and incorporated into appropriate databases for cod in waters off Iceland and Scotland, respectively.

In Iceland, a total of 17363 sexually mature adult cod were tagged and released on various spawning grounds around the country (Areas 1-9, Fig. 2.1) using conventional dart tags between 1991-1999 (Table 3.3, Fig. 3.1). Similarly, a total of 2583 juvenile cod were tagged and released during this period (Fig. 3.2), while 1007 adult cod were released with Data Storage Tags (DSTs) between 1995-1999 (Table 3.3). These data will constitute the majority of the archived Icelandic tagging database. At present, all the archived conventional tag-recapture data have been entered into an ORACLE database on a UNIX system, with the transfer of DST data from text and EXCEL files currently occurring. In addition, historical tag-recapture data from 1948-1986 (Jónsson 1996) are available for analysis, although there are concerns about the validity of comparing these data with the more recent data because of differences in research objectives and sampling strategies. Before 1991, individual cod were tagged without any clear consideration for life history stage or tagging location. In contrast, since 1991 the Marine Research Institute has conducted specific tagging experiments of adult cod on spawning grounds, and juvenile cod on feeding grounds to determine homing behaviour and spawning site fidelity.

Table 3.3. *Archived tagging data of juvenile and adult cod tagged using conventional tags, and DSTs in waters off Iceland, 1991-1999. (see Fig. 2.1 for identification of areas)*

Area	Juvenile tags	Juvenile recaptures	Adult tags	Adult recaptures	Adult DSTs	DST recaptures
1	337	70	185	70	9	5
2	652	70	1727	560	27	15
3	1594	152				
4			571	206		
5			577	204		
6			4471	1795		
7						
8						
9			9832	2002	950	269
Total	2583	292	17363	4837	1007	289

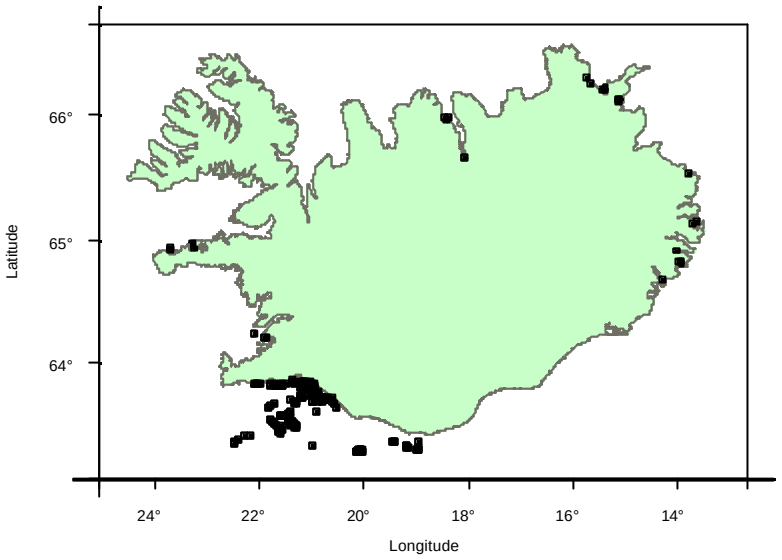

Figure 3.1. *Distribution of archived mature cod tag releases between 1991 and 1999.*

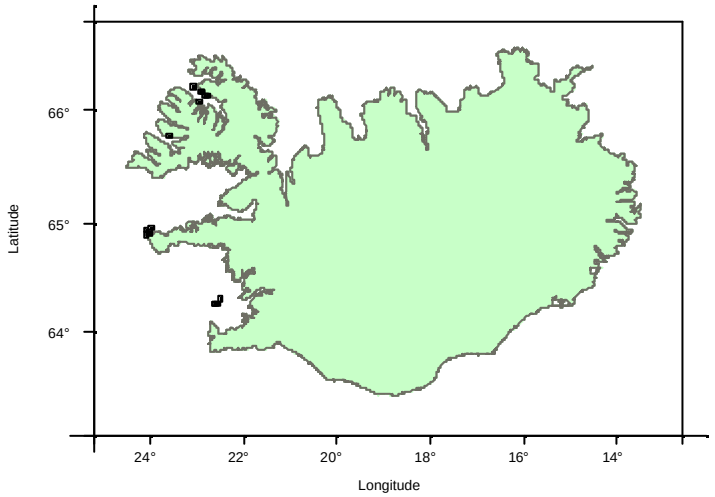

Figure 3.2. *Distribution of archived juvenile cod tag releases between 1991 and 1999.*

In 2002, new tagging experiments were conducted at spawning and nursery locations throughout Iceland and Scotland where previously there were limited data. In Iceland, a total of 3986 adult cod were tagged and released on spawning grounds off the north and east coasts using conventional dart tags and DSTs (Table 3.4, Fig. 3.4), while 3856 juvenile cod were

tagged and released on nursery grounds off the north and north-west coasts (Table 3.4, Figs. 3.4 and 3.5).

Table 3.4. *Tagging data of juvenile and adult cod tagged using conventional tags, and DSTs in waters off Iceland, 2002.*

Area	Juvenile tags	Juvenile recaptures	Adult Tags	Adult recaptures	Adult DSTs	DST recaptures
1						
2	1900	36				
3						
4	1956		1258	121	82	16
5			737	48	66	5
6						
7						
8			684	61	92	12
9			951	73	116	4
Total	3856	36	3630	303	356	37

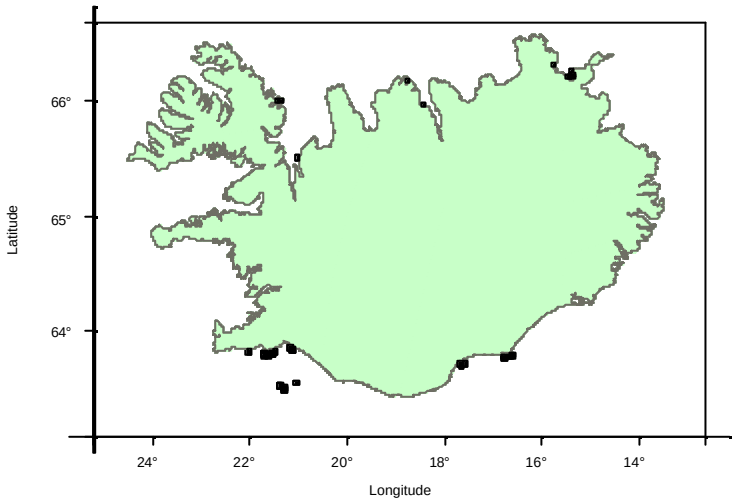

Figure 3.4. *Distribution of mature cod tag releases in 2002.*

In June 2002, a total of 1900 juvenile cod (< 40cm in length) were tagged and released in Breiðafjörður (Area 2 in Fig. 2.1; Fig. 3.5). Of these, 940 were double tagged and 880 fin-clipped for DNA analysis. An additional 200 juvenile cod were sampled for age/size structure and sex composition. In January 2003, a total of 21 fish had been recaptured from this experiment, mostly from similar locations where they were released.

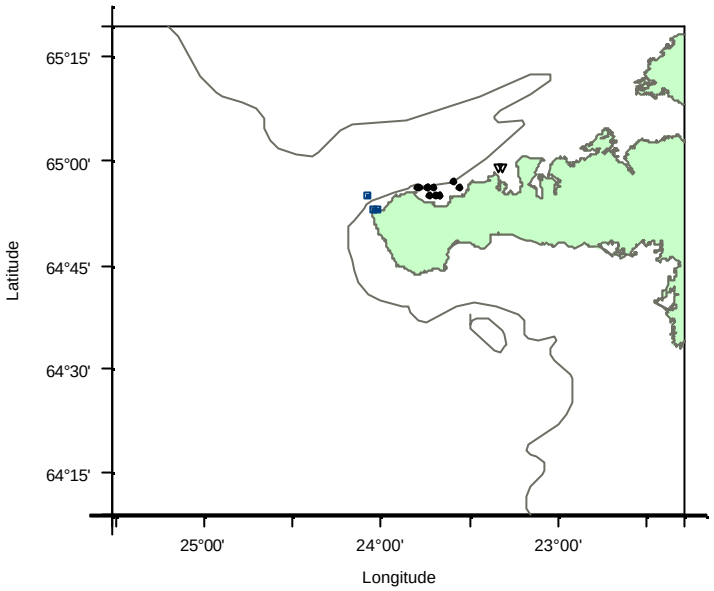

Figure. 3.5. *The three tagging areas in Breiðafjörður. In Grundarfjörður (triangle) a total of 42 immature cods were tagged; in Ólafsvík (dot) a total of 1704 were tagged and 154 in Skarðsvík (square). All tagging were performed in June 2002.*

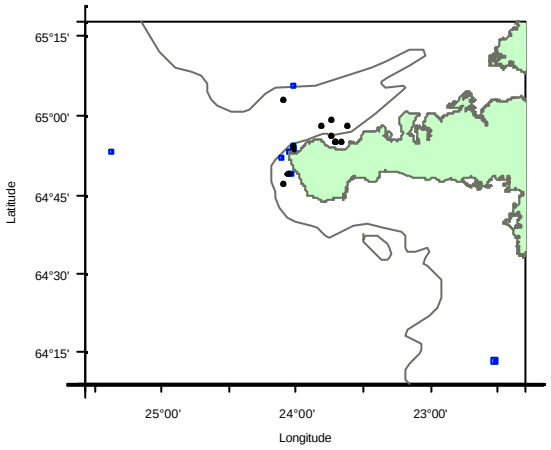

Figure 3.6. *Total of 21 cods have been recaptured since June 2002. Fishes tagged in Ólafsvík are labeled as dot and fishes tagged in Skarðsvík are labeled as square.*

In November 2002, a total of 1981 juvenile cod were tagged and released in Húnaflói (Area 4 in Fig. 2.1; Fig. 3.6). Of these, 817 were double tagged and 963 fin-clipped for DNA analysis. Similar to the June experiment, an additional 200 juvenile cod were sampled for age/size structure and sex composition. The fish were captured with shrimp trawls and placed in seawater tanks with a continuous influx of seawater until the fish recovered. Fish in good condition were subsequently tagged and released.

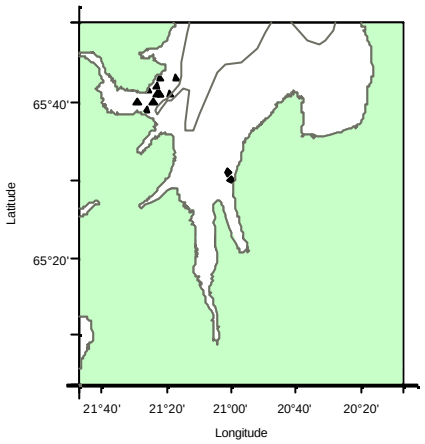

Figure 3.7. *The two tagging areas in Húnaflói (Area 4 in Fig. 2.1): Steingrímsfjörður (triangle) where a total of 1283 immature cod were tagged and Miðfjörður (diamond) where a total of 698 immature cod were tagged in November 2002.*

MLA:
In Scotland, two archive tagging databases are available for analysis, one with tagged cod release data from 1958-1978 (N=16384), and the other with recapture data from 1960-1987 (N=7049) from releases in 1960-1984. Data coverage includes the following areas: West Orkney, Shetland, Moray Firth, Solan, Inner Hebrides, South Minch and Clyde (Fig. 3.3).

All databases are in a form that enable release and recapture information to be examined by area, year, month and fish length.

Tag recovery rates for cod in waters off Iceland and Scotland respectively, will provide an indication of homing characteristics and home ranges, where these patterns will be investigated following completion of the archived databases. Historical tag-recapture data from 1948-1986 (Jónsson 1996) have indicated that there is considerable evidence of spawning site fidelity in Icelandic cod; thereby providing a foundation for the homing investigations.

FRS's research vessel *Clupea* was used to conduct two dedicated tagging surveys in February and March 2002, in the northern North Sea and off the west coast of Scotland (Table 3.5). The areas investigated were determined from the initial findings of WP1, and concentrated on areas which had been historically important for cod of spawning size during the spawning season. The first survey began on the 12th February, and ended on the 24th February. However, the cruise was hampered by bad weather conditions resulting in a loss of 6 working days. The second cruise started on the 9th March, and ended on the 17th March, and trawling efforts were concentrated in waters off Shetland and the Moray Firth.

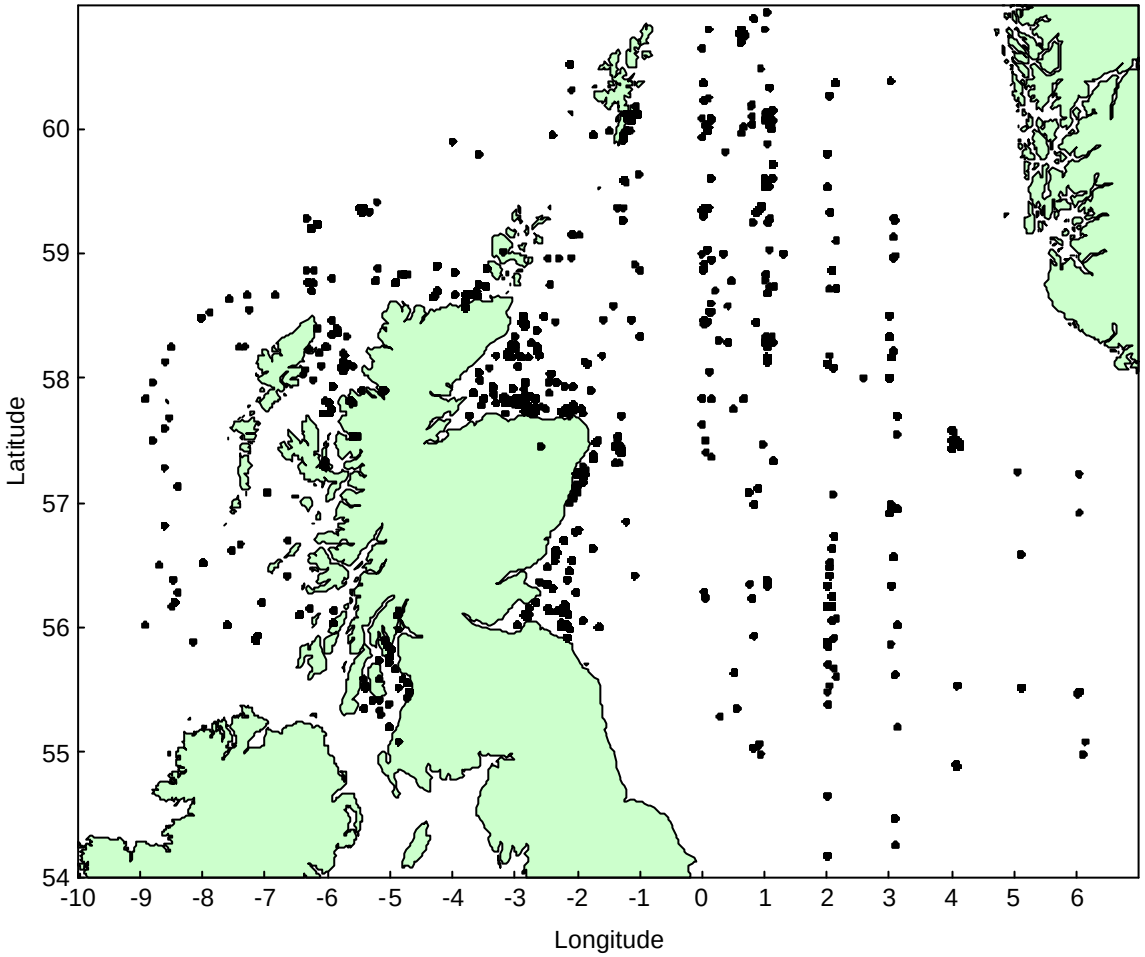

Figure 3.8. *Distribution of archived cod tag releases between 1958 and 1978*.

Table 3.5. *Summary statistics from FRS's tagging cruises off Scotland, Feb-March 2002.*

Number	Tagging survey		Total
	0302C	0402C	
Hauls	22	19	41
Cod caught	28	196	224
DST releases	10	123	133
Lotek DST releases	7	43	50
Star-Oddi DST releases	3	80	83
Floy tag releases	2	18	20
Fin-clips collected	16	55	71
Gills collected	13	145	158
Ovaries preserved	12	56	68
Otoliths for ICPMS	3	22	25

For live fish capture the BT 158 Jackson Rock hopper trawl was modified to include a PVC liner in the cod-end, retaining 1 m^3 of seawater in a still-water environment. The trawl also incorporated a 70mm square mesh panel to reduce the capture of small fish. Four alcothene hoops on the cod-end supported the liner and maintained the general shape of the trawl. The modified trawl was deployed successfully throughout both cruises, and fish were clearly seen swimming within the liner as it was lifted onboard. The fish caught were in excellent condition and suitable for tagging. Significant numbers of cod were also taken by hand-line over hard reef areas. A minilogger was attached to the headline for each trawl, recording temperature every 10 seconds. The EK500 was run continuously throughout the cruises to investigate whether spawning aggregations of cod could be detected acoustically. An acoustic seabed mapping system, RoxAnn, was run in conjunction with the echosounder to investigate cod habitat. Demersal sample grabs were conducted to ground-truth RoxAnn in areas where high catch rates of cod were recorded. However, there were very few locations where cod were caught in significant numbers to be of relevance to the habitat analyses. Despite the adverse weather conditions, a total of 153 cod were successfully tagged; 133 with DSTs, and 20 with single external conventional or 'floy' tags (Fig. 3.5).

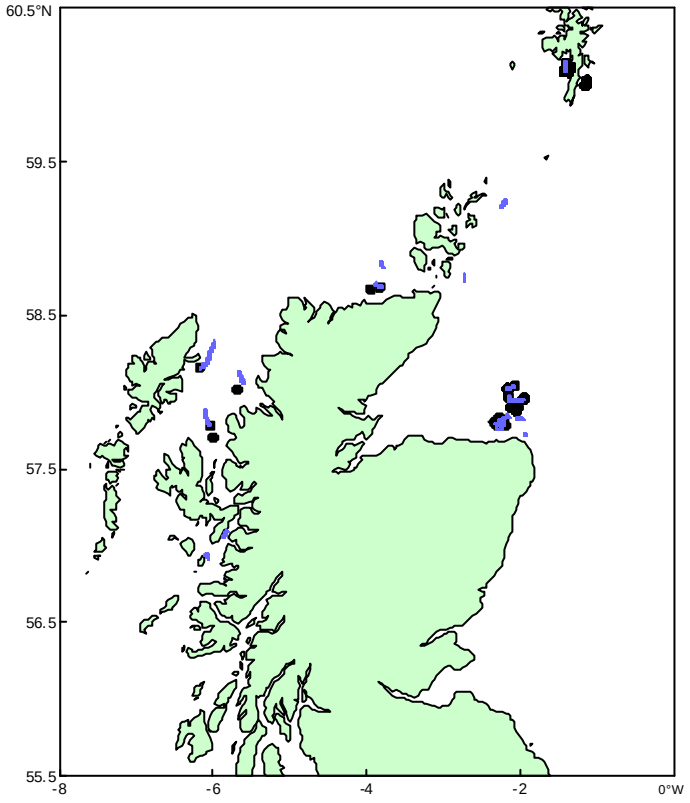

Figure 3.9 *FRS tagged cod release locations in February and March 2002 (black dots). Fishing tows are represented by blue lines.*

FRS used the DST milli tag (Fig. 3.6), manufactured by Star-Oddi, on its cod releases. To satisfy Home Office supervision regulations, an experienced staff member from CEFAS joined our cruise, and enabled a batch of 50 Lotek DSTs to be released. All released cod were measured (±1.0cm) and weighed (±1.0g), and sexual maturity noted where possible. Fin-clip samples were taken from all tagged cod for genetic analysis, and stored in plastic microtubes pre-filled with absolute ethanol. Full biological sampling was carried out on all other cod caught, and gill tissue samples taken for genetic studies. Otoliths were removed with plastic forceps and stored dry within plastic microtubes for otolith microchemistry and

age reading. Ovaries were weighed and sections of tissue fixed in 8% phosphate buffered formalin for reproductive studies.

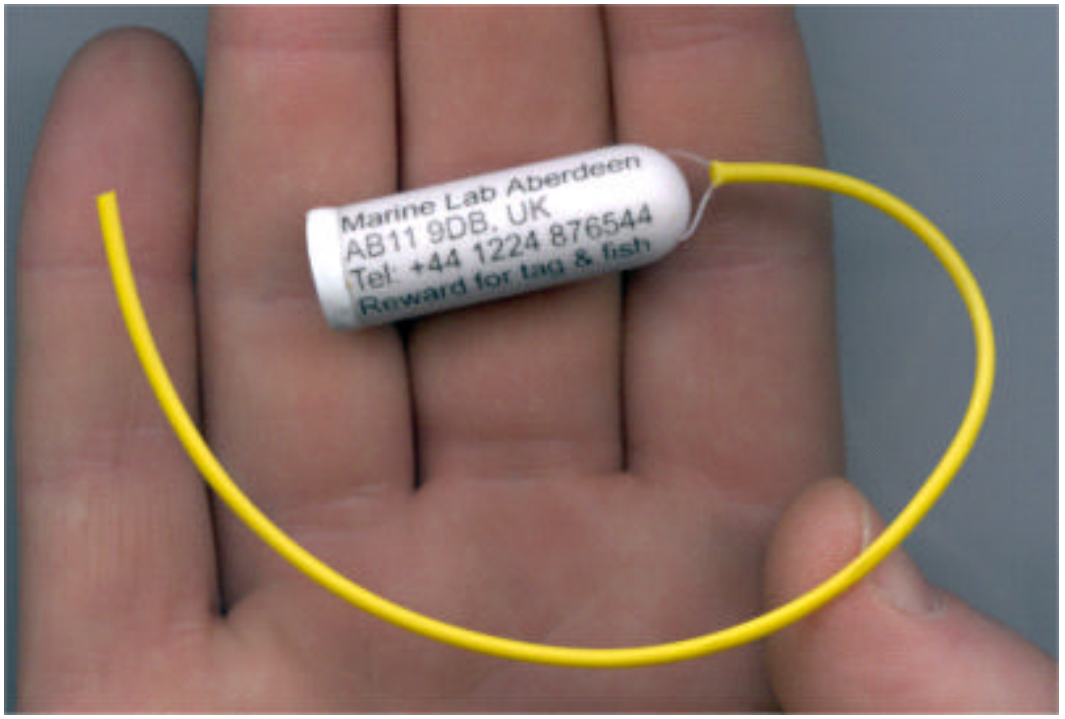

Figure 3.10 *DST milli tag used for tagging cod off Scotland.*

At present, 8 Lotek and 5 Star-Oddi DST tagged fish have been returned. Of the Star-Oddi returns, 2 of the electronic tags were missing from the returned fish. Data have been successfully downloaded from 3 tags, although the dataset collected from the third tag was incomplete due to a hairline fracture in the tag's housing which caused water leakage into the electronics. Examples of data downloaded from the DSTs are given below (Fig. 3.11).

The cod implanted with DST 1166 was released on the 17th March 2002 in the Moray Firth (57º53.932'N, 2º02.508'W). The fish was at liberty for 93 days and was recaptured on the 18th June 2002 still in the Moray Firth, around 20 miles from its release location (at 57º75'N, 2º5'W). The fish implanted with DST 1212 was released on the 10th March 2002 in the Scalloway Deeps off the west coast of Shetland (60º04.961'N, 1º22.007'W). The fish was recaptured 83 days later east of Foula (60º06'N, 1º58.5'W), 19 miles from its release location. This fish made a number of rapid dives to the bottom (75m) after tagging before descending slowly through the water column as it adjusted its depth to neutral buoyancy.

Initial analyses of the data from both fish indicate that the tagged fish made numerous forays to the seabed, presumably relating to their movements within deep trenches. Both fish spent a part of their time in the local deep water trenches. Both figures also document the seasonal rise in sea temperature in the North Sea.

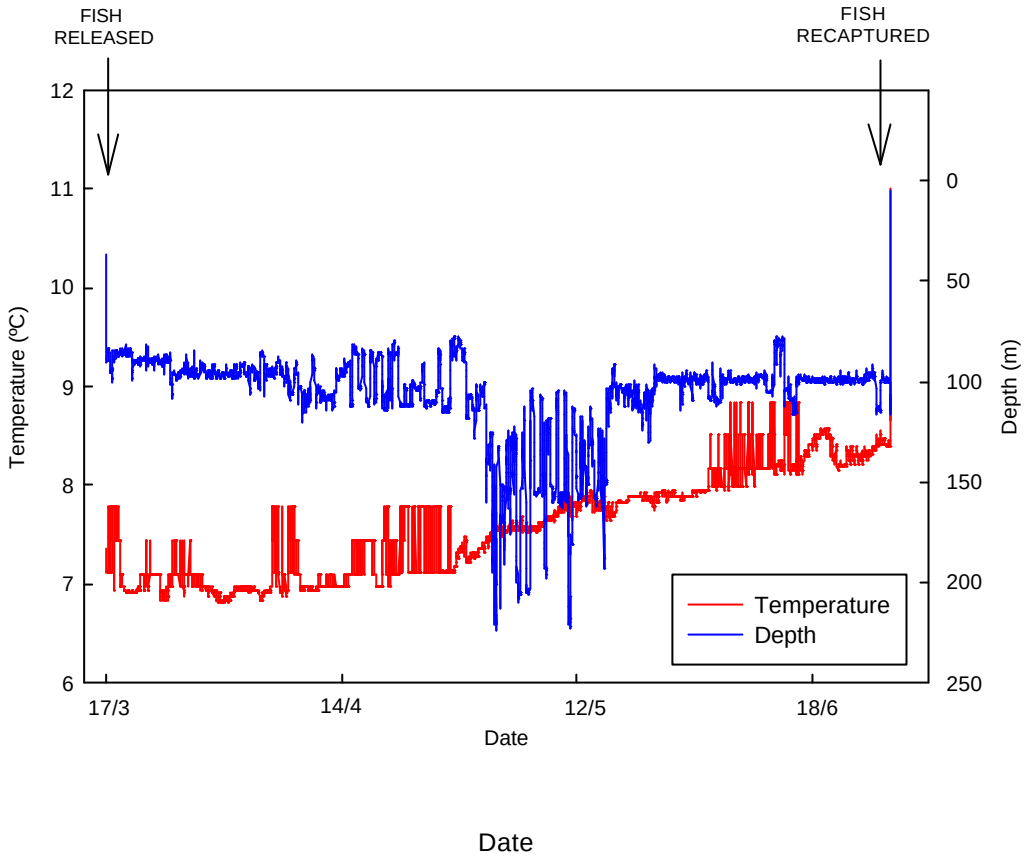

Figure 3.11. *Downloaded temperature and depth records from DST tagged fish, released in Feb-March 2002 on FRV Clupea in (a) the Moray Firth - DST1166; and (b) off Shetland – DST1212.*

Expected results and relevant corresponding milestones

The WP will result in an assessment of the migrations and homing of cod to spawning areas, and will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13).

Milestones

Progress on this workpackage is proceeding according to the timetable specified for the workpackage milestones and deliverables.

Deliverables

Archived databases for cod tagged in waters off Iceland and Scotland have been formulated. DST data for Icelandic cod are currently being transferred to the database and should be completed within the timeframe of the deliverable.

Following completion of the archived databases analysis of homing and dispersal patterns of adult and juvenile cod will occur, and be completed within the timeframe of the deliverable.

Table 3.6 *Deliverables within workpackage.*

Deliverable N^{o}	Deliverable number and title	Delivery date	Status
D7	3.1 Database of release and recovery information for cod	24	P
D26	3.2 Analysis of homing and dispersal of adult cod	36	P
D42	3.3 Analysis of dispersal and migration patterns of juvenile cod	40	P

Workpackage 4: Genetic variations among spawning components.

Start date: March 2002

End date: December 2005

N° of the partner responsible: 3

N° of other partners involved: 1, 2, 3

Table 4.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	11	0.53	24	0
Total to date	11	0.53	24	0
Total planned	38	1	34	0

Objectives and input to workpackage

Analyse microsatellite DNA and *Syp* I from samples of cod from different spawning locations, to establish the extent of genetic differentiation of spawning groups and their stability through time. Examine temporal stability by analysing the genetic composition of historical samples of cod (obtained from archived otolith collections) and correlate genetic structures with known changes in population size.

Methodology and study material

1) Spawning and late pre-spawning cod will be collected during annual surveys and by local fishing boats as well as research vessels from 8-10 spawning locations off Iceland and numerous locations in 4 main regions off the west and north of Scotland in spring 2002. Gill filaments will be preserved from at least 100 individuals per location per year.
2) Otoliths from archived samples selected from years of high and low stock sizes (up to 3 years of each) during 1960-1999, and from a subset of the same locations as the contemporary material will be located in archived collections. The aim is to collect at least 100 otoliths from each location and year.
3) DNA will be extracted from the gill filaments of cod collected during the project, and from the otoliths selected from archives.
4) The 6 selected Di, Tri- and tetranucleotide microsatellite markers and the *Syp* I locus will be screened in several year classes of cod from the various spawning locations.
5) Cod microsatellite multiplex(es) will be designed to make the screening faster and cheaper.
6) A PCR reaction with an oligonucleotide primer will be carried out for the microsatellite markers.
7) After amplification, the PCR products will be separated with gel electrophoresis using automatic sequencers, and the genotypes at the loci registered for each individual.
8) Data from both the contemporary and historical material will be loaded into a common database for analysis.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 4.1 and the deliverables within the workpackage are listed in table 4.11.

MRI:

Sampling of archived otoliths for the historical genetic analysis:

Otoliths for genetic analysis were retrieved from the archived otolith section at MRI. A total of 600 otoliths from spawning cod at 2 locations (area 9 and 2; Fig. 2.1) and 6 different time periods (e.g. 6 individual years during 1948 to present) have been retrieved and stored for further analysis. Locations were selected so that at least 100 otoliths were available for each time period (March-April in each of the 6 years) at exactly the same spawning location or as close as possible geographically.

Table 4.2. *Dates, location, depth and number of cod collected at each station during the spawning season in April 2002. All samples were collected with either gill nets or Danish seine. Gill rakers were preserved in ethanol and otoliths were stored for ageing, morphological and chemical analysis (WP 5). All cod samples were at maturity stage III (running milt or fully mature translucent eggs)*

Station	Date	Spawning site (Area, Fig 2.1)	Location	Depth	Number of cod sampled
MSK1-2002-st.1	5/4	Knarrarós (9)	63'48,49N 21'00,74V	54	12
MSK1-2002-st.2	5/4		63'48,55N 20'59,40V	54	24
MSK1-2002-st.7	6/4		63'48,68N 20'59,75V	43	7
MSK1-2002-st.8	6/4		63'48,55N 20'59,53V	51	20
MSK1-2002-st.9	6/4		63'49,10N 21'04,71V	58	15
MSK1-2002-st.19	11/4	Hálsar (8)	64'07,31N 15'42,55V	47	3
MSK1-2002-st.20	11/4		64'05,46N 15'49,98V	47	7
MSK1-2002-st.22	11/4		64'05,88N 15'50,87V	38	35
MSK1-2002-st.23	11/4		64'04,11N 16'02,42V	51	24
MSK1-2002-st.24	11/4		64'04,35N 16'00,19V	53	31
MSK1-2002-st.25	12/4	Ingólfshöfði (8)	63'45,73N 16'33,70V	65	16
MSK1-2002-st.26	12/4		63'45,92N 16'35,96V	62	40
MSK1-2002-st.27	12/4		63'45,34N 16'38,25V	71	16
MSK1-2002-st.28	12/4		63'45,51N 16'44,63V	98	28
MSK1-2002-st.31	13/4	Meðallandsbugur(8)	63'41,33N 17'40,67V	40	4
MSK1-2002-st.32	13/4		63'41,05N 17'32,88V	80	96
MSK1-2002-st.37	15/4	Selvogsbankahr. (9)	63'30,66N 21'18,54V	93	100
MGE1-2002-st.6	19/4	Eyjafjörður (4)	65'55,32N 18'25,08V	18	67
MGE1-2002-st.7	19/4		65'57,30N 18'24,95V	16	33
MGE1-2002-st.10	20/4	Miðfjörður (3)	65'26,13N 20'59,37V	60	100
MGE1-2002-st.19	23/4	Þistilfjörður (5)	66'16,76N 15'44,95V	12	98
NG1-2002-st.23	12/4	Vestmannaeyjar (9)	63'28,49N 20'00,47V	92	100
NG1-2002-st.30	15/4	Háfadjúp (9)	63'19,47N 19'30,20V	135/395	100
NOR1-2002-st.54	13/4	Breiðafjörður (2)	64'54,66N 24'00,00V	73	100
NTN1-2002-st.499	24/4	Ísafjörður	66'18,10N 23'55,10V	16/22	100
				Total	1176

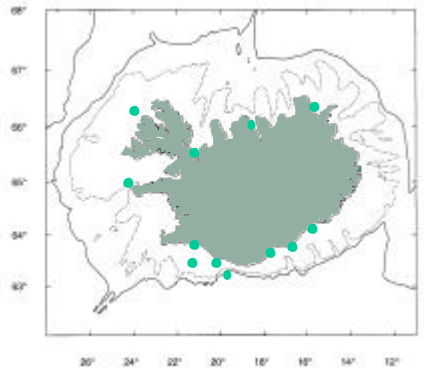

Figure 4.1 *Location of sites where spawning cod were sampled in spring 2002.*

Collection of field samples:
In the field, genetic samples were collected according to plan. In spring and summer, a total of 1176 individuals were sampled either for gills or fin-clips in pure alcohol (Table 4.2; Figure 4.1).

DNA extraction and calibration:
DNA has been extracted from gill filaments using Phenol-chloroform and Chelex-resin protocols. The latter protocol gave as good results as the Phenol-Chloroform extraction which is supposed to be the best protocol.

For the calibration of genetic markers between laboratories, a total of 100 samples from a southern location (sampled on 04.05.2000 and shipped on 15.03.2002; cruise number NALI-2000) were sent to the genetic laboratory in Denmark. In return, a total of 301 samples were received from the Danish lab (Table 4.3).

Table 4.3 *Control cod (Gadus morhua) samples sent by Partner 1-MRI to Partner 3-DIFRES.*

	Survey	Location	Sampling date	Shipment date	Sample Code	Type of sample	Number of individuals sent
Spawning	MRI	South Iceland	04.05.2000	15.03.2002	NAL1-2000	G, Bd	100
	MRI	Icelandic Farm	16.11.2002		CT2G042	G, Bd	1 control fish
Total:							**101**

Sample types: (D=DNA, G=gills in EtOH, O=Otoliths, Bd=Biological data (sex, sex maturation, length, weight).

Table 4.4. *Control cod (Gadus morhua) samples (gills in EtOH) received by Partner 1-MRI from Partner 3-DIFRES.*

	Survey	Location	Sampling date	Receiving date	Sample Code	Type of sample	Number of individuals received
Spawning	Partner 3-DIFRES	Viking bank	02.03.2002	14.05.2002	V1-2002	G, Bd	74
	Partner 3-DIFRES	North Faroe Isles	08.03.2002	14.05.2002	R1-2002	G, Bd	75
	Partner 3-DIFRES	South Faroe Isles	18.03.2002	14.05.2002	F1-2002	G, Bd	152
Total:							**301**

Sample types: (D=DNA, G=gills in EtOH, O=Otoliths, Bd=Biological data (sex, sex maturation, length, weight).

Sample analysis: The sample analysis has started and is ongoing. Preparation and developmental work has been carried out for making the screening process faster and more automated. All the necessary equipment and software are in house. The process involves the PACKARD robot in connection with PCR and the electrophoresis of samples on the ABI 377 96 well upgraded machine along with the GeneMapper Software. It is now fully developed for the mass screening of samples.
A complete protocol involving the PACKARD robot and a development of PCR-multiplexes (see below) have been processing, and will result in the next months in an easier and rapid mass screening of populations. Extraction and PCR are now run in a 384 PCR tray and the robot is handling all the chemical protocol turning around the PCR-Master mix and the loading of the samples on the ABI sequencer.

Standard PCR reactions:

94°C during 3 min
94°C during 1 min | 32 cycles
Ann t°c during 40s |
72°C during 40s |
72°C during 5 min

The annealing t°C is:

52°C for *Gmo19*, *Gmo34* and *Tch11.* This is Multiplex 1 (ML1).
50°C for *Tch5* and *Gmo8* This is ML2
54°C for *Gmo2* and *Tch14* + Gmo132 (56°C) This is ML3
46°C for *Gmo3* and *Gmo37* *This should be ML4.*

Some 45 control samples of cod have been DNA extracted (Table 4.5) and screened for 10 microsatellite loci (Table 4.6). In December Christophe Pampoulie and Magnús Örn Stefánsson visited the laboratory of Partner 3-DIFRES for further calibration and multiplex of markers and the mass screening of samples will start in the next months (see DIFRES part).

Table 4.5. Control cod (*Gadus morhua*) DNA samples extracted and analysed by Partner 1-MRI with 8 microsatellite loci. Number of individuals (n).

	Survey nation	Location	Sampling date	Survey name / Sample Code	DNA extracted (n)	*Syp* I (n)	Microsatellites (n)
Spawning	Partner 3-DIFRES	Viking bank	02.03.2002	V1-2002	15	-	15
	Partner 3-DIFRES	South Faroe Isles	18.03.2002	R1-2002	15	-	15
Feeding	MRI	South Iceland	05.04.2000	NAL1-2000	20	-	15
	MRI	South Iceland	11.11.2002	MGE1-6	67		10
	MRI	South Iceland	11.11.2002	MGE1-7	33		10
Total:					150	-	50

Table 4.6 *Microsatellite loci optimised for cod (Gadus morhua) samples by Partner 1-MRI.*

Primer	Sequences 5'=>3'	Repeat sequence	Allele Range	Number of alleles
Gmo2	R: GTGTGAGATGACTGTGTCG F: CCCTCAGATTCAAATGAAGGA	(GT)	102-204	29
Gmo8	R: TGGGGGAGGCATCTGTCATTCA F: GCAAAACGAGATGCACAGACACC	(GACA)	110-205	23
Gmo19	R: GTCTTGCCTGTAAGTCAGCTTG F: CACAGTGAAGTGAACCCACTG	(GACA)	120-220	24
Gmo34	R: GGTTGGACCTCATGGTGAA F: TCCACAGAAGGTCTCCTAA	(GACA)	80-120	8
Gmo132	R: CGAAAGGACGAGCCAATAAC F: GGAACCCATTGGATTCAGGC	(GT)	101-187	31
Tch5	R: TCGCATTGAGCCTAGTTT F: GCCTTAATATCACGCACA	(GATA)	186-280	22
Tch11	R: TCGAGTTCAGGTGGACAA F: ATCCATTGGTGTTTCAAC	(GATA)	121-193	20
Tch14	R: AAACTGATATACGCCCAACT F: CATACATTGGTCACTCTTTCTTAC	(GAAA)	124-216	23

Before the mass screening, a new control group will be defined by MRI-partner (1) to check if the calibration of the optimised microsatellite is perfect and to calibrate the new microsatellite loci chosen by the DIFRES and MRI partners. A control fish will also be run on each gel to avoid ladder or gel artefact; sufficient fin clips of this fish (n°CT2G42) will be sent by MRI-partner (1) to DIFRES-partner (3). An internal ladder will also be based on 3 to 4 known individuals for each microsatellite loci and run on each gel to be able to detect possible migration problems in the alleles or gel artefact.

MLA:

Sampling of archived otoliths for the historical genetic analysis:
Archived otolith collections (N=1101) were located from FRS research cruises in 1965, 1970, 1973, 1975 and 1976. Few otoliths are available for analysis due to the unfortunate disposal of archive collections during the 1990s. Otoliths from 1998 onwards are now archived as routine. The samples were taken from cod caught in waters around Aberdeen Bay, the Moray Firth and from inshore regions of VIa including the Clyde (see Figure 4.3). Many of the otoliths have previously been examined for age, and are thus broken in half.

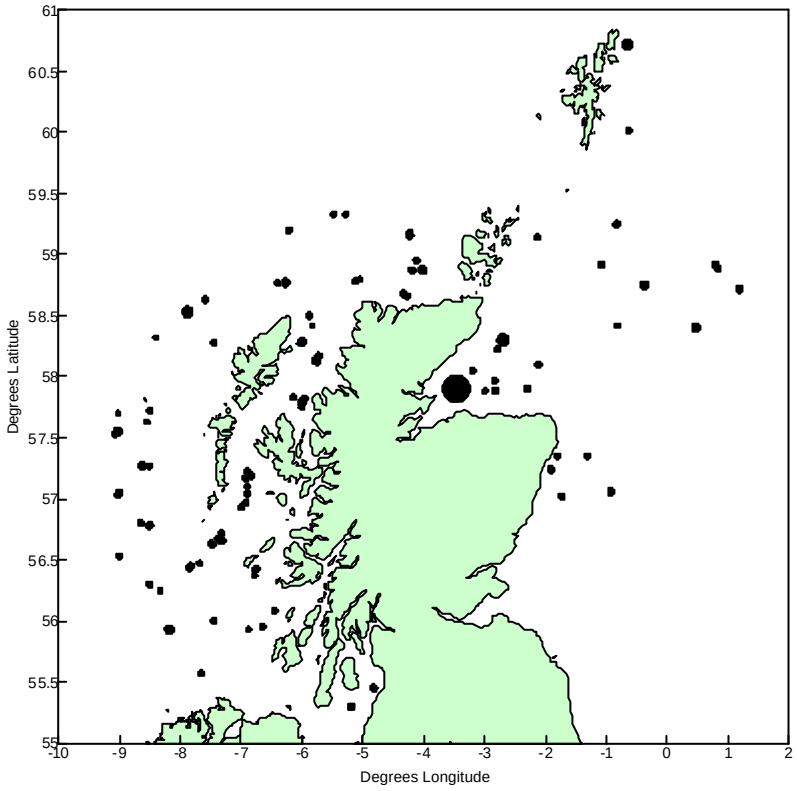

Figure 4.2. *Locations of FRS's archived cod otolith collections. Range in dot size: 1-174.*

Collection of samples for genetic analysis from spawning and late pre-spawning:
A total of 1457 cod were sampled from Scottish waters during the 2002 spawning season (Table 4.7). In each sample, information on length (±1cm), total and eviscerated wet weight (±0.1g), age (from otoliths), liver weight (±0.1g) and gonad weight (±0.1g) were collected. The incidence of parasitic infection on the gills was also noted. All sampled cod were assigned to 4 macroscopic maturity stages (immature, maturing, spawning and spent). 420 fish were found to be immature, 400 pre-spawning, 282 spawning and 207 spent/resting. Of the tagged fish releases, only 10 were distinguishable as spawning fish. Sections of ovarian

tissue for histological analysis were obtained, and preserved in 8% neutral buffered formalin. Gill tissue (N=832) was dissected with scissors and preserved in plastic micro-tubes filled with absolute ethanol. Finclips (N=158) were also extracted into vials of absolute ethanol from all tagged fish before release. In total 990 samples of tissue for genetic analysis were collected, although only 28.3% were taken from spawning fish. Numbers of pre- and post-spawning fish made up over 44.2% of these samples, a figure greater than the recommended 15% (Table 4.8). Only one area (Clyde) provided this workpackage with the required number of relevant samples. Given the low number of genetic samples taken from spawning fish, additional sampling is planned for 2003. The sampling strategy will be revised in the light of the findings in 2002; where sampling will be focussed on fewer discrete areas.

Table 4.7. *Number of cod collected from Scottish waters during the 2002 spawning season. Sample sizes include the number of cod that were measured, weighed, sexed and assigned to macroscopic maturity stages. DRC = Dedicated research cruise.*

Time period	Vessel	Sample Type	Sample Size	No. genetic samples	No. otoliths for ICPMS
12/11/01-15/11/01	*FV Helenus*	Charter	150	0	0
3/12/02-5/12/01	*FV Helenus*	Charter	10	0	0
18/1/02-5/2/02	*FRV Scotia*	DRC	220	111	219
29/1/02-30/1/02	*FV Helenus*	Charter	38	0	0
4/2/02-5/2/02	*FV Helenus*	Charter	8	0	0
12/2/02-24/2/02	*FRV Clupea*	DRC	16 (+ 12 tag releases)	25	12
25/2/02-28/2/02	*FV Fair Morn*	Charter	185	185	182
9/3/02-17/3/02	*FRV Clupea*	DRC	55 (+ 141 tag releases)	201	56
3/3/02-24/3/02	*FRV Scotia*	DRC	171	61	171
19/3/02-21/3/02	*FV Helenus*	Charter	16	15	0
25/3/02-28/3/02	*FV Helenus*	Charter	44	1	0
8/3/02	*FV Auriga*	Commercial	152	152	152
18/3/02	*FV Rivo*	Commercial	75	75	73
2/3/02	*FV Sunbeam*	Commercial	74	74	74
18/3/02	*FV Jasper*	Commercial	90	90	90
TOTALS			**1457**	**990**	**1029**

Table 4.8. *Number of cod samples collected for genetic analysis by maturity stage by area. Note low numbers of spawning (stage 3) cod*

AREA	Stage 1	Stage 2	Stage 3	Stage 4
Moray Firth	8	13	**2**	1
Orkney	1	8	**3**	0
Shetland	25	67	**19**	0
North Minch	6	2	**8**	0
South Minch	0	0	**3**	0
Clyde	9	58	**120**	1
Irish Sea	0	0	**12**	0
Central	6	12	**0**	0
Forties	0	10	**0**	1
Viking	2	21	**49**	92
Faroe	65	52	**24**	86
Butt of Lewis	2	5	**39**	0
Buchan	2	9	**1**	0
TOTALS	**126**	**257**	**280**	**181**

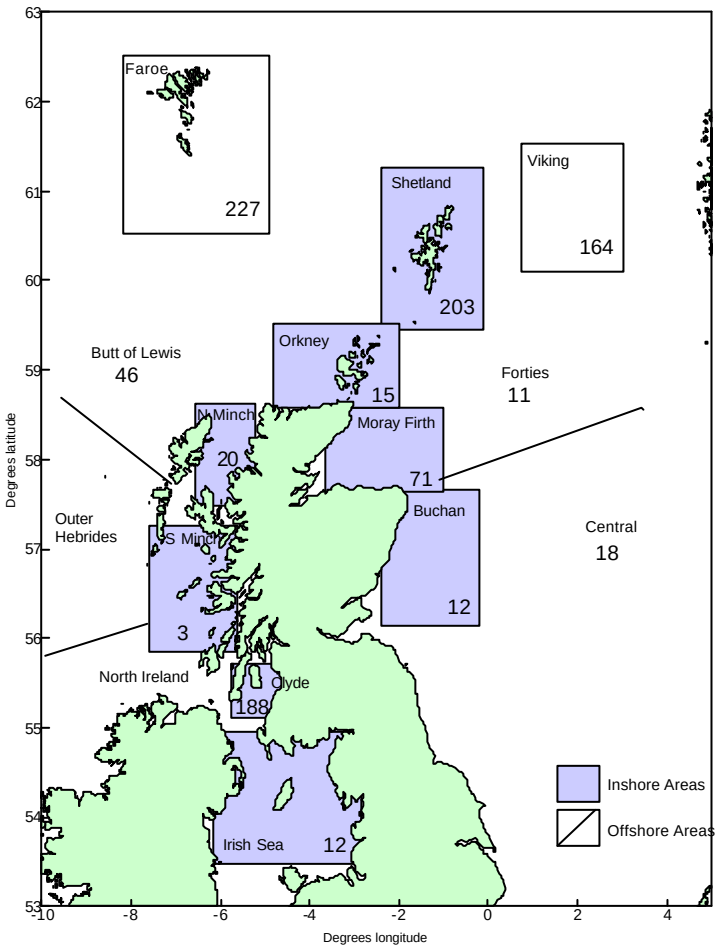

Figure 4.3 *FRS genetic sampling locations, indicating the total number of genetic samples (of all maturity stages) collected from each site during the 2002 cod spawning season.*

DIFRES:

DNA extraction from contemporary tissue and archived otoliths:

DNA was successfully extracted from tissue of contemporary cod samples (gill filaments and finclips) using the Chelex-resin method by Estoup et al. (1998). The method produced high quality DNA that could be PCR amplified (see below). The samples of extracted DNA in Chelex solution have been stored at room temperature for more than half a year without showing signs of degradation. This method will therefore be used for DNA extraction throughout the project.
The same extraction method was applied to the archived otoliths where the aim is to extract high quality DNA without damaging the otoliths. . By modification of the proteinase digestion time, it was possible to get DNA of sufficient quality and quantity for PCR amplification of short microsatellite segments without damaging the otolith. This was verified by running a number of otoliths used for DNA extraction through standard treatment for age determination including burning and polishing. There was no difference in appearance and performance between otoliths which had been subject to DNA extraction and untreated otoliths. Consequently, the Chelex-resin method by Estoup et al (1998) will also be used for extraction of DNA from archived material throughout the project.

Screening of microsatellite loci:
Twelve microsatellite loci have been screened to date (see Table 4.9). Eleven of these loci have shown consistent PCR amplification, while ten loci have produced clear bands which could be scored and interpreted on an automated sequencer. All ten loci were screened on a standard set of 46 individuals consisting of 16 individuals from Iceland, 15 from the Faroe Islands and 15 from the North Sea. The rationale for this selection of individuals was to ensure wide coverage of the geographic range of interest within METACOD and thereby also cover most of the genetic (allelic) range. Most of these ten loci were highly variable with more than 10 alleles. Only the loci Gmo 3 and Gmo 34 showed low levels of variability. None of the 10 consistently scored loci showed significant departures from HW expectations, indicating that technical problem such as "large-allele dropout", should be minimal for these loci.

Table 4.9 *Summary table of the performance of the 12 microsatellte loci screened at DIFRES.*

Microsatellite locus	Consistent PCR amplification	Clear scorable bands on an automated sequencer	Total number of alleles in 46 individuals	Significant deviations from HW expectations
Gmo 2*	√	√	10	No
Gmo 3	√	√	7	No
Gmo 8*	√	√	16	No
Gmo 19*	√	√	21	No
Gmo 34*	√	√	6	No
Gmo 37	√	√	10	No
Gmo132*	√	√	20	No
Tch 5*	√	√	16	No
Tch 11*	√	√	16	No
Tch 12	√	÷	?	?
Tch 14*	√	√	23	No
Tch 22	÷	?	?	?

The loci marked with * are currently working both at DIFRES and MRI

A calibration meeting was held on 12th December at DIFRES in Silkeborg, Denmark. The meeting included representatives from DIFRES (Einar Eg Nielsen, Dorte Meldrup and Nina Aagard Poulsen), MRI (Christophe Pampoulie and Magnus Stefansson) and the external expert Daniel Ruzzante.

The aim of the meeting was to standardise the procedure for genetic analysis and to calibrate the scoring of the microsatellite loci between DIFRES and MRI, so as to ensure the data are comparable across laboratories and can be used in a meta-analysis for cod in the Central and Northeast Atlantic. We compared the scoring of 8 loci for 46 standard individuals run in both labs. Loci were scored differently in both labs but differences were consistent across individuals and were easily eliminated by adopting common standard scores. For example at locus Gmo19 all individuals were scored with 4 extra DNA base-pairs at DIFRES compared to MRI. It was subsequently decided

1) to adopt the scoring at DIFRES as standard.

2) To supplement these 8 loci with 4 extra loci, preferably containing the two extra loci currently running at DIFRES. By having 12 loci it would be possible to sacrifice one or two loci along the course of the project should there be technical problems with them at some later time.

3) To run three standards on each electrophoretic gel consisting of an allelic cocktail from three individuals covering the whole range of alleles at that particular locus.

4) To run one known individual on each gel.

5) To ensure calibration is effective by running 39 new standard individuals in both labs for comparison.

Screening of population structure

Genetic analysis based on the 46 standard individuals revealed that there was significant genetic differentiation among the three sampled areas (see Table 10). Estimated overall Fst was 0.016.

Table 4.10 *Estimated pairwise genetic differentiation (Fst) among baseline samples (below diagonal). P- values are given above diagonal*

Sample	Iceland	Faroe Islands	North Sea
Iceland	-	0.033	0.033
Faroe Islands	0.0189	-	0.050
North Sea	0.0187	0.0095	-

Naturally these number should be interpreted with care, since they are based on a very limited number of individuals. However, it indicates that there are small, but significant, genetic differences among the three sampled regions. Iceland, Faroe Islands and the North Sea.

In summary the genetic analysis is progressing as expected. We anticipate that routine analysis of contemporary and archived samples will commence early 2003. At the same analysis of the Syp I locus will begin. Of potential concern is the fact that relatively few of the cod collected in 2002 were in spawning stage. We hope, however, that the changed sampling strategy (see above) will help solve the problems of getting sufficient samples in 2003. However, the spawning population in the area is extremely small.

Table 4.11. *Deliverables within workpackage.*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 8	4.1 Collections of cod gill filaments from spawning surveys in 2002 and 2003.	24	P
D 27	4.2 Database of genotypes for all spawning cod sampled in 2002 and 2003, and archived otolith material	36	P
D 43	4.3 Analysis of genetic differentiation within the sampled cod	40	N
D 44	4.4 Comparison of modern and historical genetic compositions of cod.	40	N

Expected results and relevant corresponding milestones

This WP will be at the heart of the project and will deliver the most valuable and comprehensive assessment of genetic structure of cod stocks in the eastern Atlantic to date. Milestones will be the completion of sample collection in 2002 and 2003 (milestones 3 and 5), and the completion of sample analysis (milestone 9). The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13), and will form the basis (i.e. definition of spawning stock characteristics) for the assessment of sub-stock composition of juveniles (WP8) and feeding aggregations (WP10).

Workpackage 5: Natural markers for the different spawning groups based on otolith elemental fingerprints and otolith shape.

Start date: March 2002

End date: December 2005

N° of the partner responsible: 1

N° of other partners involved: 1, 2

Table 5.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	9	0.41	0	0
Total to date	9	0.41	0	0
Total planned	20	7	0	0

Objectives and input to workpackage

Characterise each of the spawning groups in terms of their otolith elemental fingerprint and otolith shape, for use as a natural tag or marker in tracking subsequent movements

Methodology and study material

1) Collect and decontaminate sagittal otoliths from 100 spawning cod (2 independent samples) from each spawning location in Iceland (8-10 sites) in each of two years, North Sea (1 site), and west of Scotland (3 sites) in 2002.
2) Analyse elemental composition of one otolith from each pair for elements known to serve as natural markers: use isotope dilution ICPMS for the multi-isotopic elements (Ba, Mg, Li, Sr and Pb) and ICPMS with internal standardisation for Mn. All assays will be

blocked and randomised to eliminate sequence effects, and a cod otolith reference powder analysed at periodic intervals to insure analytical consistency.

3) Quantify shape of one otolith from each pair using FFT of a two-dimensional projection of the otolith outline, as well as measurements of otolith area, length, width, perimeter, weight, volume, circularity and rectangularity.
4) Characterise each of the spawning groups in terms of their elemental fingerprint and otolith shape, properly adjusted for variations in fish size.
5) Test for differences in elemental fingerprints and otolith shape among spawning groups using MANOVA; visualise differences using discriminant function analysis; test for classification accuracy using maximum likelihood-based stock mixture analysis. These spawning group-specific elemental fingerprints and otolith shapes are an integral part of Workpackage #10, since the stock identity of the fishery samples will be determined through comparison with the fingerprints of these reference spawning groups.
6) Embed, section and age the remaining otolith of each spawning cod.
7) Determine elemental fingerprint of juvenile stage of spawning cod by extracting the otolith core from a subsample of the otolith sections (see 6) above) with a computerised micromilling machine and assaying as per 2) above. These year-class specific juvenile elemental fingerprints form the basis for Workpackage 8, in which juvenile aggregations are linked to the their respective spawning groups in present and later life.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 5.1 and the deliverables within the workpackage are listed in table 5.4.

Sampling of spawning cod in Icelandic waters was performed during the peak of the spawning season from April 4-24, 2002 (Table 4.2). Samples were collected at 12 different places around Iceland (Fig. 4.1). At each sampling site a total of 100 mature cod were collected. At 2 stations, less than 100 mature cod were caught, resulting in lower sampling sizes (n=78 and 98). At sea, all cod were measured (total length, to the nearest centimetre), weight of the fish (whole fish and gutted), weight of liver and gonads in grams. Sex and maturity stages were also recorded for each cod. Sagittal otoliths were carefully removed from each fish, avoiding any contact with metal in case of contamination, cleaned of adhering tissue, and stored dry in paper envelopes until further analysis.

Consultation:
All methods regarding shape and elemental analysis both in this WP and WP 8 were set up under the guidance of Dr. Steven Campana, Bedford Institute, Canada. Steven visited our lab in May this year and consulted on methods and technical set up both at our lab and the laboratory at the Institute of Technology (ITI). He later provided the ITI with standard samples of dissolved otoliths to enable them to calibrate their ICP-MS analyser.

Shape analysis:
All otoliths from spring sampling 2002 have been scanned and measured in Optimas for further analysis of shape (Fast Fourier Analysis; FFT, e.g. by describing a shape in terms of cosine waves; Table5.2). The number of scanned otoliths does not match the sampling size (Table 5.2), because some of the otoliths were broken or crystallised, so it was not possible to use them. Half of the otoliths from the autumn sampling 2002 have been scanned but not measured. The otoliths were scanned using an image anlayser (Leica Qwin). The same otolith (e.g. the left one was used in all cases and oriented in a consistent manner under the microscope. For calibration of measurements, an image of a scale was stored in the beginning as well as each time when the magnification was changed. The shape will be analysed with OPTIMAS (version 6.1) using all measured parameters including area, length, width, perimeter, volume, circularity, rectangularity and the results from the FFT analysis.

Elemental analysis:
Decontamination of the otoliths from the spring sampling 2002 has started. The decontamination was performed by a 5 min sonification of the otolith in an acid-washed vial and superQ water, followed by 1 min scrubbing of otolith, triple rinse in superQ water, a 5 min sonification (twice - change water in between), and a final triple rinse in superQ water. The otoliths were then dried under a laminar flow before they were weighed to the nearest 0.1 mg. The dry decontaminated otoliths were stored dry in sealed, acid-washed polypropylene vials. The next step, the dissolvation of the otolith, which is the final step before the ICP-MS analysis, will not be initiated until the ICP-MS analyser is functioning properly and the results of test samples have been compared with controls provided by the Canadian lab.

***Table 5.2** : Status of the otolith analysis showing the number of otoliths collected during the spawning season from spawning fish (stage 3) and in the fall on the fishing grounds in Iceland in 2002.*

Location	Sampling date in 2002	Number of otoliths						
		Sampled (pairs)	Scanned	Measured	Decon-taminated	Dissolved/ ICP-MS	ageing	cored
Knarrarós (9)	April 5-6	78	78	78	50	0	0	0
Hálsar (8)	April 11	100	93	93	50	0	0	0
Ingólfshöfði (8)	April 12	100	96	96	50	0	0	0
Meðallandsbugur (8)	April 13	100	94	94	50	0	0	0
Selvogsbankahraun (9)	April 15	100	98	98	50	0	0	0
Eyjafjörður (4)	April 19	100	84	84	50	0	0	0
Miðfjörður (3)	April 20	100	88	88	50	0	0	0
Þistilfjörður (5)	April 23	98	91	91	50	0	0	0
Vestmannaeyjar (9)	April 12	100	98	98	50	0	0	0
Háfadjúp (9)	April 15	100	99	99	50	0	0	0
Breiðafjörður (2)	April 13	100	95	95	50	0	0	0
Ísafjörður (3)	April 24	100	97	97	50	0	0	0

MLA (partner 2):

Sagittal otoliths (N = 1630; N = 1029 during spawning season, see Table 5.3) were removed with plastic forceps from all cod sampled during the years sampling effort.
Where possible, these otoliths were air-dried in clean conditions and then stored dry in clearly labeled pre acid-washed plastic vials. On occasion, otoliths were preserved in paper packets. These samples required further cleaning to remove adherent tissue before storage. The otoliths were cleaned with inert forceps with a small amount of 18 mega-ohm doubly deionized water, left to air-dry and stored in plastic vials. As can be seen from Table 5.3, only 25% of the available otoliths were taken from spawning cod. Only one area (the Clyde) provided this workpackage with the required number of relevant otoliths, therefore additional sampling is scheduled for 2003.

<u>Analyze elemental composition and quantify shape of otoliths.</u>

As planned, no work has been carried out on this task as yet.

<u>Characterize each of the spawning groups in terms of their elemental fingerprint and otolith shape, properly adjusted for variations in fish size.</u>

<u>As planned, no work has been carried out on this task as yet.</u>

Determine elemental fingerprint of juvenile stage of spawning cod by extracting the otolith core from a subsample of the otolith sections.

As planned, no work has been carried out on this task as yet.

Table 5.3. *Number of cod sagittal otoliths collected by maturity stage by area. Note low numbers of spawning (stage 3) cod.*

AREA	Stage 1	Stage 2	Stage 3	Stage 4	NA	TOTALS
Moray Firth	10	13	1	1	0	25
Orkney	60	15	4	3	0	82
Shetland	50	65	8	0	5	128
North Minch	6	8	1	2	0	17
South Minch	1	1	3	0	0	5
Clyde	10	66	119	1	0	196
Irish Sea	3	31	12	1	0	47
Central	9	12	0	0	0	21
Forties	17	10	0	1	0	28
Viking	2	21	49	92	0	164
Faroe	65	52	24	84	0	225
Butt of Lewis	4	19	38	13	0	74
Outer Hebrides	0	1	0	2	0	3
Buchan	5	9	0	0	0	14
TOTALS	242	323	259	200	5	1029
% of total	23.52	31.39	25.17	19.44	0.49	

Table 5.4 *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 9	5.1 Collections of cod otoliths from spawning and juvenile surveys in 2002 and 2003.	24	P
D 28	5.2 Otolith elemental fingerprints and otolith shapes for each spawning group	36	P
D 29	5.3 Otolith elemental fingerprints corresponding to the larval/juvenile stage for specific year-classes in the spawning groups	40	N

Expected results and relevant corresponding milestones

The WP will be at the heart of the project and will deliver the most valuable and comprehensive assessment of genetic structure of cod stocks in the eastern Atlantic to date. Milestones will be the completion of sample collection in 2002 and 2003 (milestones 3 and 5), and the completion of sample analysis (milestone 9). The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13), and will form the basis (i.e. definition of spawning stock characteristics) for the assessment of sub-stock composition of juveniles (WP8) and feeding aggregations (WP10).

Workpackage 6: Growth and reproductive properties of different spawning groups

Start date: March 2002

End date: December 2005

N° of the partner responsible: 2

N° of other partners involved: 1, 2

Table 6.1. *Person-months by partner within the workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	1	0.26	0	0
Total to date	1	0.26	0	0
Total planned	6	13	0	0

Objectives and input to workpackage

Assemble and collect information on biological parameters influencing reproductive outputs and estimate total egg production by each spawning component. Construct a population abundance index that can be used to partition the total stock into spawning components.

Methodology and study material

1) Database on population parameters (size, age, condition, growth, sex stage, sex ratio, age at maturity) will be constructed for each spawning group based on data from historical surveys data collections and from annual surveys conducted during the years of the project.
2) Data from annual trawl and gill net surveys will be used to construct relative spatial abundance indices that will be used to partition the total spawning stock (based on VPA outputs) into spawning components.
3) Egg production will be estimated for each spawning group by using the egg production model developed in a previous EU-project[23]. This model is based on information on time, duration and amplitude of egg production by Icelandic cod females of different size and condition.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 6.1 and the deliverables within the workpackage are listed in table 6.2.

MRI:

In Iceland, data on length, weight, age, sex and maturity of immature and mature cod have been sampled in the spring survey (conducted in March at the beginning of the spawning season) since 1990. Additional data on length and sex exist back to 1985. These data have been subtracted from the MRI database for the years 1990-1999 and are presently being updated for the years 1985-1990 and 2000-2002. In some areas, additional data from the gill net survey as well as from routine sampling of landed catch and other research cruises conducted by the Institute will provide further information on population parameters during the most recent time periods as well as prior to 1985. Some of this data, dating as far back as 1948, have been subtracted from the data base others are being entered into the archives.

In addition, data from the sampling described in WP4 provide valuable information on the present status of length, weight, condition, age, sex and maturity in the areas sampled. More areas will be sampled in 2003. Reproductive potential will be based on these population parameters using existing fecundity relationships obtained for cod on the main spawning grounds druing 1995-2000 (Marteinsdottir and Begg, 2002).

MLA:
Samples described in WP4 have provided information (No. records=1887) on maturity in relation to length and weight at age. Histological analysis of ovaries has been conducted on 363 females to investigate spawning times and verify macroscopic staging. Fecundity was estimated from 62 specimens collected in 2002, together with a further 25 females caught in 1999 having ovaries with the late vitellogenesis stage of oocytes (greater than 520 μm). This oocyte size is reasonable for estimation of potential fecundity in cod using the auto-diametric method. Further, information on ovarian development was obtained from a histological examination of 290 cod. Further data will be collected in 2003.

Table 6.2. *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 10	6.1 Collections of gonad material, otoliths and population abundance data from spawning surveys in 2002 and 2003.	24	P
D 30	6.2 Data base on population parameters for the regional spawning components	36	P
D 31	6.3 Reproductive outputs of spawning components	36	N

Expected results and relevant corresponding milestones

The WP will deliver data on the variations in growth and reproductive parameters of cod. Milestones will be the completion of sample collection in 2002 and 2003 (milestones 3 and 5), and the completion of sample analysis (milestone 9). The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13).

Workpackage 7: Hydrodynamic and particle tracking models of egg and larval dispersal.

Start date: January 2002

End date: December 2005

N° of the partner responsible: 4

N° of other partners involved: 1, 2, 4

Table 7.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	1	0.47		12.5
Total to date	1	0.47		
Total planned	17	5	0	38

Objectives and input to workpackage

Develop fine scale hydrodynamic models of the spawning regions around southern Iceland, west of Scotland, and the north-western North Sea. Then, conduct particle tracking

simulations of the dispersal of eggs and larvae, in order to establish the extent of mixing between offspring from different spawning locations.

Methodology and study material

1) Assemble 1 km resolution gridded topographic data, tidal parameters, temperature, salinity and meteorology for south-west Iceland.
2) Assemble 1 km resolution gridded topographic data, tidal parameters, temperature, salinity and meteorology for west of Scotland/north-western North Sea.
3) Extract sea-surface elevations at fine model grid boundaries from an existing medium resolution (14 km) General circulation Model (GCM) of the North Atlantic.
4) Implement coupling of the fine scale (1 km resolution) models of the circulation in key spawning regions with the North Atlantic GCM.
5) Assemble Recording Current Meter (RCM) data for each of the fine model regions from archive databases.
6) All previous data on satellite tracking drifters released on or near the cod spawning grounds at Iceland, west of Scotland and in the north-western North Sea will be assembled and used to construct maps of trajectories and velocities.
7) Compare the fine scale model results with drift buoy and RCM data.
8) Incorporate the new GCM results into an existing particle tracking model, to simulate the dispersal of eggs and larvae from discrete spawning sites.
9) Produce indices of the extent of mixing of larvae from the different spawning sites.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 7.1 and the deliverables within the workpackage are listed in table 7.2.

IOH:
The work in WP 7 concentrated in the first year on the development of the hydrodynamic models and the collection and preparation of relevant initial and forcing data. A model system was set up that consists of a North Atlantic / Arctic Model domain in which two high resolved areas (Icelandic and Scottish waters) are embedded. The grid size varies from 75 km in remote areas (Arctic and North Atlantic) down to 2.5 km in the key regions. In order to have a smooth transition between large and small grid boxes, the grid sizes were zoomed within four steps from coarse to high resolution. The METACOD model thus consists of four nested sub-domains with increasing resolutions and an interactive coupling. The model runs simultaneously on all sub-domains. This approach is time consuming but provides the key regions with all necessary boundary values and allows even far field processes to enter consistently the key domains and vice versa.

The METACOD model is based on the well established and previously applied HAMSOM code. However, in order to handle complex bathymetries and to reproduce more realistically topographic effects on circulation and hydrography, the coding was vectorised and supplied with a vertical adaptive gridding technique. The new coding is called Vector Ocean Model and got the acronym VOM (Backhaus, in prep.). HAMSOM / VOM is a level type model but the vertical adaptive grid implies that the number of levels and the thickness depends on the topography. The METACOD grid provides a high vertical resolution in critical areas such as shallow banks, slopes and topographic obstacles. Surface and bottom following boundary layers are resolved uniformly. This allows for a better reproduction of coastal and shelf processes such as vertical stratification, stratified flows or current shear due to surface and bottom friction.

Initial data and forcing data was collected from institutional records and other sources:

- The topography was constructed basically from ETOPO 2 (NODC) and IBCAO (Int. Bathym. Chart of the Arctic Ocean) sources.
- The meteorological forcing is so far taken from a climatological year based on daily ECMWF data. This data set is cyclic and allows for multi-year runs during spin-up etc..
- Due to the very large model domain, the tides could only be considered by incorporating the body forces for individual astronomical tides into the equation of motion.
- Climatological temperature and salinity data sets were gridded and interpolated on the 3-D model grid. MRI provided IOH with seasonal mean T and S data for Icelandic waters based on multi-year observations. This data was 'fitted' at the boundary to seasonal mean global T, S data from Levitus. This work was provided by the MRI invited expert Dave Brickmann.
- Detailed freshwater runoff data is in preparation by MRI and will be incorporated soon.

Several tests were carried out in order to find the most appropriate grid resolution for the key areas. The present model version which has a resolution of 2.5 km proved to be a good compromise between the originally proposed 1 km resolution and the large amount of computer time, required for those very high resolutions. First results from the 2.5 km resolved key area around Iceland are promising and show a typical circulation that is strongly affected by eddies and the underlying topography (Fig. 7.1). The results gave confidence that the chosen resolution is sufficient to reproduce the eddy affected coastal flow and the fjord circulation.

MLA:
MLA has worked in collaboration with the remaining partners participating in this WP to collate the necessary data for the hydrodynamic modelling work and to discuss particle tracking methodology with the relevant partners. The incorporation of particle tracking modelling tools into the new general circulation model scheme, to simulate the dispersal of eggs and larvae from discrete spawning sites, is dependent on the availability of fine-resolution velocities and other environmental data. These deliverables are not due within the current reporting period. However, development work on the particle tracking models has been initiated and is progressing satisfactorily.

MRI:
During the year hydrographic data were sorted out and prepared for calculation of climatological means and gridded. Dave Brickman which works for the project in Canada calculated the climatological mean for each month of the year over a 50 year period. MRI staff consulted also on tides in connection with the Hamborg model.

Model validation and improvement will be the most important task for the next year. In this respect, the second project meeting will give the opportunity to exchange first results with experts from MRI and MLA in order to evaluate the model and to test particle tracking with the simulated flow fields. The preliminary results suggest that the simulated flow fields will be highly variable in time and space which has to be considered for the future particle tracking simulations.

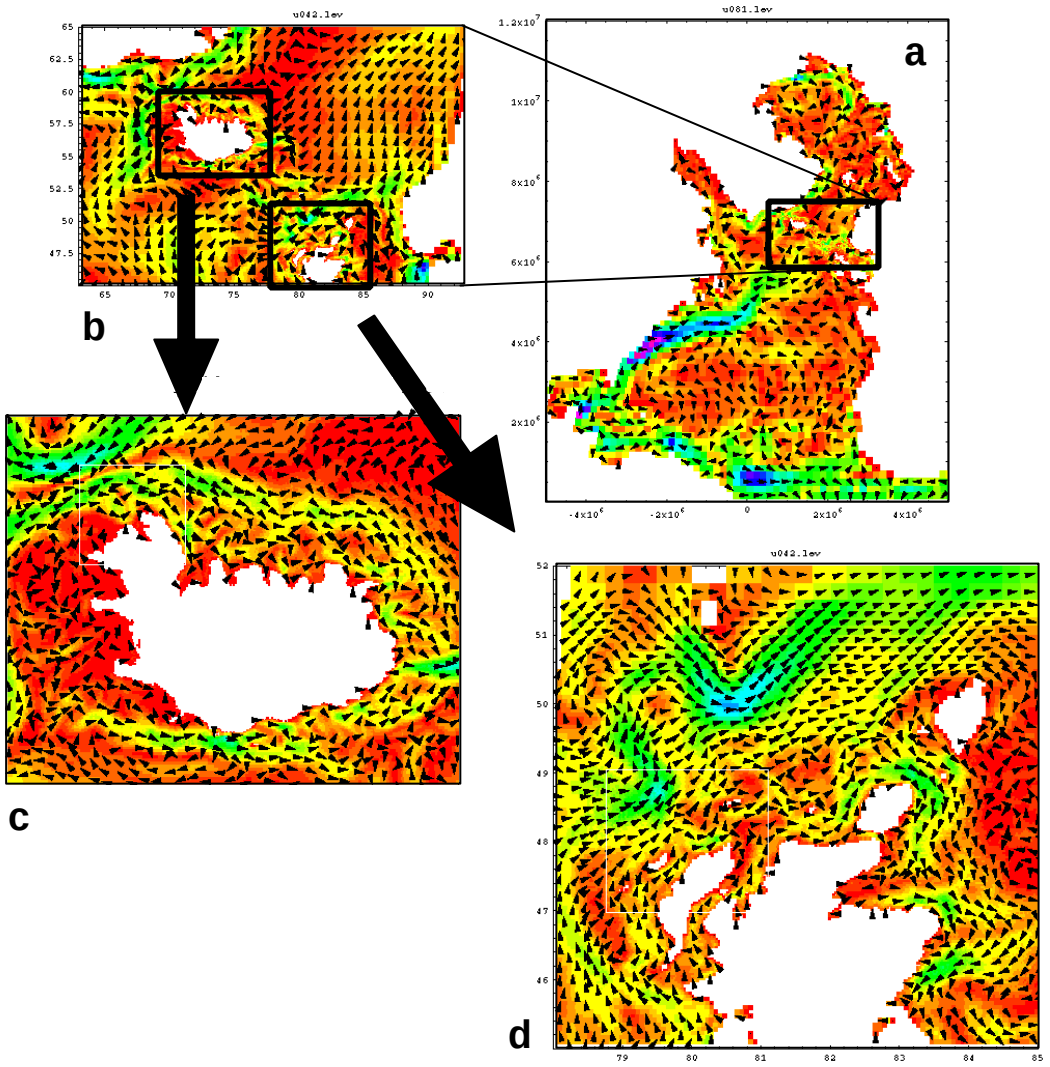

Figure 7.1 *Example for the nested model domains of the hydrodynamic METACOD model: Large basic domain (a), 2nd sub-domain (b), 4th sub-domains i.e. the key regions (c+d).*

Table 7.2. *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 3	7.1 Gridded configuration, initial, boundary and driving data for the south-west Iceland fine-resolution model region	18	P
D 6	7.2 Gridded configuration, initial, boundary and driving data for the west of Scotland/north-western North Sea fine-resolution model region	18	P
D11	7.3 Database of time and space dependent velocity observations derived from RCM and drift buoy records from Iceland and west/north of Scotland.	24	N
D12	7.4 Detailed comparison of observed velocity data with results from climatological simulations using the fine-resolution model at Iceland.	24	N
D13	7.5 Fine-resolution model simulation of velocity, temperature and salinity fields for a selected period corresponding to the field sampling of cod juveniles at Iceland in 2002.	24	N
D18	7.6 Mixing indices for eggs and larvae from spawning sites off south-west Iceland, derived from particle tracking results using the climatological and 2002 flowfields.	36	N
D19	7.7 Detailed comparison of observed velocity data with results from climatological simulations using the fine-resolution model of the west of Scotland/north-western North Sea.	30	N
D22	7.8 Fine-resolution model simulation of velocity, temperature and salinity fields for a selected period corresponding to the field sampling of cod juveniles of western Scotland/north-western North Sea in 2002.	30	N
D32	7.9 Mixing indices for eggs and larvae from spawning sites off west and north of Scotland, derived from particle tracking results using the climatological and 2002 flowfields.	36	N
D33	7.10 Fine scale model simulations of velocity, temperature and salinity fields for 2-3 selected periods for each region, including the field sampling period in 2003	36	N
D45	7.11 Particle tracking model analysis of stock mixing in 2003 for each region	40	N
D46	7.12 Particle tracking analysis of interannual variability in stock mixing indices, based on additional flowfields from each region, and comparison with North Atlantic Oscillation and other meteorological and hydrographic indices.	40	N

Expected results and relevant corresponding milestones

The WP will deliver the first fine resolution eddy-resolving flow and hydrographic simulations of the waters south and west of Iceland, and equivalent data for the west of

Scotland. These deliverables will be the input to the particle tracking models also included in the WP, and the biophysical models in WP9. Milestones are the delivery of the first fine resolution flowfields (milestones 7 and 8), and completion of the particle tracking analysis (milestone 11). Analysis of the particle tracking aspects of the WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13).

Workpackage 8: Identification of spawning group origins in mixed populations of juveniles.

Start date: August 2002

End date: December 2005

N° of the partner responsible: 1

N° of other partners involved: 1, 2, 3

Table 8.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	12.1	0.06		
Total to date	12.1	0.06		
Total planned	21	14	3	0

Objectives and input to workpackage

Conduct sampling of juvenile cod populations which the tracking models indicate should comprise fish from a mixture of spawning groups, estimate their actual composition from analysis of microsatellite DNA and *Syp* I genetic markers, otolith elemental composition and growth rates from analysis of otolith microstructure.

Methodology and study material

Classification of juveniles to their parental spawning groups.

1) Collect 100 juveniles from each of 4-6 locations per region (Iceland; west Scotland/north-western North Sea) indicated by the particle tracking model in 2002 and 2003 and identify to regional spawning components using genetic information from spawning groups (develop in WP-4).
2) Compare backcalculated hatch and spawning date distributions based on daily ageing of 2002 and 2003 juveniles, with available information on spawning time at the different spawning locations (methods developed in an earlier EU-project[23]).

Classification of juveniles to their future spawning groups.

3) Prepare otolith elemental fingerprints (from the otolith cores as developed in WP-5) of juveniles from 2-3 major aggregations per region (key locations indicated by the particle tracking model) sampled in 0-group surveys in 1996-1999 around Iceland.
4) Through comparison with elemental fingerprints of adult spawner otolith cores sampled in 2002 and 2003 (WP-5), classify the juveniles sampled in 1996-1999 as to which spawning group they recruited to in 2002 and 2003.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 8.1 and the deliverables within the workpackage are listed in table 8.4.

MRI:

A) Classification of juveniles in relation to their parental spawning groups.

Samples of pelagic 0-group cod were obtained from the annual 0-group survey conducted by the MRI in August 2002 (see Astthorsson *et al.* 1994 for methods). Samples were collected in 6 areas (Table 8.2, Fig. 4.2). On every station, samples of cod were bagged and frozen at –20 °C. No juveniles were found south of Iceland or on the main spawning grounds off the Southwest coast. In the laboratory, specimens were thawed, remeasured, oven-dried at 60 °C for 48 h and weighed to the nearest 0.1 mg. Prior to drying, lapillar and sagittal otoliths were extracted, cleaned, and mounted on glass slides with nail polish. Before viewing the otolith under a 1000 x oil immersion lens, one lapillus from each cod was polished on one side with lapping film, to render the hatch check and outer growth increments clearly visible. For otoliths from large juveniles (> 55 mm), the lapillus was removed from the glass slide with acetone and mounted on a new slide and polished again down to the core. The otolith preparation is expected to extend into the early year 2003 and the ageing of the juveniles will probably be finished in the fall the same year.

Table 8.2. *Sampling schedule of the cod juveniles, collected for otolith research in the year 2002 (see Fig. 4.2 for area division)*

Cruise	Date	Location (region)	Number of cod sampled	Analyses
B9-2002	August 8-9	Breiðafjörður (2.2)	92	Ageing
B9-2002	August 10-11	Vestfirðir (3.2)	100	Ageing
B9-2002	August 13	Húnaflói (4.1.1)	100	Ageing
B9-2002	August 15-16	Eyjafjörður (4.1.3)	20	Ageing
B9-2002	August 19	Langanes (5.2)	90	Ageing
B9-2002	August 20-21	Austfirðir (6.2)	100	Ageing
A9-1998	August 9	Vestfirðir (3)	50	Fingerprinting
A9-1998	August 13	Húnaflói (4.2.1)	16	Fingerprinting
A9-1998	August 15	Eyjafjörður (4.1.3)	50	Fingerprinting
A9-1998	August 20	Langanes (5)	50	Fingerprinting
A9-1998	August 24-25	Austfirðir (6)	86	Fingerprinting
A10-1999	August 5	Faxaflói (0)	9	Fingerprinting
A10-1999	August 6	Breiðafjörður (2)	82	Fingerprinting
A10-1999	August 12	Húnaflói (4.1.1)	150	Fingerprinting
A10-1999	August 14	Eyjafjörður (4.1.3)	100	Fingerprinting
A10-1999	August 19	Langanes (5)	41	Fingerprinting
A10-1999	August 24	Austfirðir (6)	50	Fingerprinting

Sampling for analysis of microsatellite DNA and *Syp* I genetic markers were conducted in three different cruises in October 2002 (Table 8.3). Pelagic juvenile cod was sampled in the annual 0-group survey and settled juveniles were sampled in two separate shrimp-surveys conducted in the west- and north of Iceland (Table 8.3). On board the vessels, random samples of cod were collected and preserved in a 96 % alcohol.

Table 8.3 *Sampling schedule for cod juveniles, collected for analysis of microsatellite DNA and Syp I genetic markers in year 2002.*

Cruise	Date	Location	Number of cod sampled
B9-2002	August 8-9	Breiðafjörður (2)	100
B9-2002	August 10-11	Vestfirðir (3)	100
B9-2002	August 13	Húnaflói (4.1.1)	100
B9-2002	August 15-16	Eyjafjörður (4.1.3)	100
B9-2002	August 19	Langanes (5)	100
B9-2002	August 20-21	Austfirðir (6)	100
D9-2002	October 5	Langanes (5))	100
D10-2002	October 9	Vestfirðir (3)	348

B) Classification of juveniles in relation to their future spawning groups.

In order to prepare otolith elemental fingerprints of juveniles, samples were taken from the statistical regions mentioned in section A above (Table 8.2).

Juveniles from 1995, 1998 and 1999 were selected based on available information on larval drift from the main spawning grounds (on the south coast) during these years. The larval drift was weak in 1995 and 1998 but strong in 1999. Frozen juveniles from 1998 and 1999 were thawed and the sagittal otoliths were extracted, cleaned and stored in an eppendorf tube for further chemical analysis.

All the juveniles sampled in 1995 were, at the time, dissected and the sagittal otoliths mounted in nail polish on a microscope glass slide. In order to find out whether the chemical composition of the otolith, the fingerprint, is effected by the mounting medium, a total of 50 "unknown" juveniles were dissected. One otolith of the sagittal pair was stored in eppindorf tube and the other was mounted on a glass slide for several weeks and then released in acetone and stored in eppendorf tube together with the untreated Seagate for further chemical analysis.

Otolith samples from spawning cod were collected during spring 2002 in the same regions as recorded in section A. (For location and sampling method, see WP5).

A total of 1160 otoliths from spawning cod were moulded in polyester resin blocks. Samples for fingerprinting will be acquired by cutting 1 mm slice through the otolith core and a sample retrieved from the core. The juvenile otoliths will be treated the same way. The slicing of the juvenile otolith needs to be further developed. So far 100 juveniles have been dissected and

their otoliths embedded in resin and tested for cutting/sawing. Promising results have been reported. The tests will continue until the end of the year 2002.

The elemental fingerprint will be obtained by extracting the otolith core from a subsample of the otolith sections with a computerised micromilling machine. The subsample will then be analysed for elemental composition for elements known to serve as natural markers.

MLA – North Sea and West Coast of Scotland:

The collection of 0-group cod was requested from every research cruise in 2002, from all sample areas in the North Sea and around the West Coast. However, only 76 cod of appropriate size were found. Additional trawling off Stonehaven by commercial boat gained a further 24 specimens. These low sample numbers precluded the hatch and spawning date analysis in 2002. In order to tackle this problem we propose two approaches. Firstly, all 1 – group cod will be sampled in 2003 in order to consider the 2002 year-class. Secondly, sampling will be repeated in 2003 on the 2003 year-class and an additional recruit survey of inshore areas in ICES area VIa will be conducted.

Table 8.4. *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 23	8.1 Assignment of juveniles to spawning origin based on genetic and otolith information	36	P
D 34	8.2 Determine the juvenile source of spawners sampled in 2002 and 2003.	38	P

Expected results and relevant corresponding milestones

The WP will deliver data to be used in the evaluation of particle tracking models developed in WP7, and the materials for the validation of the biophysical models in WP9. Milestones will be the completion of sample collection in 2002 and 2003 (milestones 3 and 5), and the completion of sample analysis (milestone 9). The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13).

Workpackage 9: Modelling the survival of offspring from different spawning groups.

Start date: January 2002

End date: December 2005

N° of the partner responsible: 2

N° of other partners involved: 1, 2

Table 9.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	0	1	0	0
Total to date	0	1	0	0
Total planned	8	12	0	0

Objectives and input to workpackage

Estimate the survival to juvenile stage from different spawning groups using an existing bio-physical model of dispersal, growth and mortality, calibrated using the DNA and otolith data collected from mixed juvenile populations.

Methodology and study material

1) Adapt an existing bio-physical model of the dispersal, growth and survival of cod developed in earlier EU-projects[23, 121] by incorporating the fine-resolution flow and environmental fields developed in WP7 for Icelandic and west/north of Scotland waters.
2) Set up the model to simulate the mean temporal distribution and magnitude of egg production from each spawning group over the 1990's. Seed the bio-physical model with particles at spawning locations and day through the spawning season and assign initial numbers of individuals from the egg production simulation. Track the survivors using climatological fine-resolution circulation model output. Analyse the results to determine the survival rate from each spawning group.
3) Vary the stock abundance in each spawning group homogeneously over the model region, and derive the simulated stock-recruit relationships for each sub-stock.
4) Systematically vary the relative distribution of stock abundance between sub-groups for a range of overall stock abundance, and determine the effects of interaction between the offspring from the different groups (e.g. through competition) on the individual sub-stock and the overall stock-recruit relationship.
5) Repeat 2) with year-specific hydrodynamic and environmental simulation data for 2002 and 2003, and corresponding year-specific distributions of spawning stock abundance between sub-groups.
6) Using the genetic, elemental composition and hatch date information from WP8, and the simulated time series of egg production by each spawning group distinguishable in the juvenile populations sampled in 2002 and 2003, derive the survival rate from each spawning group.
7) Compare the results of 5) and 6) for both 2002 and 2003 at both Iceland and off Scotland.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 9.1 and the deliverables within the workpackage are listed in table 9.2.

MLA:

An existing bio-physical model of the dispersal, growth and survival of cod will be modified to incorporate fine-resolution flow and environmental fields developed in WP7 for Icelandic and west/north of Scotland waters. Although the deliverable (bio-physical model implementation) is not due until the end of the second reporting period, preparatory work is already underway. This also includes frequent communication with other partners involved in modelling activities.

Table 9.2 *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 14	9.1 Biophysical model implemented with fine-resolution flow and environmental fields.	24	P
D 24	9.2 Climatological simulations of survival from different spawning groups.	36	N
D 35	9.3 Strategic analysis of simulated stock-recruit relationships for Iceland and Scottish regions	38	N
D36	9.4 Simulations of spatial and temporal patterns in cod early-life stage survival at Iceland and off Scotland in 2002 and 2003.	38	N
D39	9.5 Estimates of spatial and temporal patterns in cod early-life stage survival from juvenile sampling at Iceland and off Scotland in 2002 and 2003.	38	N
D47	9.6 Comparisons of 2002 and 2003 field estimates of survival patterns (9.5) with simulated results from deliverable 9.4.8.1: D23; Month 36 - Assignment of juveniles to spawning origin based on genetic and otolith information.	38	N

Expected results and relevant corresponding milestones

The WP will provide the fundamental basis for evaluating stock-recruit relationships for individual sub-stocks, and their interactions and hence will feed directly The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13). A major milestone will be the completion of the bio-physical modelling tasks (milestone 11). The WP will derive validation data from WP8, and rely on WP1, 4, 5, 6 and 7 for input information on spawning locations, relative distributions of egg production, and physical driving data.

Workpackage 10: Contribution of spawning groups to the harvested stock.

Start date: December 2002

End date: December 2005

N° of the partner responsible: 1

N° of other partners involved: 1, 2, 3

Table10.1. *Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	2.5	0.23	0	0
Total to date	2.5	0.23	0	0
Total planned	35	8	32	0

Objectives and input to workpackage

Examine the composition of mixed feeding aggregations generally targeted by fisheries, by quantifying the proportions of fish from the various regional spawning components using discrimination techniques developed in workpackages 4 and 5.

Methodology and study material

1) Cod feeding grounds located north-west and east of Iceland will be sampled in summer/autumn 2002 and 2003 and in 2002 off northern and western Scotland, so as to coincide with sampling from the spawning grounds during the same years.
2) A total of 200 cod will be sampled in each area, in each year. Samples will analysed with respect to DNA microsatellites (techniques developed in WP-4) and otolith shape and chemical composition (techniques developed in WP-5).
3) Using Maximum likelihood methods of Mixed Stock Analysis (MSA) and log-likelihood methods of assignment tests, the proportions of fish from the various regional spawning components that contribute to mixed aggregations found on the common feeding grounds.

Description of work conducted to date

Persons-months spent by each partner in 2002 are listed in table 10.1 and the deliverables within the workpackage are listed in table 10.5.

MRI:

Sampling of cod at the fishing grounds in Icelandic waters was performed in the period from October 1-24, 2002. Samples were collected at the two main feeding grounds west and east of Iceland (Table 10.2, Fig. 10.1). Sampling was performed on the research vessel Bjarni Sæmundsson using bottom trawl. Cruise leader was Valur Bogason. At each area a total of 263 (west area) and 265 (east area) cod were collected. In each sample, information on length (±1cm), total and eviscerated wet weight, liver weight and gonad weight were collected. All sampled cod were assigned to 4 macroscopic maturity stages (immature, maturing, spawning and spent).

***Table 10.2** : Status of the otolith analysis showing the number of otoliths collected on the Icelandic fishing grounds in 2002.*

Location	Sampling date	Number of otoliths					
		Sampled (pairs)	Scanned	Measured	Deconta-minated	Dissolved/ ICP-MS	agein g
West of Iceland	October 8–10-2002	263	263	263	50	0	0
East of Iceland	October 17–20-2002	265	265	265	70	0	0

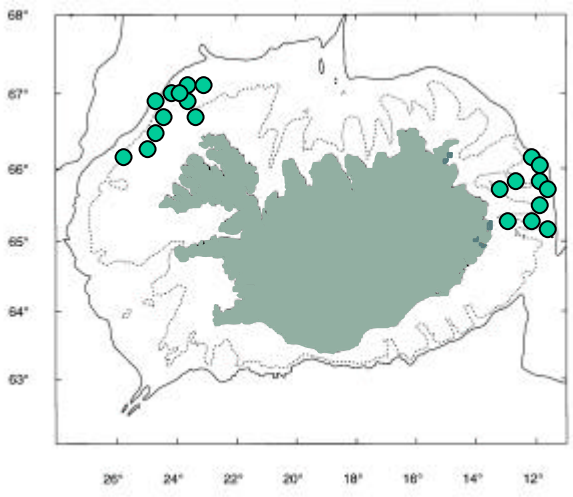

Figure 10.1 *Sampling sites for cod collected from the main fishing grounds west and east of Iceland in the fall of 2002.*

Table 10.3 *Dates, location, depth and number of cod collected at each station autumn 2002.*

Station	Date	Location		Depth	Number of cod sampled
B14-2002-st. 593	Oct 8	West of	66'10,67N 25'55,28V	271	40
B14-2002-st. 594	Oct 9	Iceland	66'15,48N 25'08,44V	126	8
B14-2002-st. 595	Oct 9		66'29,71N 24'46,40V	113	5
B14-2002-st. 596	Oct 9		66'51,35N 24'36,88V	210	50
B14-2002-st. 597	Oct 9		66'40,41N 24'20,03V	147	21
B14-2002-st. 598	Oct 9		66'43,77N 23'21,87V	139	8
B14-2002-st. 599	Oct 9		66'53,95N 23'25,96V	205	12
B14-2002-st. 600	Oct 10		67'00,15N 23'59,35V	274	40
B14-2002-st. 601	Oct 10		67'00,07N 23'45,83V	212	25
B14-2002-st. 602	Oct 10		67'03,94N 23'31,90V	230	19
B14-2002-st. 603	Oct 10		67'05,51N 23'00,22V	272	35
B14-2002-st. 663	Oct 17	East of	65'39,23N 13'07,57V	197	25
B14-2002-st. 664	Oct 17	Iceland	65'48,38N 12'36,52V	146	40
B14-2002-st. 665	Oct 17		66'15,24N 12'16,11V	261	6
B14-2002-st. 666	Oct 18		66'02,82N 12'06,45V	268	25
B14-2002-st. 667	Oct 18		65'49,48N 12'02,37V	177	25
B14-2002-st. 668	Oct 18		65'38.29N 11'32,28V	286	30
B14-2002-st. 669	Oct 18		65'18,10N 11'55,01V	219	25
B14-2002-st. 670	Oct 18		64'50,70N 11'39,04V	323	30
B14-2002-st. 671	Oct 18		65'04,99N 12'13,36V	208	40
B14-2002-st. 674	Oct 20		65'07,40N 13'03,44V	147	19
				Total	528

MLA (2): A total of 591 cod were sampled from Scottish waters during August and November 2002, primarily by research vessel surveys (1202s, 1602s & 1702s) but supplemented by commercial samples from Papa Bank in August 2002. In each sample, information on length (±1cm), total and eviscerated wet weight (±0.1g), and age (from otoliths) were collected. Additional information on liver weight (±0.1g) and gonad weight (±0.1g) was collected from the commercial samples landed at Aberdeen. The incidence of parasitic infection on the gills was noted. All sampled cod were assigned to 4 macroscopic maturity stages (immature, maturing, spawning and spent). Sections of ovarian tissue for histological analysis (n=46) were obtained, and preserved in 8% neutral buffered formalin. One sagittal otolith from each fish was removed with plastic forceps, cleaned gently and stored dry in plastic microtubes for future ICPMS analysis (n=584). Genetic tissue (n=587) was obtained from adult fish. Gill tissue was dissected with scissors and preserved in plastic microtubes filled with absolute ethanol.

Table 10.4 *Number of samples collected from Scottish waters by area in August/Nov 2002.*

AREA	No gill samples	No sagittal otoliths	No ovaries
MORAY FIRTH	7	7	0
ORKNEY	42	43	1
SHETLAND	21	21	0
NORTH MINCH	9	9	6
SOUTH MINCH	6	6	3
IRISH SEA	24	24	10
CENTRAL	50	50	0
FORTIES	71	71	0
VIKING	6	6	0
BUTT OF LEWIS	19	19	13
OUTER HEBRIDES	6	6	2
NORTH IRELAND	20	20	8
BUCHAN	13	13	0
PAPA BANK*	224	220	3
HUMBER	48	48	0
GERMAN BIGHT	19	19	0
DANISH COAST	2	2	0
TOTALS	587	584	46

***** Papa Bank is on the boundary between 6A and 4A.

Table 10.5 *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D 15	10.1 Samples of adult cod from summer autumn feeding grounds in 2002 and 2003	27	P
D 37	10.2 Analysis of genetic and otolith chemistry and shape properties for sampled cod	38	P
D 38	10.3 Analysis of genetic and otolith data, using the equivalent properties measured in fish sampled at spawning grounds, to apportion the summer feeding samples between the various spawning groups. based on genetic and otolith information.	38	N

Expected results and relevant corresponding milestones

The WP will feed into the annual re-appraisals of conceptual, mathematical and simulation models (milestones 4, 7, 10 and 13), by specifying the extent to which the fisheries exploit the different spawning groups during times of year when the fish from different sub-stocks are mixed.

Workpackage 11: Assessment of sub-stock structure of Icelandic, west of Scotland and north-western North Sea cod stocks.

Start date: January 2002

End date: December 2005

N° of the partner responsible: 2

N° of other partners involved: 1, 2, 3

Table 11.1*. Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	0.1	0.29		
Total to date	0.1	0.29		
Total planned	5	4.5	1	0

Objectives and input to workpackage

Conduct an assessment of the sub-stock structure of the Icelandic, west of Scotland and north-western North Sea cod stocks, to include estimates of the contributions of the various sub-stocks to the overall yield per recruit, and stock-recruitment relationships.

Methodology and study material:

1) Refine the initial conceptual model of sub-stock structure and dynamics using all the strands of evidence emerging from the preceding Workpackages.
2) Convert the conceptual model into a set of mathematical functions with non-linear interactions, defining the stock-recruit relationships of the individual sub-stocks and their inter-dependences.
3) Analyse the dynamic properties of this analytical system with respect to changes in overall metapopulation abundance and the distribution of that abundance between sub-stocks.
4) Combine the information on the variations in growth and maturation of fish from the different sub-stocks with the analytical stock-recruit relationships to generate a set of inter-dependent yield-per-recruit relationships for the various sub-stocks. These will be analysed to assess the productivity of the sub-stocks, and the metapopulation as a whole, with respect to variations in stock richness.

Description of work conducted to date:

Persons-months spent by each partner in 2002 are listed in table11.1 and the deliverables within the workpackage are listed in table 11.2.

The starting point for the METACOD project is the observation that within the domain of what we regard as being a unit stock of cod for assessment purposes, there are number of discrete spawning locations. On closer investigation, the fish using these sites are found to have distinctively different characteristics in terms of growth, age structure and in some cases genetics. Our hypothesis is that these spawning locations are to a degree isolated from each other such that each reflects a sub-population within the stock, and the stock is in fact a metapopulation. Our objective in devising a model of such a system is to assess the consequences for overall population dynamics of different scenarios for the connections between spawning locations.

A first draft of a model (METAFOR; deliverable 11.1; appendix 3) has been assembled where the stocks are viewed as metapopulations composed of a number of subpopulations. Each subpopulation has its own stock-recruitment relationship and the sustainability of each subpopulation will depend on the balance between its particular mortality, immigration/emigration and recruitment rates. In this first attempt, fish migration behaviour is simplified by specifying that they spend a fixed proportion of each year of mature life in the vicinity of a chosen spawning location and the reminder of the year feeding elsewhere. The chosen spawning area may vary with age or time. This part of the model needs further development, especially for cod in Icelandic waters where different units appear to have different migration behaviour (Jonsson, 1982; Begg and Marteinsdottir, 2002; Thorsteinsson, unpublished results from tagging experiments). The model allows for different rates of fishing mortality at the various spawning locations, but assumes that all fish are subject to the same fishing mortality rate during feeding. This assumption will be revisited when results from Work Package 10 on Contribution of spawning groups to the harvested stock, are available.

The conceptual model will accommodate a number of alternative scenarios concerning recruitment: 1) Recruiting fish are completely faithful or 2) imperfectly faithful to their natal spawning population; or alternatively 3) recruits are drawn at random from the pool of pre-recruit juveniles; and concerning adult migrations: 1) Recruits from particular spawning location continue to return to that location in subsequent hears; 2) individuals that recruit to non-natal spawning location gravitate back to natal units in subsequent years.

In order to compare the results from METAFOR, attempts will be made to model the dynamics of the metapopulations with another tool, GADGET (Globally Applicable Area-Disaggregated General Ecosystem Toolbox), that is being developed in another EU project "Development of structurally detailed statistically testable models of marine populations (dst). GADGET is a multi-species, multi area, multi-fleet model based on BORMICON (Stefánsson and Pálsson, 1997; Stefánsson and Pálsson, 1998) and has been used to investigate the population dynamics of many stocks and stock complexes in Icelandic waters, the Barents Sea, the North Sea and the Irish and Celtic Seas. GADGET works by running an internal model based on many parameters, and then comparing the data from the output of this model to "real" data to get a goodness-of-fit likelihood score. The parameters can then be adjusted, and the model re-run, until an optimum is found, which corresponds to the model with the lowest likelihood score. GADGET can be applied both in a simple way, including only subpopulations or in a more complex way by including also information on different fleets and other species. GADGET may prove to be especially useful in those situation where data on sub-population parameters are scarce. GADGET will also be used to provide better estimates on migration behavior. Migration in GADGET is modeled through migration matrices which represent the proportion of fish moving from one area to another in each timestep. Attempts will be made to model migration of each life stage within each sub-population.

Table 11.2 *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D1	11.1 Documented, reasoned argument for a point-of-departure conceptual model of the dynamics of sub-stock structure in Icelandic and west of Scotland cod, mathematical implementation and analysis.	3	C
D4	11.2 At the beginning of year 2, documented and justified revision of point-of-departure models from 11.1.	14	P
D16	11.3 At the beginning of year 3, documented and justified revision of models from 11.2.	27	N
D40	11.4 At the beginning of year 4, documented and justified revision of models from 11.3.	38	N
D48	11.5 Final, documented and justified versions of conceptual and mathematical models. Yield per recruit relationships for the individual sub-groups making up the metapopulations at Iceland and Scotland. Estimated relationships between metapopulation productivity and stock richness.	46	N

Expected results and relevant corresponding milestones

The first milestone in the WP will be the initial establishment of the point-of-departure models of sub-stock dynamics (milestone 1). These will be updated annually (milestones 4, 7, 10 and 13).

Workpackage 12: Development of advice on future catch and/or effort control measures.

Start date: January 2002

End date: December 2005

N° of the partner responsible: 2

N° of other partners involved: 1, 2, 3

Table 12.1*. Person-months by partner within workpackage*

Partner	1 MRI	2 MLA	3 DIFRES	4 IOH
2002	0	0	0	0
Total to date	0	0	0	0
Total planned	6	5.4	1	0

Objectives and input to workpackage:

Develop advice on how catch and/or effort control measures might be structured in space and time to both manage the population abundance at the scale of whole stock, and conserve or hasten the rebuilding of sub-stock structure.

Methodology and study material:

1) Run a probabilistic simulation of the temporal dynamics of a metapopulation in which the underlying stock-recruitment relationship is provided by the interacting sub-stock models developed in WP11, and comparing this with equivalent results obtained with a single homogeneous stock-recruitment relationship.
2) Repeat the probabilistic simulations for harvesting strategy scenarios which involve systematic variations in both integrated catch or mortality, and the rules governing the distribution of integrated catch across sub-stocks.
3) Repeat the probabilistic simulations beginning with a collapsed sub-stock structure and varying the magnitude and distribution of catches from surviving sub-units, to estimate probabilities of restoring stock richness.

Description of work conducted to date:

Persons-months spent by each partner in 2002 are listed in table12.1 and the deliverables within the workpackage are listed in table 12.2.

The first task to be performed with the METAFOR model was to explore its dynamics under the simplest possible test conditions (deliverable 12.1; appendix 6). To do this, the system was set up with

- 3 natal sub-populations,
- identical weight and maturity at age profiles for each sub-population (Table 1 in appendix 6),
- identical fishing mortality rate at age in each spawning areas, and during spawning, feeding and immature phases – *i.e.* the default rate was used throughout (Table 1 in appendix 6),
- identical stock-recruitment parameters for each spawning area.

After initial investigation it was decided to run these tests in deterministic mode rather than complicate the issues by implementing bootstrap procedures.

Initial numbers at age were taken from the STEREO reanalysis of ICES assessment working group outputs for North Sea and west of Scotland cod stocks. The numbers at age on 1 January for the combined stocks were averaged over the years 1990-1999 (corresponding to the averaging period for weight, maturity and fishing mortality data). These data (Table 1) were then used to set up the initial whole stock numbers at age in the METAFOR model. For the first runs of the model, these numbers were then distributed evenly across the three natal sub-populations, i.e. one third to each population. Three contrasting straying scenarios were devised to test the model performance (see appendix 6 for results of modelling runs):

Scenario 1: all fish remain 100% faithful to their natal spawning area throughout their life.

Scenario 2: up to age 3 fish in each natal population are uniformly distributed with respect to spawning area *i.e.* one third of the fish in each natal population are affiliated to each spawning area. Between ages 4 and 6 the fish gravitate to their natal spawning area so that from age 6 onwards all fish are 100% faithful.

Scenario 3: the fish in each natal population remain uniformly distributed across spawning areas throughout their life.

First results from the experiments with the METAFOR model have illustrated some important points that need special attention (see appendix 6 for additional details).

First of all it is clear that we need to focus on considering how stock-recruit relationships at the sub-stock level relate to stock-recruit relationships at the whole population level. In particular, we need to reach an understanding of the level at which density dependence

operates in such systems. Most likely, we need to devise a stock-recruitment function which includes both local and global (whole stock) egg production as independent variables.

Secondly, we need to consider all major environmental aspect of spawning areas which may influence their attractiveness to fish and possibly override any innate natal instincts, particularly in response to changes in overall population numbers.

Thirdly, we need to consider very carefully the basis for sub-stock structure in weight and maturity at age, since these will influence the egg production per fish at each spawning site. Assembly of all data in WP 2 and 6, both from the archives and other sources is therefore vital for improvement of estimates on reproductive potentials for the different spawning units.

Finally, the model is clearly very sensitive to the parameterisation of straying. Straying can rapidly erode any differences in abundance between components of the stock. An important area for investigation will be the extent of sub-stock structure in weight, maturity, mortality or recruitment parameters needed to overcome the eroding effects of straying and maintain sub-stock differences in abundance. In one sense this is encouraging since it means that our research could have a big influence on the understanding of whole-stock population dynamics. However, it is vital that we develop a clear understanding of the patterns of straying and how this may change with age. In this regard results from WP 3 on juvenile behaviour will be especially valuable.

Table 12.2 *Deliverables within workpackage*

Deliverable N°	Deliverable number and title	Delivery date	Status
D2	12.1 Initial version of bootstrap simulations and first-draft advice, based on the point-of-departure models produced by WP11 (deliverable 11.1).	4	C
D 5	12.2 First update of simulations and draft advice at start of year 2.	18	N
D17	12.3 Second update of simulations and draft advice at start of year 3	27	N
D41	12.4 Third update of simulations and draft advice at start of year 4.	39	N
D49	12.5 Comparison of the probability of stock collapse for a given harvesting strategy, assuming either a homogeneous population or a structured metapopulation – final version.	47	N
D50	12.6 Estimates of the harvesting strategies which result in equal probability of collapse for both the homogeneous and structured populations – final version.	47	N
D51	12.7 Estimates of the relationship between the magnitude and configuration of catch that optimise the probabilities of conserving stock richness and biomass, and initial guidelines as to how the system could be managed by constraining the spatial distribution of fishing effort – final version.	47	N
D52	12.8 Estimates of the probability of restoring stock-richness under scenarios of limited harvesting on a collapsed stock – final version.	48	N

Expected results and relevant corresponding milestones

The first milestone in the WP will be the initial establishment of the point-of-departure models of sub-stock dynamics (milestone 1). These will be updated annually (milestones 4, 7, 10 and 13)

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3. PARTICIPANTS

List of participants

Partner no	Name of Institute	Short name	Address	Name of Contact and E-mail	Telephone	Fax
1	Marine Research Institute	MRI	Skulagata 4 P.O.Box 1390 121 Reykjavik Iceland	Gudrun Marteinsdottir runa@hafro.is	354 – 552-0240	354-562-3790
2	Fisheries Research Services, Marine Laboratory	MLA	101 Victoria Rd AB11 9DB Aberdeen, UK	Peter Wright P.J.Wright@marlab.ac.uk	44 1224 295436	44-1224-295511
3	Danish Institute for Fisheries Research	DIFRES	Vejlsoevej 39 8600 Silkeborg Denmark	Einar Eg Nielsen* een@dfu.min.dk	(45) 89 21 31 15	45- 89 21 31 50
4	University of Hamburg, Institut fuer Meereskunde	IOH	Troplowitzstr. 7 D-22529 Hamburg Germany	Ingo Harms harms@ifm.uni-hamburg.de	49 (0) 40 42838 4206	49 (0) 40 560 5724

*Einar Eg Nielsen has taken over all responsibilities from Daniel Ruzzante, since Daniel moved to Canada

Partner 01: **The Marine Research Institue (MRI), Reykjavík, Iceland**
Scientific team: Prof. Gudrun Marteinsdottir (leader, project co-ordinator), Dr. Anna K. Danielsdottir, Mr. Hedinn Valdimarsson, Dr. Christophe Pampouli, Mr. Vilhjalmur Thorsteinsson, Mr. Bjorn Gunnarsson, Mr. Hoskuldur Bjornsson, Mrs. Ingibjorg Jonsdottir, Mr. Kristinn Saemundsson, Mrs. Adalbjorg Jonsdottir, Dr. David Brickman (invited expert); Dr. Gavin Begg (invited expert), Dr. Steve Campana (invited expert).

Partner 02: **FRS Marine Laboratory Aberdeen (MLA), United Kingdom**
Scientific team*:* Dr. Peter Wright (leader), Dr. Alejandro Gallego, Dr. Mike Heath, Mr. Phil Kunzlik, Mr. Coby Needle, Mr. Iain Gibb, Mrs. Fiona Gibb..

Partner 03: **Danish Institute for Fisheries Research, Denmark (DIFRES)**
Scientific team: Einar Eg. Nielsen (leader), Dr. Daniel Ruzzante (invited expert), Ms. Karen-Lise Mensberg, Ms Dorte Meldrup.

Partner 04: **Institut fur Meereskunde, University of Hamburg, Germany (IOH)**
Scientific team: Dr. Ingo Harms (leader), Prof. Jan Backhaus and and Kai Logemann.

4. PROJECT MANAGEMENT AND CO-ORDINATION

Names of Lead contractors

NAME OF LEAD CONTRACTOR	PARTNER NO	WORK PACKAGE NO
Gudrun Marteinsdottir	1	Project Co-ordinator; WP 1, 3, 5
Anna K. Danielsdottir	1	10
Bjorn Gunnarsson*	1	8*
Gavin Begg*	1	3*
Mike Heath	2	9, 11, 12
Peter Wright	2	2, 6
Einar Eg Nielsen*	3	4
Ingo Harms	4	7

* Changes from Technical Annnex - New lead contractors. Einar Eg Nielsen has taken over the lead of WP 4 after Daniel Ruzzante moved to Canada. Bjorn Gunnarsson and Gavin Begg have taken over the lead of WP 8 and WP3 from Gudrun Marteinsdottir, respectively, e.g. in order to distribute the work load more evenly.

Meetings in 2002:

First Annual Progress Meeting in, Aberdeen 31/1-1/2 2002 (See Appendix 1).

Calibration meeting between Partner 1 and 3 in Silkeborg, Denmark, 9-11 December (see Appendix 2).

In addition, several local meetings have been conducted by each partner in order to plan and coordinate actions by each team.

Meetings anticipated in 2003:

Second Annual Progress Meeting in Selardalur, Iceland, 26-28/5

The need for additional meetings between individual partners during the coming year will be discussed at the Annual Meeting in Iceland.

5. EXPLOITATION AND DISSEMINATION ACTIVITIES

Presentations given in 2002:

Björn Gunnarsson, Héðinn Valdimarsson and Gudrun Marteinsdóttir. 2002. Spatial and Temporal Abundance, Age and Hatch-Date Distributions of Icelandic Larval and Pelagic Juvenile Cod in Relation to Currents Observed with Surface Drifters. 37th European Marine Biology Symposium. Reykjavík, 5-6 ágúst

Guðrún Marteinsdóttir. 2002. METACOD, the role of sub-stock structure in the maintenance of cod metapopulations. Annual Working Group of Recruitment Processes, ICES Headquarters, Copenhagen 18-19 April 2002**.**

Presentations anticipated in 2003:

Pampoulie, C., Stefánsson, M.Ö., Marteinsdóttir, G. and Daníelsdóttir, A.K. Annual meeting of the American Fisheries Society (AFS) (Québec, Canada), 10
to 14 of August 2003. Genetic structure of Icelandic cod (*Gadus morhua*): the spawning units andtheir contribution to the stock.

Gudrun Marteinsdottir. Can we improve stock recruitment relationships by including information on maternal effects? 27th larval fish Conference in Santa Cruiz, CA, USA

Gudrun Marteinsdottir, Introductions on MEATCOD will be give at Rutgers University, NJ, USA in July and the Long Marine Lab, Santa Cruiz in August.

Appendix 1: Minutes from the first progress meeting

First meeting sponsored by
FRS Marine Laboratory Aberdeen
Thursday 31st January – Friday 1st February 2002

Minutes

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1. Welcome and Introductions

2. Timetable and important dates

The first deliverables are in Month 4, 6 and 12.

Reporting schedule:

December 20th 2002 – draft reports to co-ordinator
December 20th 2002 – cost statements to co-ordinator
January 30th 2003 – Report to the Commission
8-9 May 2003 or 12-13 May 2003 – 2nd meeting

As there are not many deliverables within the first year, it was proposed that the first meeting of all participants could be delayed until May 2003 in Iceland. A meeting regarding sampling protocols will be required before this, perhaps at the start of November 2002, with one participant from each institute attending. The standardization of sample collection protocol for the genetics work was deemed crucial, as most of the samples are being taken in Year 1. Immediate concerns for the trips leaving within the next few weeks will be addressed during this meeting.

Informal clustering with other projects:
Metacod
Hergen
Codtrace (the identification of cod stocks on a large geographical scale)

Potential dates of meetings include:
2003 May- with Codtrace
2004 – Spain
2005- All project meetings

3. Working arrangements

The compatibility of software was viewed as a historical problem, but all participants foresee no problems in this area.

4. Publicising the project

- Logo, Webpage & CD: Iceland will take responsibility for these items.

The webpage may include a restricted page for project members, containing meeting notes and presentations. A group photo was taken for inclusion to the webpage.

In addition to publications in peer reviewed journals, model runs will be demonstrated in an animated format on a CD and/or on the Web site. Animated model outputs will for example include hydrodynamic changes, drifter track routes, migration of spawners, daily egg production and particle tracking of eggs, larvae and juveniles form the individual spawning units.

Action required: Artistic input, ideas and pictures to be e-mailed to Gudrun!

- Conferences & ICES working groups

Any talks given or meetings attended relating to METACOD should be assembled for inclusion in the final report. Participants should be aware of other similar projects starting-up (e.g. Cododyssey), and thought should be given to where they could be integrated with METACOD.

5. Workpackage Discussions

A brief discussion of each workpackage took place, outlining the aims, deliverables and potential problems with the work plan. One important point to come out of these discussions was the importance of standardising the methodologies.

WP1 Past and present day spawning locations of cod
Presentation by Gudrun Marteinsdottir

The aims and deliverables were presented (Pg. 5 of the technical annex). Problems discussed included the lack of maturity stage information within the log book data, and the fact that there appeared to be many (at least 10) spawning grounds. It is hoped that local knowledge from the fishermen will help to spatially resolve these sites. The term stock-richness is widely used in the technical annex and has several possible meanings. With reference to this WP it can be defined as the number of spawning sites. The problem of partitioning numbers of spawning cod in certain areas to abundance estimates was raised. The Stereo project made use of a prevalence index, but this cannot fully account for annual variation in spawning location.

Action required: The need to agree on a rule on how to partition the numbers of spawning cod to areas was identified.

WP2 Relationship between stock-richness, catch and stock biomass
Presentation by Peter Wright and Coby Needle

The aims and deliverables were presented (Pg. 6 of the technical annex). There has been no intensive investigation into cod spawning sites in Scotland, and most of the information has been derived from historic egg surveys and research vessel surveys. The Butt of Lewis and the Moray Firth have been identified in the literature as sites with high concentrations of cod, but their relative importance as spawning sites has not been investigated. The RVR database samples one cod per 1cm length class and therefore negates any attempt to show trends in spawning cod abundance over a temporal scale. The available tag data is encouraging as it suggests that structure does exist in cod stocks. There is also recent genetic evidence that some stocks are genetically isolated.

Discussion focused on the methodology for assessment of spawning stock biomass.

Catch and effort data for North Sea cod, haddock and whiting were collated by Pope and Macer (1996), and used in a VPA to estimate abundance of these stocks from 1920 onwards. However, they used exclusively English data series, pertaining mostly to the southern North Sea. Data on Scottish, Norwegian and other relevant fisheries will need to be collated for a similar exercise to be carried out in the areas of relevance to METACOD. The methodology used by Pope and Macer forms a good starting point for generating catch and effort estimates, once data are available.

Data to be used in Icelandic waters will include data from the ground fish survey, the gill net survey (all spawning sites south and west of the country as well as north of the country in recent years), as well as logbooks and landed catch.

Action suggested: The ICES planning meeting for cod and plaice egg surveys was mentioned, efforts will be made to liase with the participants (CEFAS).

WP3 Tagging studies to determine spawning site fidelity and migrations of adult and juvenile fish
Presentation by Gudrun Marteinsdottir

The aims and deliverables were presented (Pg. 7of the technical annex). Methodologies 4 & 5 apply to Iceland only.
The Scottish survey leaves in a few weeks time, with 118 Data Storage Tags, and an additional 40 Lotec tags from CEFAS. Historical tag data is available from the 1950s to 1984. It was noted that Scottish tag recovery rates are unlikely to be useful for estimating mortality but should give an idea of homing characteristics and home ranges. New tagging experiments will be conducted, including tagging of juveniles and spawning cod especially in the Southeast and Northern area of Iceland, areas with little data at present.

WP4 Genetic variations among spawning components
Presentation by Daniel Ruzzante

Spawning aggregations
The sampling requirements of this WP were discussed (Pg. 8 of the technical annex). For both countries, the following data should be collected for all samples: Location name, Collection Year, Collection Month, Collection day, Lat deg, Lat min, Long deg, Long min, Sample number, Fish ID, Length, Sex, Mat, Age (otoliths), Weight.

Genetic samples are to be collected from spawning fish (male or female), defined as Stage 6 fish (with hydrated oocytes in the ovary). If numbers of spawning fish are low then the samples can be complimented with fish from Stages 5 (pre-spawning) and 7 (spent), but they should not make up more than 15% of the total collected. The absolute minimum number of samples per location is 50. Iceland will process its genetic samples, and samples collected in Scotland will be processed in Denmark. The importance of equipment standardisation and sampling methodology was re-iterated.

Scotland
The dedicated Scottish survey will sample 5 offshore areas and 7 inshore areas in March 2002, and will collect between 100-200 genetic samples from spawning fish per location in 2002. In total, 1200-2400 samples potentially. Some addition sampling in 2003 may also be possible but this was not promised in the technical annex. Even with this additional sampling, it is thought unlikely that the number of Scottish samples will exceed the agreed maximum (i.e. 2400).

Iceland
Iceland is to sample 8 locations per year (2 offshore and 6 inshore areas). Temporal replication will be possible on 2 offshore sites, with both locations being sampled both years. Year 2 sampling will be adapted after the analysis from Year 1 is known, meaning that some of the inshore areas may also be replicated. Iceland will collect 100 samples per location in April and May 2002 and 2003 from gill net and commercial seining boats.

Outlier samples
Additional samples are to be sought from locations outwith both countries' study areas, from commercial fleets sampling in the Faroes, Iceland and Bergen Bank. These samples will be brought back on ice. All tissue samples will be cut in two and copies sent to the relevant institute.

Actions required:

FRS:
- to liase with the Scottish commercial fleet to collect 100 cod from Faroe (e.g. Vessel – Sunbeam. Contact: John Garioch).
- to sample the 100 cod from Faroe and send one genetic tissue to Iceland (to Anna), and one to DIFRES.
- to collect 100 genetic samples from Bergen Bank in February/March 2002 to send to DIFRES.
- to collect 100 genetic samples of Scottish cod and send to Anna.

ICELAND:
- Anna is to send 100 offshore genetic samples (again, from one bit of tissue halved) from Iceland to DIFRES.

BOTH:
- A meeting is to be arranged after the samples have been collected between the two genetic groups (FRS, DIFRES and Iceland) in order to standardise techniques and assess progress – potentially at the start of November 2002.

Archived otoliths

No elemental fingerprint work is to be done on the archived otoliths, the samples are for genetic work only. The ideal template for a good study design would be 50 otoliths from 2 spawning locations, taken from 6 points in time (i.e. decades). Total No=600. These samples should be collected from fish over the full age range. Another scenario would be to collect samples from 3 spawning locations (50 otoliths per location) collected from 4-5 temporal points. Total No=600-750.

A potential problem with the collection of archived otoliths may be the lack of useable tissue on the otoliths. Scotland has recently disposed of many archived samples, although CEFAS has agreed to provide their archive samples from the West Coast. It may also not be possible to locate any location data from very old samples (i.e. 1910-1920s otoliths). Iceland has many otoliths available both within and between years, and will prioritize samples from spawning grounds.

Actions required:

- All archived otoliths are to be located and catalogued (by area [ICES square] and by decade) and the information sent to Daniel by March 2002. If haul location is known, the relevant lat/long position data should be gathered.
- More otoliths should be set aside than the required number, as many otoliths may be unsuitable for analysis.
- A meeting should be arranged between DIFRES technical staff and Iceland before these analyses start.

<u>WP5 Natural markers for the different spawning groups based on otolith elemental fingerprints and otolith shape</u>
Presentation by Gudrun Marteinsdottir

The aims and deliverables are on Pg. 10 of the technical annex. Discussion focused on the potential difficulty of comparing results between the 2 laboratories. Further discussion between both groups will be necessary, with the possibility that all samples may be processed by one lab. Iceland will compare 200 core samples in 2002/2003 with samples from

1996/1997. Scotland has no comparative samples available. Plastic forceps must be used when extracting the otoliths for future elemental analyses.

Actions required:

- Elemental work – Peter and Gudrun are to discuss which laboratory is doing what, and the
- microsatellite loci has to be agreed by Daniel and Anna. Protocols have to be drawn up by March 2002. Samples may be sent between the two labs for cross-comparison, although this may prove inconsequential if each machine gives unique results.
- A meeting with both FRS/Dunstaffnage and Iceland may be required to standardise methodology relating to the ICPMS process.
- Peter is to investigate the possibility of FRS further preparing the otoliths before sending them to Dunstaffnage Marine Laboratory for analysis, with the view to reduce their charges.
- Otolith shape analysis – Gudrun, Gavin and Peter to discuss protocol.
- Cores - Gudrun is to write a memo relating to the methodology, and who is analysing the samples.

<u>WP6 Growth and reproductive properties of different spawning groups</u>
Presentation by Peter Wright

The aims and deliverables were presented (Pg. 10 of the technical annex). Available data may be limited, but it has highlighted some radical changes that have occurred over the last few decades (e.g. fish in 1999 were mature at 25cm). The problem of partitioning abundance spatially was raised once again.
Egg production estimation (using Beth's STEREO model) has been parameterised by south coast Icelandic cod, and should be re-parameterised for Scottish cod.

<u>WP7 Hydrodynamic and particle tracking models of egg and larval dispersal</u>
Presentation by Ingo Harms and Jan Backhaus

<u>Day One Summary</u>: The aims and deliverables are on Pg. 11 of the technical annex. This workpackage leads into WP8. It is hoped that tomorrow's discussion will clarify the following: topography (1 km resolution stated as a deliverable), tides, 3-D temperature and salinity, meteorology and drift issues.
The model output, grid configuration and parameters have also to be resolved. A new adaptive vertical grid model will be tested in METACOD. The potential outputs of such a model were demonstrated by an animation sequence. Such graphics may be included on the web page, or available on CD.

<u>OMG meeting (DayTwo) Summary</u>:

Key points to discuss:

1. grids and domains for HD models (horizontal and vertical resolution)
2. HD model output (time resolution, data exchange)
3. availability and use of observational data for forcing and validation
4. general configuration of particle tracking models
5. exchange of information, possible OMG meeting

1. Model grids and domains

Hedinn gave a presentation of observational data available and relevant processes in order to decide about domains and grids. The data situation around Iceland is good. Buoy and drifter

data are a valuable help for the decision about domain and grid. It is also helpful for validation.

Actions: Alejandro and Hedinn will check for similar data around Scotland.

The domain of the Icelandic model should cover the region between the coastline and 500m isobath. The grid should have the highest possible resolution. Hamburg is free to choose the optimal grid configuration. The same criteria should be applied for the Scottish model. Areas of no interest (depths > 500m) will be blanked out.

Action: Hamburg will make suggestions for domains and grids to OMG and Gudrun by summer 2002.

2. Model output

Due to high resolution and expected eddy activity, the time resolution of output can not be decided yet.

Action: Hamburg to make suggestions to the OMG and decide then.

The standard output variables are u, v, w (3-D flow field), sse, t and s. t and s can be output on coarser time steps than the dynamics. Output formats will be settled later.

Options:

- Output of horizontal and vertical diffusivity (eddy) coefficients for climatological or other simulations.
- A tidal atlas can be produced by Hamburg.

3. Observational data

Hamburg will take care of topographic data sets, apply them in HD models and make suggestions to OMG.

The Icelandic t and s database should be used for the METACOD purpose. David will try to use t and s data to design a **gridded** climatological data set. Hamburg will deliver the topography, Hedinn will deliver t and s data to David.

HD models need good freshwater runoff data, Hedinn will take care of that. All other forcing data (ECMWF / NCEP/NCAR) will be implemented by Hamburg.

For validation, the t, s data base from around Iceland and t, s data around Scotland will be used for climatological simulations. Further validation tools are current meter and ADCP data which are frequently available from around Iceland (Hedinn). Alejandro will check for current data around Scotland, Hedinn to help.

4. Particle tracking models

Alejandro is in charge for Scotland, David for Iceland. Both models seem to be quite similar. Alejandro and David will discuss further details.

5. Exchange of information, possible OMG meeting

Options:

- comparing both model results for the same region and merging into one model later in the project
- have an OMG meeting at short notice in late autumn (Hamburg, David needs travel funds from Iceland!).

The OMG group will exchanges information within an e-mail group: harms@ifm.uni-hamburg.de, backhaus@dkrz.de, hv@hafro.is, brickmand@mar.dfo-mpo.gc.ca, a.gallego@marlab.ac.uk, runa@hafro.is.

WP8 Identification of spawning group origins in mixed populations of juveniles
Presentation by Gavin Begg

The aims and deliverables were presented (Pg. 13 of the technical annex). The micro-satellites are already developed, thus the first results could be ready in 12-18 months. These genetics results will effectively be a test on the particle tracking model. The possibility of obtaining outlier samples was discussed.

Genetic samples (gill or fin clip) should be preserved in 96-98% ethanol. If the whole juvenile is to be preserved, the ethanol in the sample tube must be changed the following day. Plastic forceps must be used when extracting the otoliths for future elemental analyses.

Scotland
Scenario One:
Sampling will be concentrated in 2 areas on the West Coast (northern 6A and Southern 6A) and 2 areas in the North Sea (East of Shetland and East Coast of Scotland). The NS samples will be collected from the Groundfish survey in August 2002 and in January 2003. The 6A samples will be collected from a cruise in November 2002. A minimum of 100 samples will be collected from 0+ - 1+ group cod per location.
Scenario Two:
Only 2 locations will be chosen (i.e. one in 6A and one from the North Sea) and the surveys will aim to collect as many fish as possible from the two areas. The decision on which location is sampled will depend somewhat on the results of the particle tracking analysis.

As the juveniles collected will also be sampled for otolith microstructure (using the lapilliae) and for IPCMS (using the sagittae), the genetic samples will be collected from previously frozen fish.

Iceland
Samples of pelagic 0+ group will be collected from 4 to 5 locations during an 0+ group survey in August 2002 and 2003. Samples for genetic analysis will be selected from these on the basis of particle tracking results from STEREO and METACOD (if available) in each of 2002 and 2003, N= 100 per location. Total No=800-1000 over two years.

100 juveniles per location will also be sampled for age and hatch date by microstructure analysis. The sagittal otoliths from these fish will be used for elemental fingerprint work. 50-100 0-group from 2 locations in 1996 and 1997 will be used for elemental fingerprint work. Total No sampled for elemental fingerprinting=600.

WP9 Modelling the survival of offspring from different spawning groups
Presentation by Alejandro Gallego

The aims and deliverables were presented (Pg. 14 of the technical annex). The presentation gave an overview of the biophysical model, showing the inputs & environmental factors, the

stages of the model (egg stage, pelagic stage, settlement processes) and the potential outputs. The model has been developed for STEREO, and as such there are no anticipated problems with developing the framework. Modelled data from large geographical areas over long periods of time has been found to represent the observed data fairly well. Issues of vertical migration were raised, and will be discussed within the OGM group. Iceland is to run the model for 2002 and 2003 with different stock structure simulations.

WP10 Contribution of spawning groups to the harvested stock
Presentation by Gavin Begg

The aims and deliverables were presented (Pg15 of the technical annex).

Scotland
A minimum of 200 genetic samples are to be collected from two areas on the boundary between 6A and 4A in the July/August 2002. These samples will be collected from one RV survey, but may be supplemented by commercial vessel samples. The possibility of collecting samples from observer trips was raised, but the extra effort required at sea may be prohibitive. Un-gutted whole cod may therefore be brought back to FRS for sampling. These fish should be caught as late into the vessel's voyage as possible. The possibility of using market sampled fish will be investigated, using results from a recent FRS study into tissue freshness.

Early indications from the genetics work of existing stock structure between areas will help plan for any 2003 sampling surveys.

Iceland

Two main fishing banks in the NW and SE will be sampled in October 2002 and 2003. Iceland has a budget for 400 genetic samples only, and so 200 samples will be collected from the two locations in 2002. Alternatively, only one location will be sampled for 200 fish, but over the two years.

Action required:
Gudrun will investigate whether additional money can be raised to repeat the Icelandic sampling and analysis in Year 2.

WP's11 & 12 Assessment of sub-stock structure of Icelandic, west of Scotland and north-western North Sea cod stocks. Development of advice on future catch and/or effort control measures

Presentation by Coby Needle

These 2 workpackages have been grouped together, Pgs. 16-17 of the technical annex. If data collection and analyses have been successful in all the feeder packages, this workpackage should run well, as the standard techniques are available at present.

Draft notes on WPs 11 & 12

1. We anticipate that most of the substock assessment inputs that we require will come from WPs 1–10 (with particular emphasis on WP 6). Hence quantities such as egg production, maturity-at-age, weights-at-age, age-length keys and spawning time/duration will be derived from substock modelling.
2. However, landed weight and catch numbers-at-age will not generally be available at the substock level. There are at least two options for generating these numbers, both of which should be implemented in the exploratory phase:

- Use survey-based assessment methods to generate a relative abundance index for each substock, then (optionally) scale by an overall abundance measure (from a whole-stock VPA, perhaps).
- Use survey indices by area to partition whole-stock catch into substocks, then use standard catch-based assessment methods at the substock level.

3. Standard techniques are available for both historical assessment and probabilistic projections. However, these will have to be modified to account for annual mixing between substocks. Exchange rates will be taken from tagging studies, and will hopefully have associated uncertainty to allow for stochasticity in projections.
4. It seems likely that not all required inputs will be available for all substocks in all years. Hence, various algorithms to "fill-in" the missing data will be explored: possibilities might include nearest-neighbour means or time-series smoothing. The sensitivity of final model output (I,e, advice to management) to the fill-in method used will be tested.
5. Whole-stock analyses will be performed concurrently, and an assessment made of whether the resultant scientific advice would be significantly different if based on the various substock or whole-stock analyses. This will be the final test of whether substock structure needs to be accounted for in fisheries management for North Sea, West of Scotland and Icelandic cod.
6. Scenario modelling will follow on naturally from the model-building exercise: however, it is important that we do not lose sight of the fact that this will be required.

Action required: Mike, Phil Coby and Peter are to meet and discuss this work package. A draft document should be available before Month 4's deliverable.

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Appendix 2: Minutes from the calibration meeting

Silkeborg Calibration meeting with partners 1 and 3 (Denmark)

Silkeborg, Denmark 9 to 11th of December 2002

List of Meeting Participants:
Daniel Ruzzante (Department of Biology, Dalhousie University)
Dortre Meldrup (Danish Institute for Fisheries Research)
Einar Eg Nielsen (Danish Institute for Fisheries Research)
Christophe Pampoulie (Marine Research Institute- Iceland)
Magnús Örn Stefánsson (Marine Research Institute- Iceland)

Opening and introductions:
Each partner quickly introduced his laboratory and the people involved in each country on the Metacod project.

Meeting Objectives:
Comparison of the methods (extraction, PCR etc)
Calibration of microsatellite loci
Choose a list of supplementary microsatellite loci
Decision taken to avoid technical problems
Objective for the meeting of May 2003
Discuss of extraction protocols for otoliths

Comparison of the methods (extraction, PCR etc):
The methods used by the two laboratories are based on studies done by O'Reilly et al. (2000) and Miller et al. (2000). The PCR conditions are consequently similar but varied at some points from one laboratory to another. For example, the MRI has developed PCR-multiplexes while DIFRES has developed single-PCR protocol. The sequencer automates are different but this does not affect the results which did not show any inconsistency.

Calibration:
Eight microsatellite loci have been run in each laboratory on 45 individuals randomly chosen from samples coming from Faroe Isles, Iceland and Norwegian Sea. Genotypes have been assessed and compared between laboratory. Then, the MRI decided to adjust the values found in Iceland to the one observed in Denmark. For that, the MRI has to add or remove a certain number of base pairs on the scoring of the genotypes they did (Table 1).

Table 1. Correction of the genotypes scored in Iceland for 8 microsatellite loci.

Correction for calibration		
Gmo2	+1	bp
Gmo8	+5	bp
Gmo19	+4	bp
Gmo34	+3	bp
Gmo132	+2	bp
Tch5	0	bp
Tch11	0	bp
Tch14	-2	bp

Choose a list of supplementary microsatellite loci:
Because some of the microsatellite used seemed to be unperfected, we decided to increase the number of microsatellite loci we will use, in order to obtain a list of 12 to 15 perfect microsatellite loci, e.g., which will not show any unexplainable Hardy-Weinberg equilibrium

due to technical problems such as null alleles. Consequently, we chose 4 new microsatellite loci (Table 2) and decided to take contact with other people working on this topic to obtain supplementary loci.

Table 2. New microsatellite loci.

Gmo35	R: CCTTATCATGTACGTTGTTAAC F: GGAGGTGCTTTGAAGATG	(ACC)	55	110-145	12
Gmo36	R: GGTGATGGAGGCTCTAGT F: ACCGCAT(G/C)CCCTTTTCA	(GGT)	50	170-210	13
Tch12	R: AGTACAGCTTGATTGTTTCTGGG F: CAATTTGTCAGCCTCTGTTACC	(GGTT)	50	122-146	12
Tch16	R: TGCTGACCTGATGATTGG F: GCCCATCGTTCTATTCTC	(GTCT)	54	86-98	5

Decision taken to avoid technical problems:

Because condition can change in a laboratory and influences the migration rate of the alleles, we decided

1) to use a control fish in each microsatellite gel in order to avoid migration rate change. The DNA of this fish will be amplified and scored with each single PCR. The allele size of this fish will be known and used as a standard. This will help us to determine whether any problems occur during the PCR or during the migration process on a microsatellite gel.

2) to use internal markers composed of several individuals for which the size of the alleles will be known. This will avoid any ladder and migration problem during the running of a microsatellite gel.

Objective for the meeting of May 2003:

We decided that all the protocols and techniques used in the laboratories should run as a routine before the annual meeting planned in May 2003 in Iceland. Each partner (DIFRES & MRI) should then be able to bring results on the new control group we chose (30 individuals). The comparison of the genotypes of this new control group will be done through email between Dorte Meldrup and Christophe Pampoulie. The matrix and the correction for the new microsatellite loci should be finished around April. Each partner should then be able to start the mass screening and to present some results before the annual meeting. If no problems are detected for this new control group, then mass screening will be officially optimised and protocols will be established.

Appendix 3:

METACOD workpackage 11, deliverable 11.1

A Conceptual model of cod metapopulation dynamics, and description of version 1 of a computational model

M Heath, FRS Marine Laboratory, Aberdeen

Introduction

The starting point for the METACOD project is the observation that within the domain of what we regard as being a unit stock of cod for assessment purposes, there are number of discrete spawning locations. On closer investigation, the fish using these sites are found to have distinctively different characteristics in terms of growth, age structure and in some cases genetics. Our hypothesis is that these spawning locations are to a degree isolated from each other such that each reflects a sub-population within the stock, and the stock is in fact a metapopulation. Our objective in devising a model of such a system is to assess the consequences for overall population dynamics of different scenarios for the connections between spawning locations.

The conceptual model

In the model set out here we view the stock as a metapopulation composed of a number of sub-populations. Here, we define a sub-population as being made up of individuals which were all born at the same spawning location, regardless of where they subsequently spawn as adults. Hence we refer to the sub-populations as natal populations.

Each spawning location has a natal population associated with it. Fish from other natal populations may spawn there, but their offspring then belong to the 'local' natal population for the rest of their lives. The consequences for the overall population dynamics of varying the degree of faithfulness to natal spawning areas is one of the key properties of the model which we shall wish to explore.

We simplify the migration behaviour of fish by specifying that they spend a fixed proportion of each year of mature life in the vicinity of a chosen spawning location, and the remainder of the year feeding elsewhere. We allow for different rates of fishing mortality at the various spawning locations, but assume that all fish are subject to the same fishing mortality rate during feeding. Thus different natal populations will be potentially exposed to different intensities of exploitation depending on the degree of natal loyalty.

The sustainability of each natal population will depend on the balance between its particular mortality and recruitment rates. In our definition of a sub-population, recruits to each natal population are the survivors from the 'home' spawning location of that natal unit, regardless of the affiliation of the parents. In this iteration of the model we assume that each spawning location has its own self-contained stock-recruitment relationship, where the 'stock' component is all of the eggs produced at a

given location. Note however, that the recruits need not necessarily subsequently spawn at their natal location. This aspect of the model will be a particular area for development since there is a case for assuming that the density dependence inherent in standard stock-recruitment functions acts at the whole stock level, and not at the local spawning unit level, depending on the degree of mixing of early life stages from different locations.

Our conceptual model must accommodate a number of **alternative** scenarios underlying the structure of the metapopulation:

Concerning recruitment:

1. Recruiting fish are completely faithful to their natal spawning population. This may be achieved by some innate memory imprinted in early life, or simply by physical segregation of larvae and juveniles from different spawning locations. The consequences for population dynamics depend on the extent to which stock-recruitment processes are self-contained for each spawning location.

2. Recruiting fish are imperfectly faithful to their natal spawning population. A degree of innate memory imprinted in early life, or physical segregation of larvae and juveniles from different spawning locations means that many fish end up returning to their natal spawning area, but a proportion stray elsewhere and spawn at different locations. In this iteration of the model, straying is completely prescriptive, but an alternative which will be explored later is that straying is density dependent. The implication for population dynamics is a degree of coherence between the recruitment time series of the various sub-units regardless of any systematic spatial differences in early life survival.

3. Recruits to each spawning unit are drawn at random from the pool of pre-recruit juveniles. The consequence of this would be that there should be no genetic differences between sub-units and any phenotypic differences are due purely to environmental exposure.

Concerning adult migrations:

1. Once individuals have recruited to a particular spawning location they continue to return to that location in subsequent years, regardless of their natal origin.

2. Individuals which recruit to non-natal spawning units gravitate back to natal units in subsequent years. Hence the proportion of natal-faithful fish increases with age within a year-class.

The computational model

Structure of the model

In this iteration, we adopt an age-structured cohort approach to specifying the computational model. We define a number (***P***) of age structured sub-populations. Each sub-population contains all fish with the same natal origin (***n***, ***n***=1 to ***P***). At any time, the mature fish in each sub-population will be affiliated to one or more of the spawning locations (***j***, ***j***=1 to ***P***). Thus, ***j***=***n*** indicates fish which are faithful to their natal origin. Juvenile fish are considered to be in a nursery area (***j***=0).

Thus, in a given year (***y***) and month (***m***) each population is composed of numbers of mature and immature individuals (***N***=numbers at the end of each month ***m*** in year ***y***) distributed over a number of annual age classes (***a***) and over the ***j*** adopted spawning areas ($N_{(n,y,m,a,j)}$). The distribution with respect to ***j*** reflects the degree of straying to non-natal spawning areas.

Basic assumptions

We make a number of assumptions in implementing this first iteration of a computational model based on the above concepts:

1. During the feeding period all mature fish are subjected to the same fishing and natural mortality rates regardless of natal origin or past/future affiliation to a spawning location.

2. All immature fish are subjected to the same fishing mortality rate regardless of natal origin or future affiliation to a spawning location.

3. During the spawning period all fish in a particular spawning area are subjected to the same fishing and natural mortality rates. Fishing mortality rates may differ between spawning locations.

4. Fish may change their spawning affiliation on an annual basis.

5. Fish of a particular natal origin retain a characteristic weight and maturity at age profile regardless of their subsequent choice of spawning location.

6. Each spawning location has a self-contained Ricker stock-recruitment relationship. The parameters of the relationship may differ between locations.

Mortality

All fish are subjected to the same natural mortality rate, which varies with age and month ($M_{(a,m)}$). We need to identify the months during which fish are exploited in the spawning areas ($X_{(j,m)}$, ***X***=1 or 0 to signify spawning or feeding respectively), the age-specific fishing mortality rate in each spawning area ($Fs_{(j,y,a)}$), the age-specific fishing morality during the feeding period ($Ff_{(y,a)}$), and the age-specific fishing mortality rate on immature fish ($Fi_{(y,a)}$). The timing of migrations between spawning and feeding areas need not be the same for each spawning area.

The default values of spawning area, feeding and immature fishing mortality rate are the whole stock annual age-specific values averaged over 1990-1999 arising from the STEREO reanalysis of North Sea and west of Scotland cod assessment outputs.

Natural mortality rates are calculated at each time step from the exponential functions of age derived in the STEREO project. Briefly, an exponential function was fitted to the annual age specific predation mortality rates for cod emerging from the North Sea multi-species VPA which were subsequently used as natural mortality rates by the

ICES assessment working group. The specific integral of this function then provides the natural mortality experienced over any given age interval:

$$M_{(a,m)} = ((1.0977/(-0.8685+1))*(a_2^{(-0.8685+1)} - a_1^{(-0.8685+1)})$$

where a_1 and a_2 are the start and end ages of the interval in question, measured in years. So, for age a, to calculate the mortality rate applicable over month m, $a_1=a+((m-1)/12)$ and $a_2=a+(m/12)$.

Growth, maturation and fecundity

For each population, we need to define the mean weight at age at spawning time ($W_{(n,y,a)}$), the proportion mature at age ($Q_{(n,y,a)}$), the sex ratio ($V_{(a)}$), which as default will be 0.5 for all ages, and the parameters of a fecundity-weight relationship.

In this iteration of the model, we define fecundity in terms of total wet weight based on a relationship derived for Icelandic cod in 1996 (STEREO project):
$Fec_{(n,y,a)} = 87.0414 * (W_{(n,y,a)} * 1000 / 1.15)^{1.248}$ where **W**=total weight (kg).

The default weight and maturity at age values are the 1990-1999 average for the combined North Sea and west of Scotland cod stocks, as derived in the STEREO reanalysis of assessment outputs.

Spawning

We shall need to specify a spawning month (m_s). In the middle of that month, the mature females which have adopted each spawning area will shed their annual egg production, calculated as the sum over all natal origins of female fecundity. The model will need to accommodate differences in spawning months between sub-units.

Natural mortality at age between start and mid-point of spawning month m_s is given by

$$Mmid_{(a,ms)} = ((1.0977/(-0.8685+1))*((a+((m_s-1)/12))^{(-0.8685+1)} - (a+((m_s-0.5)/12))^{(-0.8685+1)})$$

And the numbers of spawning female fish of age a in year y for a given spawning location j are given by

$$Nspawning_{(n,y,ms,a,j)} = \exp(\ln(Q_{(n,y,a)}*V_{(a)}*N_{(n,y,ms-1,a,j)}) - Mmid_{(a,ms)} - ((Fs_{(j,y,a)})/12)/2)$$

Population egg production in year y for a given spawning location j, ($EP_{(y,j)}$) is thus:

$$\sum_{n=1}^{n=P} \sum_{a=0}^{a=a_{max}} Nspawning_{(n,y,m_s,a,j)} * Fec_{(n,y,a)}$$

Straying

We shall need to explore a variety of deterministic and stochastic schemes for representing straying. However, each should be based on generating an array ($S_{(n,y,a,j)}$)

which specifies the proportion of mature fish of natal origin ***n*** and age ***a*** which have adopted spawning area ***j*** in year ***y***. Hence, for each combination of ***y***, ***n***, and ***a***,

$$\sum_{j=1}^{j=P} S_{(n,y,a,j)} = 1$$

Recruitment

In a given month each year (m_r), numbers of recruiting individuals age 0 will be assigned to each natal population. Initially, these will all be associated with spawning area j=0 which is considered to be a nursery pool.

A separate stock-recruitment reationship will need to be specified for each spawning area. Each of these will parameterised in terms of the number of survivors relative to the total number of eggs produced in a given spawning area. The natal origin of the recruits will be the area in which they were spawned, regardless of the natal origin of the parents.

For this iteration of the model we have specified a Ricker-type stock recruitment relationship for each spawning location. The default parameter set for each relationship is given by fitting a Ricker curve to the paired values of annual egg production and survivors at the end of August for the combined North Sea and west of Scotland cod stocks, as produced by the reanalysis of ICES assessment outputs conducted during the STEREO project. In this reanalysis, natural mortality rates were revised from those used by the ICES working groups responsible for stock assessments, and year-specific maturity at age data substituted for the time-independent values used by the working groups. Hence, the default number of recruits to natal population ***n*** in year ***y*** was given by:

$$N_{(n,y,m_r,0,0)} = (2.917 * 10^{-5}) * (EP_{(y,n)}) * e^{-(1.1697 * 10^{-11}) * (EP_{(y,n)})}$$

Updating the population

The time step for the simulation is one month. Initial numbers at age corresponding to those on 1 January are loaded into the array $\boldsymbol{N_{(n,y,m,a,j)}}$ with the dimension ***y***=1 and ***m***=0. Then, at each time step, for each natal population and spawning area the numbers of mature and immature individuals present in each age class are reduced according to the appropriate natural mortality rate and fishing mortality rate. Month-specific fishing mortality rates are simply the annual rate divided by 12. Month-specific natural mortality rates are calculated as described earlier. Hence,

For mature fish:

If $\boldsymbol{X_{(j,m)}} = 1$ then $\boldsymbol{Nmature_{(n,y,m,a,j)}} = \exp(\ln(\boldsymbol{Q_{(n,y,a)}} * \boldsymbol{N_{(n,y,m-1,a,j)}}) - \boldsymbol{M_{(a,m)}} - (\boldsymbol{Fs_{(j,y,a)}})/12)$
If $\boldsymbol{X_{(j,m)}} = 0$ then $\boldsymbol{Nmature_{(n,y,m,a,j)}} = \exp(\ln(\boldsymbol{Q_{(n,y,a)}} * \boldsymbol{N_{(n,y,m-1,a,j)}}) - \boldsymbol{M_{(a,m)}} - (\boldsymbol{Ff_{(j,y,a)}})/12)$

For immature fish:

$\boldsymbol{Nimmature_{(n,y,m,a,j)}} = \exp(\ln((1-\boldsymbol{Q_{(n,y,a)}}) * \boldsymbol{N_{(n,y,m-1,a,j)}}) - \boldsymbol{M_{(a,m)}} - (\boldsymbol{Fi_{(j,y,a)}})/12)$

$N_{(n,y,m,a,j)} = Nmature_{(n,y,m,a,j)} = Nimmature_{(n,y,m,a,j)}$

Recruits are introduced in the month m_r specified for this process.

Spawning area affiliations for the coming spawning season need to be assigned in advance of the first appearance of fish in any of the spawning areas, ie. at a time when all fish in the stock are in feeding state. For convenience, this is carried out in month m_r at the same time as recruits are added to the populations.

After 12 months, the simulated numbers in age class a, month m=12 are transferred to age class a+1 and month m=0, to form the initial conditions for the next year of simulation.

Output

For each simulation year, the programme outputs the total numbers of fish at age on 1 January associated with each spawning area, and the total number in each natal population.

Programming

The model outlined above was coded in BASIC for ease of development, and is stored in the file METAFOR.BAS

Initial data and parameters are passed to the model by means of an ASCII file produced by a separate programme – INITIAL.BAS

Having established the basic principle of the model, the next phase will be to thoroughly discuss the concepts amongst the project partners. This will lead to a second iteration of the model which will probably be recoded in FORTRAN. At this stage, we shall incorporate stochastic properties in order to take account of uncertainty in the parameters of the system.

Appendix 4: Intital Program code

```
'*************************************************************************************************
'Programme INITIAL.BAS to generate initial conditions and forcing data for METAFOR
programme

'M Heath, FRS Marine Laboratory, Aberdeen, SCOTLAND

'Updated:          9 January 2003
'*************************************************************************************************


'WHEREVER YOU SEE the FOLLOWING LINE.....
'#########################################################################
'YOU NEED TO PROVIDE VALUES WHICH WILL CONFIGURE THE METAFOR RUN


'#########################################################################
'Number of spawning sub-units
Nnatal%=3
'#########################################################################


'#########################################################################
'Number of age classes
nAGE%=10
'#########################################################################


'#########################################################################
'Number of simulation years
Nyear%=6
'#########################################################################


Nspawn%=Nnatal%

'Define initial (1 January) numbers at age array for each sub-unit (natal x age x spawing area)
dim dynamic Na!(Nnatal%,nAGE%,Nspawn%)

'Define an array to hold the whole stock numbers at age
dim dynamic Nwhole(nAGE%)

'define an array to hold various scaling factors from time to time - gets reused several times
dim dynamic p(nAGE%)

'Define strays at age array for each sub-unit (unit x year x age x spawing area)
'Spawning area 0 is a nursery pool
dim dynamic S(Nnatal%,Nyear%,nAGE%,Nspawn%)

'Define fishing mortality rate arrays
'Spawning area 0 is a nursery pool
dim dynamic Fs(Nspawn%,Nyear%,nAGE%) : 'Annual fishing mortality rate on matures in
spawing areas
dim dynamic Ff(Nyear%,nAGE%)         : 'Annual fishing mortality rate in feeding phase
dim dynamic Fi(Nyear%,nAGE%)         : 'Annual fishing mortality rate on immatures
dim dynamic WholeF(nAGE%)            : 'Whole stock annual F at age

'Define array to hold migration and spawning timings for each spawning area
dim dynamic z%(Nspawn%,12) : 'Set to 1=in spawning area, 0=feeding

'Define array to hold spawning month for each spawning area
dim dynamic SpawnM%(Nspawn%)
```

```
'Define arrays to store weight and proportion mature at age data for each sub-unit
dim dynamic W(Nnatal%,Nyear%,nAGE%)
dim dynamic Q(Nnatal%,Nyear%,nAGE%)

'-----------------------------------------------------------------------------------------------------------
'START OF DATA SETUP

'First set up the straying array
'We assume that the pattern does not vary with year
'Within each natal class and age class the sum over all spawing areas is 1.0

'#############################################################################
'Set the straying scenario you want to use
Scenario%=3
'#############################################################################

'-------------------------------------------------------------
'Scenario1 - fish are perfectly faithful to their natal area
if Scenario%=1 then
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
for s%=1 to Nspawn%
if n%=s% then
        S(n%,y%,a%,s%)=1
else
        S(n%,y%,a%,s%)=0
end if
next s%
next a%
next n%
next y%
end if
'-------------------------------------------------------------
'Scenario 2 - fish are initially uniformly distributed but gravitate back to natal with age
if Scenario%=2 then
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
for s%=1 to Nspawn%
if a%=1 then S(n%,y%,a%,s%)=1/Nspawn%
if a%=2 then S(n%,y%,a%,s%)=1/Nspawn%
if a%=3 then S(n%,y%,a%,s%)=1/Nspawn%
if a%=4 then
        if n%=s% then S(n%,y%,a%,s%)=0.6
        if n%<>s% then S(n%,y%,a%,s%)=(1-0.6)/(Nspawn%-1)
end if
if a%=5 then
        if n%=s% then S(n%,y%,a%,s%)=0.85
        if n%<>s% then S(n%,y%,a%,s%)=(1-0.85)/(Nspawn%-1)
end if
if a%>=6 then
        if n%=s% then S(n%,y%,a%,s%)=1
        if n%<>s% then S(n%,y%,a%,s%)=0
end if

next s%
next a%
next n%
next y%
end if
```

```
'-------------------------------------------------------------
'Scenario 3 - fish are always uniformly distributed across spawning areas
if Scenario%=3 then
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
for s%=1 to Nspawn%
S(n%,y%,a%,s%)=1/Nspawn%
next s%
next a%
next n%
next y%
end if
'-------------------------------------------------------------

'Now set the initial total numbers at age on 1 January for each natal population

'Using average 1990-1999 North Sea plus West coast cod population, total numbers in the
whole stock
'Taken from the STEREO revised VPA analysis for 1 January
'Nwhole(1)=316928.0824*1000
'Nwhole(2)=138731.1118*1000
'Nwhole(3)=39552.11081*1000
'Nwhole(4)=9197.855936*1000
'Nwhole(5)=2984.800471*1000
'Nwhole(6)=981.1481241*1000
'Nwhole(7)=376.5031553*1000
'Nwhole(8)=122.3334146*1000
'Nwhole(9)=48.02112394*1000
'Nwhole(10)=17.5309294*1000

'Stationary population after 1200 years running with NS+6a weighted average W, maturity and
F
'scaled by 1.084, taken from the STEREO revised VPA analysis for 1 January
Nwhole(1)=366367.3181*1000
Nwhole(2)=148831.3644*1000
Nwhole(3)=39370.01149*1000
Nwhole(4)=8740.611718*1000
Nwhole(5)=2301.290685*1000
Nwhole(6)=697.5076826*1000
Nwhole(7)=220.3897595*1000
Nwhole(8)=65.91782413*1000
Nwhole(9)=20.85628287*1000
Nwhole(10)=6.346897276*1000

'Scale the total numbers to thousands
for ii%=1 to nAGE%
Nwhole(ii%)=Nwhole(ii%)/1000
next ii%
'Now apportion theses across the natal populations assuming constant proportions with age,
' and then across the spawning areas according to the scenario set up in the straying array
'#############################################################################
'Here provide the proportional distribution of the stock across natal units
p(1)=0.1 : p(2)=0.6 : p(3)=0.3
'p(1)=0.33333 : p(2)=0.33333 : p(3)=0.33333
'#############################################################################
for n%=1 to Nnatal%
for a%=1 to nAGE%
for s%=1 to Nspawn%
Na!(n%,a%,s%)=Nwhole(a%)*p(n%)*S(n%,1,a%,s%)
next s%
next a%
```

```
next n%


'Now set up an array of weight at age data
'Using average North Sea weight (kg) at age data for 1990-1999
'W(1,1,0)=0.085
'W(1,1,1)=0.6741
'W(1,1,2)=1.0295
'W(1,1,3)=2.1303
'W(1,1,4)=3.9954
'W(1,1,5)=6.3169
'W(1,1,6)=8.1771
'W(1,1,7)=9.726
'W(1,1,8)=10.8667
'W(1,1,9)=12.3456
'W(1,1,10)=13.3274

'Using numbers weighted average of NS and 6A weight at age for 1990-1999 from STEREO
W(1,1,0)=0.085
W(1,1,1)=0.672788125
W(1,1,2)=1.040281028
W(1,1,3)=2.160393263
W(1,1,4)=4.031281645
W(1,1,5)=6.332338753
W(1,1,6)=8.168985918
W(1,1,7)=9.714629393
W(1,1,8)=10.8667
W(1,1,9)=12.3456
W(1,1,10)=13.3274

'Distribute these uniformly across years and vary slightly between natal units
'###############################################################################
'Here provide the scaling factors for the weight at age in each natal unit
'relative to the whole stock value
'p(1)=1.0 : p(2)=1.1 : p(3)=0.95
p(1)=1.0 : p(2)=1.0 : p(3)=1.0
'###############################################################################
for n%=1 to Nnatal%
for y%=1 to Nyear%
for a%=0 to nAGE%
W(n%,y%,a%)=W(1,1,a%)*p(n%)
next a%
next y%
next n%

'Now set up an array of proportion mature at age data
'Using ICES WG North Sea maturity at age data
'Q(1,1,0)=0
'Q(1,1,1)=0.01
'Q(1,1,2)=0.05
'Q(1,1,3)=0.23
'Q(1,1,4)=0.62
'Q(1,1,5)=0.86
'Q(1,1,6)=1.0
'Q(1,1,7)=1.0
'Q(1,1,8)=1.0
'Q(1,1,9)=1.0
'Q(1,1,10)=1.0

'Using numbers weighted average of NS+6A and variable maturity data
'taken from the STEREO VPA reanalysis and averaged over 1990-1999
Q(1,1,0)=0
```

```
Q(1,1,1)=0.005691557
Q(1,1,2)=0.121047257
Q(1,1,3)=0.406328435
Q(1,1,4)=0.781419314
Q(1,1,5)=0.957266497
Q(1,1,6)=0.979025623
Q(1,1,7)=1.0
Q(1,1,8)=1.0
Q(1,1,9)=1.0
Q(1,1,10)=1.0
'Distribute these uniformly across years and vary slightly between natal units
'#########################################################################
'Here provide the scaling factors for the maturity at age in each natal unit
'relative to the whole stock value
'p(1)=1.0 : p(2)=1.1 : p(3)=0.95
p(1)=1.0 : p(2)=1.0 : p(3)=1.0
'#########################################################################
for n%=1 to Nnatal%
for y%=1 to Nyear%
for a%=0 to nAGE%
Q(n%,y%,a%)=Q(1,1,a%)*p(n%)
if a%>=7 then Q(n%,y%,a%)=1.0
if Q(n%,y%,a%)>1.0 then Q(n%,y%,a%)=1.0
next a%
next y%
next n%


'#########################################################################
'Enter an overall scaling factor for fishing mortality - used to adjust the overall level of
'mortality to balance the recruitment generated by the Ricker SR relationship
Fscaling=1.084
'#########################################################################
'Using whole stock annual F, numbers weighted average of NS and 6A from STEREO VPA
reanalysis
WholeF(0)=0
WholeF(1)=0.096129449
WholeF(2)=0.764784026
WholeF(3)=1.045356718
WholeF(4)=0.955931627
WholeF(5)=0.870311472
WholeF(6)=0.863249773
WholeF(7)=0.93726682
WholeF(8)=0.9035801
WholeF(9)=0.9540741
WholeF(10)=0.8767764

'Now set up an array of spawning area fishing mortality rates
'Using scaled average North Sea whole stock F at age data for 1990-1999
'#########################################################################
'Here provide the scaling factors for the whole stock fishing mortality at age
'during spawning relative to the overall annual fishing mortality rate
'p(0)=1.25 : p(1)=1.25 : p(2)=1.25 : p(3)=1.25 : p(4)=1.25 : p(5)=1.25
'p(6)=1.25 : p(7)=1.25 : p(8)=1.25 : p(9)=1.25 : p(10)=1.25
p(0)=1.00 : p(1)=1.00 : p(2)=1.00 : p(3)=1.00 : p(4)=1.00 : p(5)=1.00
p(6)=1.00 : p(7)=1.00 : p(8)=1.00 : p(9)=1.00 : p(10)=1.00
'#########################################################################
for aa%=0 to nAGE%
Fs(1,1,aa%)=WholeF(aa%)*p(aa%)*Fscaling
next aa%
'Distribute these uniformly across years and vary slightly between spawning areas
'#########################################################################
```

```
'Here provide the scaling factors for the Fishing mortality at age in each spawning area
'relative to the whole stock value
'p(1)=1.0 : p(2)=1.1 : p(3)=0.9
p(1)=1.0 : p(2)=1.0 : p(3)=1.0
'#########################################################################
for s%=1 to Nspawn%
for y%=1 to Nyear%
for a%=0 to nAGE%
Fs(s%,y%,a%)=Fs(1,1,a%)*p(s%)
next a%
next y%
next s%

'Now set up an array of feeding phase fishing mortality rates
'Using scaled average North Sea whole stock F at age data for 1990-1999
'#########################################################################
'Here provide the scaling factors for the whole stock fishing mortality at age
'during feeding relative to the overall annual fishing mortality rate
'p(0)=0.9 : p(1)=0.9 : p(2)=0.9 : p(3)=0.9 : p(4)=0.9 : p(5)=0.9
'p(6)=0.9 : p(7)=0.9 : p(8)=0.9 : p(9)=0.9 : p(10)=0.9
p(0)=1.00 : p(1)=1.00 : p(2)=1.00 : p(3)=1.00 : p(4)=1.00 : p(5)=1.00
p(6)=1.00 : p(7)=1.00 : p(8)=1.00 : p(9)=1.00 : p(10)=1.00
'#########################################################################
for aa%=0 to nAGE%
Ff(1,aa%)=WholeF(aa%)*p(aa%)*Fscaling
next aa%
'Distribute these uniformly across years
for y%=1 to Nyear%
for a%=0 to nAGE%
Ff(y%,a%)=Ff(1,a%)
next a%
next y%

'Now set up an array of immature fishing mortality rates
'Using scaled average North Sea whole stock F at age data for 1990-1999
'#########################################################################
'Here provide the scaling factors for the whole stock fishing mortality at age
'during immature period relative to the overall annual fishing mortality rate
'p(0)=1.0 : p(1)=1.0 : p(2)=0.9 : p(3)=0.8 : p(4)=0.7 : p(5)=0.7
'p(6)=0.7 : p(7)=0.7 : p(8)=0.7 : p(9)=0.7 : p(10)=0.7
p(0)=1.00 : p(1)=1.00 : p(2)=1.00 : p(3)=1.00 : p(4)=1.00 : p(5)=1.00
p(6)=1.00 : p(7)=1.00 : p(8)=1.00 : p(9)=1.00 : p(10)=1.00
'#########################################################################
for aa%=0 to nAGE%
Fi(1,aa%)=WholeF(aa%)*p(aa%)*Fscaling
next aa%
'Distribute these uniformly across years
for y%=1 to Nyear%
for a%=0 to nAGE%
Fi(y%,a%)=Fi(1,a%)
next a%
next y%

'Define the migration patterns of fish using the various spawning areas
'Assume uniform across spawning areas
'Set to 1=in spawning area, 0=feeding
z%(1,1)=1
z%(1,2)=1
z%(1,3)=1
z%(1,4)=1
z%(1,5)=0
z%(1,6)=0
```

```
z%(1,7)=0
z%(1,8)=0
z%(1,9)=0
z%(1,10)=0
z%(1,11)=0
z%(1,12)=0
for s%=1 to Nspawn%
for m%=1 to 12
z%(s%,m%)=z%(1,m%)
next m%
next s%

'Set the spawning month for each spawning area
SpawnM%(1)=3
SpawnM%(2)=3
SpawnM%(3)=3



'-------------------------------------------------------------------------------------------------


'AND finally to output the data to a file which will be read into METAFOR
dr$="c:\d\d\EUproj~1\METACOD\Fmodel\"
Open dr$+"Modelpar.dat" for output as #1

print""


'Output a header and the basic info on number of years to simulate, number of populations
'and number of age classes
print#1,"Initial_conditions_and_parameter_file_for_METAFOR.BAS"
print#1,"Number_of_simulation years"
print#1,Nyear%
print#1,"Number_of_populations"
print#1,Nnatal%
print#1,"Number_of_age_classes"
print#1,nAGE%

print#1,"Initial_numbers-at-age_data (thousands)"
print "Writing Initial_numbers-at-age_data"
'Output the initial numbers at age - list by natal area, spawning area and age
for n%=1 to Nnatal%
for s%=1 to Nspawn%
for a%=1 to nAGE%
print#1,Na!(n%,a%,s%)
next a%
next s%
next n%

print#1,"Straying_array"
print "Writing Straying_array"
'Output the straying array - list by year, natal area, spawning area and age
for y%=1 to Nyear%
for n%=1 to Nnatal%
for s%=1 to Nspawn%
for a%=1 to nAGE%
print#1,S(n%,y%,a%,s%)
next a%
next s%
next n%
next y%
```

```
print#1,"Fishing_mortality_in_spawning_areas"
print "Writing Fishing_mortality_in_spawning_areas"
'Output the spawning area F - list by year, spawning area and age
for y%=1 to Nyear%
for s%=1 to Nspawn%
for a%=1 to nAGE%
print#1,Fs(s%,y%,a%)
next a%
next s%
next y%

print#1,"Fishing_mortality_during_feeding"
print "Writing Fishing_mortality_during_feeding"
'Output the feeding area F - list by year and age
for y%=1 to Nyear%
for a%=1 to nAGE%
print#1,Ff(y%,a%)
next a%
next y%

print#1,"Fishing_mortality_on_immatures"
print "Writing Fishing_mortality_on_immatures"
'Output the immature F - list by year and age
for y%=1 to Nyear%
for a%=1 to nAGE%
print#1,Fi(y%,a%)
next a%
next y%

print#1,"Weight_at_age_data"
print "Writing Weight_at_age_data"
'Output the weight at age data - list by year, natal area and age
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
print#1,W(n%,y%,a%)
next a%
next n%
next y%

print#1,"Maturity_at_age_data"
print "Writing Maturity_at_age_data"
'Output the proportion mature at age data - list by year, natal area and age
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
print#1,Q(n%,y%,a%)
next a%
next n%
next y%

print#1,"Migration_pattern"
print "Writing Migration_pattern"
'Output the migration pattern - list by spawning area and month
for s%=1 to Nspawn%
for m%=1 to 12
print#1,z%(s%,m%)
next m%
next s%

print#1,"Spawning_months"
```

```
print "Writing Spawning_months"
'Output the spawning month - list by spawning area
for s%=1 to Nspawn%
print#1,SpawnM%(s%)
next s%

print "Finished writing data"

close(1)

end
```

Appendix 5: METAFOR Program Code

```
'*************************************************************************************************
'Programme METAFOR.BAS Metapopulation stock simulation model for the EU-METACOD project

'M Heath, FRS Marine Laboratory, Aberdeen, SCOTLAND

'Updated:          9 January 2003
'*************************************************************************************************

dr$="c:\d\d\EUproj~1\METACOD\Fmodel\"
Open dr$+"Modelpar.dat" for input as #1
input#1,header$
input#1,dum$
input#1,Nyear%
input#1,dum$
input#1,Nnatal%
input#1,dum$
input#1,nAGE%

'---------------------------------------------------
'Natural mortality is defined by the function:
'M = (Mc/(Mb+1))*(A2^(Mb+1) - A1^(Mb+1))
'For Cod:
Mc=1.0977 : Mb=-0.8685
'Hence for a given month m the mortality rate of age a is:
'(Mc/(Mb+1))*( ((a+(m/12))^(Mb+1)) - ((a+((m-1)/12))^(Mb+1)) )
'---------------------------------------------------
'Fecundity = FecC *(W*1000/GutR)^FecE - from Icelandic cod data 1996 (W=Total Wt in Kg)
GutR=1.15 : FecC=87.0414 : FecE=1.248
'---------------------------------------------------
'Sex ratio - age and area independent
SexR=0.5
'---------------------------------------------------
'Number of spawning sub-units
'Nnatal%=3
Nspawn%=Nnatal%
'---------------------------------------------------
'Number of age classes
'nAGE%=10
'---------------------------------------------------
'Number of simulation years
'Nyear%=8
'---------------------------------------------------
'Parameters of stock-recruit relationships (Ricker)
'Recruits = Ra * (TotEggs/1000) * exp(-Rb*TotEggs/1000)
dim dynamic Ra(Nspawn%)
dim dynamic Rb(Nspawn%)
Ra(1)=2.917e-2
Rb(1)=1.1697e-8
Ra(2)=2.917e-2
Rb(2)=1.1697e-8
Ra(3)=2.917e-2
Rb(3)=1.1697e-8
'---------------------------------------------------
'Recruitment month
Rmonth%=8
'---------------------------------------------------
```

```
'Define numbers at age array for each sub-unit (year x month x age x spawing area)
'Month=0 holds the initial conditions for a given year - ie. input at start or transfer from end of
previous year
dim dynamic Na!(Nnatal%,Nyear%,12,nAGE%,Nspawn%)

'Define array to hold egg production from each sub-unit x spawning area
dim dynamic Eggs(Nnatal%,nAGE%,Nspawn%)

'Define strays at age array for each sub-unit (unit x year x age x spawing area)
'Spawning area 0 is a nursery pool
dim dynamic S(Nnatal%,Nyear%,nAGE%,Nspawn%)

'Define fishing mortality rate arrays
'Spawning area 0 is a nursery pool
dim dynamic Fs(Nspawn%,Nyear%,nAGE%) : 'Annual fishing mortality rate on matures in
spawing areas
dim dynamic Ff(Nyear%,nAGE%)         : 'Annual fishing mortality rate in feeding phase
dim dynamic Fi(Nyear%,nAGE%)         : 'Annual fishing mortality rate on immatures

'Define array to hold migration and spawning timings for each spawning area
dim dynamic z%(Nspawn%,12) : 'Set to 1=in spawning area, 0=feeding

'Define array to hold spawning month for each spawning area
dim dynamic SpawnM%(Nspawn%)

'Define arrays to store weight and proportion mature at age data for each sub-unit
dim dynamic W(Nnatal%,Nyear%,nAGE%)
dim dynamic Q(Nnatal%,Nyear%,nAGE%)

'Define array to store number of recruits from each spawning area
dim dynamic Recruits(Nspawn%)

'Define array to store number of eggs produced in each spawning area
dim dynamic TotEggs(Nspawn%)

'Define a couple of temporary storage arrays
dim dynamic Temp(Nnatal%)
dim dynamic Nimm(Nnatal%)
dim dynamic Nimmx(Nnatal%)
dim dynamic Nmat(Nnatal%)
dim dynamic Nmatx(Nnatal%)
dim dynamic Nspawn(Nnatal%)


'-------------------------------------------------------------
'START INPUT INITIAL CONDITIONS AND FORCING DATA

'Input initial numbers at age data
input#1,dum$
print "Reading ";dum$
for n%=1 to Nnatal%
for s%=1 to Nspawn%
for a%=1 to nAGE%
input#1,Na!(n%,1,0,a%,s%)
next a%
next s%
next n%

'Input straying array data
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
```

```
for n%=1 to Nnatal%
for s%=1 to Nspawn%
for a%=1 to nAGE%
input#1,S(n%,y%,a%,s%)
next a%
next s%
next n%
next y%

'Input spawning area F
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
for s%=1 to Nspawn%
for a%=1 to nAGE%
input#1,Fs(s%,y%,a%)
next a%
next s%
next y%

'Input feeding area F
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
for a%=1 to nAGE%
input#1,Ff(y%,a%)
next a%
next y%

'Input immature F
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
for a%=1 to nAGE%
input#1,Fi(y%,a%)
next a%
next y%

'Input weight at age data
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
input#1,W(n%,y%,a%)
next a%
next n%
next y%

'Input proportion mature at age data
input#1,dum$
print "Reading ";dum$
for y%=1 to Nyear%
for n%=1 to Nnatal%
for a%=1 to nAGE%
input#1,Q(n%,y%,a%)
next a%
next n%
next y%

'Input the migration pattern
input#1,dum$
```

```
print "Reading ";dum$
for s%=1 to Nspawn%
for m%=1 to 12
input#1,z%(s%,m%)
next m%
next s%

'Input the spawning month list
input#1,dum$
print "Reading ";dum$
for s%=1 to Nspawn%
Input#1,SpawnM%(s%)
next s%

Print "Finished reading input data"

close(1)

'FINISH INPUT OF INITIAL CONDITIONS AND FORCING DATA
'---------------------------------------------------------------
FOR Y%=1 to Nyear%

  FOR M%=1 to 12

        'Check whether this is a recruitment month and if so calculate recruits and add them
to the data set
        'and then reassign the spawning associations for each natal stock using the straying
array
        if M%=Rmonth% then
        'Clear the Egg production array
                FOR jj%=1 to Nspawn%
                TotEggs(jj%)=0
                NEXT jj%
        'Sum the egg production at age from the previous spawning month
                FOR jj%=1 to Nspawn%
                FOR kk%=1 to Nnatal%
                FOR ii%=0 to nAGE%
                TotEggs(jj%)=TotEggs(jj%)+Eggs(kk%,ii%,jj%)
                NEXT ii%
                NEXT kk%
                NEXT jj%
        'Calculate numbers of recruits using the spawning area specific S-R relationship
                FOR jj%=1 to Nspawn%
                Recruits(jj%)=Ra(jj%)*(TotEggs(jj%)/1000)*exp(-
1*(Rb(jj%)*TotEggs(jj%)/1000))
                NEXT jj%
        'These recruits then become natal to their spawning area and associated with the
nursery pool j%=0
                for n%=1 to Nnatal%
                Na!(n%,Y%,m%,0,0)=Recruits(n%)
                next n%


        'Finally, reassign the spawning associations for the coming season for each natal
population.
                'This only works if ALL fish are subject to the same feeding pHase F at age
when the
                'reassignment takes place.
                'First sum over spawning areas for each age class of each natal population
                IF Y%<Nyear% then
                FOR aa%=0 to nAGE%-1
                        for nn%=1 to Nnatal%
```

```
                    Temp(nn%)=0
                    next nn%
                for jj%=0 to Nspawn%
                for nn%=1 to Nnatal%
                Temp(nn%)=Temp(nn%)+Na!(nn%,y%,m%,aa%,jj%)
                next nn%
                next jj%
                'Now reallocate this total according to the stray distribution for age aa%+1 and
year y%+1
                for jj%=0 to Nspawn%
                for nn%=1 to Nnatal%
                Na!(nn%,y%,m%,aa%,jj%)=Temp(nn%)*S(nn%,y%+1,aa%+1,jj%)
                next nn%
                next jj%
                next aa%
                end if


        end if


  FOR j%=0 to Nspawn%

   FOR A%=0 to nAGE%

        'Check whether mature fish are in the spawning area j% or feeding, and assign fishing
mortality value
        if z%(j%,M%)=1 then Fmat=Fs(j%,Y%,A%)/12
        if z%(j%,m%)=0 then Fmat=Ff(Y%,A%)/12
        if j%=0 then Fmat=0
        Fimm=Fi(Y%,A%)/12

        'Calculate natural mortality rate for this age and month
        NatMat = (Mc/(Mb+1))*( ((A%+(M%/12))^(Mb+1)) - ((A%+((M%-1)/12))^(Mb+1)) )

        if M%<=Rmonth% and A%=0 then goto Skip1
        'For each natal population - Calculate numbers at age for this age, spawning area,
month and year
        for nn%=1 to Nnatal%
        'Previous month Immature numbers at age
        Nimm(nn%)=(Na!(nn%,Y%,m%-1,A%,j%))*(1-(Q(nn%,Y%,A%)))
        'Previous month Mature numbers at age
        Nmat(nn%)=(Na!(nn%,Y%,m%-1,A%,j%))*(Q(nn%,Y%,A%))
        'Apply mortality rates
        Nimmx(nn%)=0 : Nmatx(nn%)=0
        if Nimm(nn%)>0 then Nimmx(nn%)=exp(log(Nimm(nn%))-(Fimm)-(NatMat))
        if Nmat(nn%)>0 then Nmatx(nn%)=exp(log(Nmat(nn%))-(Fmat)-(NatMat))
        Na!(nn%,Y%,m%,A%,j%)=Nimmx(nn%)+Nmatx(nn%)
        next nn%
        Skip1:

        if j%=0 or A%=0 then goto Skip2
        'Check whether this is a spawning month and if so calculate egg production using
mature numbers at mid month
        if M%=SpawnM%(j%) then
        NatMatMid = (Mc/(Mb+1))*( ((A%+((M%-0.5)/12))^(Mb+1)) - ((A%+((M%-
1)/12))^(Mb+1)) )

        for nn%=1 to Nnatal%
        'Previous month Mature numbers at age
        Nmat(nn%)=(Na!(nn%,Y%,m%-1,A%,j%))*(Q(nn%,Y%,A%))
        if Nmat(nn%)>0 then
```

```
                Nspawn(nn%)=exp(log(Nmat(nn%))-(Fmat/2)-(NatMatMid))
        else
                Nspawn(nn%)=0
        end if
        Eggs(nn%,A%,j%)=Nspawn(nn%)*SexR*FecC*((W(nn%,y%,a%)*1000/GutR)^FecE)
        next nn%
        end if
        Skip2:

NEXT A%

NEXT j%

NEXT M%

        'Transfer population at end of month 12 into the initial conditions for the next year
        'incrementing age by 1 of course
        if y%<Nyear% then
        for aa%=0 to nAGE%-1
        for jj%=0 to Nspawn%
        for nn%=1 to Nnatal%
        Na!(nn%,y%+1,0,aa%+1,jj%)=Na!(nn%,y%,12,aa%,jj%)
        next nn%
        next jj%
        next aa%
        end if

NEXT Y%

open dr$+"Foutput.csv" for output as #1

'Sum over spawning areas.....
print#1,"Sums over spawning areas"
print#1,""
for j%=1 to Nspawn%
for A%=1 to nAGE%
print A%;
print#1, A%;
for Y%=1 to Nyear%
print ",";
print#1,",";
Areasum=0
for nn%=1 to Nnatal%
Areasum=Areasum+Na!(nn%,Y%,0,A%,j%)
next nn%
print Areasum;
print#1, Areasum;
next Y%
print""
print#1,""
next a%
print""
print#1,""
next j%

'Sum over natal units.....
print#1,"Sums over natal units"
print#1,""
for nn%=1 to Nnatal%
for A%=1 to nAGE%
print A%;
print#1, A%;
```

```
for Y%=1 to Nyear%
print ",";
print#1,",";
Areasum=0
for j%=1 to Nspawn%
Areasum=Areasum+Na!(nn%,Y%,0,A%,j%)
next j%
print Areasum;
print#1, Areasum;
next Y%
print""
print#1,""
next a%
print""
print#1,""
next nn%

close(1)

end
```

Appendix 6:

METACOD workpackage 12, deliverable 12.1

First experiments with the METAFOR model

M Heath, FRS Marine Laboratory, Aberdeen

The first task to be performed with the METAFOR model was to explore its dynamics under the simplest possible test conditions. To do this, the system was set up with

- 3 natal sub-populations,
- identical weight and maturity at age profiles for each sub-population (Table 1),
- identical fishing mortality rate at age in each spawning areas, and during spawning, feeding and immature phases – *i.e.* the default rate was used thoughout (Table 1),
- identical stock-recruitment parameters for each spawning area.

After initial investigation it was decided to run these tests in deterministic mode rather than complicate the issues by implementing bootstrap procedures.

Initial numbers at age were taken from the STEREO reanalysis of ICES assessment working group outputs for North Sea and west of Scotland cod stocks. The numbers at age on 1 January for the combined stocks were averaged over the years 1990-1999 (corresponding to the averaging period for weight, maturity and fishing mortality data). These data (Table 1) were then used to set up the initial whole stock numbers at age in the METAFOR model. For the first runs of the model, these numbers were then distributed evenly across the three natal sub-populations, ie. one third to each population.

Table 1. *Configuration and initial conditions, averaged over 1990-1999 from the STEREO reanalysis.*

Age	Weight (kg)	Proportion mature	Initial whole stock numbers at age (thousands)	Whole stock annual fishing mortality rate
0	0.085	0		0
1	0.673	0.006	316928.082	0.096
2	1.040	0.121	138731.112	0.765
3	2.160	0.406	39552.111	1.045
4	4.031	0.781	9197.856	0.956
5	6.332	0.957	2984.800	0.870
6	8.169	0.979	981.148	0.863
7	9.715	1.000	376.503	0.937
8	10.867	1.000	122.333	0.905
9	12.346	1.000	48.0211	0.954
10	13.327	1.000	17.531	0.877

Three contrasting straying scenarios were devised to test the model performance:

Scenario 1: all fish remain 100% faithful to their natal spawning area throughout their life.

Scenario 2: up to age 3 fish in each natal population are uniformly distributed with respect to spawning area *i.e.* one third of the fish in each natal population are affiliated to each spawning area. Between ages 4 and 6 the fish gravitate to their natal spawning area so that from age 6 onwards all fish are 100% faithful.

Scenario 3: the fish in each natal population remain uniformly distributed across spawning areas throughout their life.

Case 1: Basic test results

Because the fishing mortality rates are applied uniformly across the sub-populations and the initial populations are set equal, the expectation was that:

- all the natal sub-populations would follow the same numbers at age trajectory over time, regardless of the straying scenario,
- the numbers at age affiliated to each spawning area should equal the numbers at age in each natal population,

These expectations were realised by the results, indicating that the coding correctly represented the conceptual model. However, the simulated population was not stationary over time *i.e*. the simulated numbers at age were not constant, but increased and eventually attained a stationary state at higher numbers than the initial conditions.

The lack of stationarity indicated that the annual recruitment rate implied by the combination of Ricker parameters and initial numbers at age, maturity and weight data, was less than the annual loss rate implied by the sum of natural and fishing mortality rates. To test this, a scaling factor was applied to the fishing mortality at age values. The population state was summarised by outputting the mature biomass on 1 January each year. As the scaling factor was increased, so the mature biomass of the final stationary population decreased (Figure 1). However, beyond a scaling factor of 1.09 the population declined to extinction.

It was clearly necessary for further testing of the model to supply initial numbers at age which were consistent with the whole population mortality rate. Thus, the model was run for 1200 years with straying scenario 1 and a fishing mortality scaling factor of 1.084. With this scaling factor, the population underwent a series of damped oscillations with decreasing amplitude over time, eventually settling to a mature biomass which was close to the initial conditions. After 1200 simulation years the amplitude was less than 0.001% of the 20 year average value. Comparison of the stationary population numbers at age and the initial population showed that the latter had higher numbers in the oldest age classes and fewer in the youngest (Figure 2). The average numbers at age over the final 20 years of the long-term simulation were then taken as initial conditions for future runs of the model. These are referred to as the "acclimatised initial conditions". Restarting the model with acclimatised initial conditions produced a stationary population throughout the run, regardless of straying scenario.

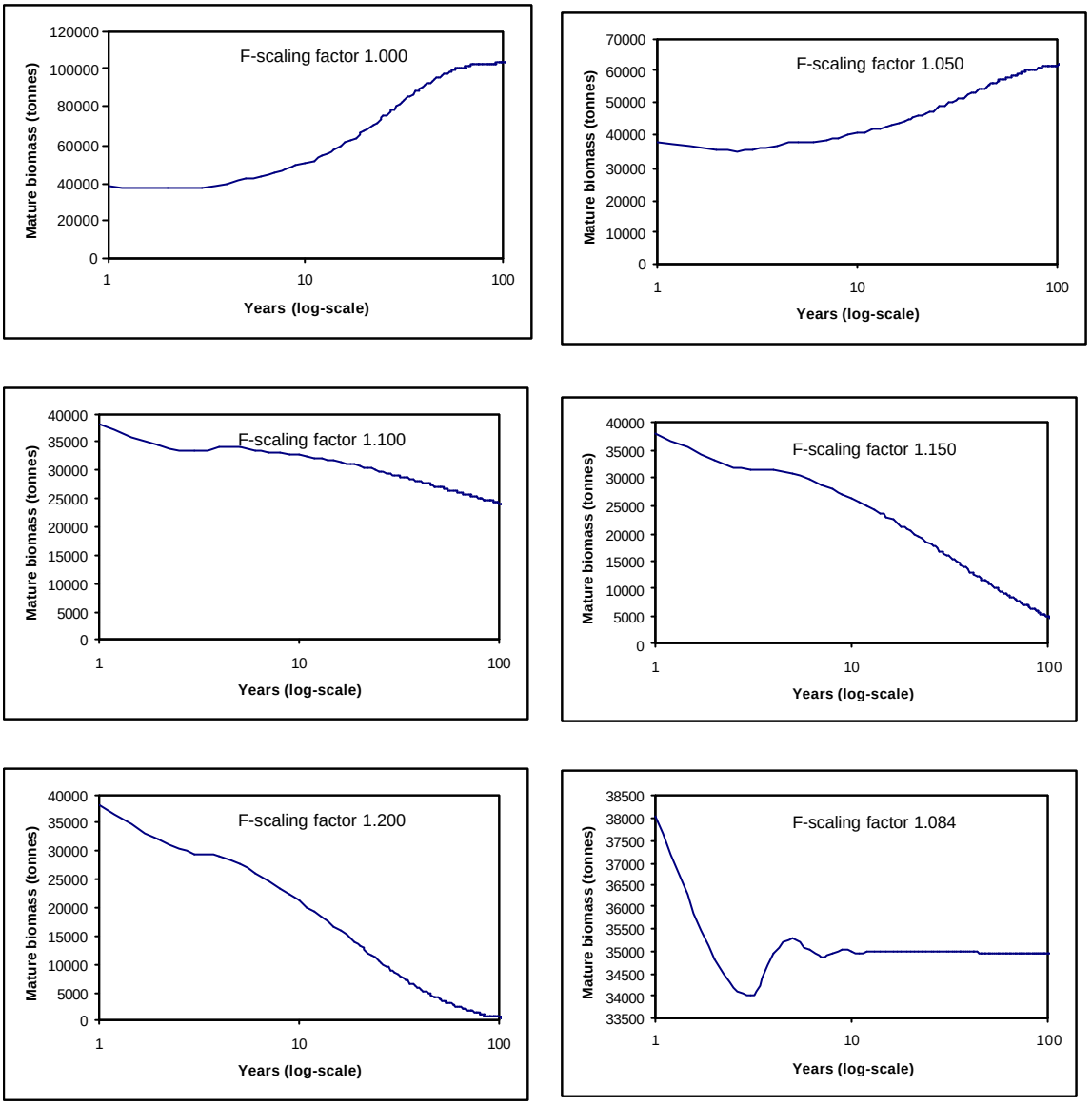

Figure 1. *Trajectories of simulated sub-population mature biomass for different values of the fishing mortality scaling factor. Simulations carried out with straying scenario 1 and initial whole stock numbers at age from the STEREO reanalysis.*

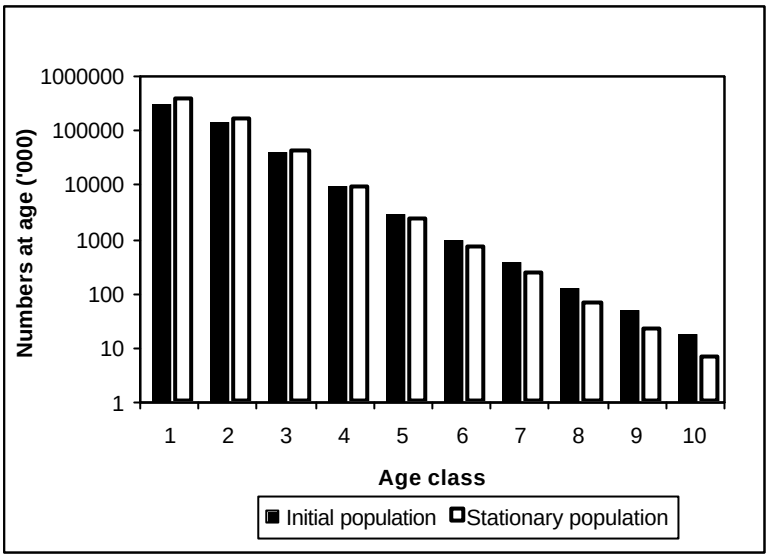

Figure 2. *Comparison of whole population numbers at age in the initial conditions derived from the STEREO reanalysis, and the average over the final 20 years in the near-stationary population after 1200 simulation years with an F-scaling factor of 1.084.*

Case 2: Effects of varying the size of the natal populations .

In the next set of runs, the acclimatised initial whole population numbers at age were unevenly distributed across the natal populations, in the proportions 10%, 60%, 30%, and the model run with each of the three straying scenarios. The F-scaling factor of 1.084 established in case 1 was retained for case 2.

Since the recruitment and mortality parameters remained the same across the entire stock, the expectation was that the differences in initial numbers and biomass between the natal populations would gradually be eroded and that all three sub-populations would eventually equilibrate.

With straying scenario 1 (100% faithful to natal spawning areas), the numbers and biomass in each natal population equalled the numbers and biomass affiliated to each spawning area throughout the model run. Initial differences between the populations decayed only slowly (Figure 3). However, the whole stock mature biomass declined during the run indicating that the population as a whole was no longer stationary.

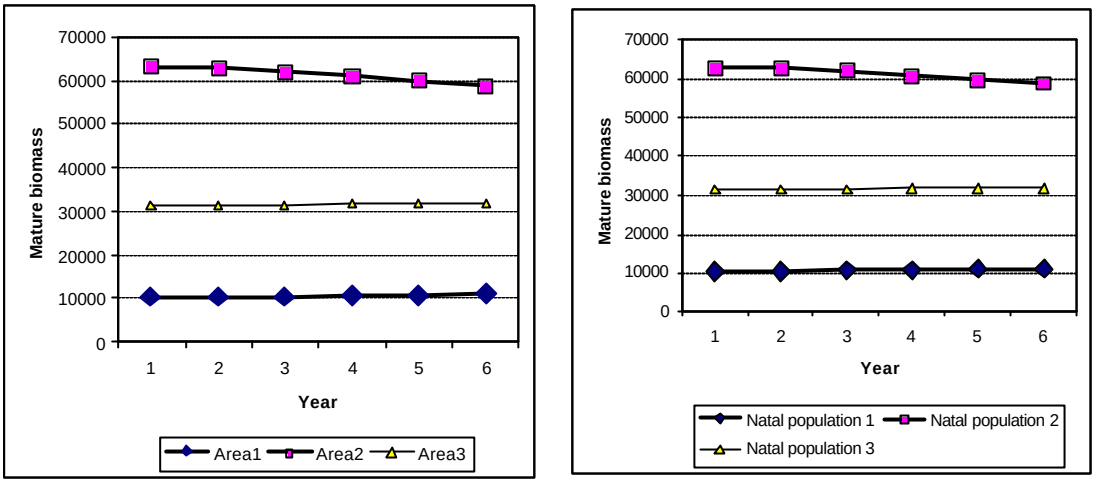

Figure 3. *Simulated changes in mature biomass a) affiliated to each spawning area, and b) in each natal population for case 2, straying scenario 1.*

With straying scenario 2 (fish gravitate back to natal spawning areas beyond age 4), natal population biomass was not the same as the biomass associated with corresponding spawning areas. Biomass affiliated to each spawning area rapidly equilibrated within 6 years. Differences in biomass between natal populations decayed more slowly (Figure 4), but very much quicker than with straying scenario 1. Whole stock mature biomass decline slightly during the run but less than with scenario 1.

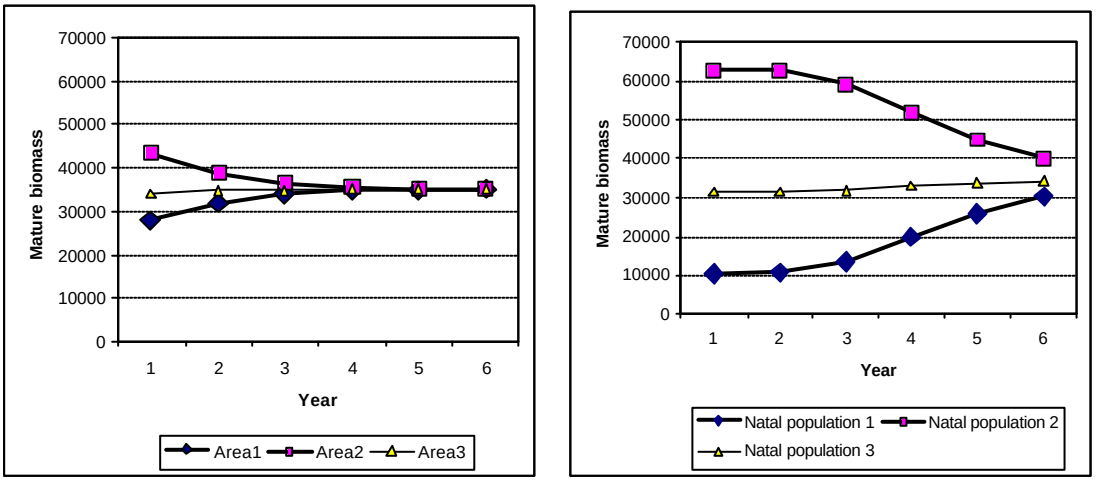

Figure 4. *Simulated changes in mature biomass a) affiliated to each spawning area, and b) in each natal population for case 2, straying scenario 2.*

With straying scenario 3 (fish distribute evenly across spawing areas), the biomass affiliated to each spawning area was the same in the initial conditions and remained so throughout the run. Differences in biomass between natal populations decayed away slightly quicker than with straying scenario 2 (Figure 5). Whole stock mature biomass remained constant throughout the run.

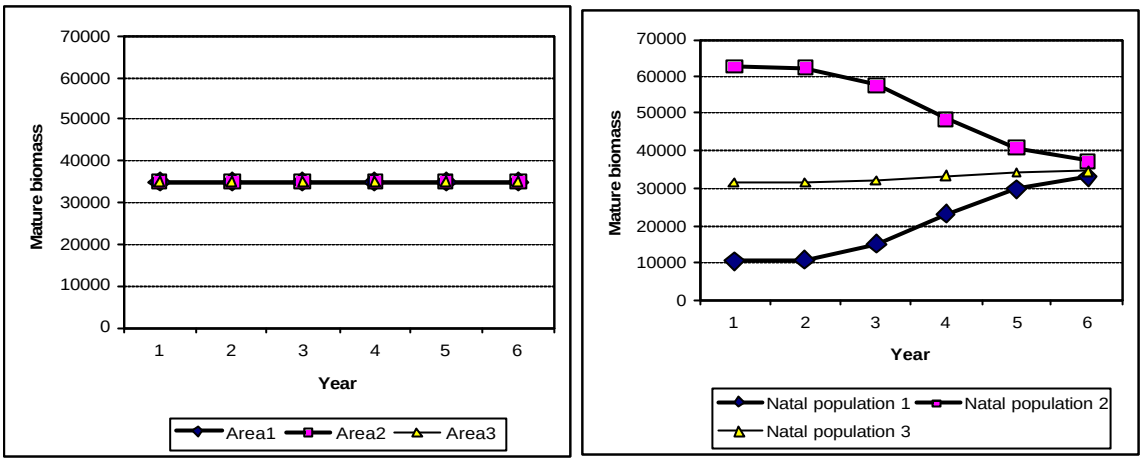

Figure 5. *Simulated changes in mature biomass a) affiliated to each spawning area, and b) in each natal population for case 2, straying scenario 3.*

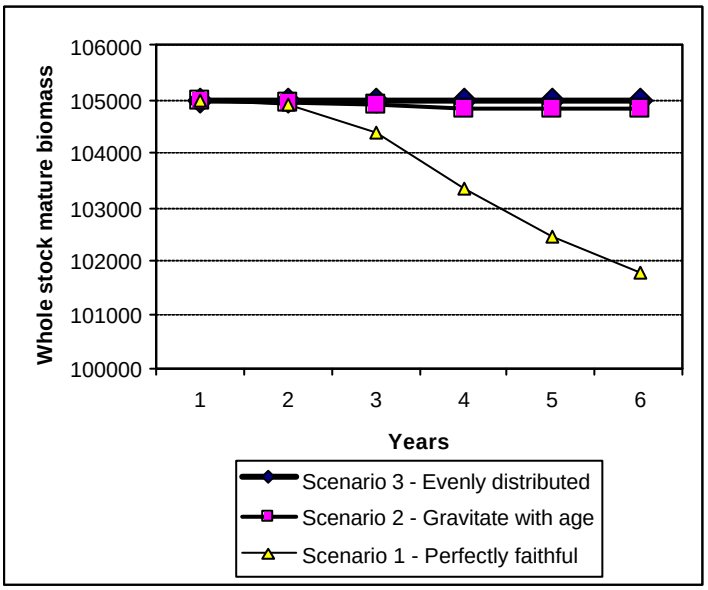

Figure 6. *Simulated changes in whole stock mature biomass for case 2 runs with different straying scenarios.*

Conclusions

The results from these very simple configurations of the model illustrate some important points which will need to be considered for further development, and which should focus the research activity.

1. Case 1 runs with acclimatised initial conditions produced stationary results at the whole stock level, but this was not true for all case 2 runs with the same whole-stock initial conditions and mortality rates (Figure 6). The sole difference between case 1 and case 2 was the initial distribution of the whole stock across natal populations. The key to this result lies in the way that stock-recruit relationships are portrayed in the model. Note that in case 2 with

straying scenario 3, in which the initial numbers affiliated to each spawning area were equal, the simulated whole stock mature biomass was stationary. However, as the natal populations become more tightly bound to individual spawning areas (scenario 1 being the most extreme instance), so the simulations diverge from stationarity. The reason for this effect is that the stock-recruitment relationship is non-linear, and hence the number of recruits per egg declines as the value of egg production increases. Thus, the total number of recruits to the stock as a whole depends on the distribution of egg production across spawning areas.

The above results indicate that we need to focus on considering how stock-recruit relationships at the sub-stock level relate to stock-recruit relationships at the whole population level. In particular, we need to reach an understanding of the level at which density dependence operates in such systems. Most likely, we need to devise a stock-recruitment function which includes both local and global (whole stock) egg production as independent variables.

2. In this iteration of the model, fish are attracted, or not, to a given spawning location solely on the basis of their natal origin. The simple results produced so far show that, under these circumstances, the only way that differences between natal populations and spawning areas can be sustained in the long-term is through consistent differences in stock-recruitment parameters and/or fishing mortality rates. Clearly we need to consider other environmental aspect of spawning areas which may influence their attractiveness to fish and possibly override any innate natal instincts, particularly in response to changes in overall population numbers.

3. Given the complicated nature of the relationship between individual spawning area and whole population stock-recruit relationships outlined in (1) above, we need to consider very carefully the basis for sub-stock structure in weight and maturity at age, since these will influence the egg production per fish at each spawning site.

4. The model is clearly very sensitive to the parameterisation of straying. Straying can rapidly erode any differences in abundance between components of the stock. An important area for investigation will be the extent of sub-stock structure in weight, maturity, mortality or recruitment parameters needed to overcome the eroding effects of straying and maintain sub-stock differences in abundance. In one sense this is encouraging since it means that our research could have a big influence on the understanding of whole-stock population dynamics. However, it is vital that we develop a clear understanding of the patterns of straying and how this may change with age.

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