

Fishing-induced neutral and adaptive evolution

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Introduction

Fishing can alter the genetic composition of harvested stocks through two processes: *selection* and *genetic drift*.

Studies based on neutral molecular markers have shown increasing genetic drift rates correlated with a *loss of neutral genetic diversity*.

This has implication for population conservation for three reasons:

- Link with demographic properties [1]
- Link with fitness [2]
- Link with functional genetic diversity (and population adaptive potential) [3]

Field observations, experiments & theoretical models have shown that fishing might induce *adaptive evolution in life-history traits*.

However, no gene coding for these has been identified in wild harvested fish yet

- Role of selection Vs phenotypic plasticity and drift controversial
- Effect on additive genetic diversity unknown

Questions

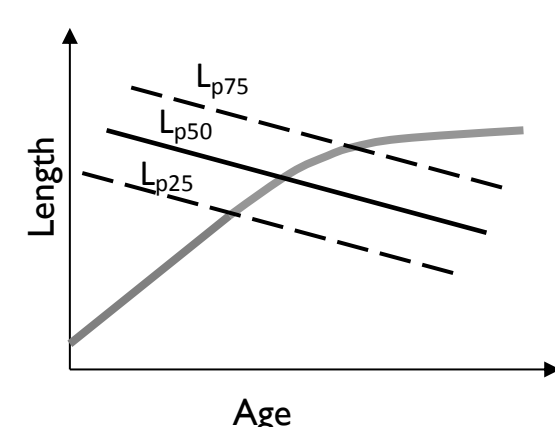
1. How is neutral genetic diversity affected by fishing and is it indicative of demographic changes?
2. What is the effect of fishing on the genetic variance of quantitative traits?
3. What is the relative contribution of neutral and adaptive evolution in genetic changes of quantitative traits and are neutral and quantitative genetic temporal changes correlated?

Method

We develop an *individual-based eco-genetic model* [4] with *gametic inheritance*.

Individual genotypes comprise a set of *neutral loci* to assess neutral evolutionary dynamic and a set of *functional loci* to assess the combination of neutral and adaptive evolutionary dynamics of life-history traits. Functional loci code for five life-history traits:

- Juvenile growth rate
- Two traits for growth investment at adult stage
- Two traits for Probabilistic Maturation Reaction Norm (intercept and slope)



Population genetic diversity is measured using effective population size, N_e [5], additive genetic variance of quantitative traits, and expected heterozygosity [6].

Summary

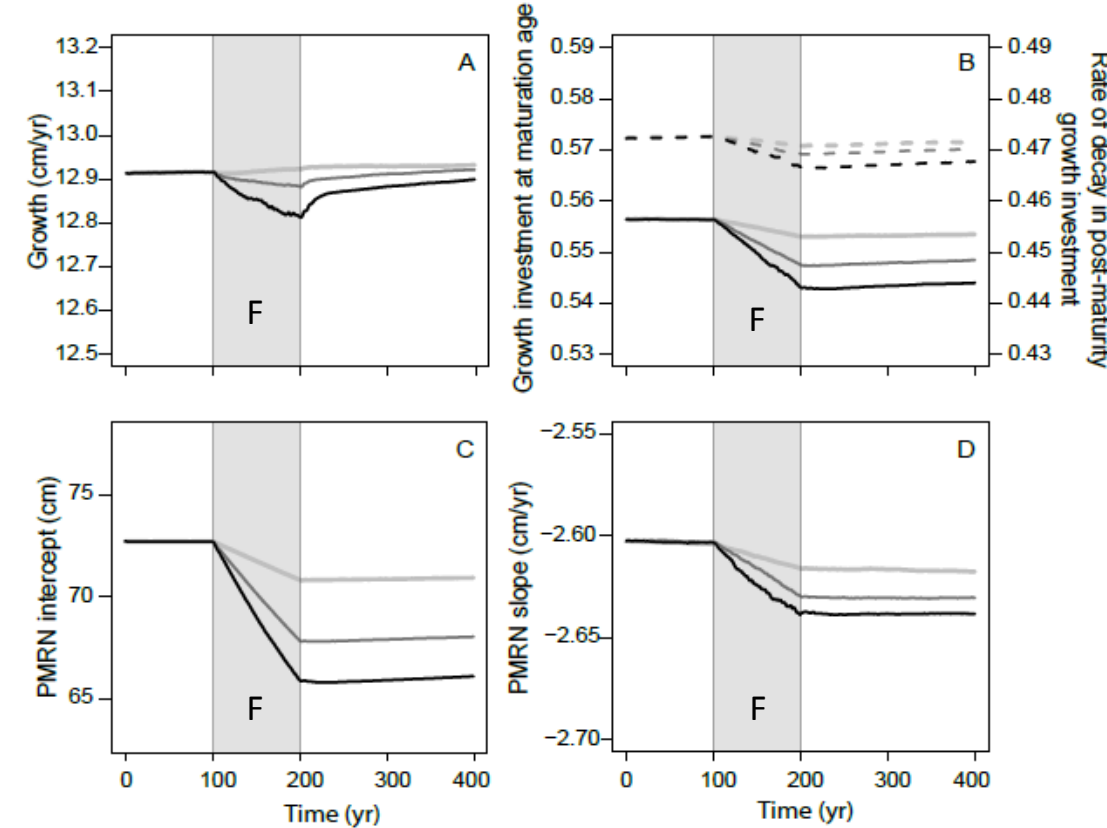
- Fishing reduces neutral genetic diversity as measured by effective population size, which is co-varying linearly with important population demographic features.
- Fishing induces an erosion of functional genetic diversity, which can prevent life-history traits from recovering when fishing pressure stops.
- The contribution of selection to functional genetic diversity erosion clearly dominates that of genetic drift for traits related to maturation, but not for others.

Together, our results suggest that effective population size and neutral genetic diversity could be respectively used as indicators of population demography and functional genetic diversity for fish stock management.

Results

Results are presented for different fishing intensities, from weak (light-grey line) to strong (dark grey-line). The grey-shaded area delimits the start and the end of fishing.

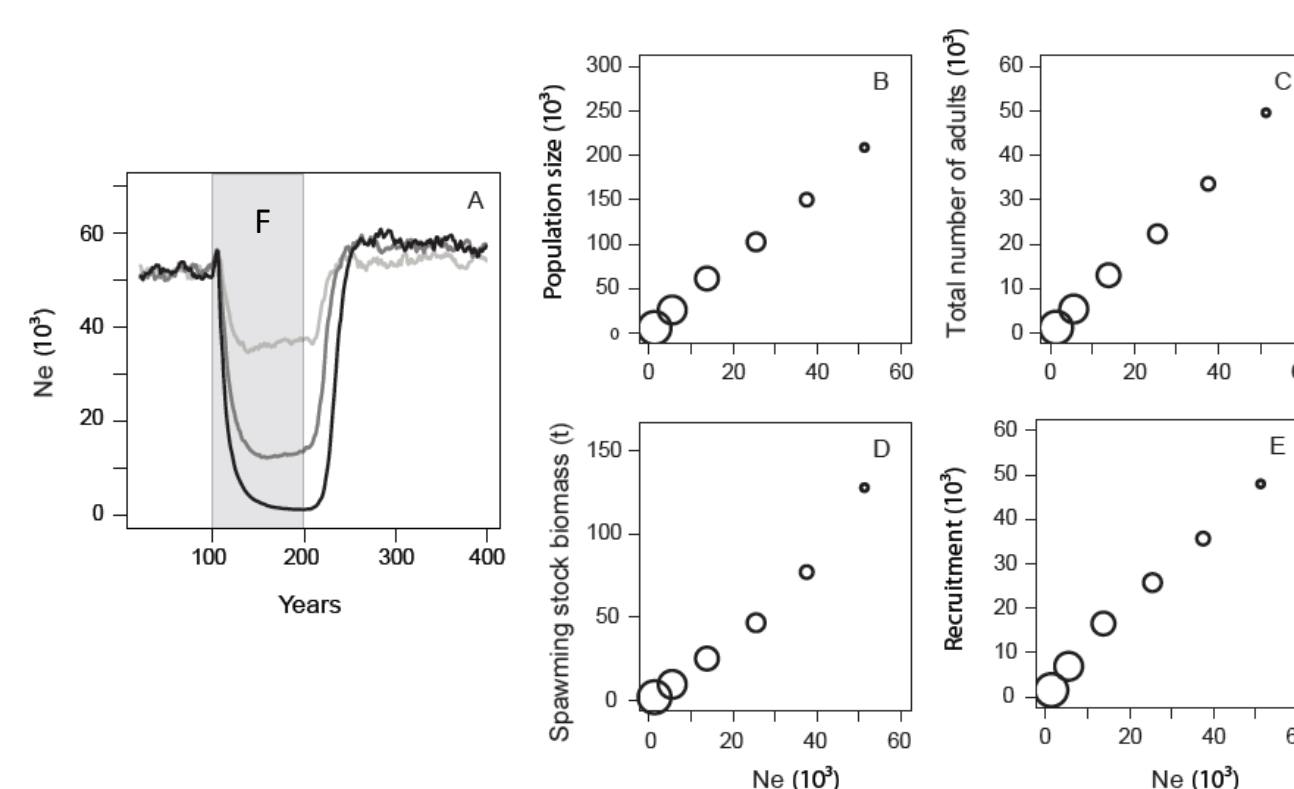
Genetic means of life-history traits



As harvesting occurs, the mean genotypic values of all life-history traits decrease.

When fishing stops, juvenile growth rate almost recovers within the next 200 years, while all other genetic changes remain.

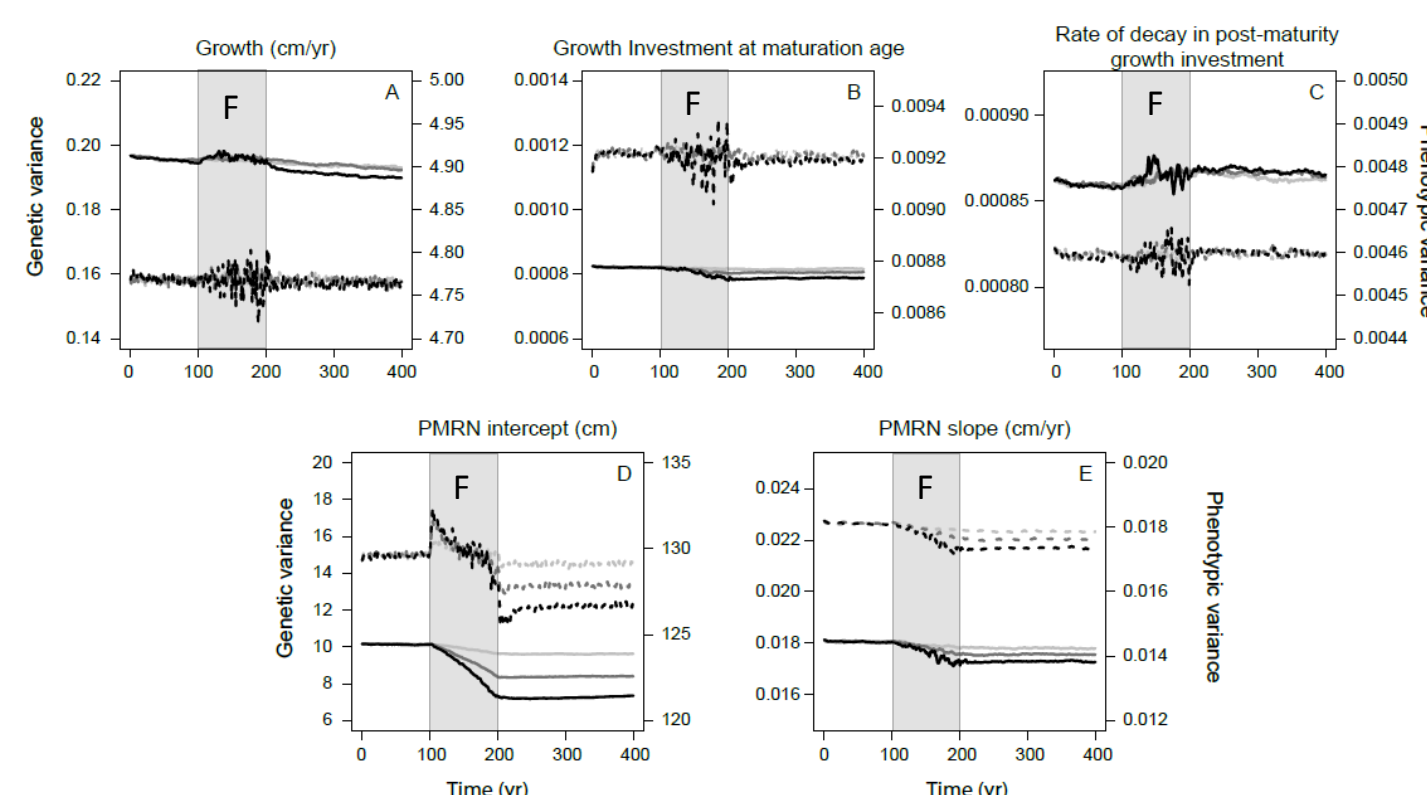
1. Neutral genetic diversity and relationship with demography



(A) Fishing reduces neutral genetic diversity (measured by effective population size, N_e). The higher the fishing intensity, the stronger the decrease.

(B,C,D,E) Effective population size after 100 years of fishing (fishing intensities are proportional to the size of circles) co-varies positively with many population demographic properties

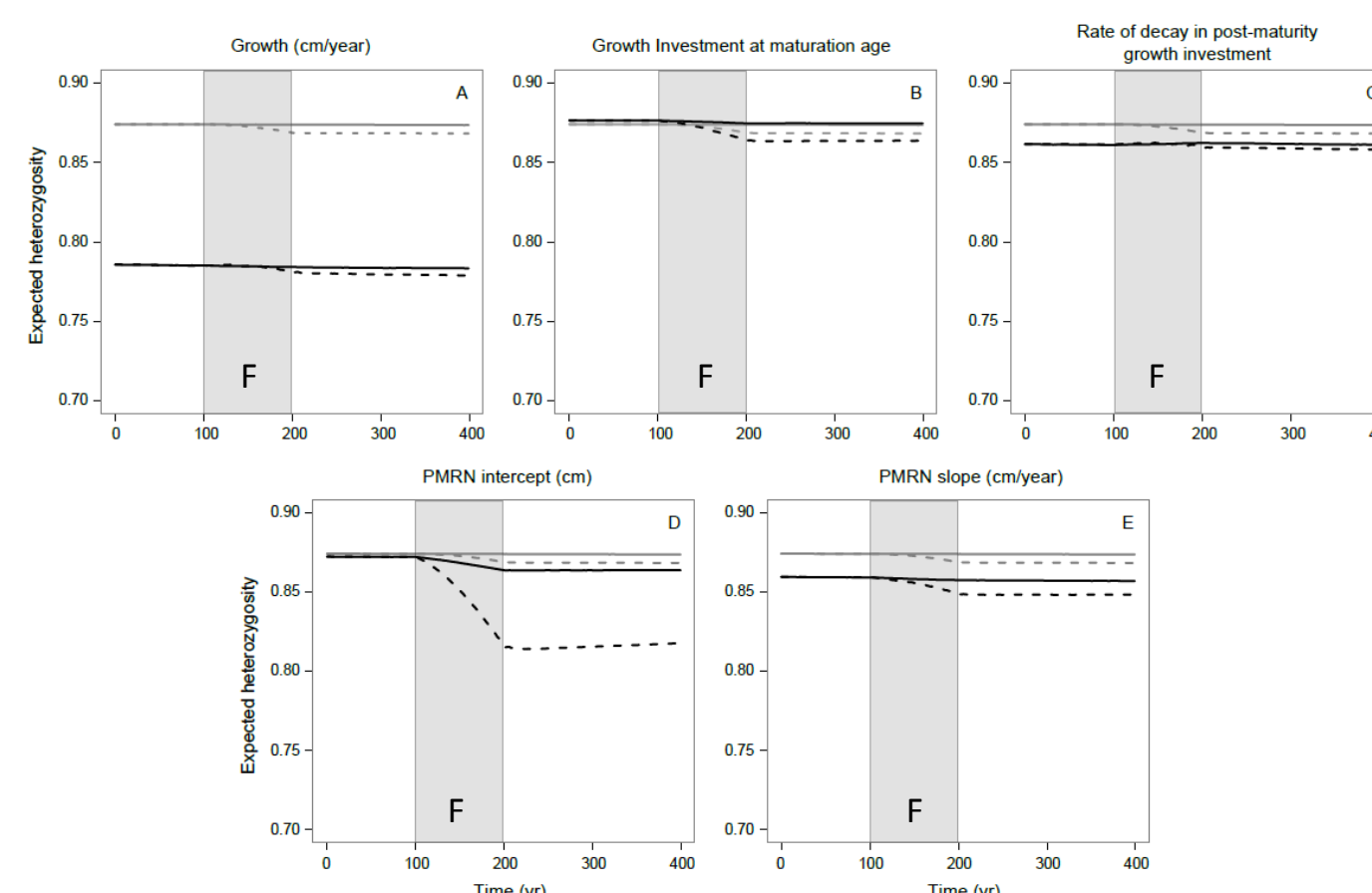
2. Genetic and phenotypic variances of life-history traits



Full lines: genetic variances
Dashed lines: phenotypic variances

Fishing decreases long-term functional genetic and phenotypic diversity of maturation-related traits

3. Relative contributions of drift Vs. selection to loss in functional genetic variability



Grey lines: neutral loci
Black lines: functional loci
Full lines: light fishing intensity
Dashed lines: high fishing intensities

Compared to heterozygosity neutral loci, a stronger decrease is observed in the heterozygosity of loci coding for PMRN intercept (D) due to stabilizing selection.

References & Acknowledgements

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This study was supported by the European Commission, as part of the Specific Targeted Research Project on “Fisheries-induced evolution” (FinE, contract number SSP-2006-044276)

