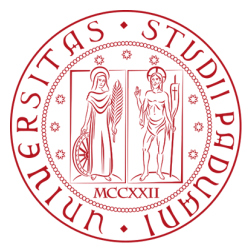




WSCS - Student Subunit
December 19th, 2023

Sturgeons in Italy

historical background,
current activities and new
insights



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Historical Background

3 autochthonous **sturgeon species** were historically present **in Italy**:

Two belong to the genus ***Acipenser***

One belongs to the genus ***Huso***



Acipenser sturio
European sturgeon



Acipenser naccarii
Adriatic sturgeon



Huso huso
Beluga sturgeon

Historical Background

Nowadays

A. sturio

European sturgeon

H. huso

Beluga sturgeon

are considered **Regionally Extinct**

RE

Multiple **factors** led to their **disappearance**

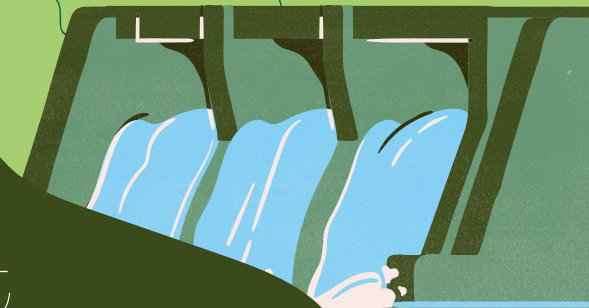


pollution



overfishing

habitat
degradation



Alien
species

Historical Background

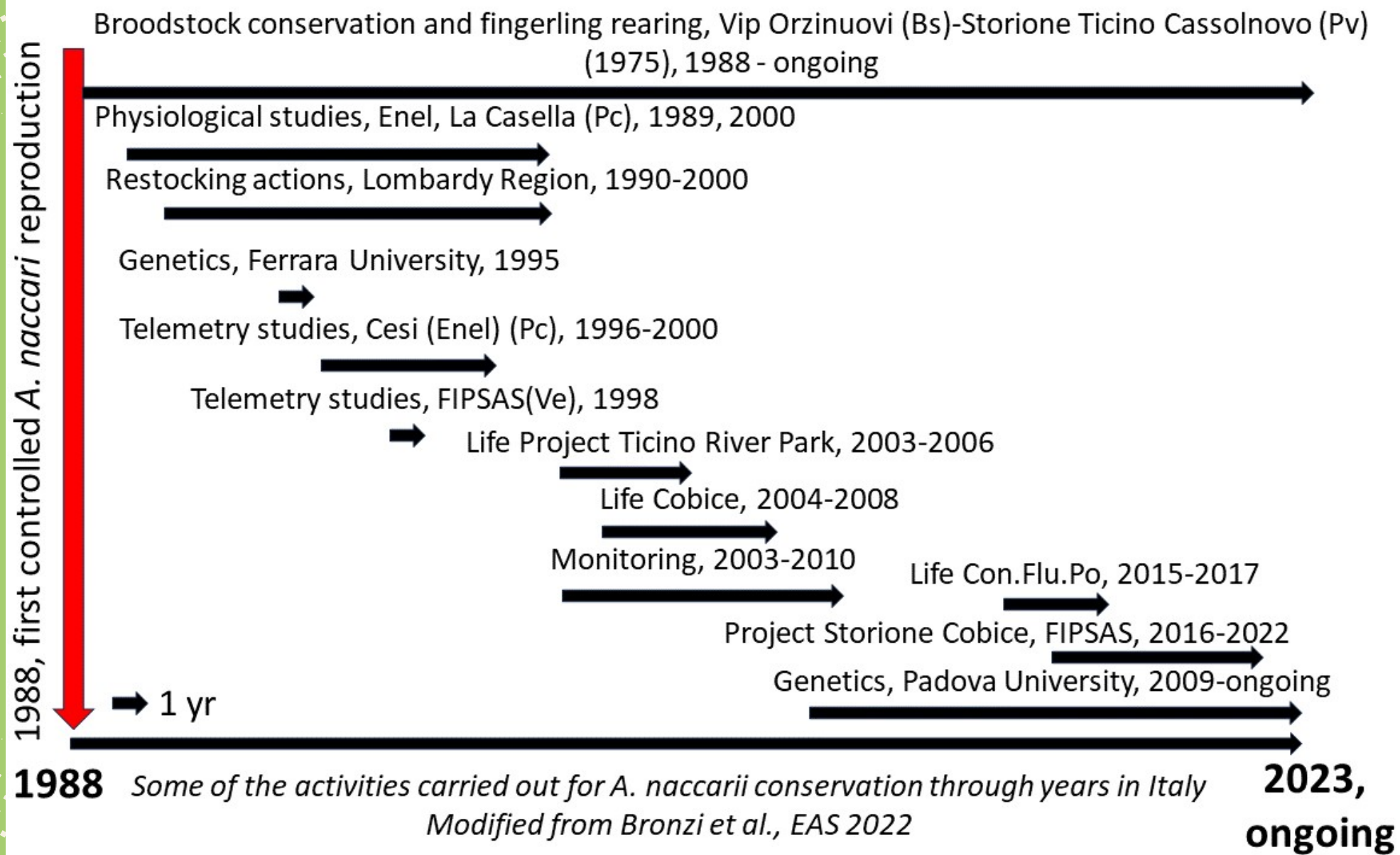


A. naccarii

Is present in some **Italian rivers**

All **reintroduced animals** are descended from a **single stock** of wild animals, **caught** in the **70s**

Showed **localised** but encouraging **signals of natural reproduction**



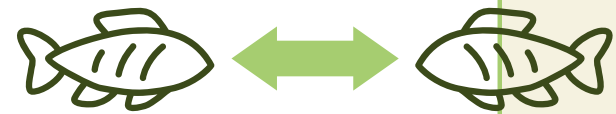


Padua University

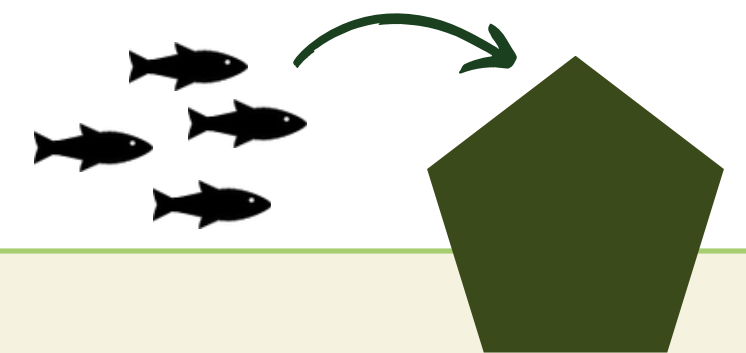


What do we do?

- **Relatedness** analysis
- **Species** identification
- **Hybrids** detection
- **Development** and **application** of **molecular markers**



- Establishment of **breeding plans**
- **Reintroduction** and **restocking** activities



Conservational Efforts





Complete genetic characterization of Adriatic and Beluga sturgeon

- **Generic screening** of the existing breeders
- **Preserve** most of the residual **genetic diversity**
- Animals taken from **aquaculture facilities**



A. naccarii



H. huso



- Investigation of **purity, relatedness** and **geographical origin** 
- **Support to reintroduction** activities in the **Po Valley rivers**

Ongoing projects



MIPS

Multiallele Intron Polymorphisms

Ongoing projects



Alternative category of **nuclear markers** developed in our laboratory

Informative for **molecular ecology studies**



- Nuclear loci with bi-parental inheritance
- Highly-variable
- Flanked by more conserved exon regions
- Amplifiable by PCR
- Potentially highly transferable



MIPS

Multiallele Intron Polymorphisms

Identification of species and interspecific hybrids

Optimization of data analysis **pipelines** for **polyploids species** analysis



Ongoing projects

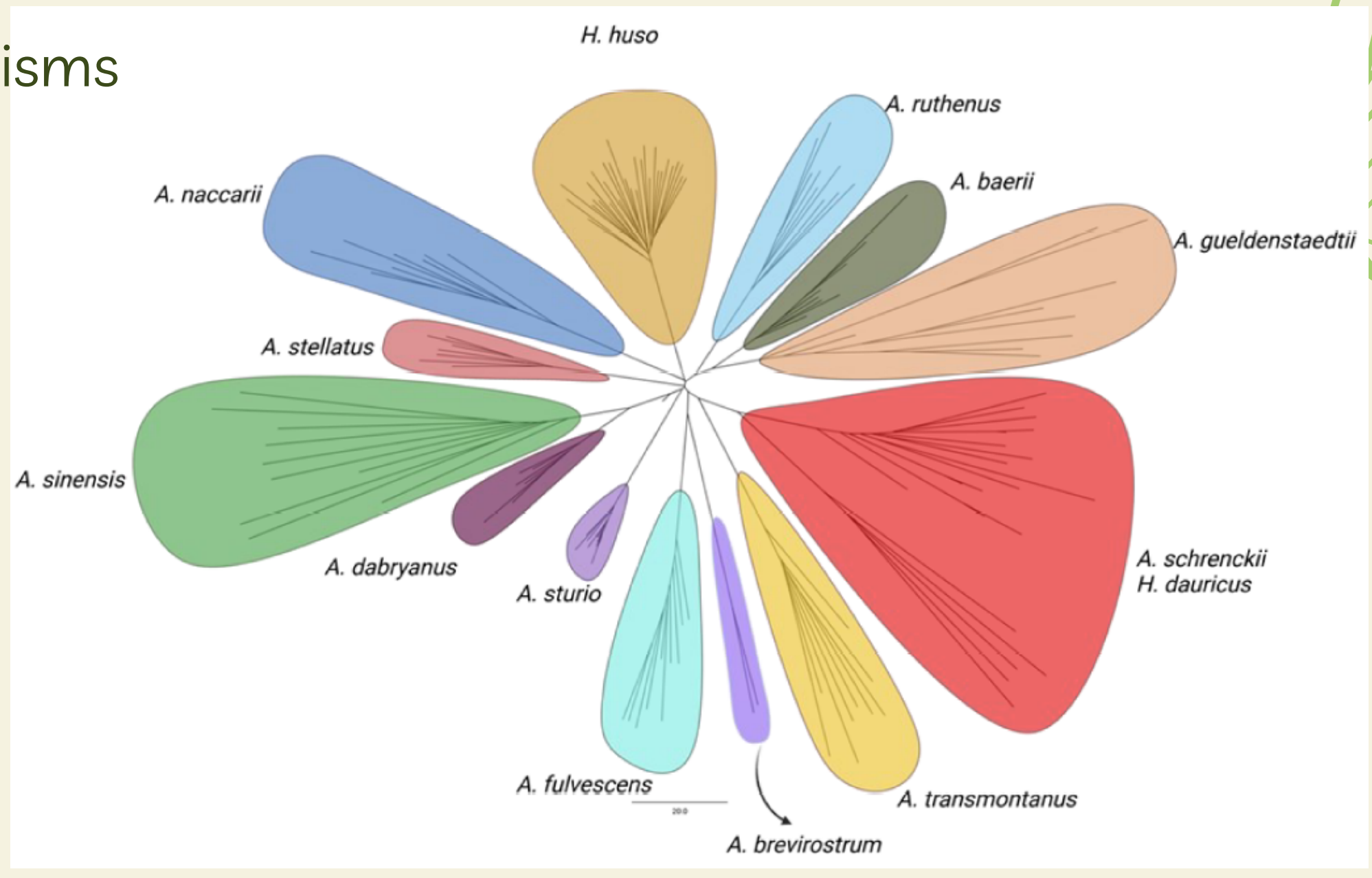


Figure 8 Neighbor-Joining tree based on the number of allelic differences among species for the 18 best characterize intronic *loci*. The genotypes at each *locus* were converted into presence/absence data for each allele. The data were then transformed into a sequence consisting of the T and A bases, to be an input file for the MEGAX software.



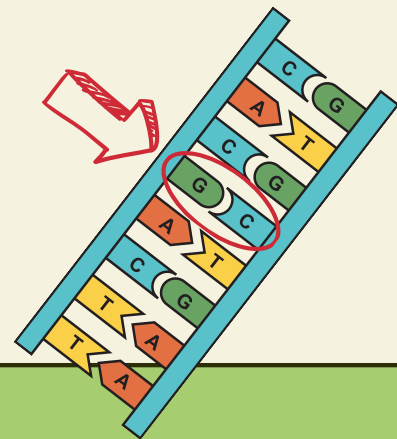
Ferrara University

What do we do?



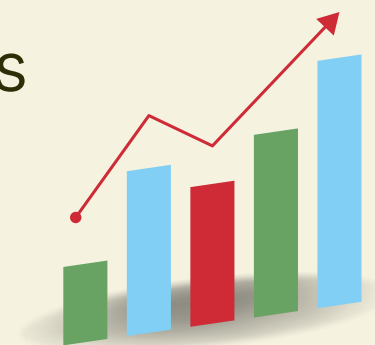
Bioinformatics

- De novo assembly to obtain a high-quality **reference genome**
- **SNP calling**



Population genomics

- **Genetic diversity** and **inbreeding level**
- **Demographic** reconstructions
- **Mutation load** estimations
- Forward **simulations**

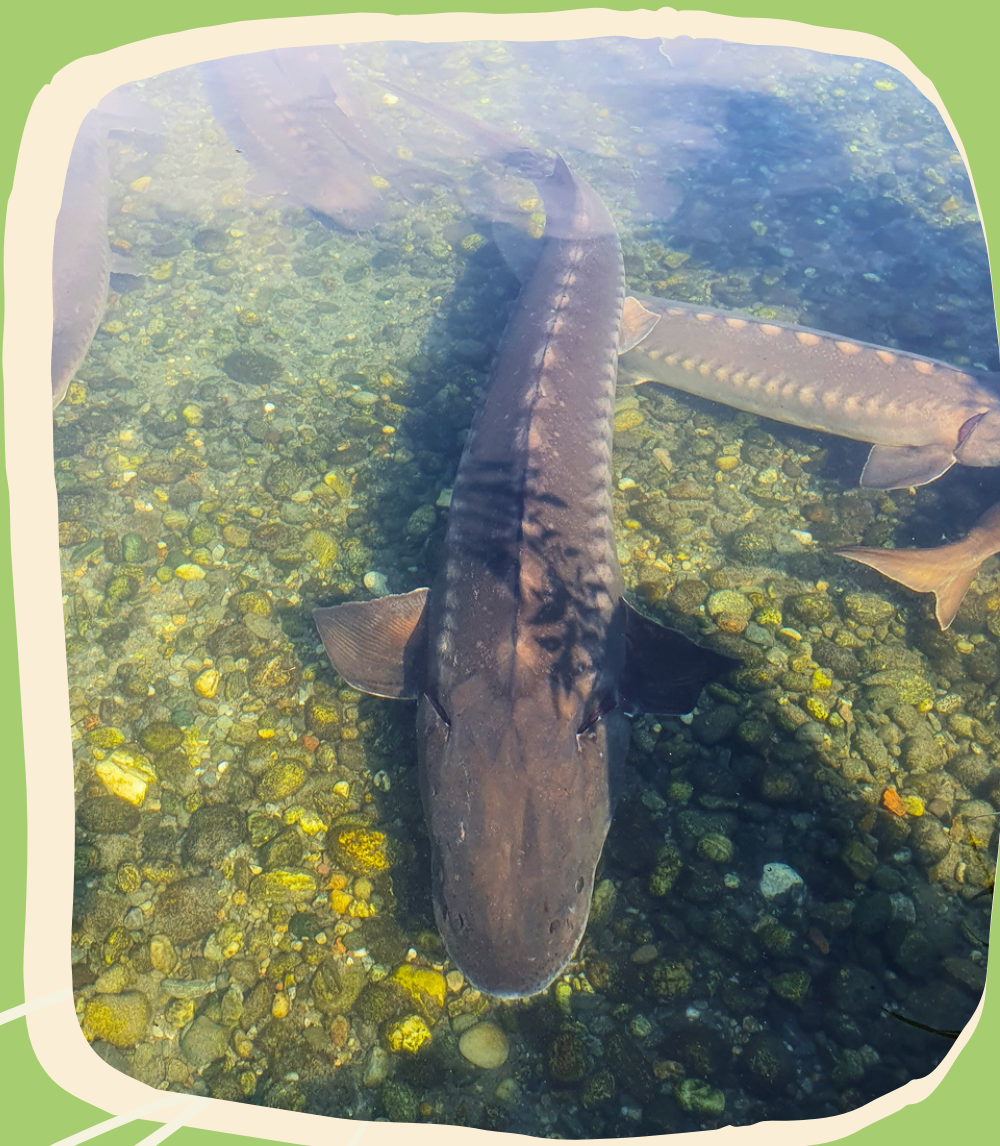


Conservation genomics



High quality reference genome for *A. naccarii*

Ongoing projects



Sequencing data

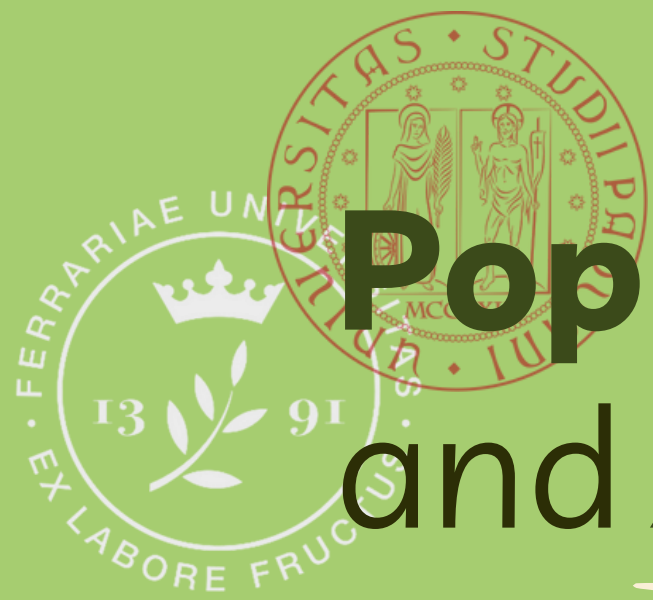
- **PacBio** HiFi reads
- **Arima Hi-C** reads
- **Illumina** reads



Aims

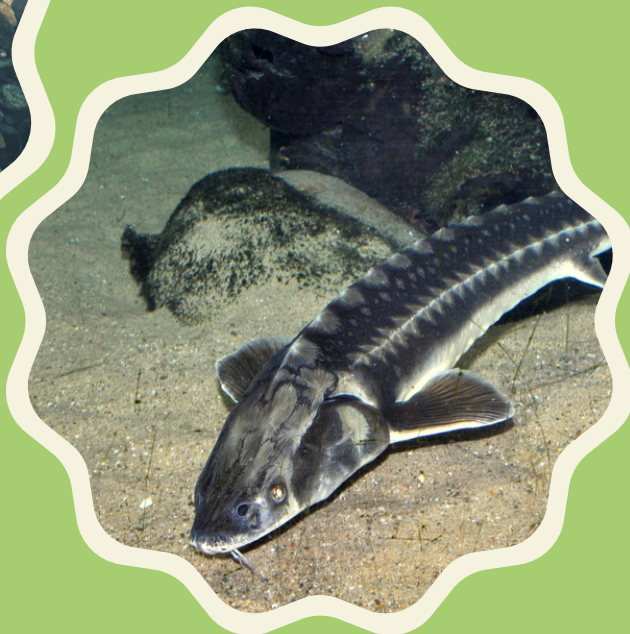
- Develop **tetraploid-specific pipelines** for genome assembly
- Obtain a **chromosome-scale reference genome** with a high completeness





Population genomics of *A. naccarii* and *A. gueldenstaedtii*

Ongoing projects



Genomic data

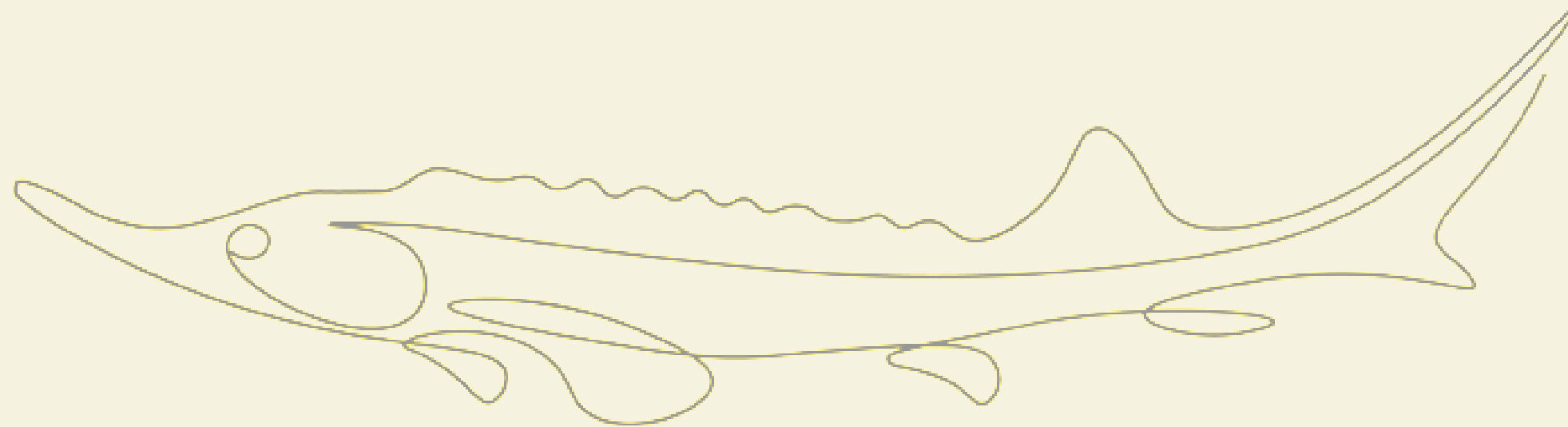
- 18 **Adriatic surgeons** (small population)
- 10 **Russian sturgeons** (large population)

Aims

- **Comparing** genetic diversity, inbreeding levels, and mutation load
- Make **predictions on the risk of extinction** of *A. naccarii*
- Develop **conservation strategies** for *A. naccarii*



Thanks for your attention



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