Population structure and genetic diversity in the Eurasian shad, *A. alosa* and *A. fallax*: Implications for Conservation

Alosa alosa: Allis Shad

Alosa fallax: Twaite Shad

Stephen SABATINO, Paulo ALEXANDRINO (U. of Porto, Portgual)

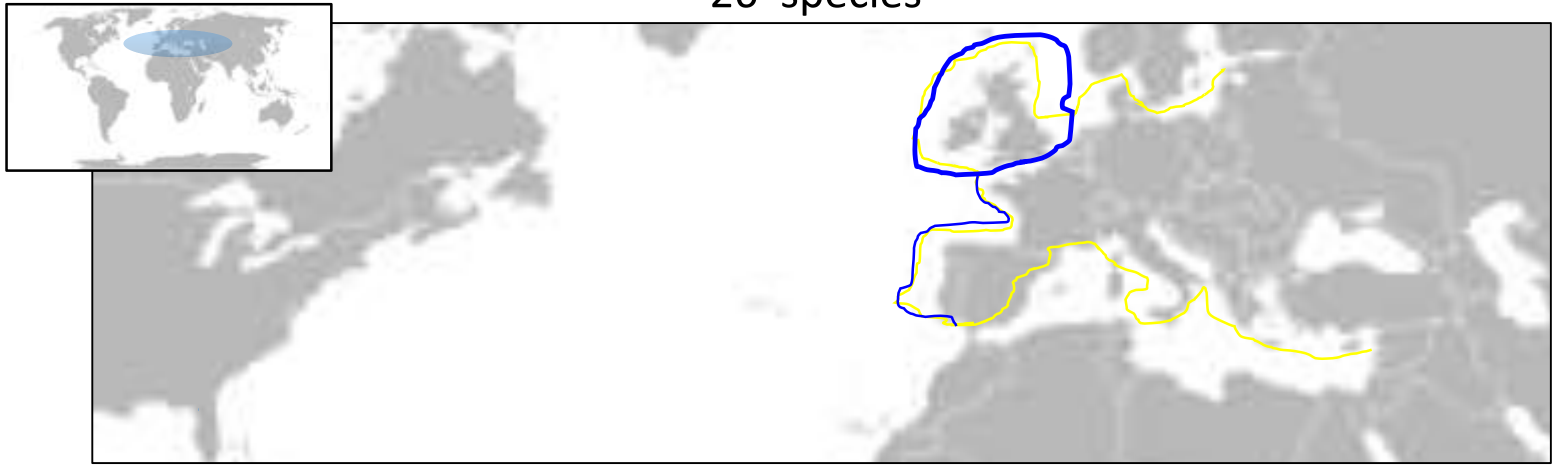
Allis shad
A. alosa

Twaite Shad
Alosa fallax

Family Clupeidae	>300 species: sardines, hilsa, anchovy, herring	Worldwide distribution, MOSTLY tropical Asia
	Usually 10–30 cm Up to 75cm (*Alosa*)	Coastal, marine, brackish some anadromous or freshwater (i.e. *Alosa*)
	Important fisheries	Generally planktivores, important primary/secondary consumers, ecosystem indicators

Genus *Alosa* (River Herrings)
26 species

Eurasia (20 species)



Closely related ~ 1–2% sequence divergence at mtDNA loci, <1% at nuclear loci

Variation in size, feeding strategies, migratory patterns and the number of times they reproduce in a lifetime

A. alosa (Allis shad)

- Eastern Atlantic
- Lakes in Portugal

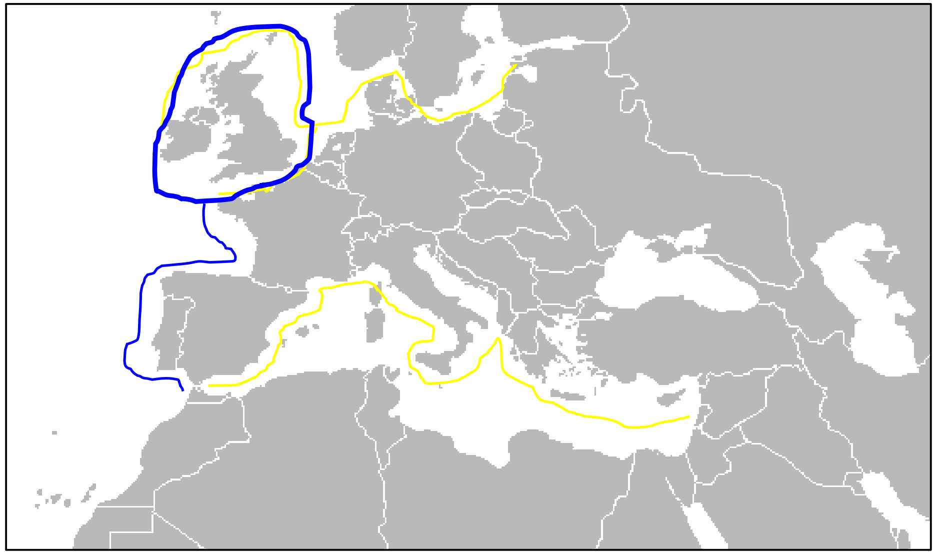
A. fallax (Twaite shad)

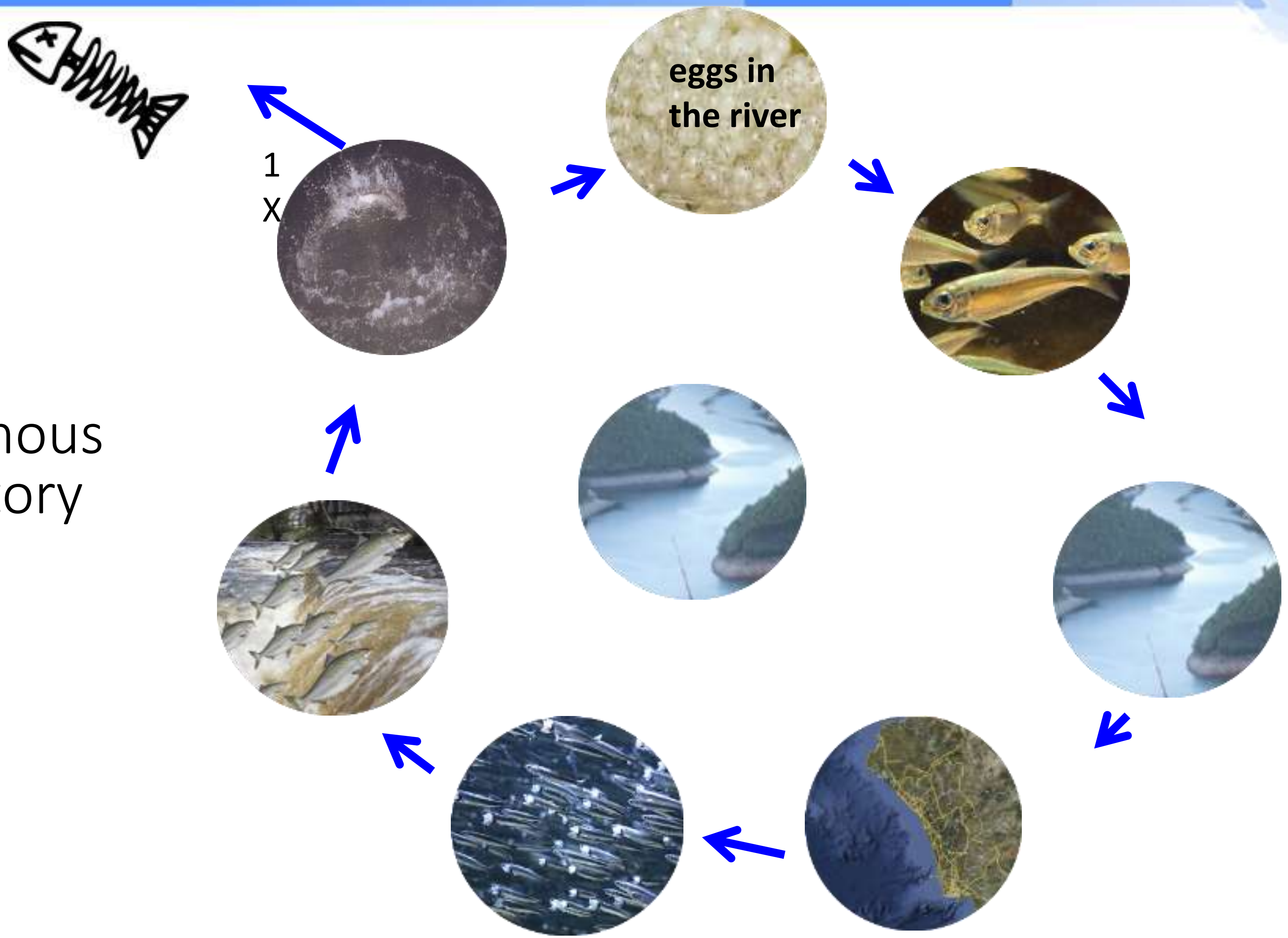
- Eastern Atlantic and Mediterranean
- Lakes in Ireland, Italy, Montenegro

A. alosa

A. fallax

	A. alosa	*A. fallax*
Adult Size	45-85cm	20-40cm
# Gill Rakers/ Feeding Mode	115-160 Planktivores	40-65 Omnivores
# of Spawnings	1 (Semelparous)	2-7 (Iteroparous)
Spawning Site	Upper rivers: 100 – 1200km	Lower rivers: 50-300km

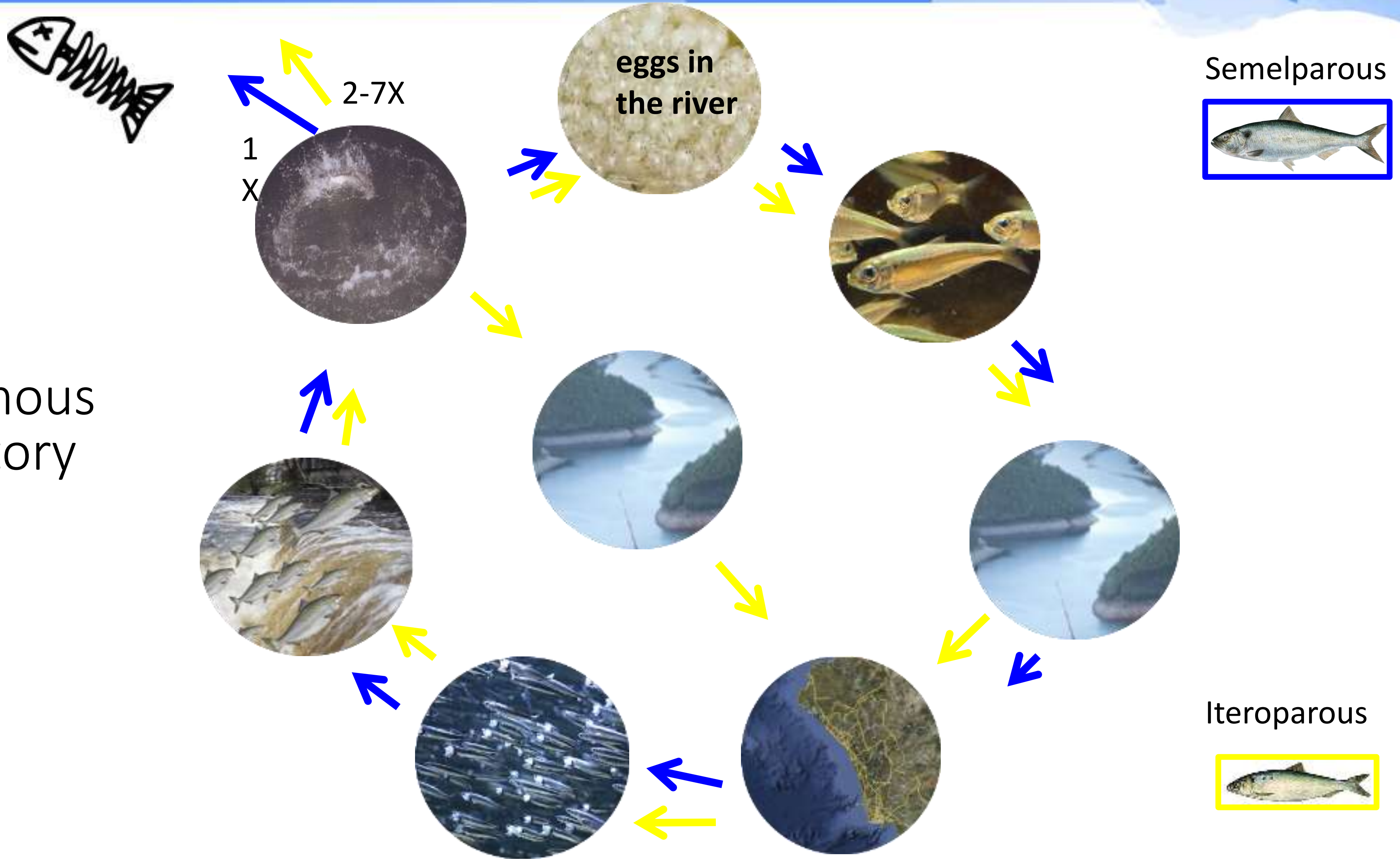




Semelparous

Anadromous Life History

Anadromous Life History



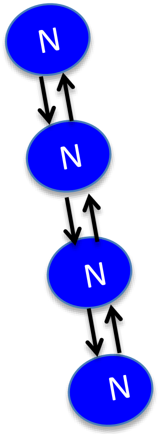
Anadromous fish species often return to their natal drainage, or one nearby, to spawn

"Homing"

Homing can promote population structure

Straying from natal drainage is often local

"Straying"



Can lead to a "**Stepping-Stone**" mode of dispersal and isolation-by-distance

A. alosa

BIGGER

MIGRATES FAR

SPAWNS 1X

PLANKTIVORE

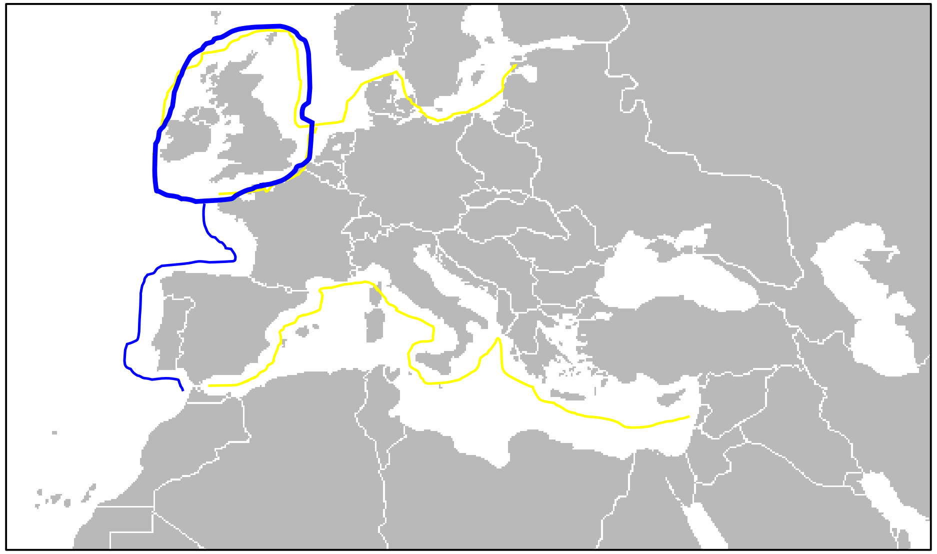
A. fallax

SMALLER

MIGRATES LESS FAR

SPAWNS > 1

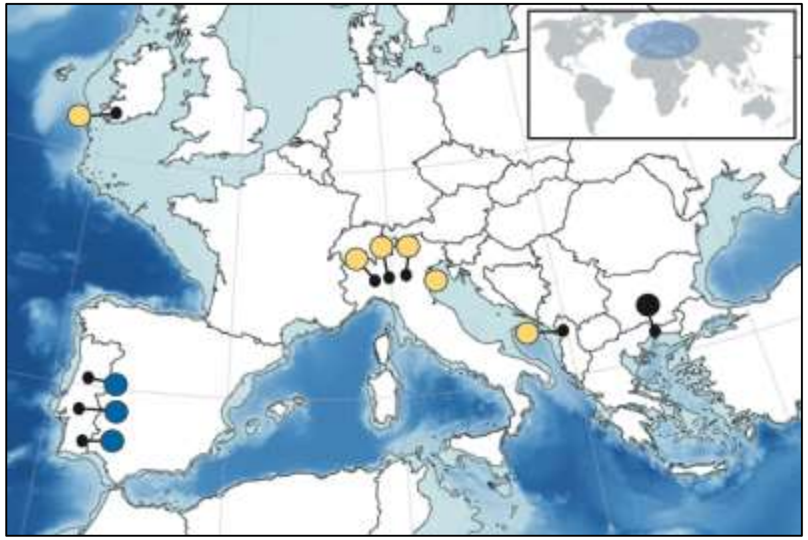
OMNIVORE



Landlocked Populations

Castelo de Bode, Portugal

Lake Killarney, Ireland

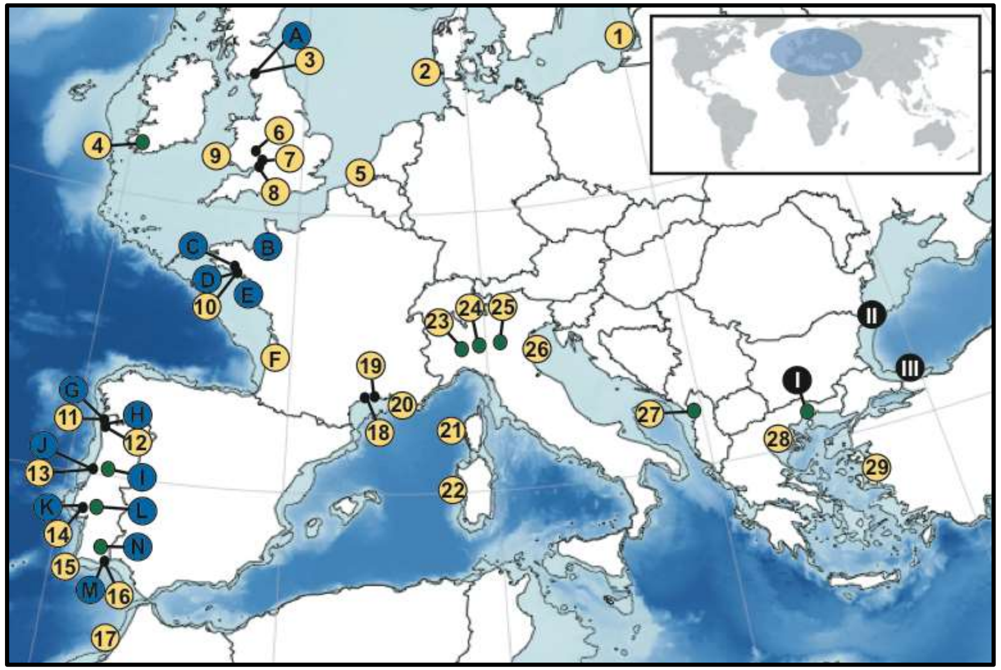


- Smaller than anadromous relatives
- *A. fallax* tend to become planktivores
- Some evidence that *A. alosa* can be iteroparous

A. alosa

A. fallax

Sampling



10 anadromous, 3 landlocked *A. alosa* populations

26 anadromous, 4 landlocked *A. fallax* populations

landlocked

Methods: Population Genetic Analyses

21 microsatellite loci, 13 populations of *A. alosa*, 550 individuals

18 microsatellite loci, 30 populations of *A. fallax*, 750 individuals

-Pairwise F_{ST}

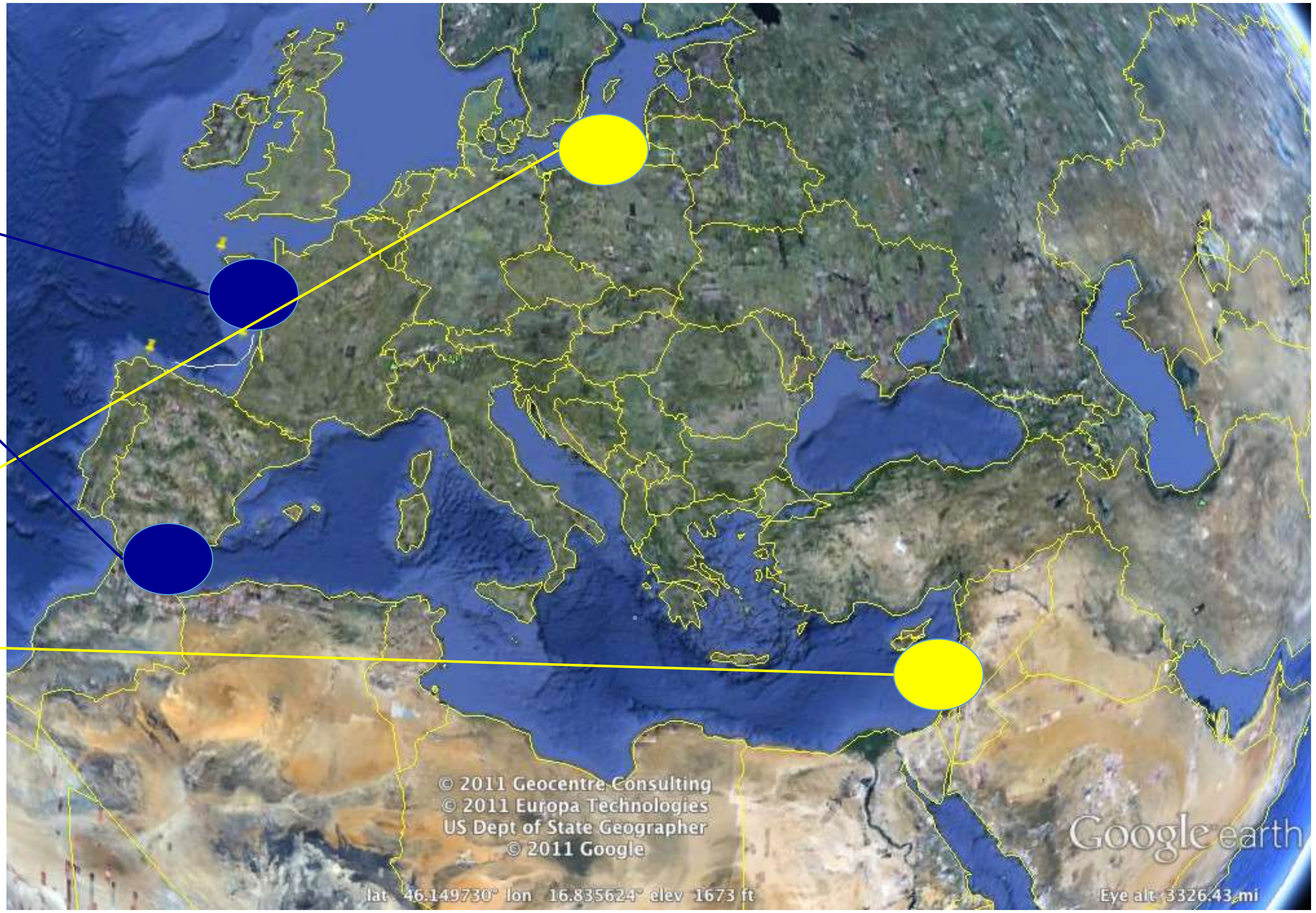
-BAPS: Bayesian cluster analysis (Corander et al. 2004)
-Location used as a prior

-MSA using ONCOR (ONCOR: Kalinowski et al. 2007)
-Leave-one-out-test

F_{ST} between the two most geographically distant populations in *A. alosa* and *A. fallax*

A. alosa
F_{ST}: 0.075

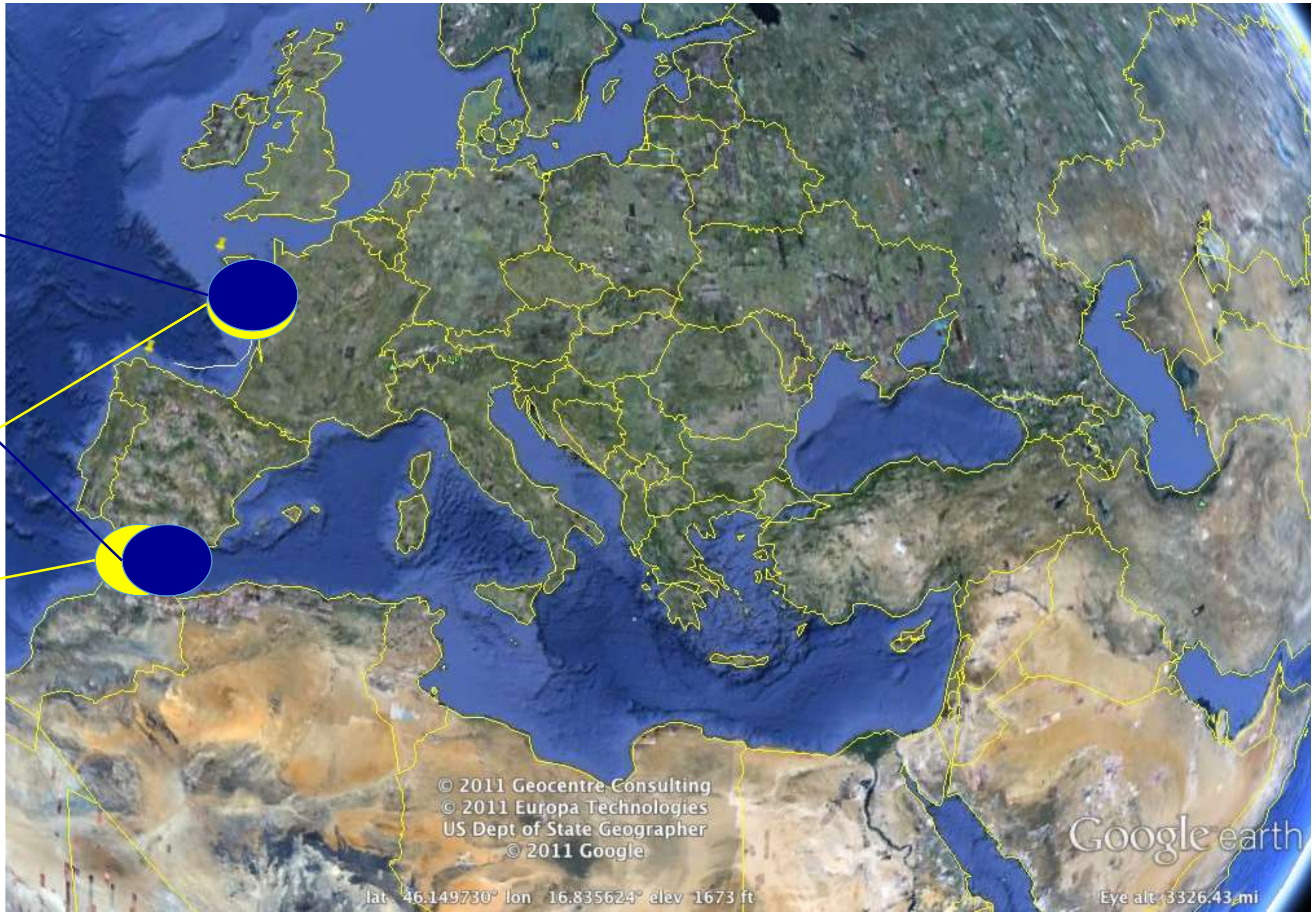
A. fallax
F_{ST}: 0.590



F_{ST} between the two most geographically distant populations in *A. alosa* and *A. fallax* in the same range

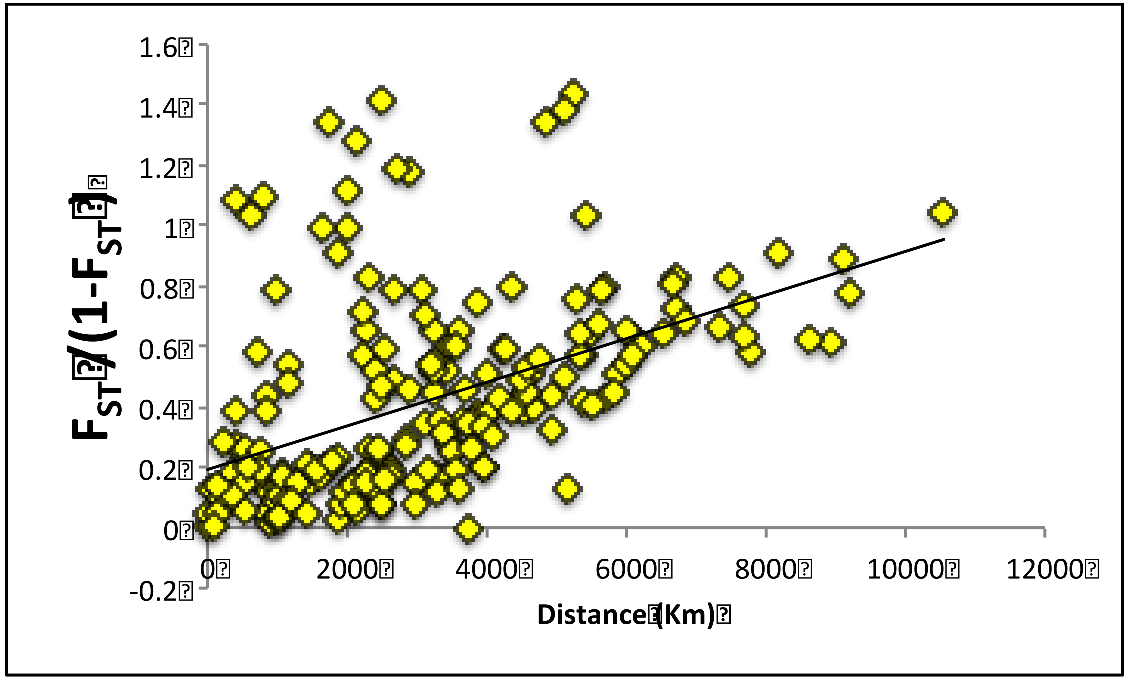
A. alosa
F_{ST}: 0.075

A. fallax
F_{ST}: 0.140



Isolation By Distance

Entire range

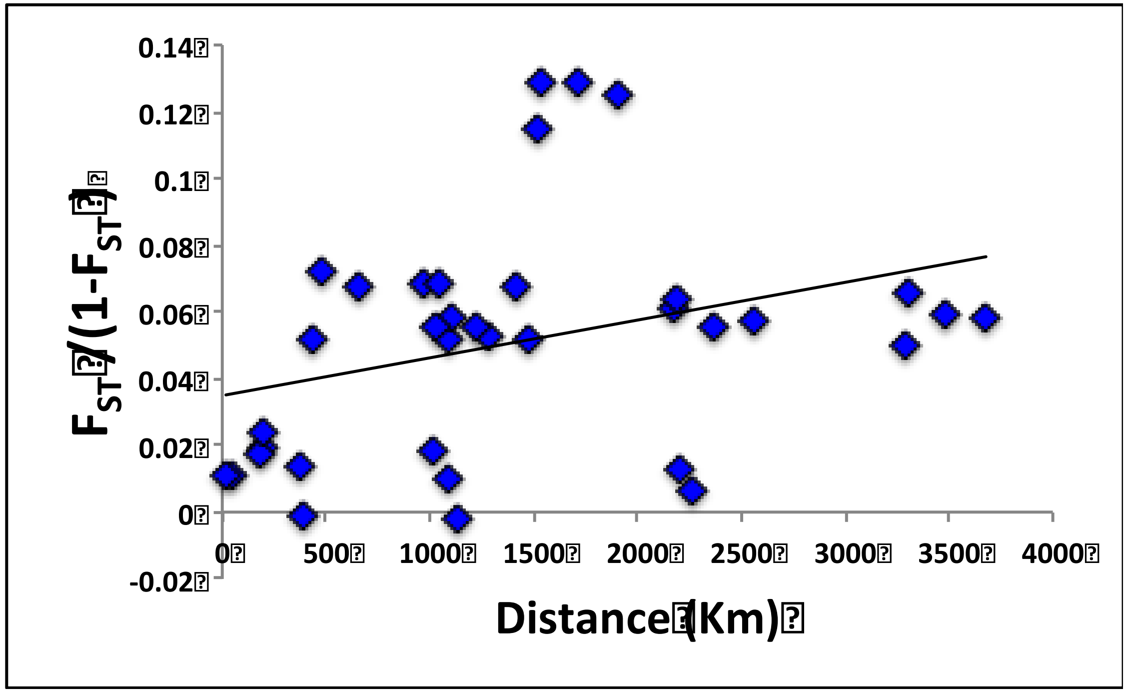


A. fallax

***r* = 0.377 (*p* = 0.008)**

Isolation By Distance

Entire range



A. alosa

***r* = 0.329 (*p* = 0.082)**

Conclusions about spatial scale of population structure

- About 2x genetic structure among *A. alosa* populations as *A. fallax* over the same geographic distance

- Isolation by distance in *A. fallax* and perhaps *A. alosa* may be due to similar patterns of straying in both species (i.e. "stepping stone"), but more populations of *A. alosa* must be studied

Life History and Population Structure

- **Migration at sea**
  - *A. alosa* have the capacity to, and may, go further at sea than *A. fallax* to reach rich feeding grounds associated with a planktivore diet
- **Semelparity versus iteroparity**
  - *A. alosa* stay at sea much longer, could stray further from natal drainage by chance
  - *A. fallax* must return to their natal rivers each spawning season…costly to stray too far

Life History and Population Structure

Assuming:

1) Similar homing capacities in *A. alosa* and *A. fallax*

2) They colonized the North Atlantic around the same time after the glaciers receded

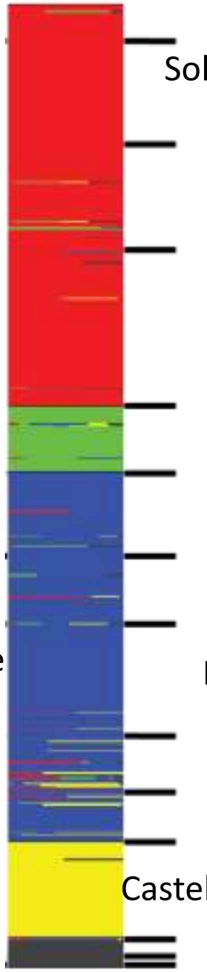
Then:

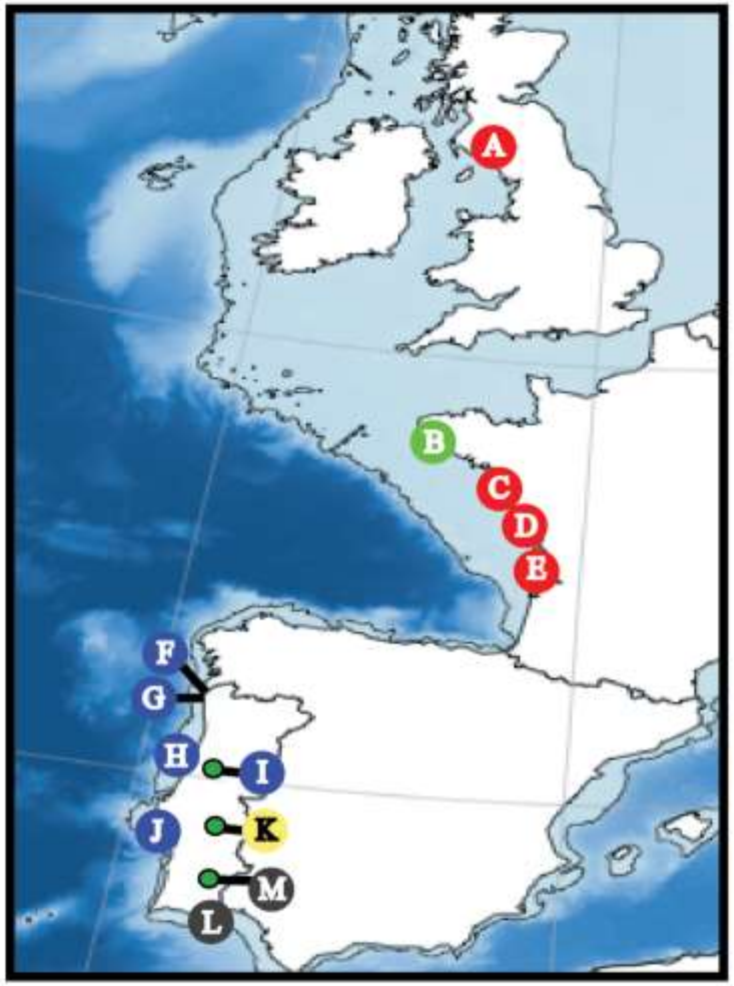
Life history may explain the higher level of population structure in *A. fallax* (iteroparous) compared to *A. alosa* (semelparous)

Anadromous and landlocked average (F_{ST})

	Species	Anad.	Land.	History
	*A. alosa*	0.07	0.09	Manmade populations, last 70 years or earlier
	*A. fallax*	0.30	0.53	Natural, at least since recorded history and probably much older (~ post-Pleistocene)

A. alosa

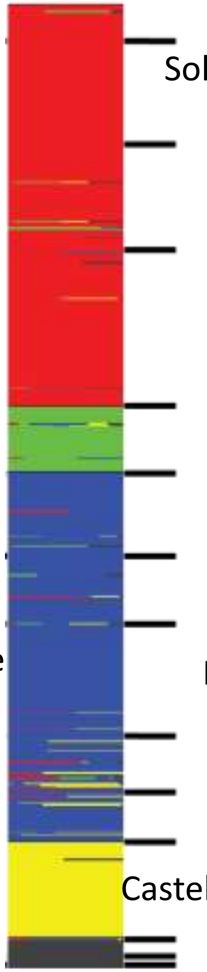


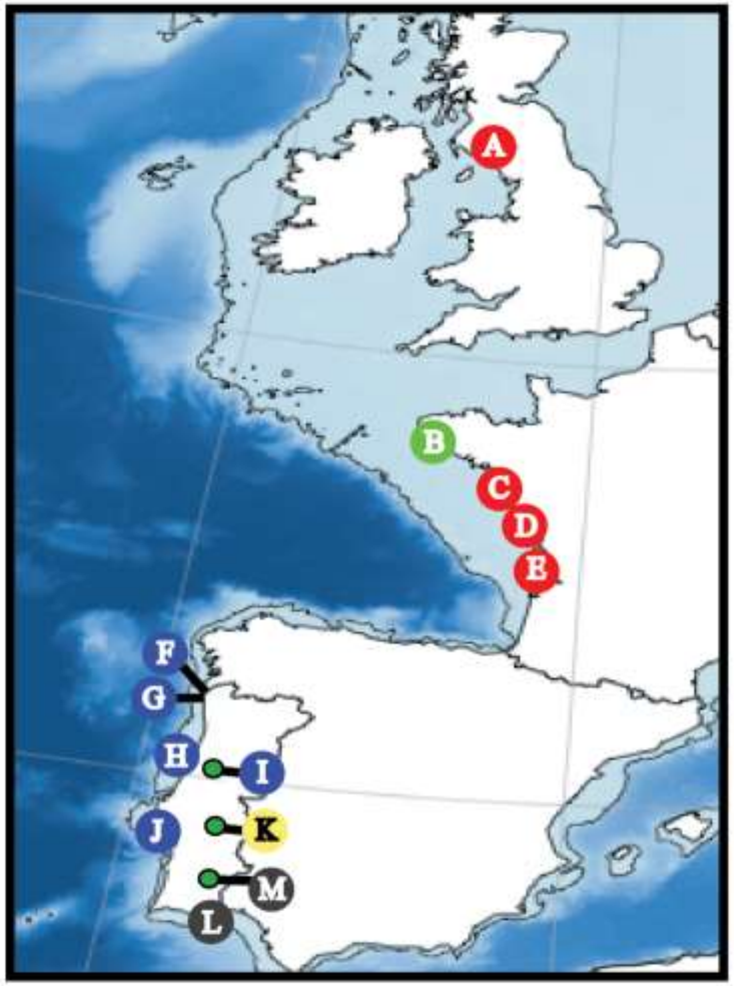


BAPS Cluster analysis
K (# of clusters) = 5

Mixed Stock Analysis

A. alosa

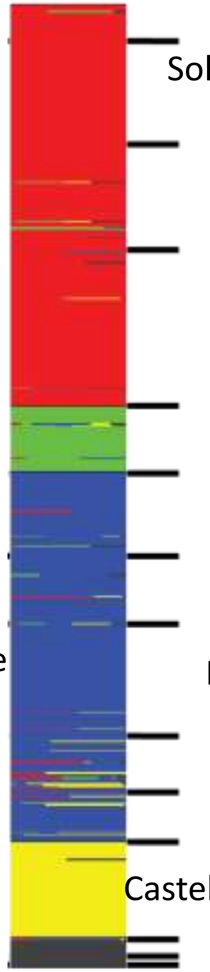


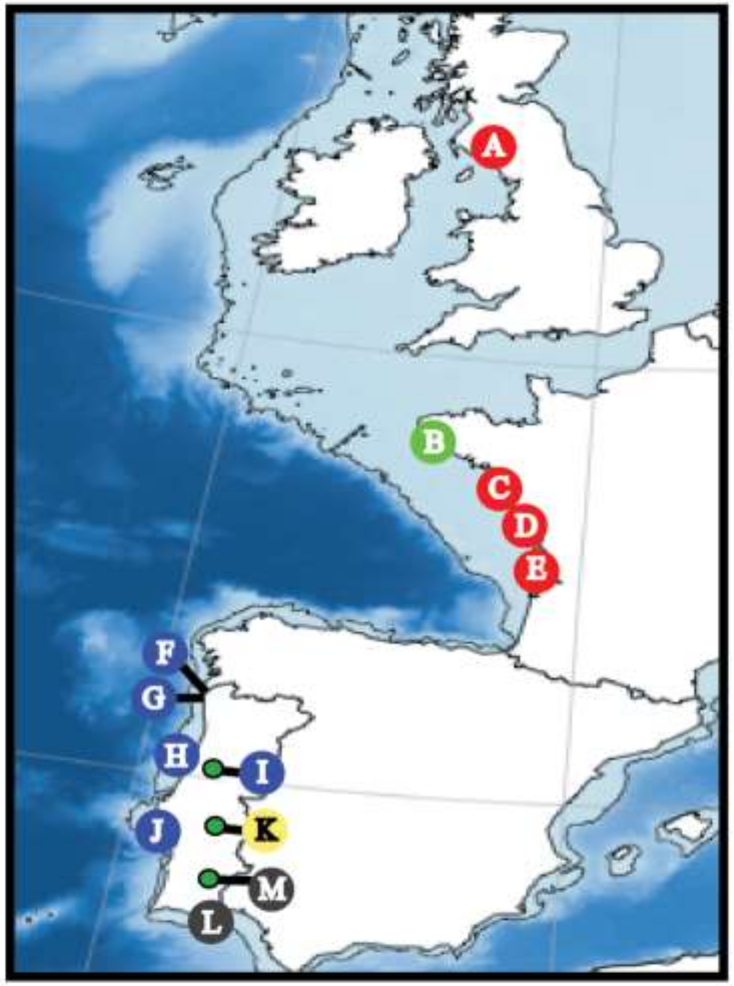


% Correctly
Assigned to
population

Mixed Stock Analysis

A. alosa

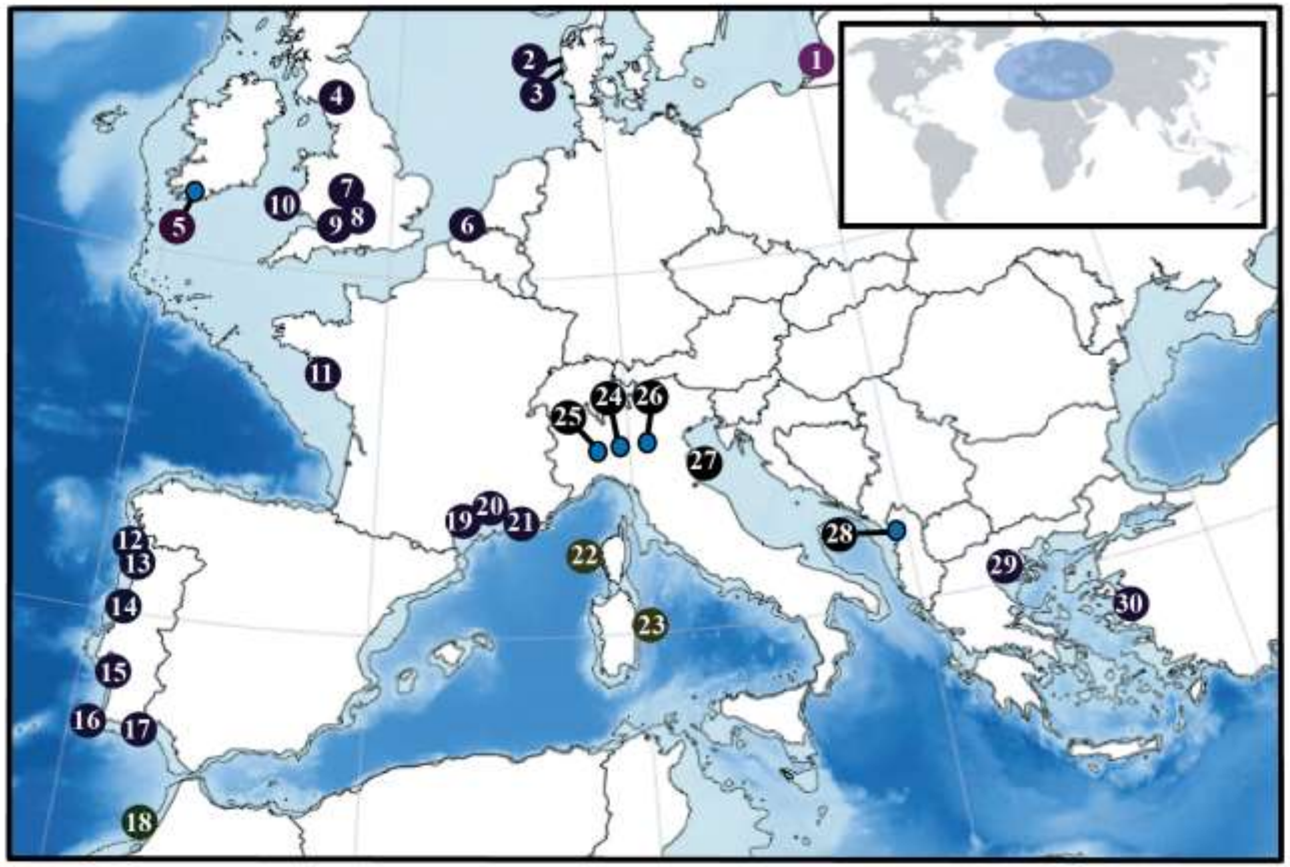




% Correctly Assigned to **cluster**

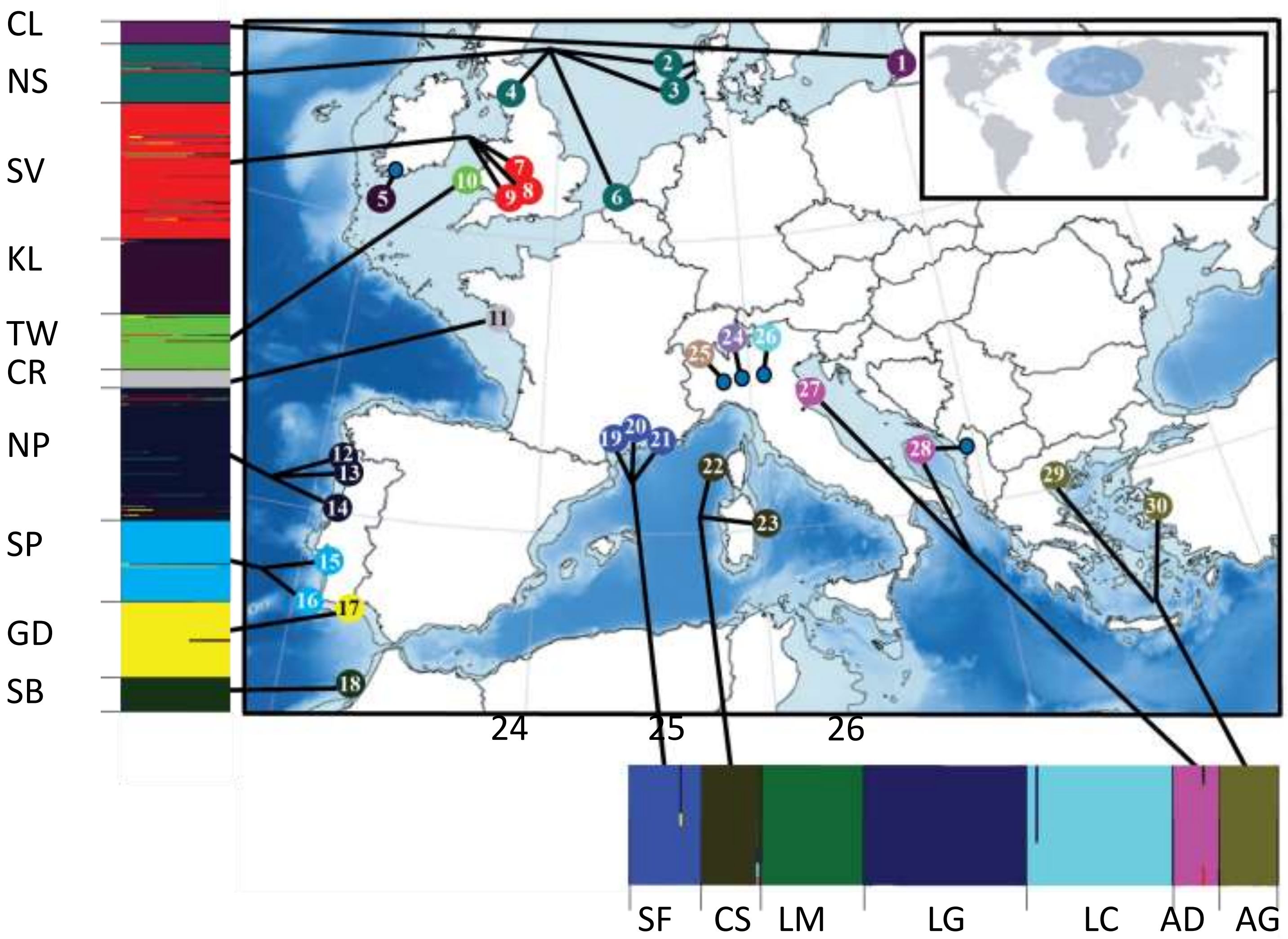
A. fallax

1	Curonian Lagoon	100.00%
2	Solway Firth	25.00%
3	Lake Killarney	90.00%
4	Scheldt Estuary	63.60%
5	Severn River	90.00%
6	Towy River	95.20%
7	Charente River	80.00%
8	Minho River	62.90%
9	Lima River	59.10%
10	Mondego River	36.40%
11	Tejo River	63.60%
12	Mira River	93.30%
13	Guadiana River	85.00%
14	Sebou River	100.00%
15	Rhone River	70.00%
16	Aude River	86.70%
17	Tavignano River	100.00%
18	Lake Maggiore ¢	100.00%
19	Lake Como	100.00%
20	Lake Garda	97.50%
21	Lake Skadar	100.00%
22	Pinios River	100.00%
23	Izmir Bay	100.00%



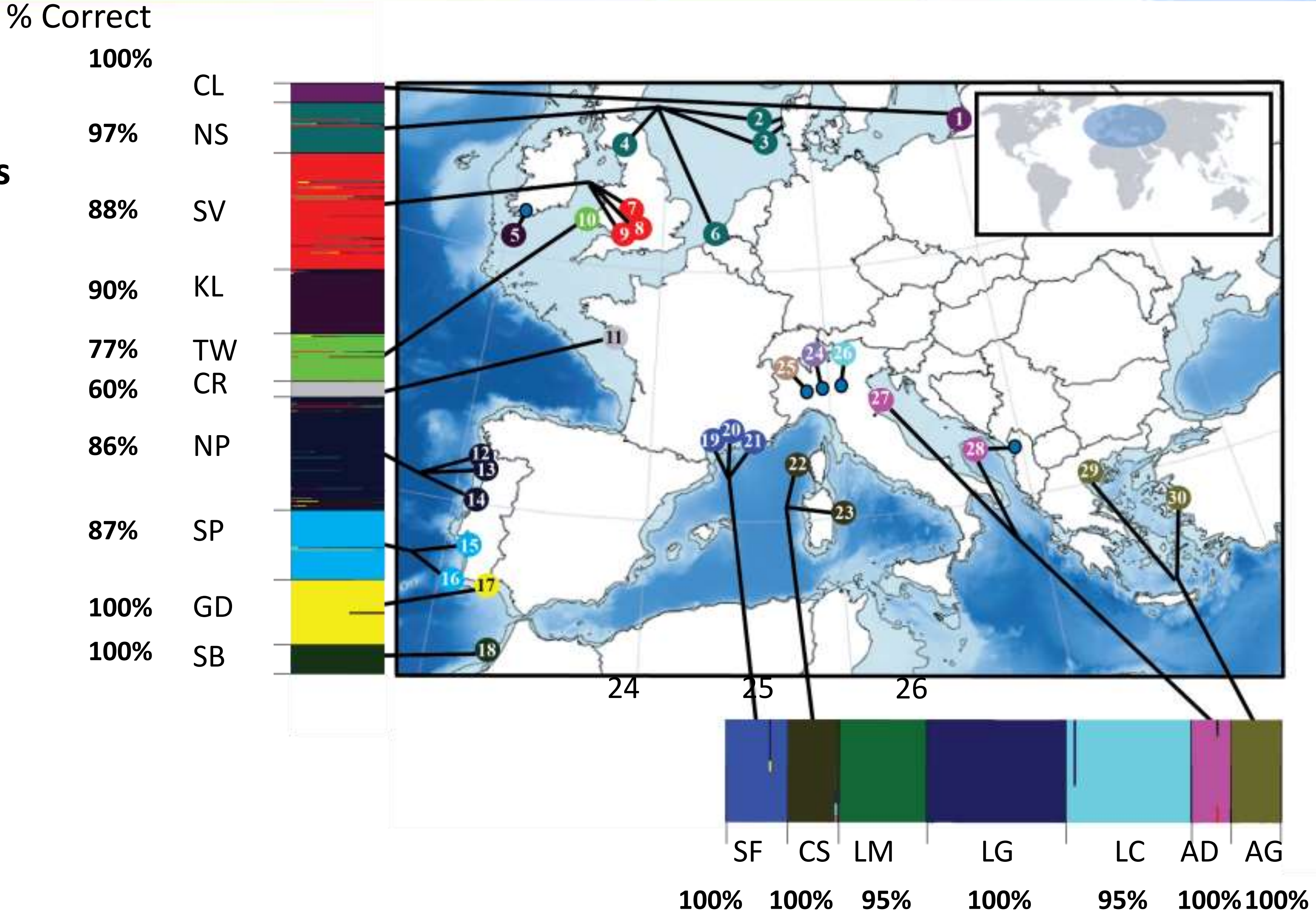
Mixed stock analysis
% Correctly Assigned to **population**

BAPS Cluster analysis
K (# of clusters) = 17



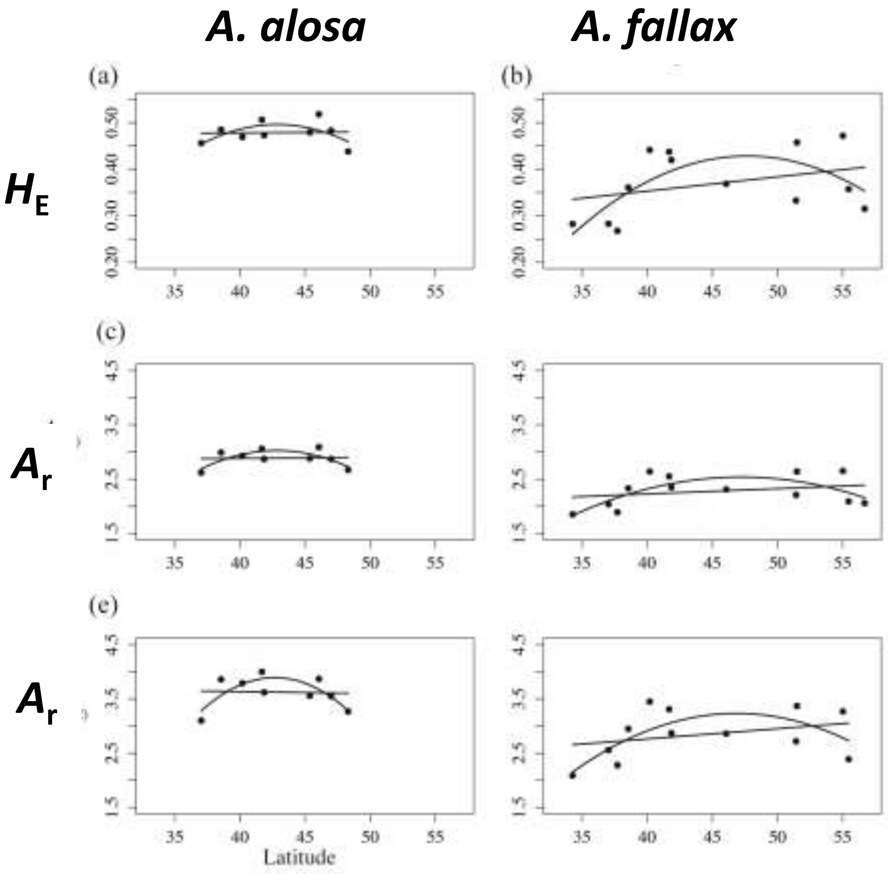
A. fallax

BAPS Cluster analysis
K (# of clusters) = 17



A. fallax

Genetic Diversity and latitude

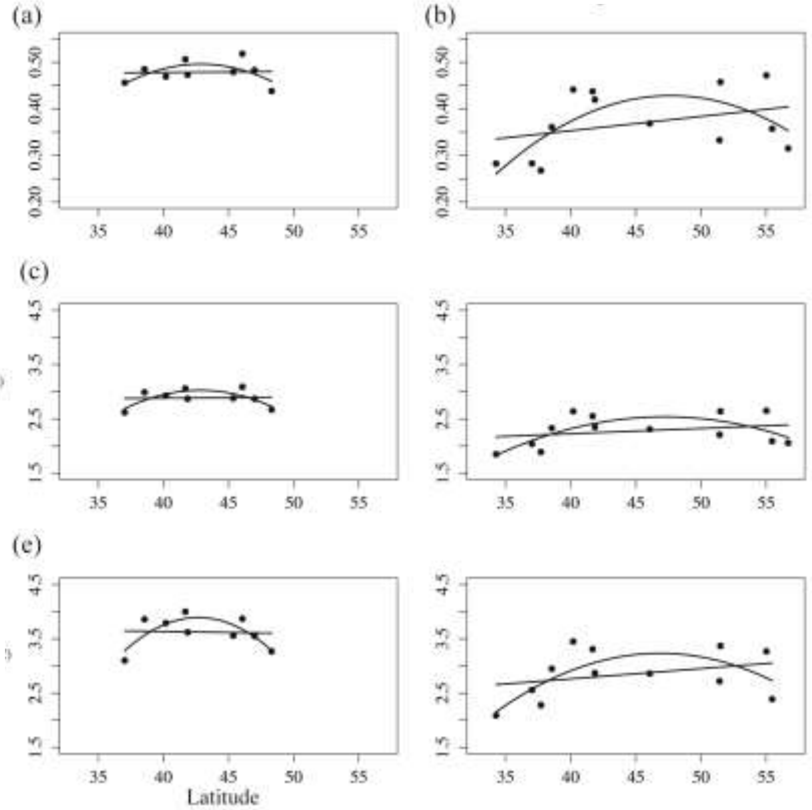


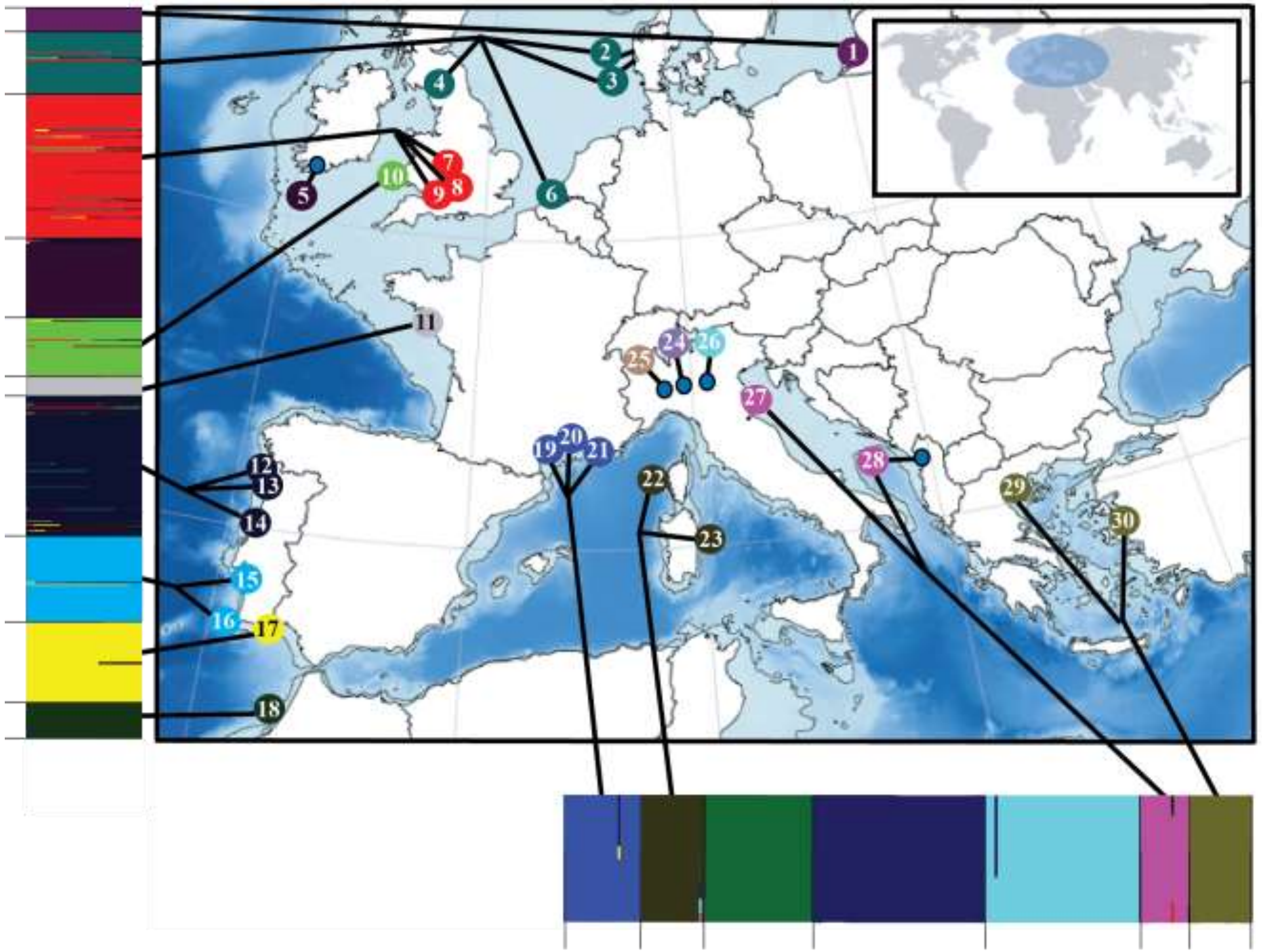
A. alosa *A. fallax*

H_E

A_r

A_r



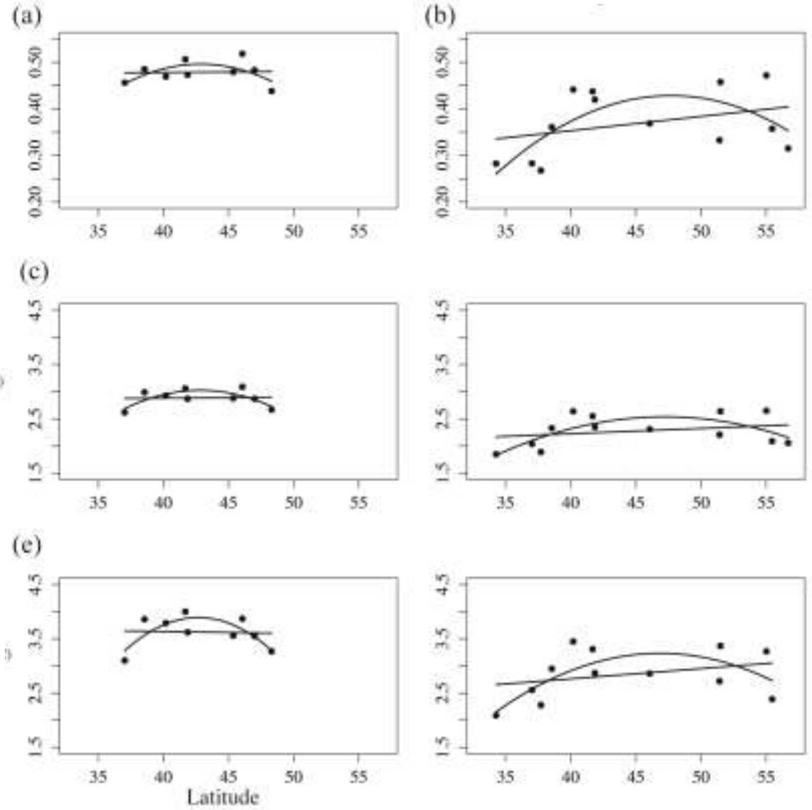


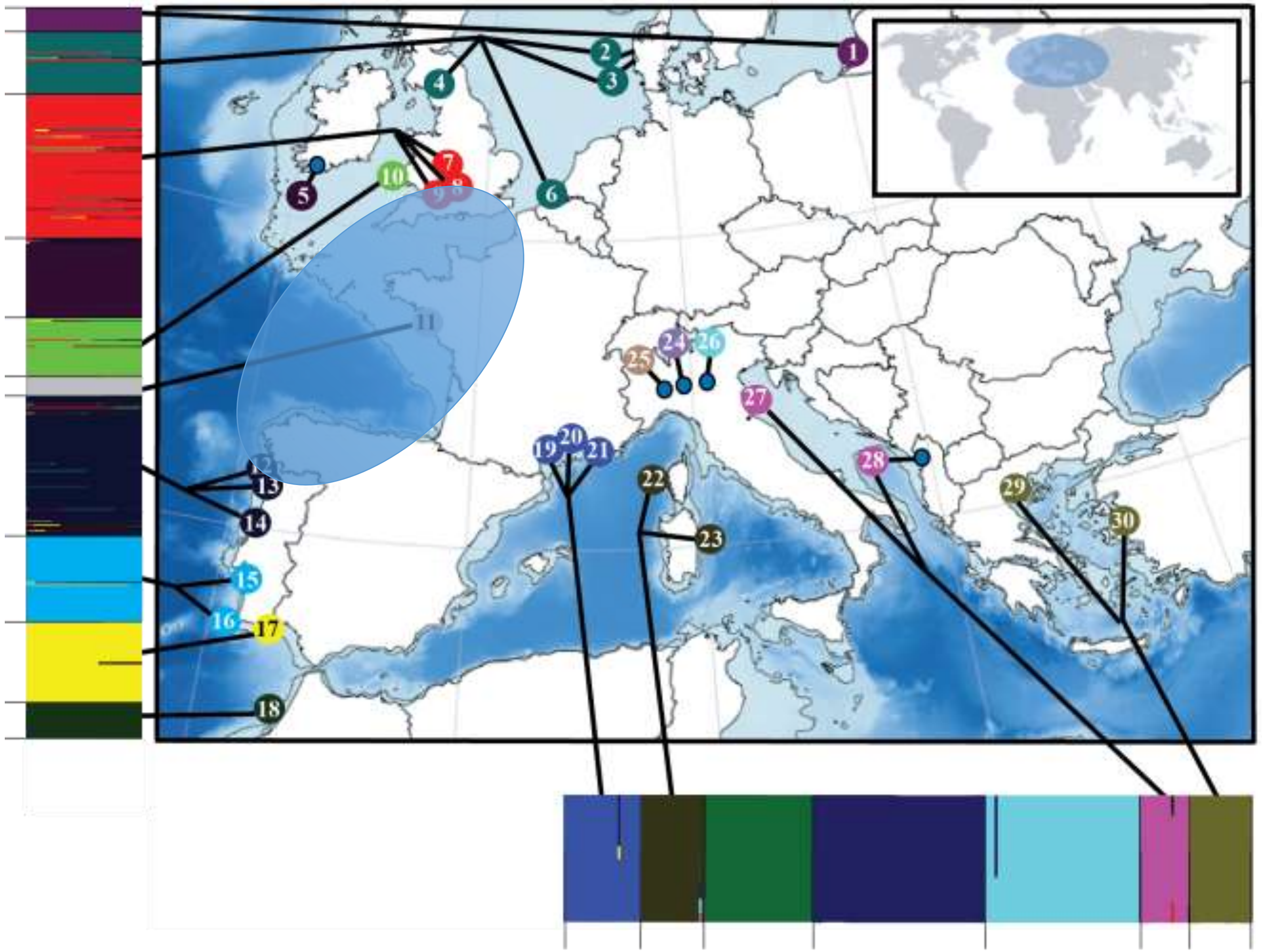
A. alosa *A. fallax*

H_E

A_r

A_r





Summary

- Population structure was about twice as high in anadromous *A. fallax* than *A. alosa*, possibly due to life history differences between them

- Landlocked populations of each species show the greatest genetic differentiation, should be conservation priorities

- The capacity to assign individuals from mixed stocks to their spawning locations using these 18+ microsatellite loci varied among drainages from 12 — 100%

- Generally high (60—100% in *A. fallax*, 88—100% in *A. alosa*) capacity to assign individuals to their genetic cluster
  - In general, genetic clusters span distances of a few hundred kilometers
  - Poor assignment is for populations/clusters that appear truly admixed
  - Clusters may provide a preliminary basis for management units for each species

Summary

- Cluster analysis may be useful for incorporating meta-population dynamics into conservation strategies for *Alosa*

- Non-linear patterns of genetic diversity in the Atlantic
  - Higher in the center of their Atlantic ranges
  - Spatial patterns of genetic diversity should be taken into account when devising conservation strategies for *Alosa*

Ongoing work: Transcriptome analysis

- 74 SNP loci from coding regions of the genome
- Similar patterns of population differentiation among populations within *A. fallax* and *A. alosa*
  - MSA: Equal or worse power to assign individuals to population compared to (~ 20) microsatellite loci
  - Useful for hybrid analysis, 20 msats are probably not enough

Ongoing work: Genome analysis

- Dozens of interesting genes associated with adaptation to a completely freshwater life cycle

- Selection on genes associated with osmoregulation, long distance migrations, the capacity to navigate long distances at sea (brain size and function) – LIFE HISTORY

- Likely that adaptive genes associated with different life histories will be identified and help in conservation planning for *Alosa*

Paulo Alexandrino

Jolita Dilyte

Rui Faria

Walt Eanes, Michael Bell and Stephan Munch

Members of CIBIO/InBio, Portugal, especially, Sandra Alfonso and Susana Lopes

Many generous, hardworking fishermen and researchers that helped with sampling

Our funding agencies