Can genetic data be used as a decision-support tool to guide restoration of fish connectivity in salmonid streams?

The example of the Sûre river catchment (Belgium, Wallonia)

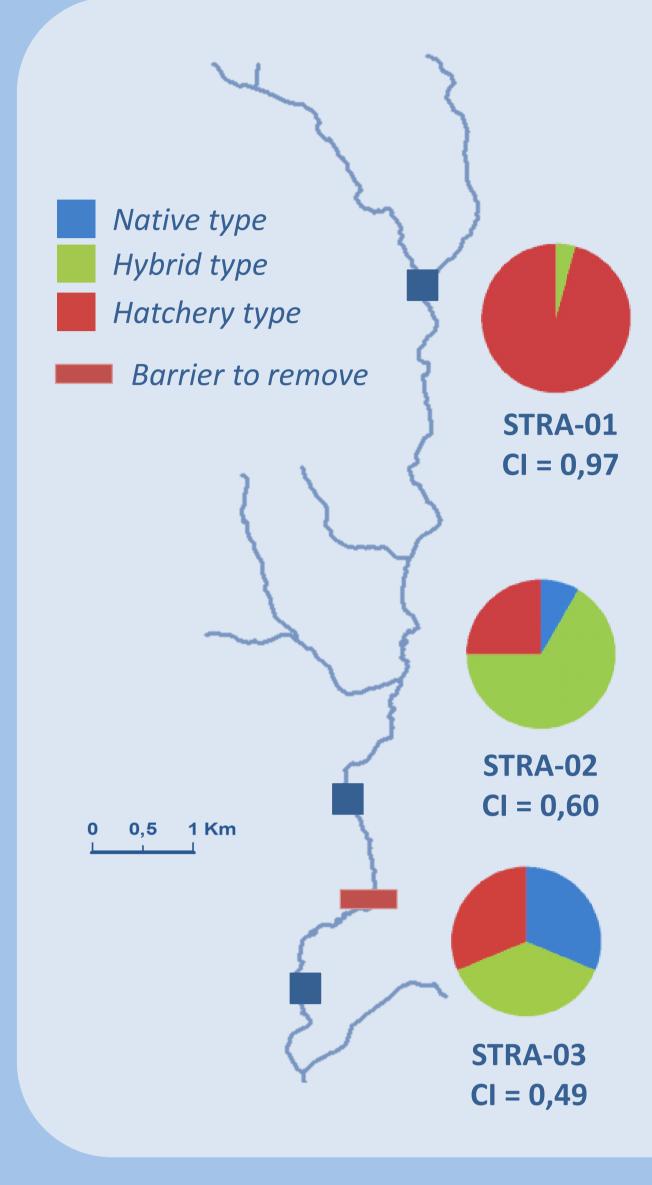


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Background

In addition to restraining access to spawning grounds or causing migration retard, longitudinal barriers are known to be responsible for genetic risks in isolated fish populations. Therefore, the conservation of migratory spawning species like brown trout (Salmo trutta) implies restoration of stream connectivity. On the other hand, Belgium's rivers have been intensively stocked in past decades using domesticated trout from hatcheries. Interactions between wild and stocked fish may result in the introgression of native gene pools, potentially causing fitness alterations and population decline. From this point of view, physical barriers may sometimes contribute to preserve native populations from the influence of domesticated material.



Case 1: The Strange river

On the Strange River, native populations were missing upstream of an impassable barrier (h = 1,4m) but were present downstream. The disappearance of native trout in the upper stretches being probably linked to a heavy oil episode followed by intensive hatchery pollution restocking in the late 90's. Restoring connectivity at the weir was validated since it did not threaten any remnant autochthonous population, while furthermore allowing downstream potentially better adapted native fish (35% of the population) to recolonize the upper stretches.

Project goals

Within the MigraSûre project, genetic characteristics of brown trouts living up- and downstream of longitudinal barriers were investigated and used as prioritizing tool for connectivity restoration actions. The ideas were to:

- preserve native populations from genetic drift / inbreeding due to isolation;
- avoid introgression risks in reconnected populations by possible hatchery/hybridized fish from downstream.

Material & Methods

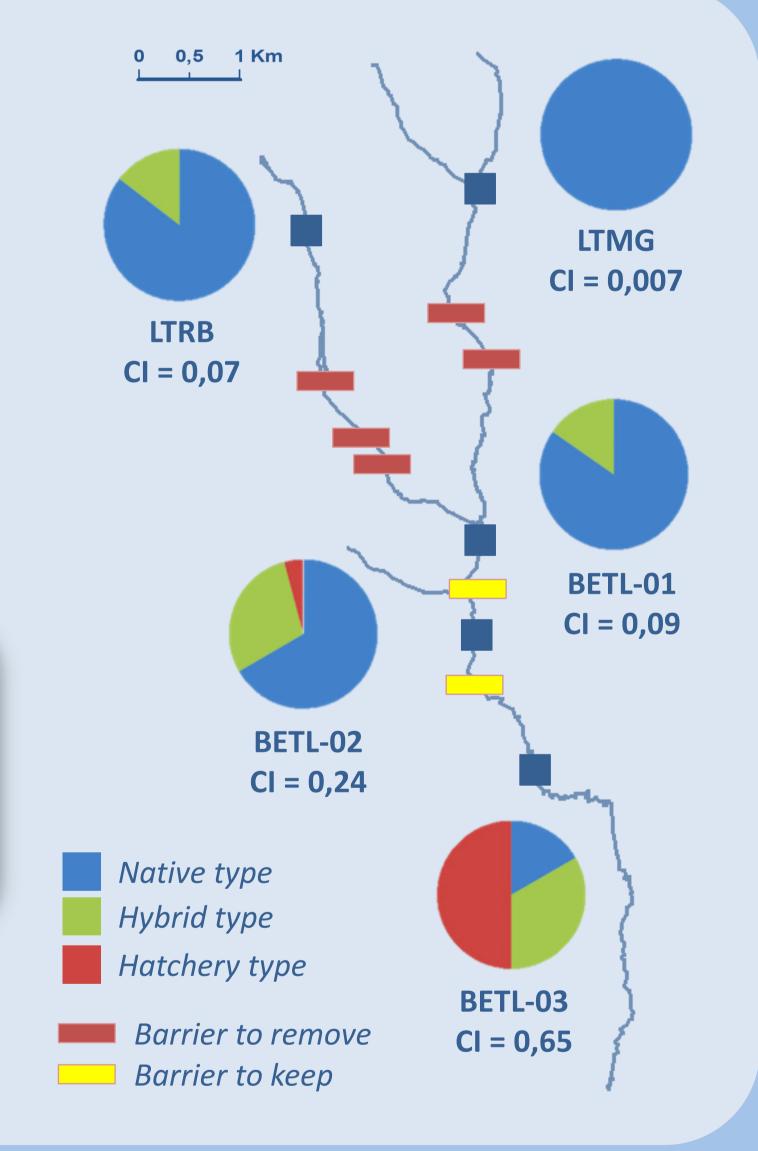


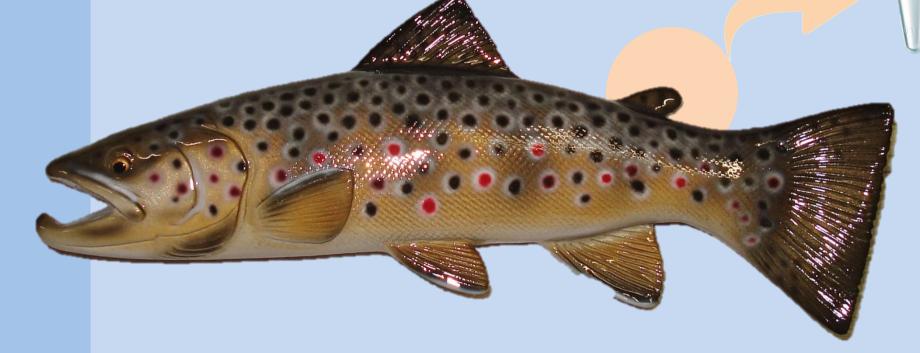


A rock-ramp fishway (5% slope) has been built with 12 transverse ridge rocks forming a series of pools and small falls (0,1 m).

Case 2: The Betlerbaach river

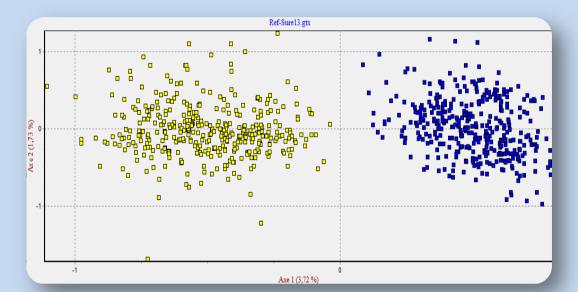
On the Betlerbaach river system, upstream tributaries were shown to host small preserved native populations while fish living downstream of an impassable road crossing culvert displayed high hatchery introgression. Here, the decision was made to maintain the most downstream barrier to avoid any input of domestic material within native populations. We rather focused on reconnecting upstream native populations to each other in order to limit inbreeding and genetic drift.





Field sampling

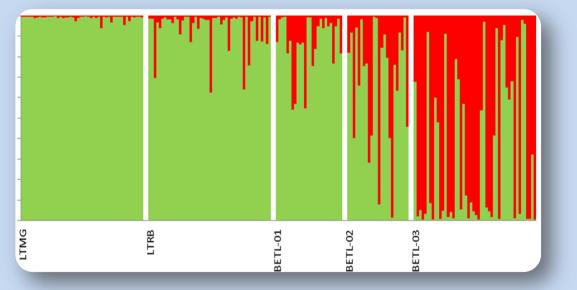
- 1655 fish from 45 river sites.
- 398 fish from 8 hatcheries.



DNA sequencing based on

12 microsatellite markers.

Factorial Correspondence Analysis confirms 2 genetic groups (native vs. hatchery).



Bayesian assignment Each fish is assigned to the cluster for which it has the highest likelihood: native (green) vs. hatchery (red).



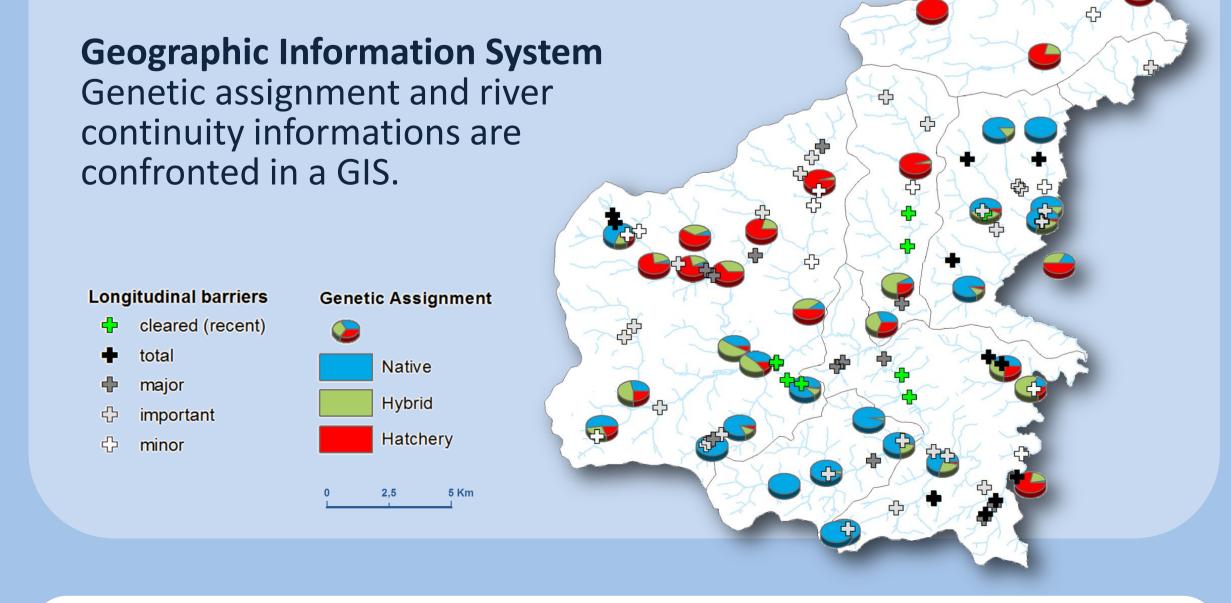
Upstream road crossings have been improved for fish passage and the canalized stream has been uncovered. Downstream barriers were preserved.

Conclusion and outlook

Many studies have shown the evolutive importance of preserving native populations of brown trout as part of the intraspecific genetic diversity. As introgression by domestic material from hatcheries is known to alter naturally selected genotypes, we made

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the choice to maintain several migration obstacles in order to preserve native populations. This was considered the more adequate solution until other conservation measures dealing with hatchery stocking are implemented.

Sources

Laikre L. et al., 1999. Conservation genetic management of brown trout (Salmo trutta) in Europe. Report by the concerted action on identification, management and exploitation of genetic resources in the brown trout (*Salmo trutta*), "TROUTCONCERT"; EU FAIR CT97-3882.

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Contact and acknowledgements

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