



# Population level effects of reduced fecundity in the fish species perch (*Perca fluviatilis*) and the implications for environmental monitoring

Niklas Hanson

Department of Plant and Environmental Sciences, University of Gothenburg, Box 461, S-405 30 Göteborg, Sweden

## ARTICLE INFO

### Article history:

Received 4 March 2009

Received in revised form 24 April 2009

Accepted 24 April 2009

Available online 30 May 2009

### Keywords:

Environmental monitoring

Population modelling

Pseudo extinction

Biomarkers

## ABSTRACT

A 40% reduction in relative gonad size in perch (*Perca fluviatilis*) has been observed over that past two decades at the Swedish national reference site Kvädöfjärden. This biomarker response could be interpreted as a reduction in fecundity and increased risk of local extinction. However, abundance estimates from the same area has not provided any evidence of a reduction in population size. In the present study, a matrix population model was developed to investigate if a reduction in fecundity can be expected to have long term effects on population viability for perch and to evaluate the probability to detect such effects through abundance estimates. The model was parameterized from 17 years of population data from Kvädöfjärden as well as from other studies on perch. The model included density dependence and environmental stochasticity. The results indicated that a reduction in fecundity that is in level with the observed reduction in relative gonad size in Kvädöfjärden will cause a substantial risk for local extinction. The risk that the population will fall below 20% of the carrying capacity within 50 years is 44% when the fecundity is reduced by 40%. However, due to variability in abundance measurements it will take some time before a reduction in gonad size leads to statistically significant effects on the population. If the fecundity is reduced by 40% successively over a 10-year period, the probability to detect this through abundance estimates within 10 years is less than 50%. The results of the present study clearly show that relevant biomarkers have an important role in environmental monitoring as early warning signals, preferably in combination with measurements at higher levels of biological organization.

© 2009 Elsevier B.V. All rights reserved.

## 1. Introduction

Human activities have caused damage to many ecosystems around the world (e.g., Hughes and Tanner, 2000; Jackson et al., 2001; Tilman and Lehman, 2001). According to a study by Halpern et al. (2008), as much as 41% of the world's oceans are strongly affected by human activities. One of the most important factors that contribute to the degradation of aquatic ecosystems is pollution. The effect of pollution is most important in human dominated parts of the world, such as heavily populated coastal areas. However, due to widespread use of chemicals and long range transport of contaminants, even remote areas like the polar regions are affected by anthropogenic chemicals (Chapman and Riddle, 2005).

Environmental monitoring is performed to get information on the distribution of contaminants in the environment, to assess the present contamination load and to evaluate environmental effects of pollution. The level of contaminants in the aquatic environment can be determined by chemical analyses of water, sediment and biota. A drawback with this method is that it only shows those

chemicals that are measured. Hence, unknown and unexpected chemicals may be missed. Furthermore, the presence of contaminants does not mean that the organisms are affected. Biomonitoring is an alternative strategy that focuses on organisms instead of chemicals. A common example of biomonitoring that can provide information about pollution is to examine the species composition of a certain community. In the aquatic environment, e.g., community structure for benthic macrofauna (Ingole et al., 2006) and fish community assemblages (Aguilar et al., 2004) have been used to characterize environmental stress. This type of qualitative analysis of fauna is, however, often time consuming. Therefore, biotic indices based on the presence or absence of certain indicator species are often used to simplify monitoring (Roberts et al., 1998; Bustos-Baez and Frid, 2003). The use of bioindicators and indicator species can be useful for environmental monitoring when the types of contaminants are not known. However, the use of bioindicators and indicator species will only respond once changes have become measurable at the population and community levels. Furthermore, populations and communities are affected by numerous factors other than pollution and can change also in situations when the environment is stable. This means that the data may be too noisy to detect effects, and that it often is difficult to establish causal relationships for those effects that are found.

E-mail address: [niklas.hanson@dps.gu.se](mailto:niklas.hanson@dps.gu.se).

Although the most relevant effects of toxic exposure are found on the levels of the population, community or ecosystem, initial effects will appear on the biochemical level, when the toxic chemical first interacts with the cell or its components. The effect may then manifest through the levels of biological organization and, eventually, affect growth, reproduction and survival of the organism. By measuring sub-organismal responses (biomarkers), an early warning for effects at the population level may be achieved. Biomarkers include physiological and biochemical responses to environmental pollution. Many biomarkers offer high precision and can point out a chemical, or a group of chemicals, that is likely to be causing the observed response. Biomarkers have been used extensively on fish populations to assess environmental status of various recipients (Munkittrick et al., 1994; Larsson et al., 1999; Aas et al., 2000; de la Torre et al., 2002; Hanson et al., 2009a). The reliability of biomarkers as early warning signals for effects at higher levels is, however, debated (McCarty and Munkittrick, 1996; Forbes et al., 2006).

In Sweden, biomarkers in the fish species perch (*Perca fluviatilis*) have been used for more than 25 years to evaluate the environmental impact of pulp mills (Andersson et al., 1988), metal industry (Larsson et al., 1984) landfills (Noaksson et al., 2005) and large population centres (Linderoth et al., 2006) as well as to examine the status at, presumed, clean reference sites (Hansson et al., 2006). In several cases, biomarker responses have indicated that the reproductive capacity of perch is impaired. At the Swedish reference site Kvädöfjärden, which is located on the Swedish Baltic coast, the gonad somatic index (GSI, Gonad weight  $\times$  100/somatic weight) decreased by 40% between 1988 and 2002 (Sandström et al., 2005). Analyses of other biomarkers have indicated that exposure to polycyclic aromatic hydrocarbons (PAHs) is contributing to this effect (Hanson et al., 2009a,b). Another example where physiological responses indicate impaired reproductive capacity in perch is a study along a gradient to the city of Stockholm. Here, it was found that GSI values were approximately 40% lower in the central parts of the city compared to a reference site 52 km east of the city centre (Linderoth et al., 2006). Furthermore, the frequency of sexually mature females in the size range 190–390 mm was reduced by up to 50%. The lake Molnbyggen, in central Sweden, is exposed to leachate water from a public refuse dump. Here, gonad size was found to be reduced by 80% compared to a reference lake in a neighbouring watershed (Noaksson et al., 2001). The frequency of sexually mature females in the catches was only 24.7% in Molnbyggen compared to more than 95% at the reference lake. In a study of seven lakes that were exposed to public refuse dumps, five had reduced numbers of sexually mature females (Noaksson et al., 2005). Reduced gonad size and delayed maturity suggest that reproduction is negatively affected and that the perch populations are at risk. However, despite the high number of studies that have shown physiological effects on reproduction, few studies have been able to show population level effects on perch that can be associated with environmental pollution. For example, during the same period as the relative gonad size has been reduced by 40% in Kvädöfjärden, abundance estimates of perch suggest that the population size has been stable or even increasing (Sandström et al., 2005). Therefore, it can be argued that GSI values are not reflecting fecundity or that fecundity has limited impact on the population size. The latter could, e.g., be explained by a strong density dependence on survival so that the reduction in fecundity is compensated by increased survival of recruits as well as adults. However, it is likely that environmental factors, such as water temperature and food availability, are important for the development of the perch population. If the reduction in gonad size (and fecundity) occurs during a period that is otherwise favourable for the perch, the population size may remain unaffected. It is also possible that the population is affected but that noise from other sources, such as natural environmental variation

or measurement error, are causing so much variation in abundance estimates that effects are missed. If the annual variation in estimated population size is considerable, it may take many years to detect an average long term decline of, e.g., 5% per year. The decline is still, however, highly ecologically significant as it will drive the population towards extinction. Important questions that need to be answered when a strategy for environmental monitoring is chosen include; Are sub-organismal responses ecologically relevant? and Are population level measurements sensitive enough to detect relevant effects? Today, satisfactory answers to these questions are not available.

In the present study, a population model of perch was used to evaluate the effects of reduced gonad size and delayed maturity. Data from the Swedish national reference site Kvädöfjärden were used to parameterize the model and for vital rates that could not be estimated from this data set, the literature was searched for previous studies on perch. The aim was to develop a model that was well representative for perch in northern Europe, although not perfectly matching any specific population. The model was used to examine the effects of reduced fecundity and delayed sexual maturation as well as to establish the probability to detect population level effects by abundance estimates from catches with gill nets (as used in Kvädöfjärden).

## 2. Method

### 2.1. Model development

An age-structured matrix population model was developed based on age-specific survival rates and fertility values for female perch. The exclusion of males in the model is valid as long as they are not limiting for the population growth, e.g., due to strongly male biased mortality. Survival rates were parameterized from a 17-year data set of catches from the reference site Kvädöfjärden, on the Swedish Baltic coast. The data were collected within the Swedish Environmental Monitoring Programme, which is funded by the Swedish Environmental Protection Agency. Sampling was performed in August each year, rendering a projection interval in the model of 1 year. The female perch were divided into age classes 0+, 1+, 2+, etc. Age class 0+ consists of perch that were born in the spring the year of sampling, 1+ were born 1 year earlier, and so on. Besides this data set, data from other studies on perch were also included to parameterize the model.

The survival probability is the proportion of a given age class that survives for one time step and the fertility value is the average number of surviving descendants from the females of a specific age class during one time step. Survival rates and fertility values are referred to as vital rates. Age dependent vital rates are inserted in the Leslie matrix ( $M$ ). By multiplying the Leslie matrix ( $M$ ) with the age class density vector ( $n$ ) of time  $t$ , the age class density vector of time  $t+1$  is given ( $n_{t+1} = M \times n_t$ ). This renders a discrete model where the number of individuals in each age class is given at each time step. In a deterministic model without density dependence, the vital rates (survival rates and fertility values) are equal for all years and, hence,  $M$  is constant. The dominant eigenvalue of  $M$  is equal to the asymptotic growth rate ( $\lambda$ ) (Caswell, 2001). In a deterministic model, without density dependence, the matrix multiplication results in exponential population growth. For  $\lambda > 1$ , the population will increase exponentially in size and for  $\lambda < 1$ , the population will decline and approach extinction.

If random variations in vital rates are allowed, the model is termed a stochastic model. A stochastic model is used to simulate natural fluctuations in the growth of a population due to environmental variation (e.g., water temperature and food availability). The stochastic population growth rate ( $\lambda_s$ ) is the geometric mean population growth over a time period (Caswell, 2001). However,  $\lambda_s$

Download English Version:

<https://daneshyari.com/en/article/4377765>

Download Persian Version:

<https://daneshyari.com/article/4377765>

[Daneshyari.com](https://daneshyari.com)