Genetic structure of nase, *Chondrostoma nasus*, and common barbel, *Barbus barbus* (Teleostei, Cyprinidae) populations in South Belgium rivers: toward a rational management of conservation restocking.

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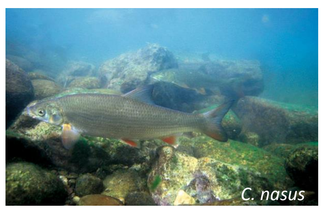
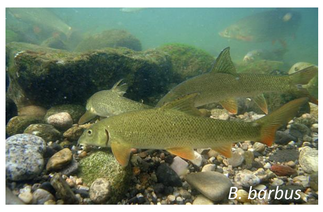
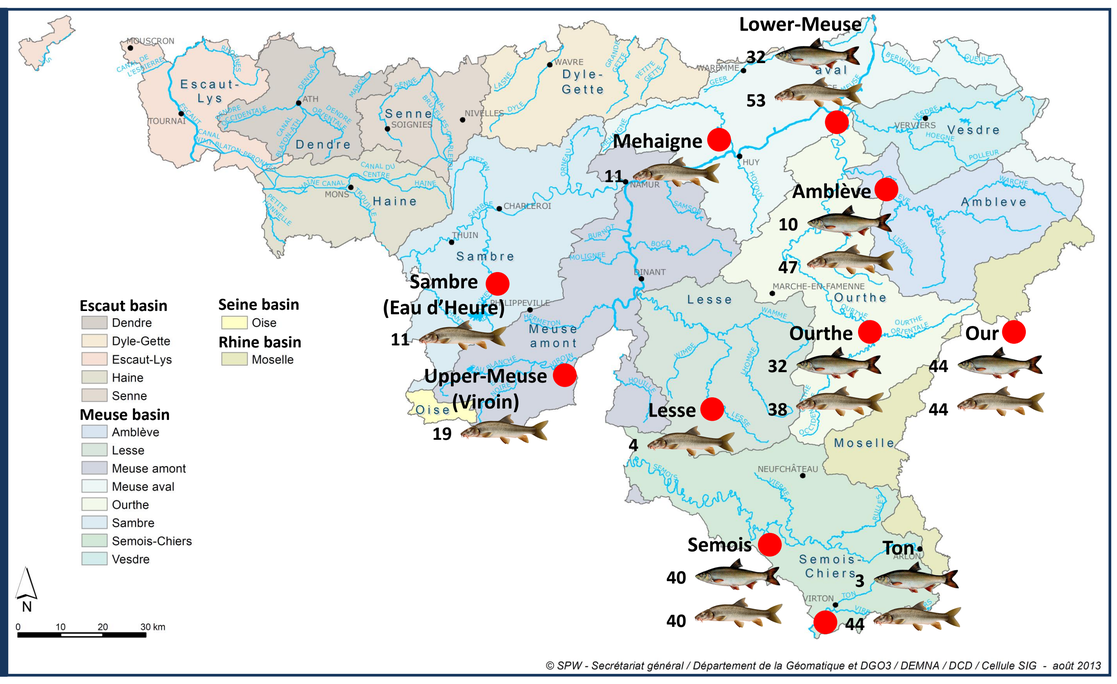
BACKGROUND





Nase (*Chondrostoma nasus*) and common barbel (*Barbus barbus*) are two rheophilic cyprinid fish naturally present in the Belgian Meuse and Rhine basins. During the last decades, some local dramatic declines in their populations have been reported in South Belgium rivers. However, recent improvements in terms of water quality and habitat fragmentation allow considering as realistic a rational restocking plan of these two species. Restocking operations for a conservation purpose have to be based on the knowledge and the use of wild type genetic strains. Therefore, the aim of this study was to characterize the genetic structure and diversity of nase and common barbel populations in South Belgium rivers.

SAMPLING



GENETIC ANALYSES

Nase (*Chondrostoma nasus*)

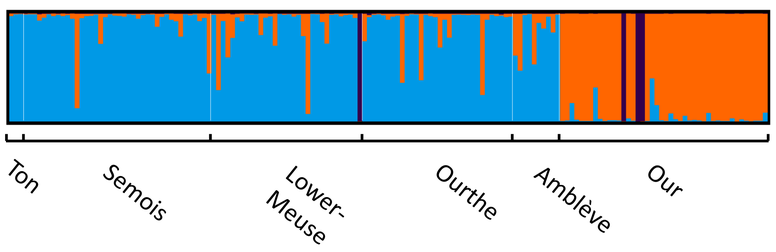
Dilpoid species

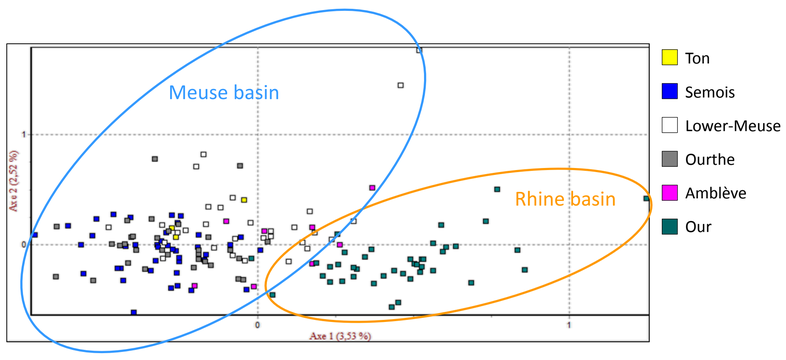
Total number of individuals = 161

24 microsatellite markers

(*BL1-2b, BL1-30, BL1-84, BL1-153, LleA-029, LleA-071, LleC-090, LceC1, Lsou19, BL1-98, BL2-114, LleA-150, Lsou05, Lsou08, Lsou29, Lsou34, Ppro132, CnaB-030, CnaD-112, CtoA-247, CtoA-256, CtoE-249, LCO3, Rser10*; described by Dubut et al., 2010)

Clusters inferred with STRUCTURE software, after the Evanno correction (K = 3). The colour composition of the vertical lines represent the cluster membership of each sample.





Plot of the factorial correspondence analysis showing the proximity between each individual genotype based on the microsatellite allele frequencies (GENETIX software).

Genetic diversity at each cluster

	N	N_a	A_r	H_O	H_E	F_{IS}
K1	106	7,29 (4,02)	3,34	0,64	0,69	0,034 < **0,065** < 0,094
K2	41	5,79 (2,92)	3,47	0,66	0,67	-0,033 < **0,006** < 0,044
K3	4	3,17 (2,08)	2,46	0,41	0,49	-0,256 < **0,196** < 0,524

N: Number of samples, N_a: Mean number of alleles (Standard deviation), A_r: Allelic richness, H_O: Observed heterozygosity, H_E: Expected heterozygosity, F_{IS}: Inbreeding Coefficient (with 95% confidence intervals) (diveRsity pack).

Genetic differentiation between clusters

G_{ST} \ F_{ST}	*K1*	*K2*	*K3*
K1		0,017 < **0,023** < 0,030	0,151 < **0,184** < 0,250
K2	0,034 < **0,044** < 0,057		0,170 < **0,203** < 0,262
K3	0,252 < **0,286** < 0,340	0,287 < **0,318** < 0,364	

Above diagonal: F_{ST} ; below diagonal: G_{ST} (values with 95% confidence intervals) (diveRsity pack).

3 genetic clusters

→ **K1** = major cluster mainly characterizing Meuse basin populations (high genetic diversity, low differentiation vs K2)

→ **K2** = major cluster mainly characterizing Rhine basin (Our) population (high genetic diversity)

→ **K3** = minor cluster highly differentiated (relic individuals?)

Common barbel (*Barbus barbus*)

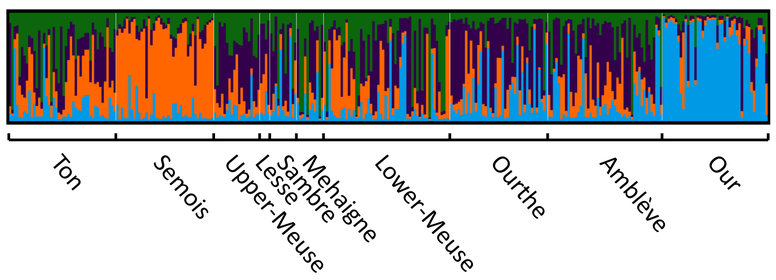
Tetraploid species

Total number of individuals = 311

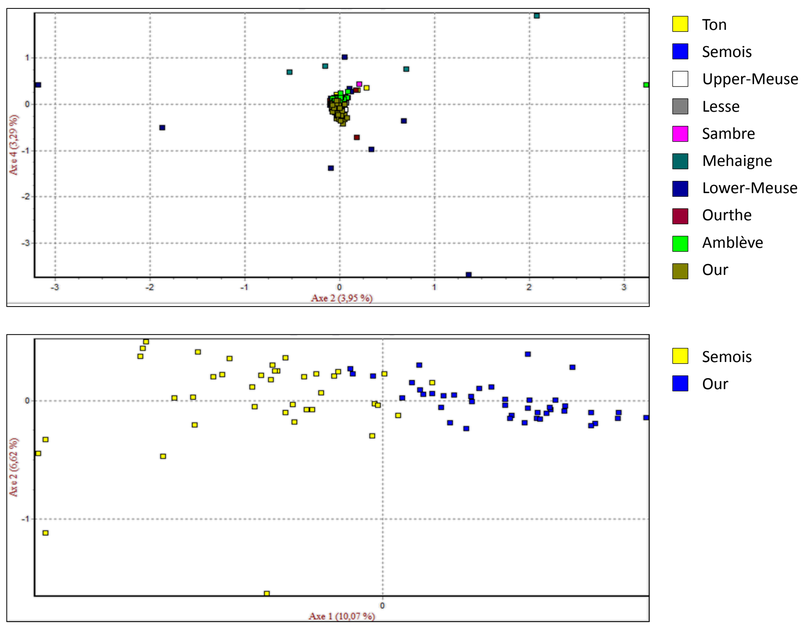
18 microsatellite markers with a likely disomic inheritance

(*Barbus28, Barbus32, Barbus37, Barbus4, Barbus11, Barbus21, Barbus26, Barbus27, Barbus31, Barbus47, Barbus55, Barbus56, Barbus57, Barbus63, Barb59, Barbus39, Barbus50, Barbus62*; described by Chenuil et al., 1999 and Gettová et al. , 2013)

Clusters inferred with STRUCTURE software, after the Evanno correction (K = 4). The colour composition of the vertical lines represent the cluster membership of each sample.



- **4 genetic clusters showing low structuring and high diversity**
- **Admixture of different genetic lineages**
- **Smooth separation between more differentiated Semois and Our populations** (GST = 0,088, Atetra software)



Plots of the factorial correspondence analysis showing the proximity between each individual genotype based on the microsatellite allele frequencies (GENETIX software).

CONCLUSIONS

Apart from some uncommon peculiar individuals (*K3*), nase populations show a clear genetic structure with a differential genetic clustering between fish originating from the Meuse basin and those originating from the Rhine basin. These two groups are moderately separated, suggesting possible gene flows between populations.
Barbel populations are genetically weakly structured, probably due to restocking operations performed in the 80' and 90' with different genetic lineages. Populations from the Semois and Our rivers are more genetically characterized, showing less admixture than the other populations.
These results will serve as a basis for broodstock management in a new conservation restocking plan for nase and common barbel in South Belgium rivers.

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