How many stocks could there be?
Spatial organization of yellow perch in Lake St. Pierre

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Introduction

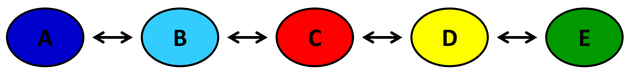
- The yellow perch (*Perca flavescens*) is an important socio-economic resource in Lake St. Pierre (LSP). A sustainable management program requires an understanding of population dynamics.
- While there is indirect evidence of spatial organization, i.e., natal site fidelity behaviour[1] and habitat use[2-3], a study using microsatellite loci on adult yellow perch revealed a single panmictic population in LSP[4].
- Colonization of LSP is extremely recent, occurring only after the retreat of the Champlain Sea *ca.* 8000 years ago[5].
- When population differentiation is low, AFLP (amplified fragment length polymorphism) markers have been found to be more powerful than microsatellites in individual-based population assignment[6].

Objectives

1. Determine which AFLP or microsatellite markers are suitable for detecting spatial organization at low levels of differentiation using simulations.
2. Determine whether several populations of yellow perch coexist in LSP using AFLP on larvae (following emergence).
3. Assess whether the genetic signal of spatial organization is blurred on adult yellow perch using microsatellites on larvae.

Materials and Methods

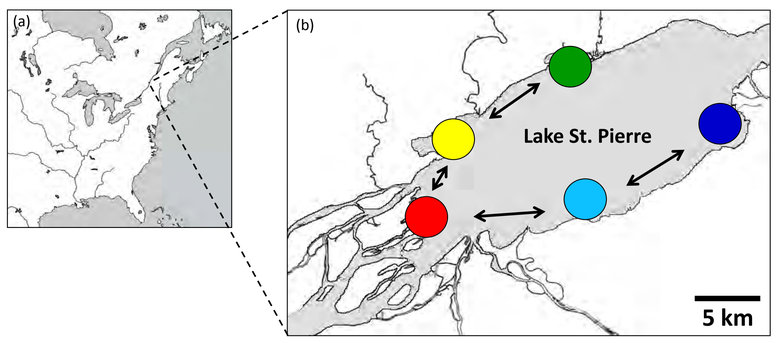
➢ **Population simulations with the stepping stone model. Assessment of the usefulness of AFLP *vs.* microsatellite markers using clustering methods (Table 1).**



N_E		3000 individuals			
Number of generations		1st step: 1000 generations (m=0.5; homogenization) 2nd step: 5000 generations (differentiation)			
Migration rate (2nd step)		from 3.10^{-4} to 10^{-1}			
				μ	**Sample size**
Microsatellites	SMM	100 loci	9 alleles	5.10^{-5}	20 ind./pop, 10 loci
AFLP	KAM	500 loci	2 alleles	1.10^{-9}	20 ind./pop, 100 loci

Figure 1. Stepping stone model and input parameters for the simulations (EASYPOP 2.0.1).

➢ **Sampling recently emerged larvae from LSP to assess the presence of multiple spawning sites and to analyze molecular polymorphism (Table 1).**



Sampling	102 individuals from 5 sites Different years (2008 and 2009) to avoid sib sampling
Markers	9 microsatellite loci[7] and 91 AFLP loci

Figure 2. Study site: (a) Eastern North America. (b) LSP, a widening of St. Lawrence River, and sites where larvae were collected (coloured circles). Arrows represent expected migration of individuals.

Table 1. Methods used to compare individuals (AFLP *vs.* microsatellite polymorphism).

Methods making no assumption about population structure	**Phylogenetic inferences:** NJ tree based on DAS genetic distance (microsatellites) or Euclidian distance (AFLP) **Parsimony Score[8]** (p-score): assess how individuals cluster according to their group of origin (high value = random) Standardized p-score: (p-score - (# populations - 1)/(# individuals - 1))	
Methods that assume site = population	**Simulations:** Proportion of individuals correctly reassigned (p<0.05) to their population according to allele frequencies (Reassignment test: GENECLASS and AFLPOP)	**Sampled larvae:** Constrained ordination between genetic polymorphism and spatial distribution of larvae. Regression is tested using permutations (Redundancy Analysis (RDA): R package)

Results and Discussion

1. Simulations: AFLP or microsatellite loci?

- High mutation rate of microsatellite markers results in higher intra-population diversity and lower F_{ST} value than AFLP markers for the same migration rate.

All methods used revealed:

- Greater differences between AFLP and microsatellite loci when the migration rate is higher than 0.001.
- More successful assignments with AFLP loci, especially at low levels of differentiation.

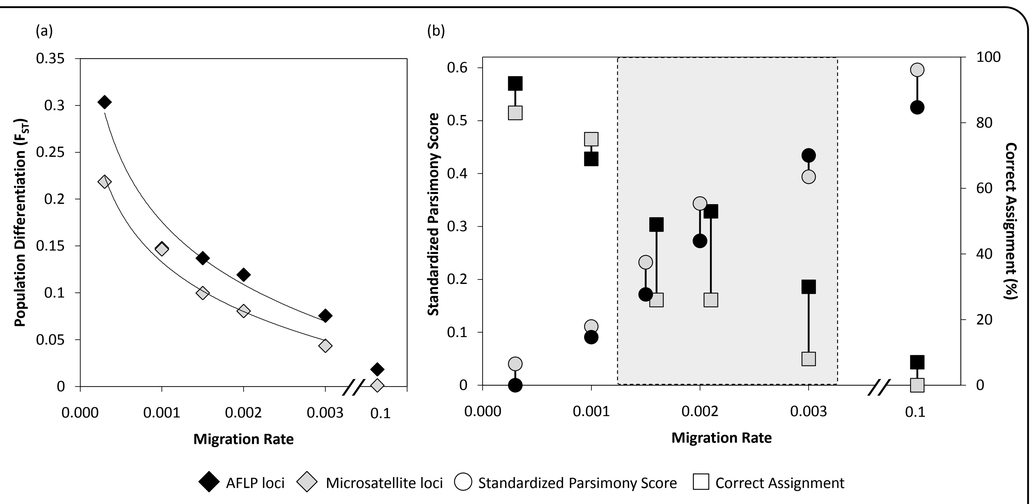


Figure 3. (a) Population differentiation as a function of migration rate for AFLP (black) and microsatellite (grey) loci. (b) Standardized parsimony score (circles) and proportion of correct assignment (squares) as a function of migration rate for AFLP and microsatellite loci.

2. Clustering larvae using 91 AFLP loci

- Observed F_{ST} = 0.058
- Standardized parsimony score = 0.14
- RDA *p-value* = 0.001

AFLP loci confirm the spatial organization of multiple populations. Individuals are more genetically similar within a site than among sites.

3. Clustering larvae using 9 microsatellite loci

- Observed F_{ST} = 0.003
- Standardized parsimony score = 0.54
- RDA *p-value* = 0.7

Microsatellite loci failed to detect spatial organization in larvae and revealed a single panmictic population, as observed in adults.

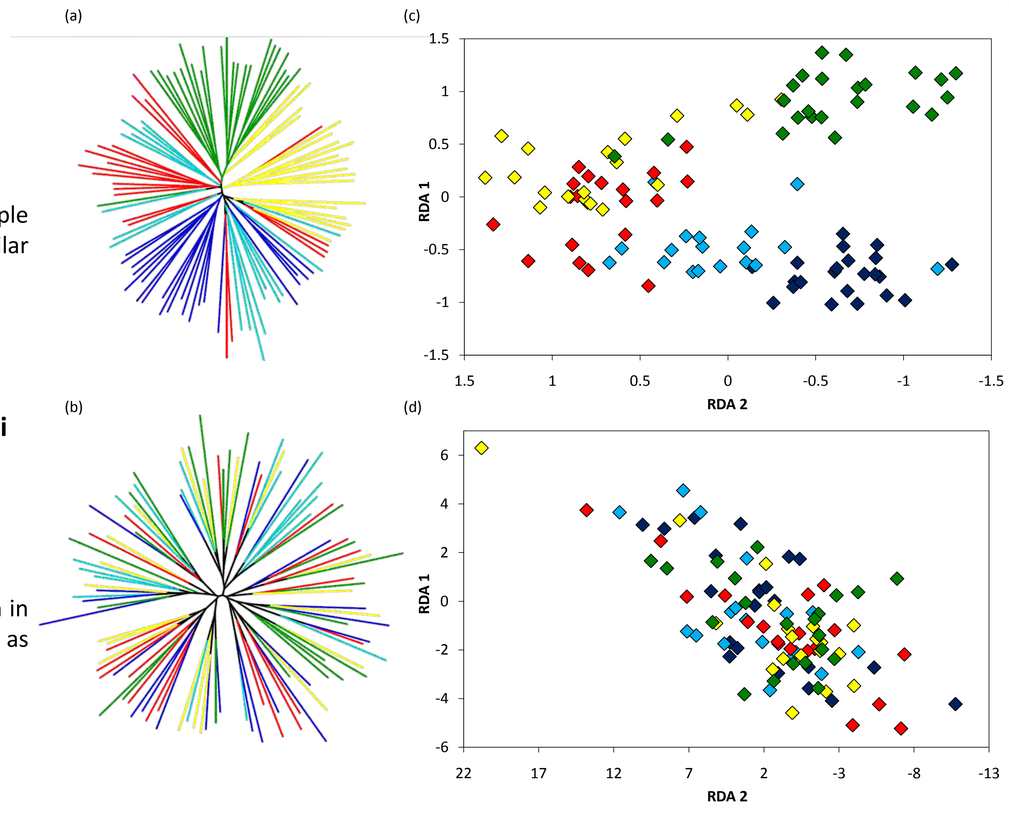


Figure 4. Dendrograms obtained using AFLP (a) and microsatellite loci (b). RDA plots obtained using AFLP (c) and microsatellite loci (d) as a function of sampling sites. Each colour represents a sampling site.

Conclusions

- A limited number of AFLP markers is more useful than a limited number of microsatellites to detect spatial organization at low levels of genetic differentiation.
- A genetic organization of yellow perch in LSP is detected when using AFLP loci on larvae, which is consistent with the evidence of natal site fidelity observed in this species.

Conservation implications:

- Management of multiple spatially organized populations.
- Identification and protection of spawning sites.
- Assessment of population dynamics and the contribution of spawning sites.

References

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Acknowledgements

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