
**Genetic structure of 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.

### Nase (*Chondrostoma nasus*)

**Dilpoid species**

- Total number of individuals = 161
- 24 microsatellite markers

**Common barbel (*Barbus barbus*)**

**Tetraploid species**

- Total number of individuals = 311
- 18 microsatellite markers with a likely disomic inheritance

### Genetic Structure

#### Nase (*Chondrostoma nasus*)

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

#### Common barbel (*Barbus barbus*)

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

### Genetic diversity at each cluster

<table>
<thead>
<tr>
<th>K</th>
<th>N</th>
<th>A</th>
<th>H_e</th>
<th>H_o</th>
<th>F_{ST}</th>
</tr>
</thead>
<tbody>
<tr>
<td>K1</td>
<td>106</td>
<td>7.93</td>
<td>3.14</td>
<td>0.56</td>
<td>0.515 &lt; 0.005</td>
</tr>
<tr>
<td>K2</td>
<td>46</td>
<td>5.79</td>
<td>3.47</td>
<td>0.66</td>
<td>0.601 &lt; 0.005</td>
</tr>
<tr>
<td>K3</td>
<td>4</td>
<td>3.17</td>
<td>3.06</td>
<td>0.65</td>
<td>0.634 &lt; 0.005</td>
</tr>
</tbody>
</table>

- Number of samples, N: Mean number of alleles (Standard deviation).
- A: Allelic richness.
- H_e: Shannon diversity.
- H_o: Observed heterozygosity.
- F_{ST}: Fst-coefficient.

**Genetic differentiation between clusters**

<table>
<thead>
<tr>
<th>K1</th>
<th>K2</th>
<th>K2</th>
<th>K3</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.031 &lt; 0.047</td>
<td>0.602 &lt; 0.605</td>
<td>0.511 &lt; 0.515</td>
<td></td>
</tr>
<tr>
<td>0.295 &lt; 0.308</td>
<td>0.581 &lt; 0.574</td>
<td>0.471 &lt; 0.465</td>
<td></td>
</tr>
</tbody>
</table>

Above diagonal: F_{ST} between diagonal: R_{ST}(values with 95% confidence interval) (parentheses).

### 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.