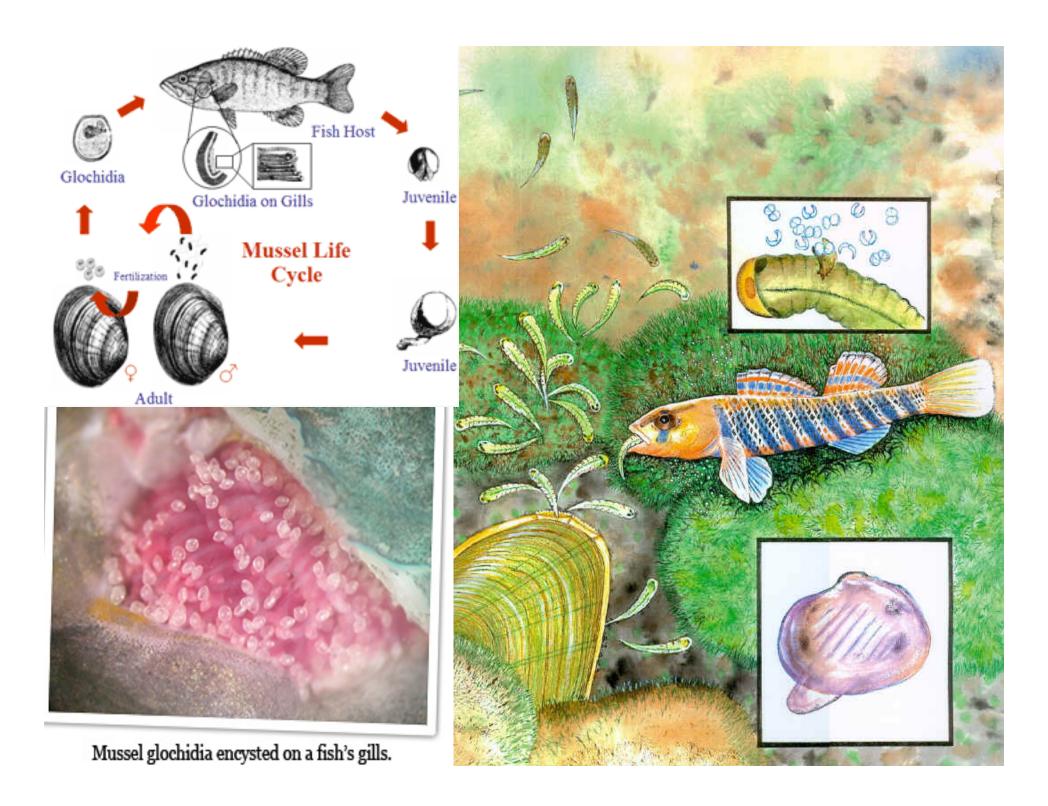
Freshwater mussels;
State of the art & Barcoding

Stefan Lundberg Swedish Museum of Natural History Stockholm Sweden

December 3, 2014
Department of Aquatic
Resources, Drottningholm







Diversity of freshwater mussels:

Approx. 1000 species estimated worldwide

United States: 304 spp.

Africa: 96 spp. China: 60 spp.

Europe: 16 spp.

Essential components of rivers and streams.

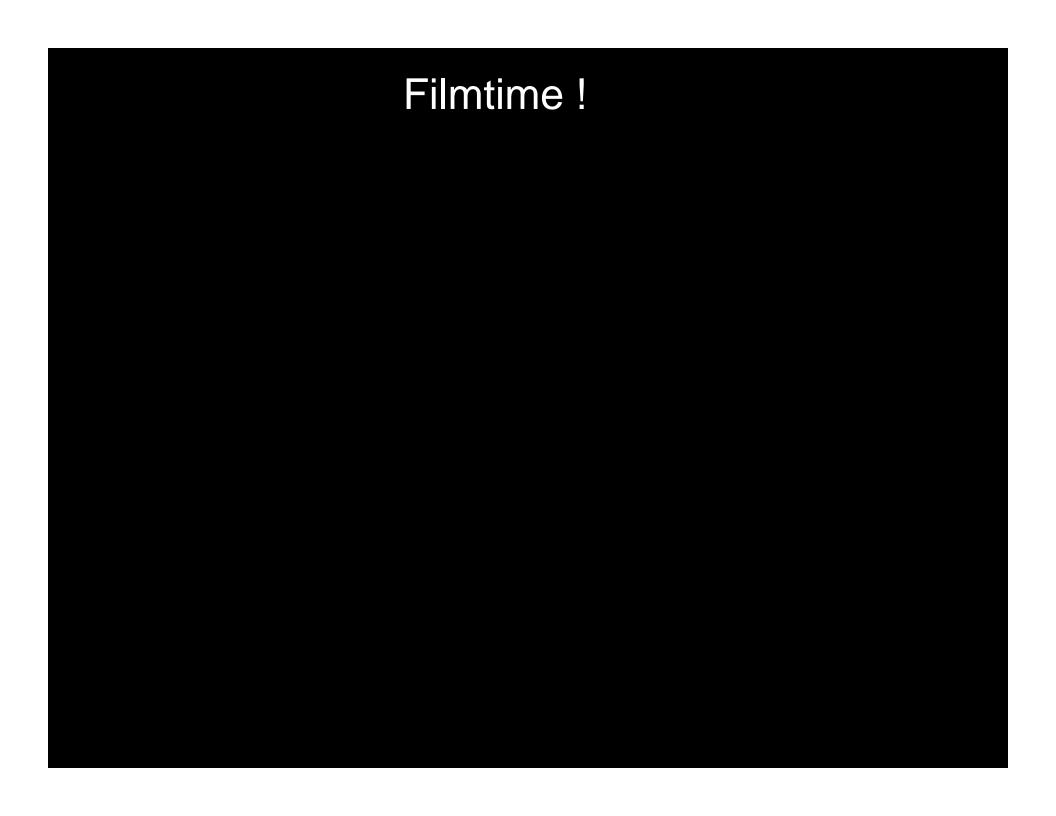
By their siphoning actions, mussels filter bacteria, algae, and other small particles, which make them one of the few animals that improve water quality.

Serve as a food source to many species of fish, reptiles, birds, and mammals.

The outer shell of a live mussel is usually covered by aquatic insects, algae, and plants.

The empty shell functions as a nesting site for small fish like bullhead etc.





Freshwater mussels (Bivalves) in Sweden

7 native species

2 introduced

Stormussior Stormussion



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Zebra mussel – different shell-morphs



Threats!

Freshwater bivalves of the Superfamily Unionoidea provide important ecosystem functions and services, yet many of their populations are in decline.

Pollution

- eutrophication
- acidification
- toxics

Biotope degradation

- cleaning for timber floating etc.
- siltation
- water regulation

Decreased host fish populations

decreased connectivity



Background – work with freshwater mussels in Sweden

Investigations of freshwater pearl mussels started in the middle of the 1980's

Mostly follow-up after lime-treament

The first survey and monitoring work was performed in a small scale

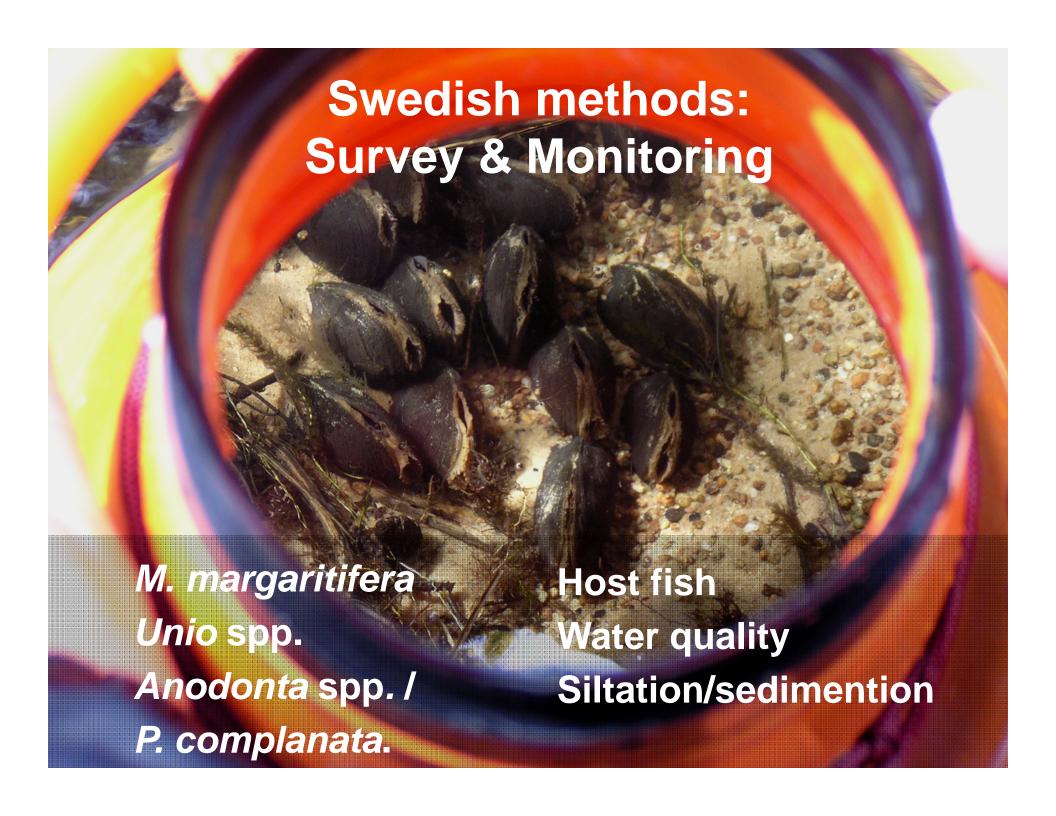
A defined method for monitoring of freshwater pearl mussel estblished in 1991. Modified 1996 and 1999.

Since 2010 there is a complete method for monitoring both *Unio* spp., *Anodonta* spp. */ P. complanata* and *M. margaritifera* (3 different parts)

- 1. *M. margaritifera* in stream waters
- 2. Unio spp. and Anodonta spp. / P. complanata in stream waters
- 3. Unio spp. and Anodonta spp. / P. complanata in lakes









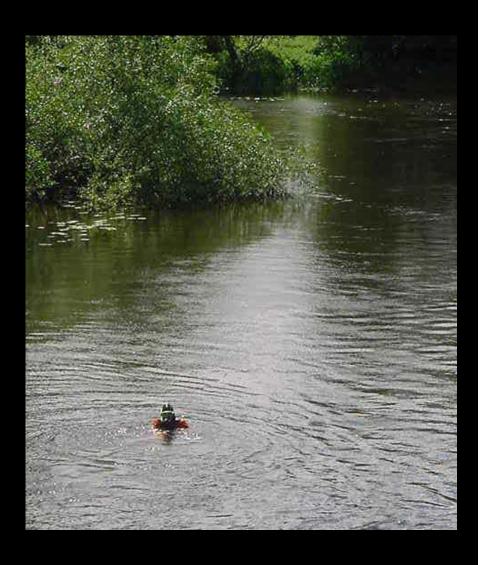




If a water course consists of parts which are difficult to investigate, diving is recommended.

An advantage with diving is that the search for juvenile mussels becomes more effective.

Diving





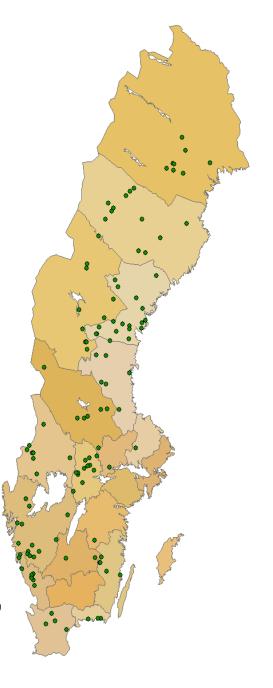


127 streams monitored by the Swedish standard method





The result gives information on the range, density, number and reproduction



Double Uniparental Inheritance (DUI)

Unionoid freshwater mussels are holders of an unusual mitochondrial DNA inheritance mechanism (Double Uniparental Inheritance) in which males have mitochondria inherited by both the maternal and paternal ancestors.

Standard maternal inheritance of mtDNA is a rule in the animal kingdom. The most notable exception from this rule is the doubly uniparental inheritance (DUI) system discovered in some bivalve species. Under DUI, females pass their mtDNA (F-type) to the offspring, but heteroplasmic males pass one of their mtDNAs only to their sons.

Thus the paternal mtDNA (M-type) is present mainly in the germline of males.

DUI occurs when both mothers and fathers are capable of transmitting mitochondria to their offspring.

DUI occurs in some bivalve molluscs, in which two mitochondrial genomes are inherited, one through eggs, the other through sperm.

Molecular studies

Ribosomal genes (ITS region) were compared to mitochondrial) genes (CO1).

DNA profiles (Barcodes) for unionid mussels were identified.

The method can also be used to identify mussel larvae (glochidia) on fish gills.

Evaluation of ITS rDNA as a complement to mitochondrial gene sequences for phylogenetic studies in freshwater mussels: an example using Unionidae from north-western Europe

Mari Kallersjö, Ted von Proschwitz, Stefan Lundberg, Pia Eldenäs & Christer Erséus

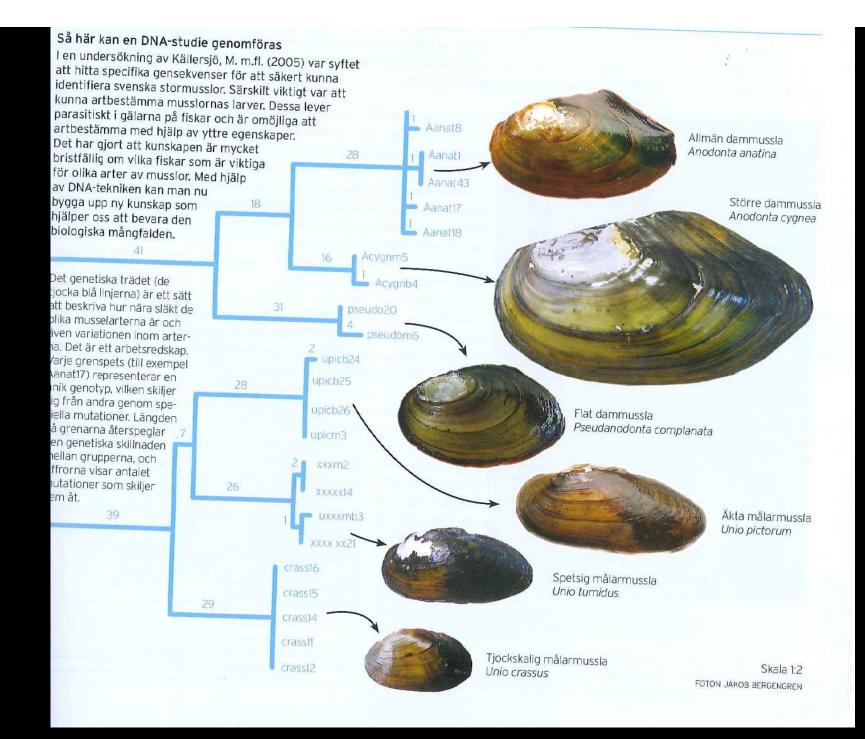
Accepted: 13 April 2005 doi:10.1111/j.1463-6409.2005.00202.x Källersjö, M., von Proschwitz, T., Lundberg, S., Eldenis, P. & Erséus, C. (2005). Evaluation of ITS rDNA as a complement to mitochondrial gene sequences for phytogenetic studies in freshwater mussels: an example using Unionidae from north-western Europe. — Zeologica Sarigaa, 34, 415–424.

Mitochondrial inheritance in the Unionidae is complex since mitochondria can be inherited from both parents. An increased rate of recombination could lead to erroneous homology assessments, which could cause problems for phylogenetic reconstruction. For this reason we investigated the possibility of using a nuclear marker, the ribosomal internal transcribed spacer region, for phylogenetic studies in the Unionidae, as a complement and comparison to two of the most widely used mitochondrial genes today. The nuclear ribosomal internal transcribed spacer region (ITS1, 5.8S, ITS2) was sequenced from 72 specimens representing six of the seven species of Unionidae mussels occurring in NW Europe: Unio pienzum, U. tumidae, U. crassus, Anodonta anatina, A. cypnea and Pseudanodonta complanata. Sequences from Margaritifera margaritifera were used as an outgroup. The ITS sequences of all species were found to have low intragenomic and infraspecific variation. Compared to mitochondrial genes (165 and COI) they show an intermediate genetic diversity. Phylogenetic analyses produce tree topologies that are congruent with those resulting from analyses of the mitochondrial sequences. Likewise, an incongruence length difference (ILD) test showed no significant incongruence between data sets, indicating that if recombination has occurred it has not produced any conflicting patterns. Best-resolved and supported trees are obtained when gaps are treated as a fifth character state. A combined analysis of the three gene regions shows that Unio crasms and U. pictarum are more closely related than either to U. tumidus. Pseudanodonta is nested within Analouss as sister taxon to A. cygnes. Advice on how to best preserve mussel material for DNA studies is provided.

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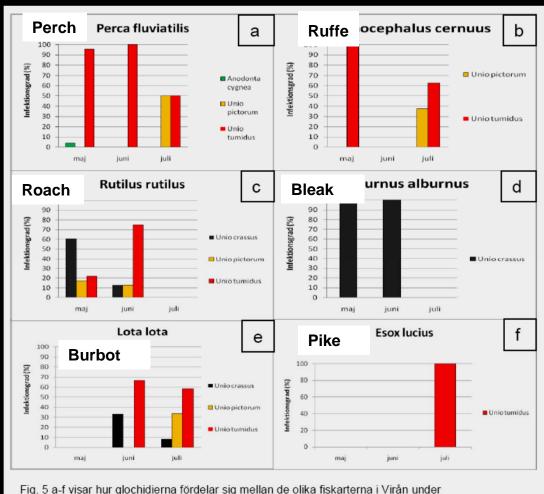
Christer Errius, Department of Zodogs, Gitcharg University, PO Box 463, SE-405-30 Götchorg. Sweden, E-mail: christer.aseus@zod.gu.te



From 2009, a DNA-barcoding approach has been used at SMNH to identify different species of freshw. mussels from glochidia recovered from naturally infested host fishes

månaderna maj, juni och juli.





Wengström, 2009

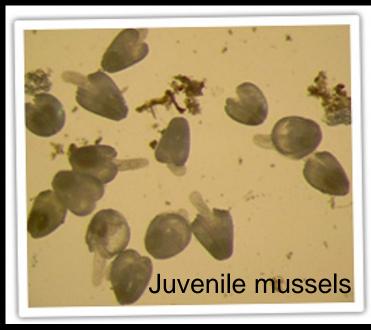


A DNA-barcoding approach to identifying juvenile freshwater mussels (Bivalvia:Unionidae) recovered from naturally infested fishes

Author(s): Sarah L. Boyer, Alexander A. Howe, Nathan W. Juergens, and Mark C. Hove

Source: Journal of the North American Benthological Society, 30(1):182-194. 2011.

Published By: The Society for Freshwater Science





Freshwater Drum (*Aplodinotus grunniens*), host to mussels from upper Mississippi River, USA.

DNA BARCODING

Identification of 'extinct' freshwater mussel species using DNA barcoding

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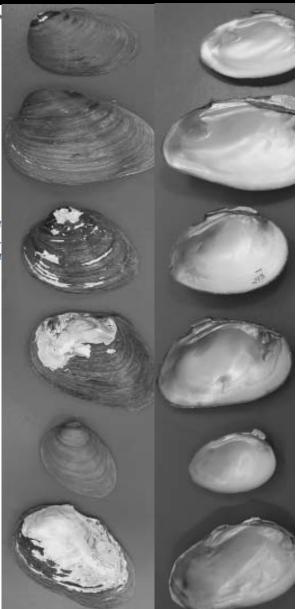
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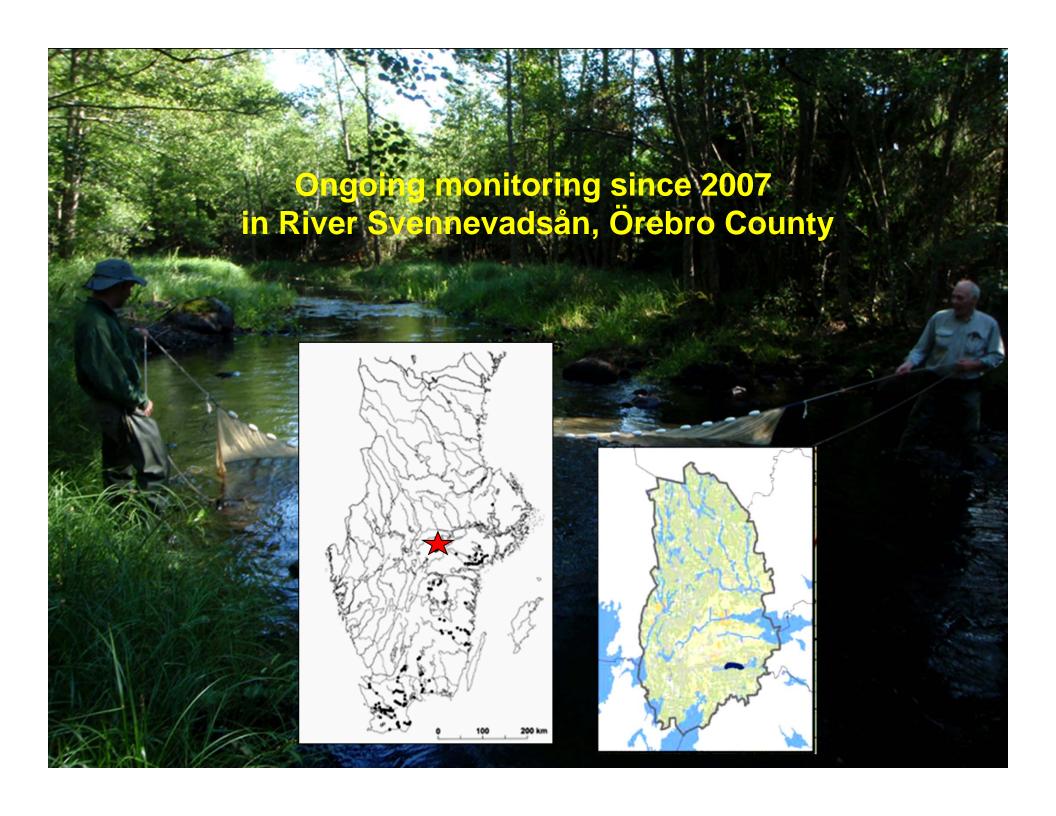
Abstract

Freshwater mollusks are highly imperiled, with 70% of the North American species extinct, endangered, or at risk of extinction. Impoundments and other human impacts on the Coosa River of Alabama, Georgia and Tennessee of the southeastern USA alone are believed to have caused 50 mollusk species extinctions, but uncertainty over boundaries among several putatively closely related species makes this number preliminary. Our examination of freshwater mussels collected during an extensive survey of the upper-drainage basin, DNA barcoding and molecular phylogenetic analyses confirm the rediscovery of four morphospecies in the genus *Pleurobema* (Unionidae) previously thought to be extinct from the upper Coosa basin. A fifth 'extinct' form was found in an adjoining basin. Molecular data show that the Coosa morphologies represent at least three species-level taxa: *Pleurobema decisum*, *P. hanleyianum* and *P. stabile*. Endemism is higher than currently recognized, both at the species level and for multispecies clades. Prompt conservation efforts may preserve some of these taxa and their ecosystem.

Keywords: cox1, endangered species, molecular barcode, Pleurobema, Unionidae

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Viable mussel-population?

