

Genetic diversity in Baltic Sea trout

- What has been done
- What should be done
- Examples from other species

Baltic sea trout: What has been done so far?

Surprisingly few published studies and with restricted geographic scope (e.g. Denmark, Bornholm, Gotland).

No comprehensive description of the overall population structuring throughout the Baltic.

Existence of major groupings and their relationship is poorly known

An incomplete list.....

Assesment of genetic status of individual populations

Monitoring

Detection of conservation units:

- Large-scale (entire Baltic Sea) and within-river genetic structure -

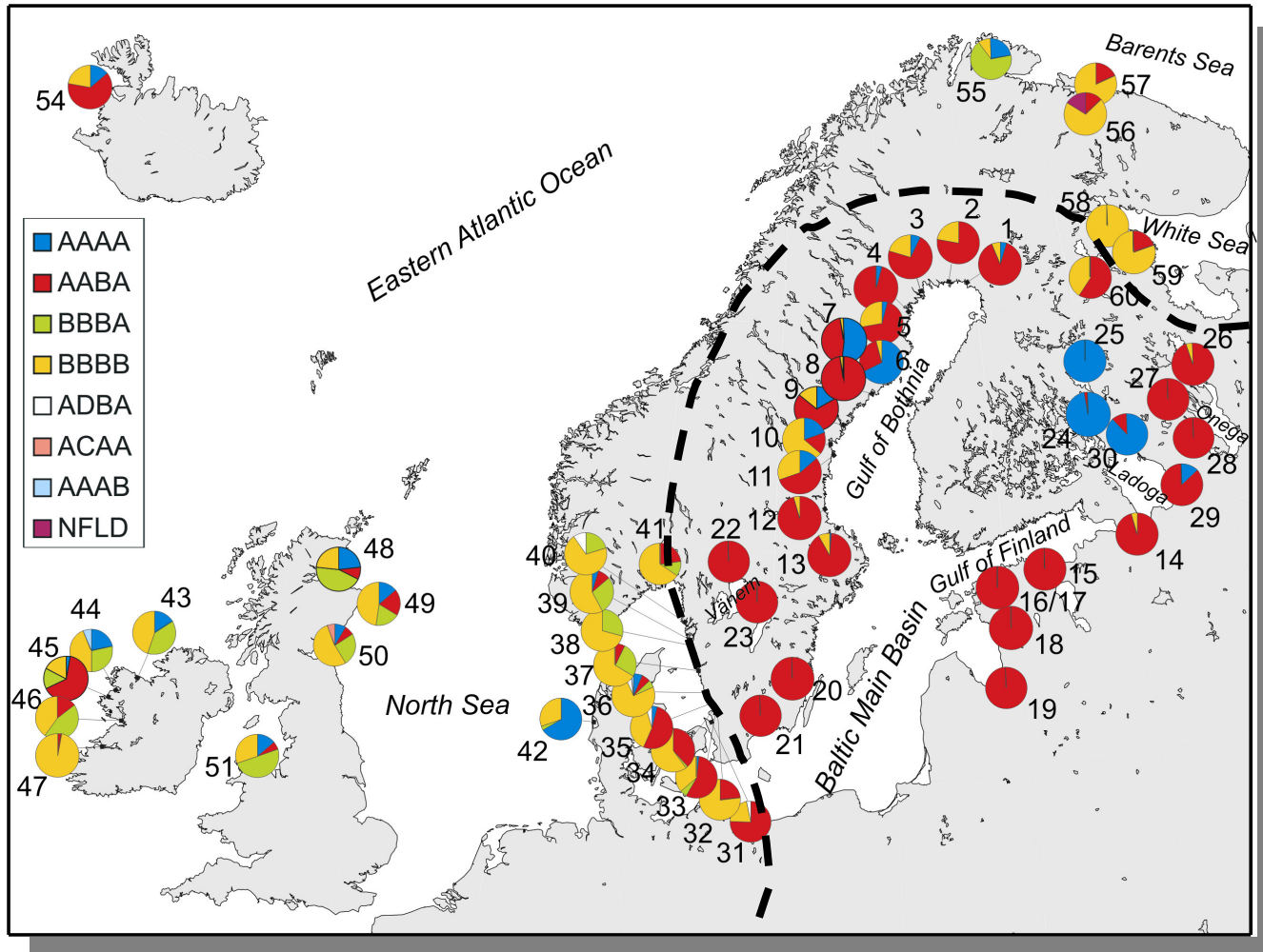
Stocking success

Stock composition – in the Sea, of spawning runs and out-migrating smolts

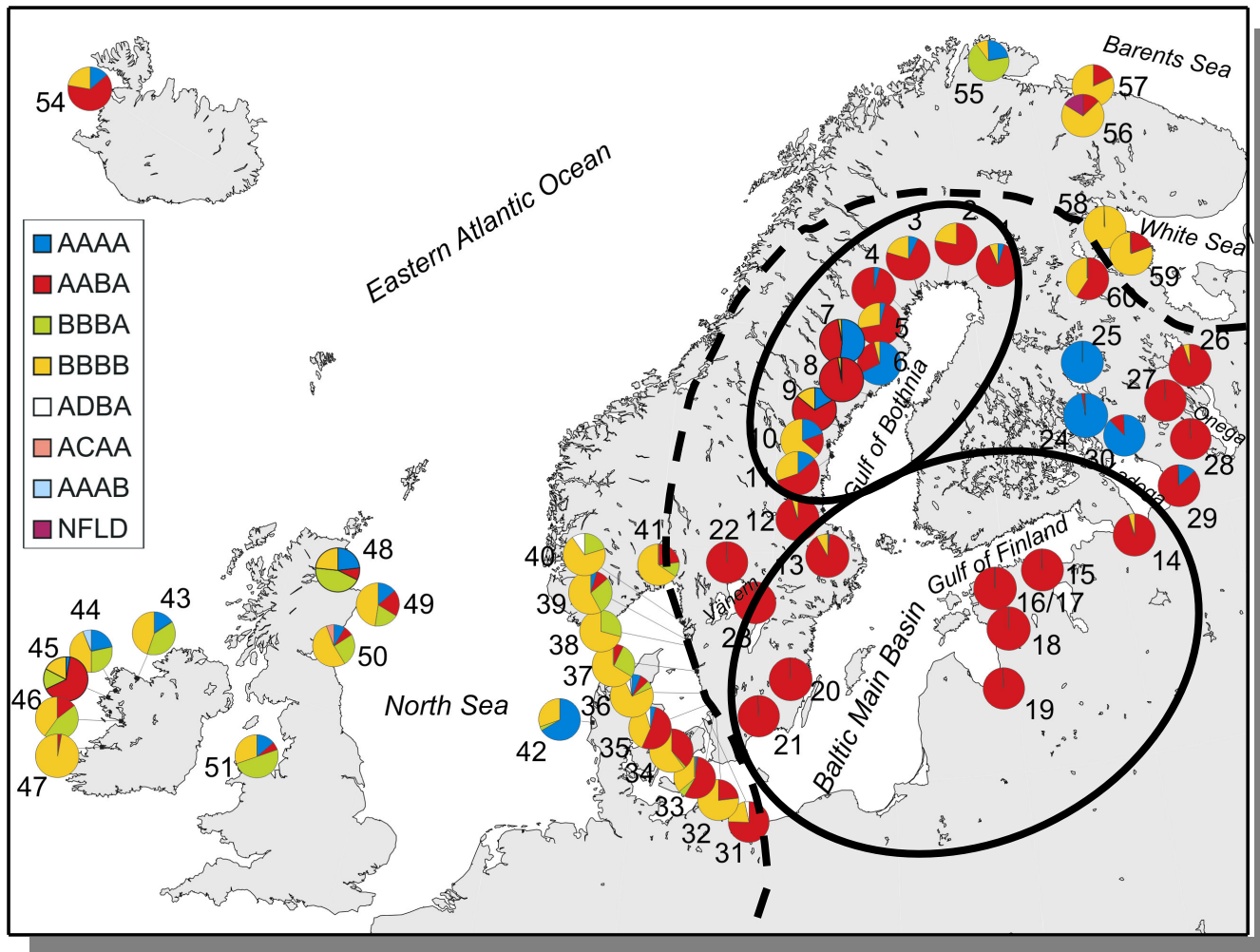
Examples from other species:

Major genetic groupings in salmon and grayling

- **Clear separation between the Baltic and Eastern Atlantic salmon populations**

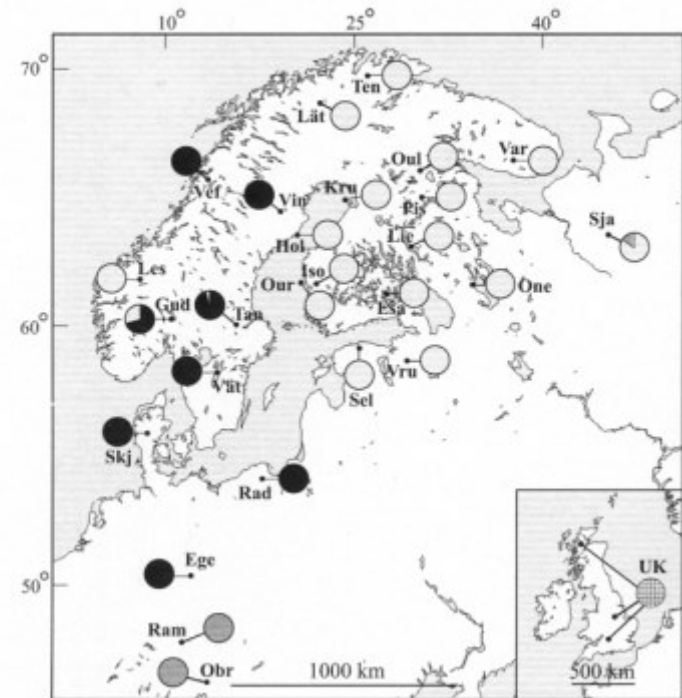


- **ND1 variation supports the hypothesis of postglacial colonization of the Baltic Sea by multiple lineages**

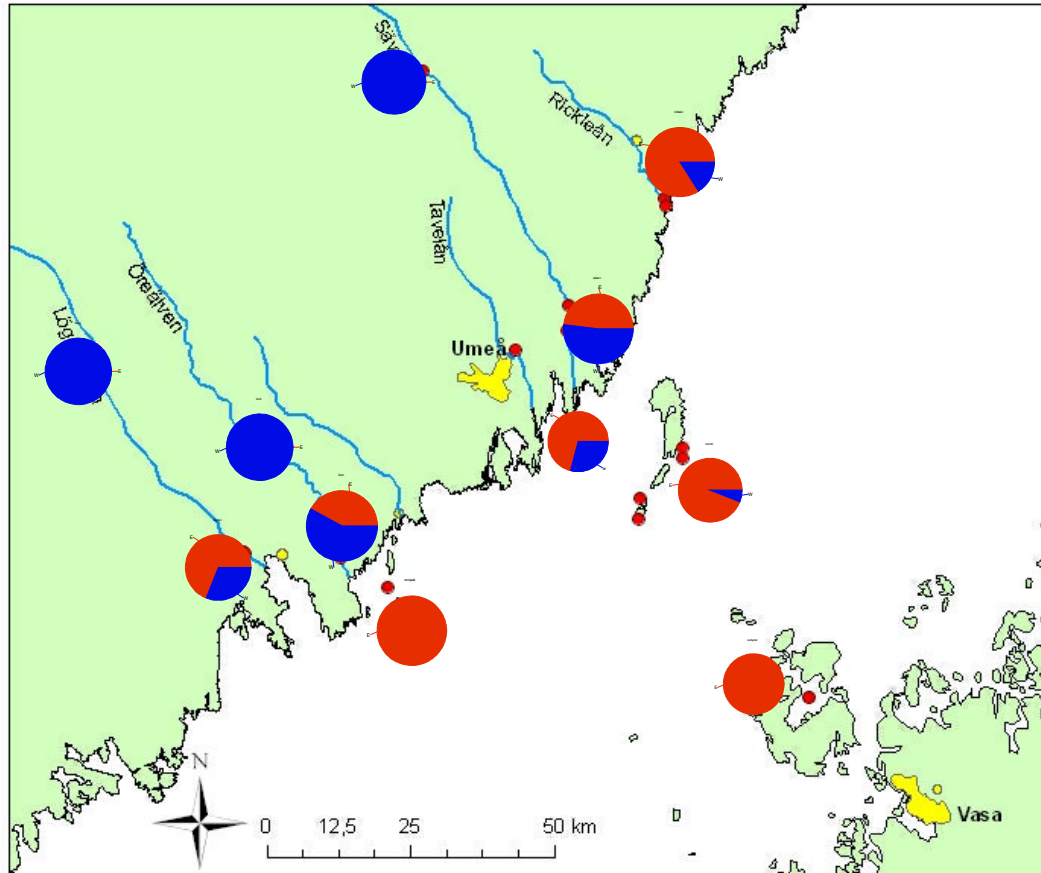


Grayling: two major lineages meet in the Baltic region

1612 M. T. KOSKINEN ET AL.



Grayling in the Bothnian sea (ongoing study)



Work on several freshwater and anadromous species (e.g. Salmon, Grayling, Perch) has shown the presence of multiple lineages in the Baltic Sea region with important implications for conservation and management.

Identifying conservation units should be important for Baltic Sea trout.

Example of use of genetic stock composition analysis:

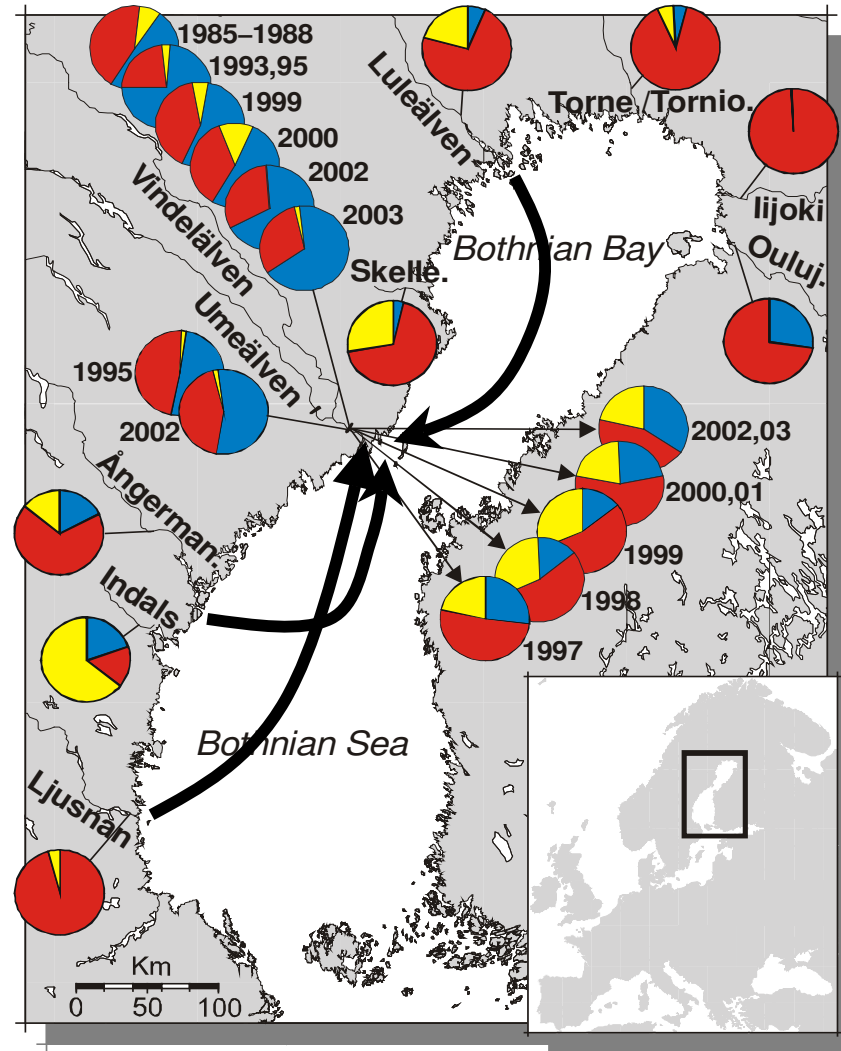
Salmon strayers in the R. Umeälven

(Vasemägi et al)

Origin of 186 strayers was assessed using Mixed-Stock Analysis

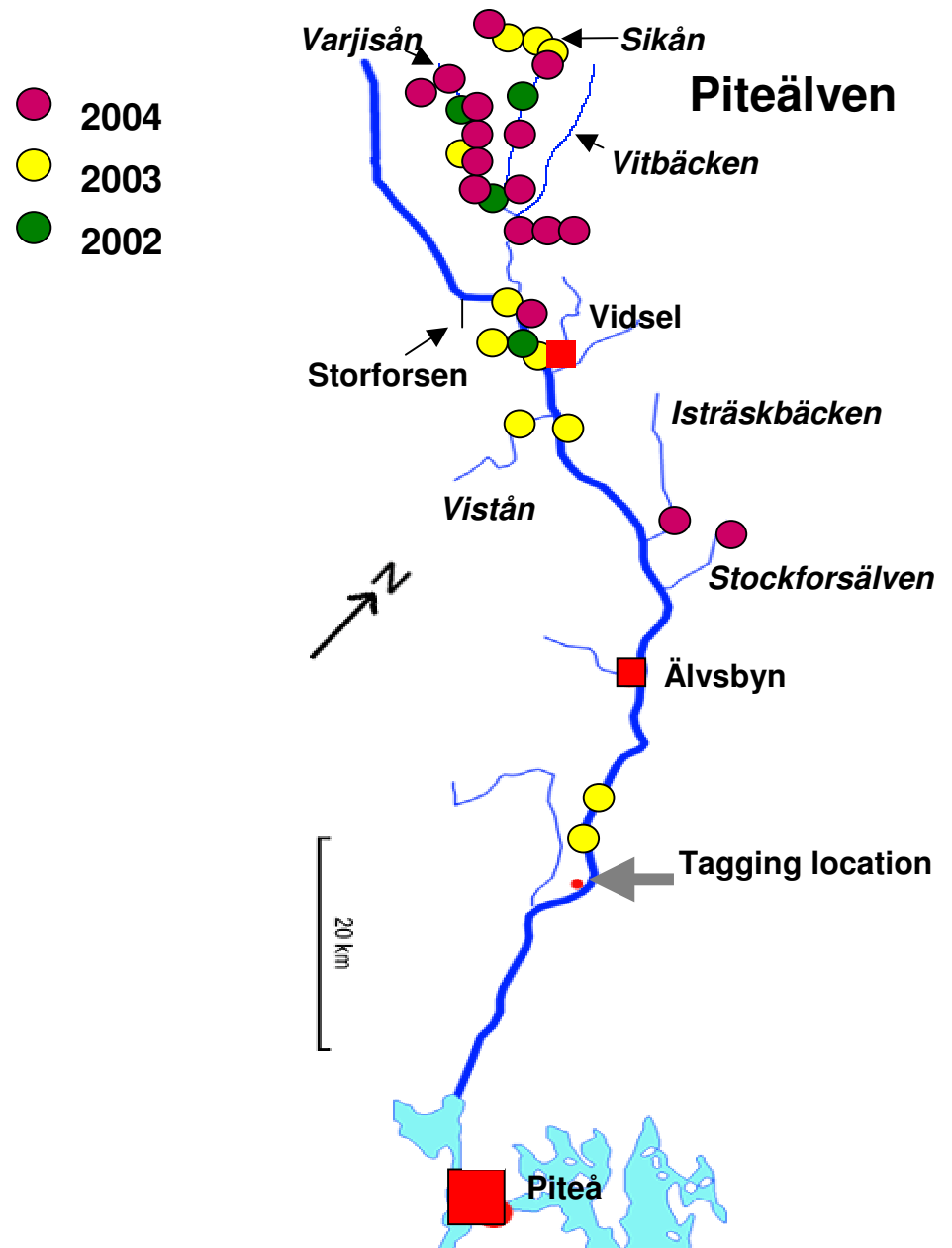
Their genotypes from 8 microsatellites and one mitochondrial marker was tested against corresponding base-line data from 8 salmon stocks.

- Majority of the fin-damaged fishes (ca 70%) originated from three non-native hatchery releases



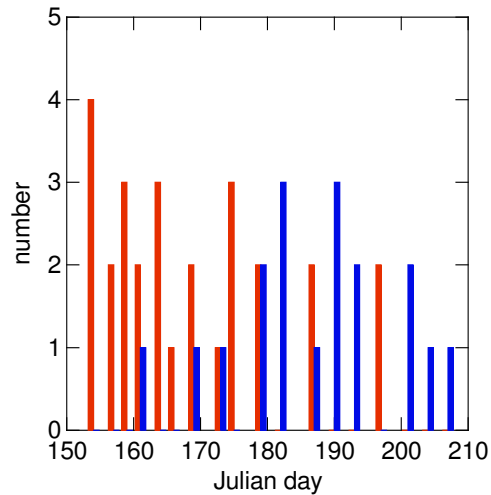
Sea trout in R. Piteälven

Analysis of microsatellite variation in upstream migrating spawners suggest sub-structuring

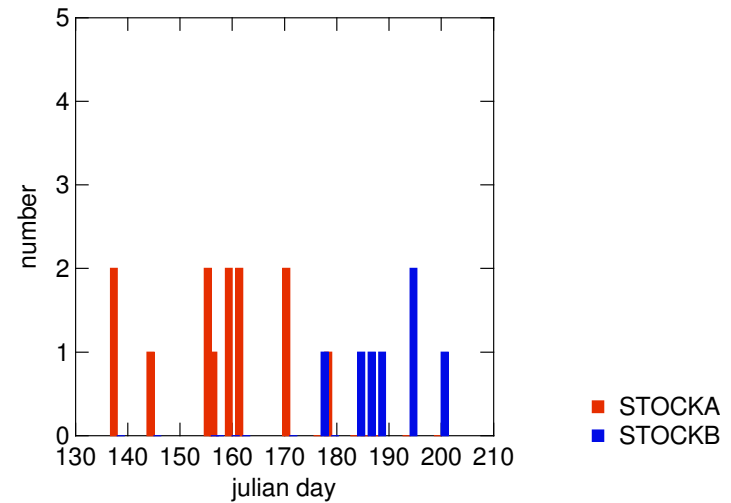


Individual assignment of salmon: Stock origin vs time of catch

2004



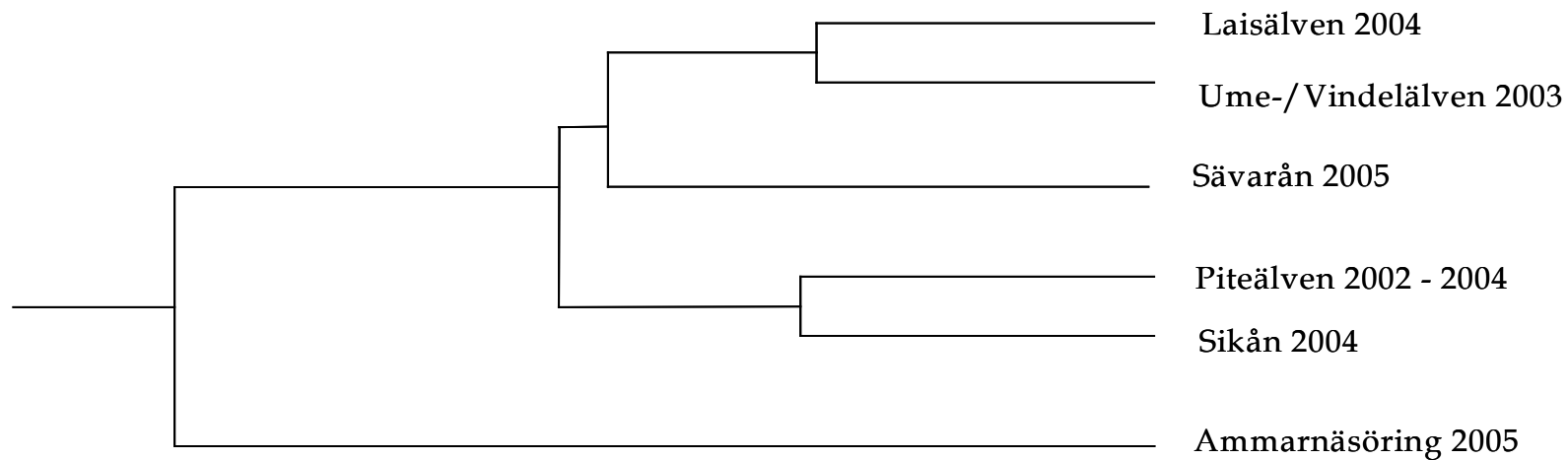
2005



Mixed Stock Analysis and related analytical tools could give valuable information on migration patterns, catch composition et c in Sea trout

Sea trout genetic studies going on in Umeå

- Diversity among Bothnian sea stocks
- Within river diversity
- Relation to resident populations
- stocking



	Laisälven	Ume-/Vindelälven	Sävarån	Piteälven	Sikån
Ume-/Vindelälven	0,030				
Sävarån	0,054	0,043			
Piteälven	0,037	0,030	0,043		
Sikån	0,081	0,072	0,100	0,032	
Ammarnäsöring	0,098	0,100	0,139	0,095	0,145

**Some work should be done on a
Baltic level:**

Agreement of common markers and protocols

Spatial distribution of genetic variation

Access to baseline data