

## **Fisheries Induced Evolution (FinE)**

**Contract N° GOCE044276**

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**Activity Report No 1**  
01 July 2007 to 31 December 2008

IIASA Contract No. 07-103

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# Executive summary

## ***Project objectives***

Today, fishing is the dominant source of mortality in most commercially exploited fish stocks. According to the United Nation's Food and Agricultural Organization (FAO), world capture fisheries have reached a ceiling, with three stocks out of four being maximally exploited or overexploited. Since all fish species were genetically adapted to the environmental conditions experienced prior to intensive exploitation, the current, drastically altered, conditions cannot possibly leave their life-history patterns unaffected. In other words, fishing not only decreases the abundance of fish, but also changes their genetic composition.

The Specific Targeted Research Project on Fisheries-induced Evolution (FinE) investigates the prevalence of fisheries-induced evolutionary changes in life-history traits of exploited fish stocks in European and North American waters. Phenotypic case studies document trends in life-history traits, including maturation, reproductive effort, and growth, relevant for the demography and productivity of exploited fish populations. Genetic analyses elucidate the genetic basis of fisheries-induced evolutionary changes suggested by phenotypic analysis. Eco-genetic models are designed for evaluating alternative hypotheses explaining the observed data; for assessing the ecological consequences of fisheries-induced evolution for the yield, stability, and recovery potential of exploited stocks; and for developing and comparing practical management options.

The FinE Project (i) unravels the mechanisms of change underlying fisheries-induced evolution, (ii) evaluates their consequences on population and fisheries dynamics, and (iii) provides recommendations for evolutionarily sustainable management. These objectives necessitates the development and application of novel methodological tools for investigating field data both at phenotypic and genetic levels, together with the setup of relevant experiments on model species and the careful construction of theoretical models suitable for complementing field data analyses and for evaluating managerial options. Earlier investigations have focused on specific aspects such as the analysis of long-term trends in phenotypic data, the investigation of temporal changes in neutral genetic markers, artificial fishing experiments, or the modelling of fisheries-induced evolutionary changes in life-history traits and their demographic consequences for exploited stocks. However, a comprehensive investigation of fisheries-induced evolution at the phenotypic and genetic level and of consequences on fish stocks dynamics are still largely missing, mostly because of the wide range of scientific expertises and approaches required for tackling these challenges.

The FinE Project combines fields of expertise as diverse as population genetics and quantitative genetics, life-history theory, population dynamics, evolutionary theory, and fisheries science. The project ensures a close integration of both empirical and theoretical lines of development in our understanding of evolutionary processes in exploited populations. The FinE Project will thereby provide the scientific basis required for designing policies and implementing management measures that can cope with fisheries-induced adaptive changes.

### ***Contractors involved***

<b>Participant number</b>	<b>Participant country</b>	<b>Participant organisation</b>	<b>Participant acronym</b>
1 (coordinator)	Austria	International Institute for Applied Systems Analysis	IIASA
2	Norway	Institute of Marine Research	IMR
3	France	French Research Institute for the Sustainable Exploitation of the Sea	Ifremer
4	Denmark	Danish Institute for Fisheries Research	DIFRES
5	Belgium	Catholic University of Leuven	KUL
6	UK	University of Wales	UW
7	UK	Fisheries Research Services	FRS
8	Norway	University of Tromsø	UT
9	Netherlands	Institute for Marine Resources and Ecosystem Studies	IMARES
10	Norway	University of Oslo	UO
11	Spain	Spanish National Research Council	CSIC
12	Portugal	Portuguese Research Institute for Agriculture and Fisheries	IPIMAR
13	Germany	Federal Research Centre for Fisheries	BFAF

### ***Subcontractors involved***

<b>Subcontractor number</b>	<b>Subcontractor country</b>	<b>Subcontractor organisation</b>	<b>Subcontractor acronym</b>
1	Iceland	University of Iceland	UI
2	Sweden	Swedish Board of Fisheries	SBF
3	Ireland	Central Fisheries Board	MI
4	Finland	Finish Game and Fisheries Research Institute	FGFRI
5	Canada	Fisheries and Oceans Canada	DFO

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***Project logo***



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## Section 1

### Project objectives and major achievements during the reporting period

#### *Overview of general project objectives*

The Specific Targeted Research Project on Fisheries-induced Evolution (FinE) contributes – in the context of the EU Programme on Integrating and Strengthening the European Research Area; Priority 8.1 on Policy-oriented Research; Activity I on Sustainable Management of Europe’s Natural Resources; and Topic 1.3 on Modernisation and Sustainability of Fisheries, including aquaculture-based production systems – to Task 2 on Fisheries-induced Changes in the Adaptive Genetic Potential of Exploited Fish Stocks. Phenotypic case studies document trends in life-history traits, including maturation, reproductive effort, and growth, relevant for the demography and productivity of exploited fish populations. Genetic analyses elucidate the genetic basis of fisheries-induced evolutionary changes suggested by phenotypic analysis. Eco-genetic models are designed for evaluating alternative hypotheses explaining the observed data; for assessing the ecological consequences of fisheries-induced evolution for the yield, stability, and recovery potential of exploited stocks; and for developing and comparing practical management options.

Today, fishing is the dominant source of mortality in most commercially exploited fish stocks. According to the United Nation’s Food and Agricultural Organization (FAO), world capture fisheries have reached a ceiling, with three stocks out of four being maximally exploited or overexploited. Since all fish species were genetically adapted to the environmental conditions experienced prior to intensive exploitation, the current, drastically altered, conditions cannot possibly leave their life-history patterns unaffected. In other words, fishing not only decreases the abundance of fish, but also changes their genetic composition.

The Fisheries-induced Evolution (FinE) Project is set up to investigate the prevalence of fisheries-induced evolutionary changes in life-history traits of exploited fish stocks in European and North American waters. The aims are to unravel the underlying mechanisms of change ranging from the phenotypic to the genetic level, to evaluate their consequences on population and fisheries dynamics, and to provide recommendations for evolutionarily enlightened management. This objective necessitates the development and application of novel methodological tools for investigating field data both at phenotypic and genetic levels, together with the setup of relevant experiments on model species and the careful construction of theoretical models suitable for complementing field data analyses and for evaluating managerial options. Earlier investigations have focused on specific aspects such as the analysis of long-term trends in phenotypic data, the investigation of temporal changes in neutral genetic markers, artificial fishing experiments, or the modelling of fisheries-induced evolutionary changes in life-history traits and their demographic consequences for exploited stocks. However, a comprehensive investigation of fisheries-induced evolution at the phenotypic and genetic level and of consequences on fish stocks dynamics are still largely missing, mostly because of the wide range of scientific expertises and approaches required for tackling these challenges.

The FinE Project combines fields of expertise as diverse as population genetics and quantitative genetics, life-history theory, population dynamics, evolutionary theory, and fish-

eries science. The project ensures a close integration of both empirical and theoretical lines of development in our understanding of evolutionary processes in exploited populations. The FinE Project will thereby provide the scientific basis required for designing policies and implementing management measures that can cope with fisheries-induced adaptive changes.

### ***Objectives for the reporting period***

As foreseen in the project plan, work performed during the first reporting period has unfolded in three dimensions. First, phenotypic case studies have been initiated to document trends in life-history traits relevant the demography and productivity of exploited fish populations. Second, genetic analyses have begun to elucidate the genetic basis of fisheries-induced evolution as revealed by some of the phenotypic case studies. Third, eco-genetic models have been devised for understanding past evolutionary changes observed in exploited stocks, and for predicting the expected impact of alternative management measures in the future dynamics of exploited stocks. The progress made in the various work packages is detailed in Sections 2 and 3 below and has involved all contractors and subcontractors of the network as described in Section 3.

### ***Problems during the reporting period***

Work on the large majority of tasks of the FinE Project is unfolding exactly as initially planned. Exceptions are Tasks 1.1 and 1.2 (analyses complete, publication pending), Task 1.4 (slightly postponed processing of otoliths), Task 1.6 (additional data requirements), and Task 2.4 (recruitment delay).

## Section 2

### Work package progress during the reporting period

#### *Work Package 1: Phenotypic Case Studies*

Start month	0								
Participant acronym	IIASA	IMR	Ifremer	FRS	UT	IMARES	CSIC	IPIMAR	(UI)
Person months per participant	4	23.4	22	14.5	18	9.8	10	4	1
Participant acronym	(SBF)	(MI)	(FGFRI)	(DFO)					
Person months per participant	1	1	1	1					

#### ***Task 1.1 Fisheries-induced changes in Atlantic cod in the Barents Sea***

Lead responsibility: IMR

#### **Objectives of the task for the reporting period**

The aim of this task is to utilize individual life-history measurements collected since 1932 to (1) quantify the changes in age and size at maturation and (2) understand the likely nature of changes in these traits.

#### **Progress towards the objectives**

The data selection and statistical analyses have been completed, and the results have been presented at various meetings.

#### **Deviations from the project's work program and corrective actions**

The deliverable is not yet available as a publication, since this publication is planned to bring together the empirical results obtained under this task with model-based results obtained under Task 3.6. The publication will be submitted once the corresponding model-based analyses are completed.

#### **Deliverables**

D3. Task 1.1: Assessment of evolutionary changes in age and size at maturation in Atlantic cod in the Barents Sea (month 6, IMR, O, PP).

The results of statistical analyses suggest that changes in age and size at maturation in Atlantic cod in the Barents Sea cannot be explained only by demographic changes caused by increased total mortality and phenotypic responses caused by faster individual growth. Thus, the results lend support to the hypotheses that the observed changes in maturation involve an evolutionary component. Results of the statistical analyses are available upon request. They will be published in an article that is planned to bring them together with the model-based results obtained under Task 3.6, which will be submitted once the corresponding model-based analyses are completed.

## Milestones

M1. Task 1.1: Data selection for the final analyses finished (month 2, IMR).

Data selection for the final analyses has been finished. The biological data cover the period 1932–2006 and include 92,693 individual observations.

## ***Task 1.2 Fisheries-induced changes in Atlantic cod in the Northwest Atlantic***

Lead responsibility: IMR

### **Objectives of the task for the reporting period**

The task here is threefold: (1) Utilizing indices of individual body condition, we want to understand the role body reserves (condition) play in the maturation of cod stocks off Newfoundland-Labrador, and whether considering changes in condition alters our conclusions about the likelihood of evolutionary changes; (2) Changes in reproductive effort in cod stocks off Newfoundland-Labrador are documented to test whether the theoretical prediction of increased reproductive effort holds; (3) We will also analyze fisheries-induced changes in maturation of Flemish Cap cod.

### **Progress towards the objectives**

The main analyses have been completed, and the results are reported in papers that have been submitted or are due to be submitted within the next 1–2 months.

### **Deviations from the project's work program and corrective actions**

Publications corresponding to deliverables D4 and D8 are not yet finished, although the results are essentially ready and have been presented at meetings. The papers are under final polishing and will be completed and submitted within next 1–2 months.

## **Deliverables**

D4. Task 1.2: Refined understanding of evolutionary changes in age and size at maturation in Atlantic cod off Labrador-Newfoundland through analysis of effects of body condition to maturation (month 6, IMR, O, PP).

We have analyzed data from three stocks, covering the time period until year 2008. The main results are as follows. (1) The interpretation that maturation changes in the study populations have an evolutionary component is unaltered by the inclusion of body condition in the analysis. (2) The tentative signs of evolutionary recovery in the data covering the time period until the year 2002 are not supported by the data with extended temporal coverage.

D8. Task 1.2: Assessment of evolutionary changes in reproductive effort in Atlantic cod off Labrador-Newfoundland (month 9, IMR, O, PP).

We have analyzed data from three stocks, covering the time period 1978–2007. Results suggest significant positive trends in males (1–2% annual increase in relative gonad

weight), while trends in females are weaker (0–1%) and generally not significant. This difference might stem from greater changes in female gonad weight during the spawning season compared to males. In males, there are signs that the positive trends have tapered off after the fishing pressure was decreased in the early 1990s.

D15. Task 1.2: Assessment of evolutionary changes in age and size at maturation in Flemish Cap Atlantic cod (month 15, CSIC, O, PP).

The evolution of PMRNs throughout the cohorts from 1977 to 2005 shows an important decreasing trend in length and age at maturation throughout this period. Moreover, changes in the growth rates of Flemish Cap cod together with fishing-mortality shifts and alterations in ecosystem structure were observed. This permits us to advance the hypothesis that genetic changes have occurred during the period of high fishing pressure at the end of the 1980s and beginning of the 1990s. This work was presented in the ‘Evolving Fish, Changing Fisheries symposium,’ of the 2008 American Fisheries Society (AFS) Congress, in Ottawa, Canada, August 17-21, 2008.

D16. Task 1.2: Comparison of maturation reaction norm estimation methods with and without distinguishing recruit and repeat spawners utilizing histological data from Flemish Cap Atlantic cod (month 15, CSIC, O, PP).

The estimation of probabilistic maturation reaction norms (PMRNs) through the so-called direct method is preferable, since calculations are based on observations of immature individuals and recruit spawners. In contrast, the so-called demographic method for PMRN estimation uses observations of recruit and repeat spawners lumped together, which requires making assumptions about equal growth and mortality rates for immature and mature individuals. Results obtained from the comparison of both methods show that both methods produce comparable results, with a correlation coefficient of 0.93. These results therefore support the idea that a potential violation of the assumptions made for applying the demographic method is not influential for the results. A manuscript on this work has been submitted to *Evolutionary Applications*.

## **Milestones**

M8. Task 1.2: Revised database (1990-2005) on Flemish Cap Atlantic cod individual measurements (month 8, CSIC).

The database was built and revised in accordance with this deliverable. In particular, data on maturity and recruit spawners were deeply revised. This involved also the revisiting of original histological slides. The CSIC database was further revised and integrated with the corresponding DFO database. (For this purpose, DFO members visited Vigo in October 2007.)

## ***Task 1.3 Fisheries-induced changes in North Sea gadoids***

Lead responsibility: Ifremer

### **Objectives of the task for the reporting period**

The objective for the reporting period was to develop models of growth trajectories and maturity ogives for North Sea gadoids (cod, haddock, whiting, Norway pout, and saithe) using data provided by the International Bottom Trawl Surveys (IBTS), as a first step before assessing evolutionary changes in age and size at maturation in these stocks using probabilistic maturation reaction norms (PMRNs) to disentangle phenotypic plasticity and genetically-determined maturation tendency.

### **Progress towards the objectives**

More progress than expected was made since the first estimates of time series of PMRNs are now available and being refined for cod and whiting, and the feasibility of the same analysis for haddock, Norway pout, and saithe is currently being assessed according to the quality of the available data.

### **Deviations from the project's work program and corrective actions**

Not applicable.

### **Deliverables**

D17. Task 1.3: Assessment of evolutionary changes in reproductive effort in North Sea cod and haddock (month 18, Ifremer, O, PP).

Reproductive investment in sub-stocks of North Sea cod and haddock were examined from data on maturity, fecundity, length, body, gonad weights, and liver weights for cod from 1967–1970, 1999, 2002, 2003 and 2008-9 and for haddock from 1977–1979, 1985, 1994–1999, 2007–2008. PMRN analysis indicated a decline in maturation at size between the 1970s and 1990s in both species. Potential fecundity for a given size also differed between years, being generally highest in the 1990s. Condition indices explained some of the variation in maturity and fecundity in addition to size, but could not explain the temporal differences. A manuscript is currently in preparation for journal submission.

### **Milestones**

M11. Task 1.3: Models for growth and maturity established for the key stocks (month 12, Ifremer).

Models for the growth trajectories and the maturity ogives of the different cohorts of cod and whiting since the mid-1960s were established. Equivalent models for haddock, Norway pout, and saithe were developed, and their quality is being assessed in order to determine the feasibility of probabilistic maturation reaction norm (PMRN) estimation.

### ***Task 1.4 Fisheries-induced changes in flatfish***

Lead responsibility: IMARES

### **Objectives of the task for the reporting period**

The objective for the reporting period was to extend the data set of back-calculated individual growth trajectories to analyse the evolutionary changes in age and size at maturation of sole.

### **Progress towards the objectives**

A sampling scheme of selected year classes of North Sea sole sampled at different age has been designed and otolith samples have been extracted. In total 61 samples (1774 fish) have been selected for DNA extraction at KUL. By December 2008, DNA has been extracted from all otoliths. 1300 otoliths have been processed of which 520 have been back-calculated (with age of more than 6 years).

### **Deviations from the project's work program and corrective actions**

Because the DNA-extraction method negatively affected the otolith, hampering the subsequent back-calculation of individual growth histories, otolith back-calculation has been delayed. The remaining part (ca. 30%) is rescheduled to be finished by March 2009.

### **Milestones**

M12. Task 1.4: Extended dataset of back-calculated individual growth trajectories established (month 12, IMARES).

The dataset of back-calculated individual growth curves is now available for 520 female North Sea sole representing different cohorts in the period from 1960 to the present.

### ***Task 1.5 Fisheries-induced changes in small pelagics***

Lead responsibility: IMR

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to study whether relatively short-lived small pelagic species show similar life-history changes as more long-lived and intensively studied demersal fish species.

#### **Progress towards the objectives**

We have collected background information and consolidated the data sources to be used in the analyses.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 1.6 Fisheries-induced changes in Atlantic salmon***

Lead responsibility: Ifremer

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to use long-term angling datasets (since the mid-1920s, with a monthly resolution from February to September) on the size of fished running salmon from several Irish rivers (Blackwater, Owenduff, and Newport) to (i) reconstruct the age of caught individuals based on the multi-modality of size distributions, (ii) devise a method for estimating probabilistic maturation (running) reaction norms (PMRNs) without information on the age and size distribution of immature individuals, and (iii) apply this

method to study the temporal trends in age and size at maturation in the salmon stocks of these three rivers.

### **Progress towards the objectives**

The method for reconstructing the age of caught individuals from multi-modal size distributions was developed and applied to reconstruct the time series of the age and size distribution of running salmon, and the method for estimating the probabilistic maturation (running) reaction norms (PMRNs) without information on the age and size distribution of immature individuals was established.

### **Deviations from the project's work program and corrective actions**

The statistical method for estimating the probabilistic maturation reaction norms (PMRNs) without information on immature individuals requires unexpected additional pieces of data to be used, namely annual survival probability, terminal fishery mortality probability, rod fishery mortality probability, and annual growth increments. Several sources for these data were identified and the data thus identified are currently being compiled in order to apply the method within one year.

### **Deliverables**

D5. Task 1.6: Assessment of evolutionary changes in age and size at maturation of Atlantic salmon in the Baltic Sea (month 6, Ifremer, O, PP).

We have analyzed data from four Finnish populations of Atlantic salmon. The data are from salmon originally tagged and released in their home rivers as smolts (juvenile salmon migrating to the sea), then captured in commercial fisheries as adults returning to spawn or as juveniles in their feeding area. The results lend some support to the hypothesis that populations that are entirely hatchery-based have changed less than populations that are partly naturally reproducing and potentially influenced by fisheries-induced evolution; the quality of data did not permit straightforward conclusions. A manuscript reporting these results has been submitted for publication.

D9. Task 1.6: Assessment of evolutionary changes in age and size at maturation of Atlantic salmon in Ireland (month 12, Ifremer, O, PP).

Because of the identification of missing pieces of information (see above), this deliverable is not yet available. Completion of the work is expected within one year.

D18. Task 1.6: Assessment of evolutionary changes in age and size at maturation and run timing of Atlantic salmon in Scotland (month 18, FRS, O, PP).

A major empirical analysis of the Scottish salmon data (from the River North Esk and from five other sites) has been completed and submitted. This work is providing crucial understanding of the dynamics and possible evolutionary changes underlying the Irish situation. Work to separate evolutionary and other causes is in progress.

## Milestones

M9. Task 1.6: Selection of stocks of salmon in Scotland for detailed analyses (month 9, FRS).

A number of Scottish stocks have been selected. Detailed analyses will focus on stocks from the River North Esk, which has been the site of scientific investigations into population structure, abundance, life-history characters, and exploitation rates since 1963. Secondary analyses will be performed using data from the River Dee.

### ***Task 1.7 Fisheries-induced changes in landlocked salmonids***

Lead responsibility: UT

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to update and finalize life-history databases for Arctic charr and whitefish, and analyze Arctic charr data to assess evolutionary changes associated with fishing mortality.

#### **Progress towards the objectives**

The life-history databases were updated, and Arctic charr data from lakes Takvatn and Fjellfrosvatn were analyzed, providing evidence of life-history changes that are consistent with evolution being driven by fishing mortality.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### **Deliverables**

D19. Task 1.7: Assessment of evolutionary changes in age and size at maturation, growth and fecundity in Arctic charr in northern Norway (month 18, UT, O, PP).

Evolutionary life-history changes have been assessed for Arctic charr populations from the experimental lakes Takvatn and Fjellfrosvatn. The assessment was based on probabilistic maturation reaction norm (PMRN) analyses indicating changes in maturation schedules consistent with fishing-induced evolution. In lake Takvatn, the size at maturation declined during intensive fishing and showed some degree of recovery during the period of suspended harvest. The probabilistic maturation reaction norm of lake Takvatn was rotated counter-clockwise relative to that of lake Fjellfrosvatn, indicating that the more intensive fishing experienced in Takvatn caused substantial evolutionary changes in this latter lake.

## Milestones

M10. Task 1.7: Updated database on environmental variables and individual measurements established (month 9, UT).

The Arctic charr and whitefish life-history databases were updated to allow analyses of phenotypic changes. The standardized and updated databases contain information on individual fish including length, weight, age, sex, and spawning status, in addition to relevant abiotic and biotic environmental data.

### **Task 1.8 Comparative analysis and synthesis**

Lead responsibility: IMR

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to utilize the growing body of empirical case studies to seek for common patterns in evolutionary responses in relation to the characteristics of fish stocks and fisheries, guided by theoretical understanding of fisheries-induced evolution and population ecology in general.

#### **Progress towards the objectives**

We have primarily worked with case studies that contribute to the dataset to be analyzed in this task.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

## **Work Package 2: Genetic Analyses**

Start month	0							
Participant acronym	IIASA	IMR	Ifremer	DIFRES	KUL	UW	IMARES	BFAF
Person months per participant	0.2	0.7	21	41.5	33.5	1	0.6	2.8

### **Task 2.1 Biological samples collection**

Lead responsibility: DIFRES

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to create a database of available historical tissue samples for wild cod populations from European fisheries institutions.

#### **Progress towards the objectives**

The data has been collected and the task has been completed.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

## Deliverables

D6. Task 2.1: Database of available historical tissue samples for cod wild populations from European fisheries institutions (month 6, DIFRES, O, RE).

A database has been created at DTU Aqua (formerly DIFRES) providing an overview of collections of cod otoliths found in fisheries institutions and universities worldwide. Samples have been recorded from Denmark, Norway, Scotland, Faeroe Islands, Iceland Greenland, and Canada. At present, access has been granted to at least a subset of samples from most areas available, and these samples form the basis for our screening of genetic changes over time.

D7. Task 2.1: Database of available historical tissue samples for sole wild populations from European fisheries institutions (month 6, KUL, O, RE).

Historical data collections for sole have been identified at CEFAS (UK), DTU Aqua (DK, formerly DIFRES) and IMARES (NL). To perform an integrated genetic-phenotypic analysis, otoliths should not be read already (burned and cracked or imbedded). Unfortunately, the Baltic Sea otoliths from DIFRES and the Irish Sea otoliths from CEFAS cannot be used for DNA extraction anymore, because they have already been processed before for age reading and are not suitable anymore for molecular work. The collection of North Sea sole otoliths from IMARES is still in a good state. Otoliths date back from the period 1957–2001 and are all kept in paper envelopes. In collaboration with IMARES (Prof. A. Rijnsdorp), we selected in total 3036 otoliths from a larger collection from the North Sea (several locations), based on the available corresponding biological information and sampling coordinates available in a database. The samples from the different years consist of a mixture of cohorts. The table below shows an overview of the number of samples from each sampling year from the North Sea. Additionally, there are 1229 historical otoliths available from the Irish Sea for the more recent period 1984–2000. These otoliths are still at IMARES and will be used as a control at a later stage only if needed.

Overview of the number of historical otoliths from the North Sea per sampling year.

<b>Year</b>	<b>N samples</b>
<b>1957</b>	88
<b>1958</b>	226
<b>1959</b>	100
<b>1966</b>	151
<b>1967</b>	100
<b>1968</b>	100
<b>1971</b>	149
<b>1972</b>	197
<b>1973</b>	50
<b>1974</b>	151
<b>1977</b>	50
<b>1984</b>	443
<b>1985</b>	56
<b>1987</b>	328
<b>1988</b>	150
<b>1989</b>	100
<b>1995</b>	349
<b>1996</b>	100
<b>1997</b>	140
<b>1999</b>	4
<b>2001</b>	4
<b>TOTAL</b>	<b>3036</b>

### Milestones

M2. Task 2.1: Documentation of long-term phenotypic trends to collect historical tissue samples from relevant cod wild populations (month 3; DIFRES).

Based on a literature search, we have documented long-term phenotypic changes in most (all) of the cod populations for which historical samples are available. For examples see Vainikka et al. (2009) and references therein.

M3. Task 2.1: Documentation of long-term phenotypic trends to collect historical tissue samples from relevant sole wild populations (month 3; KUL).

Substantial changes in growth, maturation and reproductive investment have been documented in sole in the North Sea and Eastern Channel during the 20th century. Sole became heavily exploited since the 1960s. In common sole, changes have been related to density-dependent processes and to an increase in food availability. However, recent work shows that for sole there has been a downwards shift in probabilistic maturation reaction norms (PMRNs) during the period 1963–1996, a finding that is in agreement with expectations of fisheries-induced evolution (Mollet et al. 2007). We specifically selected the North Sea population, because of the in-depth knowledge that is available about changes in its life-history traits, fishing pressure, and climate conditions.

## **Task 2.2 Baseline neutral genetic variation**

Lead responsibility: KUL

### **Objectives of the task for the reporting period**

The objective for the reporting period was to optimize DNA extractions from the historical sole otoliths, to investigate temporal changes in neutral genetic variation, and to obtain a first estimate of the effective population size of sole.

### **Progress towards the objectives**

Progress has been made according to plans and the objectives have been reached in time.

### **Deviations from the project's work program and corrective actions**

Not applicable.

### **Deliverables**

D10. Task 2.2: Database of temporal neutral genetic variation in wild cod populations (month 12, DIFRES, O, CO).

Temporal neutral genetic variation has been established in populations from the North Sea, Baltic Sea, Faeroe Islands (both Plateau and Bank populations), and Canada. These data are now available at DTU Aqua (formerly DIFRES). The already investigated populations form the core samples within our temporal investigation. The other samples from Norway (Northeast Arctic cod and Norwegian coastal cod) and Greenland will be investigated if time and resources are available. Here neutral and adaptive variation will be screened simultaneously.

D11. Task 2.2: Database of temporal neutral genetic variation in sole wild populations (month 12, KUL, O, PP).

The DNA extraction protocol has been optimized (Cuveliers et al., in press) and purifications have been carried out for 2700 otoliths from the North Sea. A total of 515 samples have already been genotyped with 15 microsatellite markers. The amplification success for the markers was 60-90%. After a first quality check, the nine best microsatellite loci were kept for first analyses. All loci were polymorphic. There was no clear decrease or increase in genetic diversity through time, although the samples from 1985 showed a lower diversity. However, the location of the samples appeared to be spread across the North Sea and therefore we plan, in the future, to select only temporal samples from the same location to exclude any spatial effects confounding the temporal patterns. We will continue the analysis of neutral genetic variation and aim at increasing the number of loci (to enable temporal QST estimates later on) and the number of genotyped samples (to enable various  $N_e$  estimations and to decrease sampling bias).

D20. Task 2.2: Estimates of temporal changes in the effective population sizes and migration patterns in wild cod populations (month 18, DIFRES, O, PP).

Estimates of effective population sizes have been established for the core temporal samples. All temporal comparisons unequivocally show temporal stability of the observed

genetic structure. Thus, there are no indications of changes in the migration pattern among populations, and effective population sizes appear to be very large. The most likely estimates derived from a number of different statistical methods of estimation suggest that the effective population sizes range in the thousands.

D21. Task 2.2: Estimates of temporal changes in the effective population sizes and migration patterns in sole wild populations (month 18, KUL, O, PP).

We have used two approaches for calculating effective population size: the moment-based temporal method (Waples 1989) and the maximum-likelihood method (Wang 2001). We used five points in time (1957, 1966, 1972, 1985, and 2007) and eight years as generation time. Preliminary estimates of both methods were comparable and varied from  $N_e = 421$  to  $N_e = 857$ . Since it is likely that generation time has evolved during the study period, we want to evaluate the estimate of generation time to improve our estimate of effective population size (the larger the sampling intervals, the better). We will compare  $N_e$  estimates made using one cohort with  $N_e$  estimates made using mixed age cohorts. Finally, we want to include any possible effects of migration by including historical samples from the Irish Sea and contemporary samples, by applying the method of Wang and Whitlock (2003).

## Milestones

M13. Task 2.2: Provision of temporal neutral genetic variation in wild cod populations (month 12; DIFRES).

The temporal development in neutral genetic variation has been established in a number of major wild cod populations throughout the species range. In general, the populations have shown a remarkable temporal stability with no indications of neutral genetic changes due to exploitation.

M14. Task 2.2: Provision of temporal neutral genetic variation in wild sole populations (month 12; KUL).

A database has been built to collect sampling locations and other important biological information, such as genetic information gathered for this project. Genotypes have been added to the database, which is available to the consortium. Initial data analyses have been carried out to evaluate neutral genetic variation.

## ***Task 2.3 Genetic variation in candidate genes***

Lead responsibility: DIFRES

### **Objectives of the task for the reporting period**

The objective for the reporting period was to investigate temporal variation in candidate genes for growth and sexual maturation over time, to establish whether selection imposed by fishing have altered gene frequencies.

### **Progress towards the objectives**

Genetic variations in candidate genes have been identified for a number of genes, and the routine screening of the distribution of genetic variation in time and space has been initiated.

### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 2.4 Quantitative genetic variation***

Lead responsibility: Ifremer

### **Objectives of the task for the reporting period**

The objectives for the reporting period were to develop (i) a method for estimating temporal quantitative genetic changes by combining data on temporal neutral genetic differentiation and data on temporal phenotypic changes, while accounting for environmental covariates that may be responsible for phenotypic changes at the same time, and (ii) a method for estimating within-population or within-generation quantitative genetic parameters (additive genetic variance, breeding values) for probabilistic maturation reaction norms (PMRNs), with these parameters being critically needed to calibrate operational eco-genetic models for predicting fisheries-induced evolution.

### **Progress towards the objectives**

A quantitative genetics model for probabilistic maturation reaction norms (PMRNs) was built by combining models for infinite-dimensional traits and threshold traits, and a statistical method for estimating the corresponding parameters was developed based on generalized linear mixed models.

### **Deviations from the project's work program and corrective actions**

The method for estimating temporal quantitative genetic changes by combining data on temporal neutral genetic differentiation and data on temporal phenotypic changes could not be developed because of the impossibility to find a postdoctoral fellow with the required expertise on whom this part of the work was supposed to rely. Measures are being taken for seeking a candidate with expertise in theoretical genetics in order to develop this methodology in the second half of the project.

### **Deliverables**

D12. Task 2.4: Statistical methods to estimate temporal quantitative genetic changes in wild populations from neutral molecular data and phenotypic data for both quantitative and probabilistic function-valued traits (month 12, Ifremer, O, PP).

Because of the lack of postdoctoral fellow with the required competences (see above), this deliverable is not yet available and will be completed at the end of the second half of the project.

D13. Task 2.4: Statistical methods to estimate within-population or within-generation quantitative genetic parameters for probabilistic maturation reaction norms (month 12, Ifremer, O, PP).

A quantitative genetic model for probabilistic maturation reaction norms (PMRNs) and the corresponding statistical method to estimate its parameters are available. An article reporting these results is currently being drafted and a condensed version of the results was included in a book chapter to be published soon (Heino et al., in press).

### **Milestones**

M15. Task 2.4: Development of new statistical methods to estimate temporal quantitative genetic changes for both quantitative and probabilistic function-valued trait from neutral molecular data and phenotypic data in wild populations, as well as within-population quantitative genetic parameters for probabilistic maturation reaction norms (month 12; Ifremer).

Because of the circumstances described above, the first part of the milestone could not yet be met. In contrast, the statistical method for estimating within-population quantitative genetic parameters for probabilistic maturation reaction norms (PMRNs) is now available.

### ***Task 2.5 Comparative analysis of neutral and adaptive genetic variation***

Lead responsibility: Ifremer

#### **Objectives of the task for the reporting period**

No objective was specified for this task for the reporting period, as work on this task will be carried out only during the second half of the project.

#### **Progress towards the objectives**

Not applicable.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 2.6 Linking adaptive genetic variation and phenotypic variation***

Lead responsibility: DIFRES

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to investigate molecular genetic variation at candidate gene loci in fish, for which maturation or growth phenotypes have already been established under controlled environmental conditions.

### **Progress towards the objectives**

Screening of genetic variation at candidate gene loci in aquaculture cod from the Faeroe Islands with known phenotypes has been initiated to establish potential links between genotype and phenotype.

### **Deviations from the project's work program and corrective actions**

Not applicable.

### **Task 2.7 Causal analysis**

Lead responsibility: KUL

### **Objectives of the task for the reporting period**

The objective for the reporting period was to unequivocally establish fishing as the main selective agent responsible for the observed adaptive genetic changes in wild exploited populations, by assessing the agreement between the fisheries-induced selection gradient and the direction of observed selective genetic changes through the link between genotype and phenotype.

### **Progress towards the objectives**

The causal analysis was scheduled for the second half of this project, as this analysis will rely on input from neutral and adaptive variation at candidate genes.

### **Deviations from the project's work program and corrective actions**

Not applicable.

## **Work Package 3: Eco-Genetic Models**

Start month	0								
Participant acronym	IIASA	IMR	Ifremer	DIFRES	KUL	FRS	UT	IMARES	UO
Person months per participant	76.5	5.4	20.7	0.5	0.5	9.5	12	0.2	16.5

### **Task 3.1 Evolutionary determination of maturation reaction norms**

Lead responsibility: Ifremer

### **Objectives of the task for the reporting period**

The objectives for the reporting period were to identify the ecological factors that are most likely to influence the evolution of maturation reaction norms and to start developing a model describing the evolutionary trajectories of maturation reaction norms under varying combinations of these factors.

### **Progress towards the objectives**

More progress than expected was made on this task, since the ecological factors most likely to influence the evolution of maturation reaction norms were identified as growth and mortality; in addition, a model for maturation reaction norm evolution under various combinations of

growth and mortality was developed, fully analyzed, and described in the draft of an article which is to be submitted very soon.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### **Milestones**

M16. Task 3.1: Decision on the environmental factors to be considered for studying the evolution of deterministic maturation reaction norms (month 12, Ifremer).

A literature review allowed to identify growth rate and mortality rate as the two main ecological factors driving the evolution of maturation reaction norms: as the costs and benefits of maturing early or late and small or large are mainly linked to the survival probability until reproduction, to adult life span, and to the effect of body size on fecundity and offspring survival, somatic growth and mortality rates are indeed expected to affect strongly the evolution of age and size at maturation.

#### ***Task 3.2 Fisheries-induced multi-trait evolution***

Lead responsibility: IIASA

##### **Objectives of the task for the reporting period**

The objective for the reporting period was to devise a conceptual and computational framework for model-based studies of multiple life-history traits in response to fisheries-induced evolution.

##### **Progress towards the objectives**

A general eco-genetic model has been devised to integrate the following life-history traits: intercept of the probabilistic maturation reaction norm (PMRN), slope of the PMRN, width of the PMRN, growth capacity, and gonado-somatic index; an article describing these results will soon appear in the journal Ecological Applications.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### ***Task 3.3 Evolutionary vulnerability of prototypical life histories***

Lead responsibility: IIASA

##### **Objectives of the task for the reporting period**

The objective for the reporting period was to establish methods for exploring and quantifying how vulnerable stocks are to fisheries-induced evolution, in dependence of their different life histories.

##### **Progress towards the objectives**

Results have been obtained in terms of a matrix, spanned by five prototypical life histories (representing fish like anchovy, cod, sharks, rays, and whales) and five life-history traits (as

described for Task 3.2), where each matrix element described the evolutionary response of the given life-history trait in the given life-history prototype to fishing and a subsequent fishing moratorium.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### **Milestones**

M17. Task 3.3: Establishment of life-history prototypes for assessing vulnerability to fisheries-induced evolution (month 12, IIASA).

Based on an extensive literature survey, key parameters were established for quantifying the average life history of species within the five considered prototypical life-history groups. For each group, parameter estimates were based on multiple sources.

### ***Task 3.4 Sex-specific dimensions of fisheries-induced evolution***

Lead responsibility: IMR

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to understand to which extent male and female life histories are expected to respond differently to fishing pressure, whether the fishing pressure directly differs between sexes or not.

#### **Progress towards the objectives**

We have consolidated our understanding of the origin of differences in male and female life histories in fish, usually seen as earlier maturation and lower asymptotic size in males compared to females.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 3.5 Fisheries-induced evolution of neutral and selected genetic markers***

Lead responsibility: Ifremer

#### **Objectives of the task for the reporting period**

No objective was specified for this task for the reporting period, as work on this task will be carried out only during the second half of the project.

#### **Progress towards the objectives**

Not applicable.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 3.6 Fisheries-induced evolution of specific stocks***

Lead responsibility: IIASA

#### **Objectives of the task for the reporting period**

The objectives for the reporting period were to secure the modelling frameworks and empirical estimates needed for devising stock-specific models of fisheries-induced evolution for the following four stocks: Northeast Arctic cod, sole in the English Channel, Arctic charr in Norwegian lakes, and Atlantic salmon in Scotland.

#### **Progress towards the objectives**

With regard to each of the targeted four stocks, substantial progress has been made in terms of establishing a computational framework for modeling fisheries-induced evolution and in terms of deriving the empirical estimates needed for calibrating the four stock-specific models.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### ***Task 3.7 Implications for stock stability and recovery potential***

Lead responsibility: IIASA

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to explore, through model based analyses, the impact of fisheries-induced evolution on the resilience of stocks.

#### **Progress towards the objectives**

An eco-genetic model has been devised and calibrated for Atlantic cod in the Northern part of its range, to quantify how environmental variability and fisheries-induced evolution interplay in the recovery of an exploited stock during a fishing moratorium; an article describing these results will soon appear in the journal *Evolutionary Applications*.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### **Milestones**

M18. Task 3.7: Conceptual summary of the potential implications of fisheries-induced evolution for stock stability and recovery potential (month 12, IIASA).

Various forms of environmental variability (affecting growth, maturation, reproduction, and mortality) have been integrated in an eco-genetic model. Studying this model has allowed us to reveal a systematic delay in the evolutionary recovery of life-history traits during a fishing moratorium in the wake of heavy exploitation. These evolutionary delays preclude stock biomass from recovering to its original level during the first few decades of the fishing moratorium.

### **Task 3.8 Economic models of fisheries-induced evolution**

Lead responsibility: UO

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to integrate eco-genetic models of fisheries-induced evolution with economic models.

#### **Progress towards the objectives**

The model has been developed, and data has been collected for the economic estimations, which are nearly finished.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

#### **Milestones**

M19. Task 3.8: Plan for integrating eco-genetic models of fisheries-induced evolution with economic models (month 12, IIASA).

This integration has been achieved by linking an eco-genetic model of fisheries-induced evolution in Northeast Arctic cod with the economic relationships describing the response of prices and demand to varying annual catch levels.

### **Task 3.9 Evolutionarily enlightened stock management**

Lead responsibility: IIASA

#### **Objectives of the task for the reporting period**

Since the objectives of this task are synthetic, they will mostly be achieved during the second reporting period.

#### **Progress towards the objectives**

Significant progress has already been made in elucidating (i) the differential evolutionary vulnerability of fish life histories, (ii) the impact of alternative fisheries regulations (regarding gear types, minimum-size limits, total allowable catches, and marine reserves), and (iii) the conditions under which evolutionary responses of fishing are particularly difficult to reverse.

#### **Deviations from the project's work program and corrective actions**

Not applicable.

### **Work Package 4: Oversight of Integrated Case Studies**

Start month	0								
Participant acronym	IIASA	IMR	Ifremer	DIFRES	KUL	FRS	UT	IMARES	UO
Person months per participant	76.5	5.4	20.7	0.5	0.5	9.5	12	0.2	16.5

### ***Task 4.1 Coordination and synthesis of case study on cod***

Lead responsibility: IMR

#### **Objectives of the task for the reporting period**

The objective for the reporting period was to ensure the integration of the case studies by a timely combination of research and results from work packages 1 to 3.

#### **Progress towards the objectives**

We have primarily worked with case studies that contribute to the knowledge basis of this task.

#### **Deviations from the project's work program and corrective actions**

Model-based analyses have progressed more slowly than planned. Work is ongoing and working sessions to address this task are scheduled for the near future.

#### **Milestones**

M4. Task 4.1: Completion of step 1 (month 3, IMR).

Step 1 aims at documenting temporal trends in life-history traits and at removing plastic components from such trends. This work is being conducted under Task 1.1; please see that task for more information. Temporal trends in life-history traits have been documented and the main plastic components have been removed through statistical analyses.

M21. Task 4.1: Completion of step 2 (month 18, IMR).

Step 2 aims at estimating fisheries-induced selection gradients. This work is being conducted under Tasks 1.1 and 3.6; please see those tasks for more information. Model development and calibration is underway, but final results are not yet available.

### ***Task 4.2 Coordination and synthesis of case study on sole***

Lead responsibility: Ifremer

#### **Objectives of the task for the reporting period**

The objectives for the reporting period were (i) to document temporal trends in life-history traits in North Sea sole and remove their plastic (environmental) components and (ii) to estimate fisheries-induced selective gradients for these life-history traits.

#### **Progress towards the objectives**

Temporal trends in probabilistic maturation reaction norms (PMRNs) in North Sea sole were assessed across 43 cohorts (1960 to 2002) together with trends in yearly growth increments; trends in energy-allocation parameters (including rates of energy acquisition, energy expenditure on maintenance, and energy expenditure on reproduction) are currently being estimated.

### **Deviations from the project's work program and corrective actions**

Fisheries-induced selection gradients on life-history traits could not be assessed because of the impossibility to find a postdoctoral fellow with the required expertise, on whom this part of the work was supposed to rely. Measures are being taken for seeking a candidate with expertise in theoretical evolutionary biology in order to develop this part of the work in the second half of the project.

### **Milestones**

M5. Task 4.2: Completion of step 1 (month 3, Ifremer).

Step 1 aims at documenting temporal trends in probabilistic maturation reaction norms (PMRNs) and yearly growth increments in North Sea sole; this was completed and will be complemented by the estimation of temporal trends in energy-allocation parameters, which is in progress.

M22. Task 4.2: Completion of step 2 (month 18, Ifremer).

Because of the lack of a postdoctoral fellow with the required expertise (see above), this milestone could not yet be met.

## Section 3

### Consortium management

#### **Work Package 5: Coordination, Integration, Dissemination**

Start month	0								
Participant acronym	IIASA	IMR	Ifremer	DIFRES	KUL	FRS	UT	IMARES	UO
Person months per participant	9.8	2	2	2	0.1	0.1	0.1	0.1	0.1
Participant acronym	CSIC	IPIMAR	BFAF	UW	(UI)	(SBF)	(MI)	(FGFRI)	(DFO)
Person months per participant	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1

#### **Research contributions, coordination contributions, and changes in responsibility**

**IIASA:** As coordinator of the FinE Project, the team has fulfilled a multitude of organisational tasks, bringing other teams together and initiating the research described in the work packages. In addition, the team has (i) participated in estimating fisheries-induced changes in the maturation of Northeast Arctic cod (Task 1.1), (ii) contributed to discussing analyses of fisheries-induced evolution in Atlantic salmon (Task 1.6) and in Norwegian salmonids (Task 1.7), (iii) co-supervised research on how environmental conditions affect evolutionary outcomes in the slopes of maturation reaction norms (Task 3.1), (iv) led research on extending eco-genetic models of fisheries-induced evolution to multiple life-history traits (Task 3.2), (v) led research on exploring the evolutionary vulnerability of prototypical life histories (Task 3.3), (vi) contributed to research on the differential response of male and female life histories to fisheries-induced evolution (Task 3.4), (vii) co-supervised research on integrating neutral and selected genetic markers into eco-genetic models of fisheries-induced evolution (Task 3.5), (viii) contributed to the development of stock-specific models of fisheries-induced evolution in Northeast Arctic cod, North Sea sole, Norwegian Arctic charr, and Scottish Atlantic salmon (Task 3.6), (ix) systematically investigated the implications of fisheries-induced evolution for stock recovery (Task 3.7), (x) co-supervised research on interfacing biological and socio-economic models of fisheries-induced evolution (Task 3.8), and (xi) contributed to various explorations of the impacts of alternative management measures on fisheries-induced evolution (Task 3.9). Furthermore, the team has (i) developed the public website of the FinE Project (Task 5.1), (ii) developed an online reprint exchanges service for the FinE Project (Task 5.1), (iii) designed a summary leaflet describing the FinE Project (Task 5.2), (iv) co-organized the annual consortium meetings of the FinE Project (Task 5.3), and (v) coordinated the preparation of this report (Task 5.6). No changes in the responsibilities assumed by or within this team have occurred.

**IMR:** The team has had lead role in statistical analyses of maturation trends in several cod populations, all strengthening the case for fisheries-induced evolutionary changes in these populations. The team has also actively been supporting many other empirical and modeling investigations. Regarding coordination and management, the team at IMR was responsible for organizing the first annual meeting (also the kick-off meeting) in Osterøy, Norway, in September 2007. The team was also an active participant in the second annual meeting in France, October 2008.

**Ifremer:** The team has (i) provided an assessment of evolutionary changes in maturation in North Sea cod and whiting based on data from the International Bottom Trawl Survey since the 1970s (Task 1.3); (ii) estimated the time series of age and size distribution of running salmon in three Irish rivers and developed a method to estimate probabilistic running reaction norms without information on immature individuals (Task 1.6); (iii) developed a quantitative genetics model for probabilistic maturation reaction norms together with the corresponding statistical method to estimate its parameters (Task 2.4); (iv) developed and analyzed a theoretical model to predict the evolutionary determination of maturation reaction norms under the influence of environmental covariation between growth and mortality rates (Task 3.1); (v) coordinated the integrated case study on sole (Task 4.2); and (vi) organized the first annual consortium meeting, which took place from October 13 to 15, 2008, in Saint Jean de Luz, France.

**DIFRES:** During the reporting period, we have collected historical cod samples from across the species range and screened neutral genetic variation in the majority of these samples to investigate the temporal genetic stability. We have developed methods for screening variation in candidate genes for growth and maturation and commenced routine screening of these genes in cod populations covering the range of the species. We have been responsible for and have been engaged in coordinating the work among partners within work package 2 and have participated in the steering committee of the FinE Project together with the other work-package leaders.

**KUL:** Molecular work has been carried out by lab technician S. Geldof and PhD student E. Cuveliers. Preliminary analyses were done by E. Cuveliers and G. Maes and a first publication was written during the first year. Coordination of the work has been done by G. Maes and F. Volckaert.

**UW:** The team has attended and contributed to the FinE annual consortium meetings, and discussed with the leader of work package 2 (E. E. Nielsen) about genetic aspects of fisheries-induced evolution, especially with regard to Tasks 2.2, 2.3, and 2.5. All other work has been carried out by a PhD student, S. van Wijk, using guppies as a model system (the latter is not included in our resources and is funded independently).

**FRS:** The team's research contributions included hosting a FinE Salmon Workshop at the Freshwater Laboratory in March 2008. Interested participants from within the FinE consortium identified traits of interest in relation to evolutionary pressures, and went on to outline a strategy to allow the analysis of these traits in the datasets available. Work has been progressing on schedule in relation to PMRN analysis, fitting of the identified traits, and the building, testing, and running of an eco-genetic model.

**UT:** New individual fish data were collected to extend the databases on Arctic charr and whitefish life histories from lakes Takvatn and Stuorajavri, and existing datasets were reorganized and scrutinized, before being collated into standardized databases ready for analysis. The Arctic charr life-history data from lakes Takvatn and Fjellfrosvatn were analyzed to assess whether changes indicative of fishing-induced evolution had occurred in these experimental lakes.

**IMARES:** The team has participated in the annual consortium meeting in Saint Jean de Luz, France, in November 2008. The team kept close contact with the team at KUL to discuss the delivery and processing of otolith samples. In collaboration with Ifremer, methods have been developed to estimate life-history parameters of individual fish from the individual growth

curves that will allow the analysis of fisheries-induced evolutionary changes to be linked to the results of the DNA analyses.

**UO:** The bio-economic model has been under developments and has been calibrated for the Northeast Arctic cod stock fishery. The biological model has been completed, and the estimations of the economic functions are near completion. We are employing an economist (A. Richter), already working on this project, to finalize the economic estimations while working at CEES for some months during the spring and summer of 2009. Finalized developments with regard to Task 3.8 are expected in summer 2009.

**CSIC:** It was possible to compare demographic PMRNs with results based on recruit spawners identified by histological means, i.e., with a precise knowledge of their maturity status. To achieve this, it was necessary to coordinate with DFO members. J. Morgan from DFO visited CSIC in Vigo in autumn 2007, while A. Pérez from CSIC spent six months at the DFO laboratory to analyze the joint database and to deal with Deliverables D15 and D16.

**IPIMAR:** Historical data on sardine length, age, and maturity were compiled from annual acoustic surveys (autumn 1984–1987, 1992, 1997–2007; spring 1986, 1988, 1996–2008) and commercial catch samples (1986–2007) collected within the spawning season in Portuguese waters. These data were used to estimate the maturation probability of 0-group individuals from each year class and to describe temporal variation in Lp50, the midpoints of the probabilistic maturation reaction norms (PMRNs) for this age group. For earlier years (early 1970s to mid-1980s), age data is still being compiled from commercial catch samples. Maturity and length data from this period were used to obtain maturity ogives and to estimate annual variation in L50, the length at 50% maturity. A small but significant linear decrease (of 0.06 cm per year) in Lp50 over time ( $p = 0.03$ ) was observed since the mid-1980s, although a low proportion of the data variance was explained by this trend ( $r^2 = 0.26$ ). The Lp50 for the 0-group and the L50 showed a strong positive correlation in corresponding years, since most individuals mature during their first year of life. If L50 is considered as a proxy for Lp50, the negative trend in maturation may have started in the late 1970s. Seasonal effects on maturation were explored, indicating that maturation probability at a given length is higher in the middle than in the beginning or end of the spawning season. There was also some indication that fish body condition and population abundance affected maturation probabilities. Further analyses will be carried out within the project to clarify the significance of these effects.

**BF AF:** We concentrated on Task 2.3 and identified, cloned, and sequenced genes related to growth and maturation in Atlantic cod. We targeted the growth hormone gene (GH) cDNA and the Ghrelin gene, designed primer pairs to amplify specific GH-gene regions from genomic DNA, and passed the sequence information to project partners.

**UI:** The team has analyzed changes in maturation of the Icelandic stock of Atlantic cod. The results suggest that there is an evolutionary component in the documented changes. These results will be utilized in the synthesizing Tasks 1.8 and 4.1.

**SBF:** The team has been working with the analysis of maturity changes in the Baltic stock of Atlantic cod, eventually contributing to the synthesizing Tasks 1.8 and 4.1. The team has also been involved in the analysis of maturation in Baltic salmon (Task 1.6).

**MI:** The team has provided expertise and data to the ongoing analyses of life-history changes in Irish populations of Atlantic salmon (Task 1.6). The team has joined the FinE Salmon Workshop in Pitlochry in March 2008 and the annual consortium meetings to foster collaboration on this task.

**FGFRI:** The team has analyzed data from four Finnish populations of Atlantic salmon (Task 1.6), yielding some support to the hypothesis that populations that are entirely hatchery-based have changed less than populations that are partly naturally reproducing and potentially influenced by fisheries-induced evolution; the quality of data did not permit straightforward conclusions.

**DFO:** The team has contributed data and participated in the analyses of life-history changes in Atlantic cod in the northwest Atlantic. These analyses revolve around questions about the nature of trends in reproductive effort and maturity, and the role of body condition in these trends.

### **Changes with regard to the project timetable and to contributions to deliverables or milestones**

**IIASA:** All milestones and deliverables for the first reporting period have been fulfilled as planned. The summary leaflet describing the FinE Project has just been completed.

**IMR:** The statistical analyses on maturation trends in Northeast Arctic cod have been completed and will be reported in the peer-reviewed literature (Task 1.1). The statistical analyses on reproductive patterns in cod stocks off Newfoundland-Labrador are slightly behind the timetable, but are now almost completed (Task 1.2). We expect that both of these deviations will be rectified within the next few months.

**Ifremer:** Deliverables D9 and D12, part of milestone M15, and milestone 22 could not be completed and have been postponed to the second half of the project.

**DIFRES:** Not applicable.

**KUL:** Not applicable.

**UW:** Not applicable.

**FRS:** Early in 2008, we discovered a key extra Irish data set that will be particularly informative. Although these data were outside the original FinE agreement, we have now negotiated access to them. They will allow (i) a direct test for fisheries-induced selection using the breeder's equation of quantitative genetics theory and (ii) improved fitting of probabilistic maturation reaction norms (PRMNs) by allowing more accurate estimates of ocean mortality. Negotiating access to these data, obtaining, and collating them have delayed progress, but this work is now well underway.

**UT:** Not applicable.

**IMARES:** The study of male probabilistic maturation reaction norms (PMRNs) has been taken up already for the spawning season of 2008. Results have been presented at the 7<sup>th</sup> International Symposium on Flatfish Ecology, November 2008, Sesimbra, Portugal.

**UO:** Not applicable.

**CSIC:** Not applicable.

**BFAF:** Not applicable.

**UI:** Not applicable.

**SBF:** Not applicable.

**MI:** Not applicable.

**FGFRI:** Not applicable.

**DFO:** Not applicable.

### **Deliverables**

D1. Task 5.1: Project web site (month 3, IIASA, O, PP).

The project website has been brought online right at the start of the FinE Project in June 2007.

D2. Task 5.2: Project leaflet (month 3, IIASA, O, PP).

The project leaflet has been completed and is currently in print.

D14. Task 5.6: Interim activity report (month 12, IIASA, O, PU).

Not applicable.

D22. Task 5.6: Mid-term activity report (month 18, IIASA, O, PU).

The first periodic activity report has been completed.

### **Milestones**

M6. Task 5.3: Kick-off meeting (month 3, IIASA).

The kick-off meeting of the FinE Project was held in Osterøy, Norway, from September 24 to 28, 2007.

M7. Task 5.5: Contacts with salient related European initiatives (month 6, IIASA).

Interfacing efforts have been extended to the Marie Curie Research Training Network FishACE (Fisheries-induced Adaptive Changes in Exploited Stocks), the Specific Targeted Research Project UNCOVER (Understanding the Mechanisms of Stock Recovery), the Network of Excellence MARBEF (Marine Biodiversity and Ecosystem Functioning), and to the 7th Framework Project FishPopTrace (The Structure of Fish Populations and Traceability of Fish and Fish Products).

M20. Task 5.3: Annual consortium meetings (months 15 and 27, IIASA).

The second annual consortium meeting was held in Saint Jean de Luz, France, from October 13 to 16, 2008. The third annual consortium meeting is planned for October 5 to 9, 2009, on Bornholm, Denmark.

## Annex

### List of project publications to date

- Arlinghaus R, Matsumura S & Dieckmann U (2009). Quantifying selection differentials caused by recreational fishing: Development of modeling framework and application to reproductive investment in pike (*Esox lucius*). *Evolutionary Applications*, in press
- Bacon PJ, Palmer SCF, MacLean JC, Smith GW, Whyte BDM, Gurney WSC & Youngson AF. Empirical analyses of the length, weight and condition of adult Atlantic salmon on return to the Scottish coast between 1963 and 2006, accepted subject to revision
- Boukal DS, Dunlop ES, Heino M & Dieckmann U (2008). Fisheries-induced evolution of body size and other life history traits: The impact of gear selectivity. *ICES CM 2008/F: 07*
- Brunel T, Ernande B, Mollet FM, Rijnsdorp AD. Coupling non-linear mixed statistical models and dynamic energy allocation models to determine the onset of maturation and related energy allocation parameters from somatic growth data, submitted
- Cuveliers EL, Bolle LJ, Volckaert FAM & Maes GE (2009). Influence of DNA isolation from historical otoliths on nuclear-mitochondrial marker amplification and age determination in an overexploited fish, the common sole (*Solea solea* L.) *Molecular Ecology Resources* 9: 725-732
- Dunlop ES, Baskett ML, Heino M & Dieckmann (2009). Propensity of marine reserves to reduce the evolutionary effects of fishing in a migratory species. *Ecological Applications*, in press
- Dunlop ES, Heino M & Dieckmann U (2009). Eco-genetic modeling of contemporary life-history evolution. *Ecological Applications*, in press
- Eikeset AM, Dunlop ES, Heino M, Godø OR, Stenseth NC & Dieckmann U. Harvest-induced evolution of multiple life-history traits in Atlantic cod, submitted
- Enberg K, Dunlop ES, Jørgensen C, Heino M & Dieckmann U (2009). Implications of fisheries-induced evolution for stock rebuilding and recovery. *Evolutionary Applications*, in press
- Hard JJ, Gross MR, Heino M, Hilborn R, Kope RG, Law R & Reynolds JD (2008). Evolutionary consequences of fishing and their implications for salmon. *Evolutionary Applications* 1: 388-408
- Heino M & Dieckmann U (2008). Detecting fisheries-induced life-history evolution: an overview of the reaction norm approach. *Bulletin of Marine Science* 83: 69-93
- Heino M & Dieckmann U (2008). Evolution and sustainability of harvested populations. In *Conservation Biology: Evolution in Action* (Carroll SP & Fox C eds.), pp. 308-323, Oxford University Press
- Heino M & Dieckmann U (2009). Fisheries-induced evolution. In *Encyclopedia of Life Sciences*. Chichester: John Wiley & Sons, in press
- Heino M, Ernande B & Dieckmann U. Reaction norm analysis of fisheries-induced adaptive changes. In *Fisheries-induced Adaptive Change* (Dieckmann U, Godø OR, Heino M & Mork J eds.), Cambridge University Press, in press

- Jørgensen C, Enberg K, Dunlop ES, Arlinghaus R, Boukal DS, Brander K, Ernande B, Gårdmark A, Johnston F, Matsumura S, Pardoe H, Raab K, Silva A, Vainikka A, Dieckmann U, Heino M & Rijnsdorp AD (2007). Managing evolving fish stocks. *Science* 318: 1247-1248
- Jørgensen C, Enberg K, Dunlop ES, Arlinghaus R, Boukal DS, Brander K, Ernande B, Gårdmark A, Johnston F, Matsumura S, Pardoe H, Raab K, Silva A, Vainikka A, Dieckmann U, Heino M & Rijnsdorp AD (2008). The role of fisheries-induced evolution – Response. *Science* 320: 48-50
- Miethe T, Dytham C, Dieckmann U & Pitchford J. Marine reserves and the evolutionary effects of fishing on size at maturation, submitted
- Mollet FM, Brunel T, Ernande B & Rijnsdorp AD. Multiple life history traits (growth, maturation and reproduction) estimated simultaneously in individuals, submitted
- Nielsen EE & Hansen MM (2008). Waking the dead: the value of population genetic analyses of historical samples. *Fish and Fisheries* 9: 450-461
- Okamoto KW, Whitlock R, Magnan P & Dieckmann U (2009). Mitigating fisheries-induced evolution in lacustrine brook charr (*Salvelinus fontinalis*) in southern Quebec, Canada. *Evolutionary Applications*, in press
- Pardoe H, Vainikka A, Thórdarson G, Marteinsdóttir G & Heino M (2009). Temporal trends in probabilistic maturation reaction norms and growth of Atlantic cod (*Gadus morhua* L.) on the Icelandic shelf. *Canadian Journal of Fisheries and Aquatic Sciences*, submitted
- Primicerio R, Amundsen PA, Heino M, Knudsen R, Svenning M & Klemetsen A. Fishing induced evolution and recovery potential of Arctic charr maturation schedules in a whole lake experiment. *Evolutionary Applications*, submitted
- Primicerio R, Amundsen PA, Heino M, Knudsen R, Svenning M & Klemetsen A (2009). Fishing induced evolution and recovery potential of Arctic charr maturation schedules in a whole lake experiment. *Ecological Applications*, submitted
- Thériault V, Dunlop ES, Dieckmann U, Bernatchez L & Dodson JJ (2008). The impact of fishing-induced mortality on the evolution of alternative life-history tactics in brook charr. *Evolutionary Applications* 1: 409-423
- Vainikka A, Kallio-Nyberg I, Heino M & Koljonen ML (2009). Divergent trends in life-history traits between Atlantic salmon of wild and hatchery origin in the Baltic Sea. *Journal of Fish Biology*, submitted
- van Walraven L, van Damme C, Mollet FM & Rijnsdorp AD. Fisheries induced evolution in growth, maturation and reproductive investment of male and female North Sea plaice *Pleuronectes platessa*. *Journal of Sea Research*, submitted