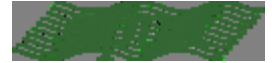
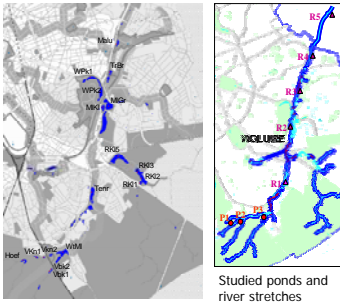


Clonal diversity and spatial genetic structure of *Potamogeton pectinatus* in pond and river populations



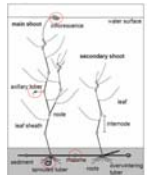
Plant Biology and Nature Management, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium

Introduction



Ponds and rivers of the Brussels Capital Region are constantly managed and maintained to obtain a healthy status of the water quality and the aquatic organisms living therein. The Woluwe catchment is an area with high levels of biodiversity and both the ponds and the river contain submerged water plants (macrophytes).

These macrophytes are an important structural and biotic element in the maintenance of a clear water status in the ponds, associated with a healthy status preventing the development of toxic cyanobacterial blooms. Macrophytes are also associated with various invertebrate aquatic animals because they provide food and shelter. Pond and river management therefore aims at the establishment of healthy stands of submerged water plants that regenerate spontaneously.



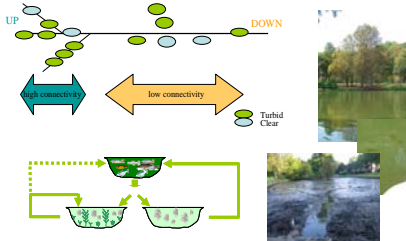
Potamogeton pectinatus

The fennel pondweed, *Potamogeton pectinatus*, is a key-stone macrophyte species that grows abundantly in the river and interconnected ponds of the Woluwe. It reproduces both clonally through persistent tubers and sexually by seeds.

Objectives

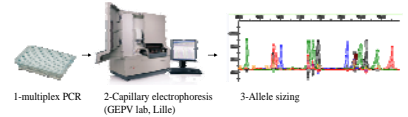
The aim of the study was to assess the level of clonality and the spatial structure of genetic diversity of *Potamogeton pectinatus* populations in relation to the habitat. Particular attention was given on the estimation of gene flow between sites along the river and among the ponds. Therefore, we analysed the genetic diversity of 354 plant shoots sampled in 2005 and 2006 at three pond and five river locations, using nine highly polymorphic microsatellite DNA markers.

Results



Year	Year1		Year2	
	N	MLG	N	MLG
Ponds	20.7	13.3	26.0	12.0
River	18.3	6.8	33.2	8.2

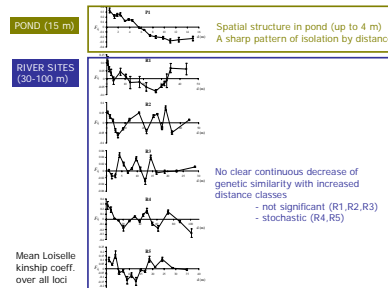
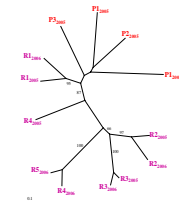
Development of a unique multiplex amplification (1 PCR réaction = 9 loci)



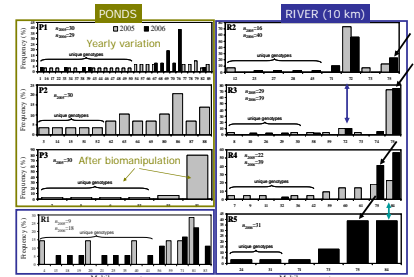
Ponds contain more MLGs than river stretches

Flow-through ponds are highly connected with the river. Clear ponds may contain macrophytes. Turbid ponds are devoid of submerged vegetation but can be biomanipulated to restore the macrophyte stands. Propagules of *Potamogeton pectinatus* allowed establishment already one year after biomanipulation.

Genetic proximity between temporal samples of the same location except for those who presented very high differences of multilocus genotype frequencies (P1 & R4). Neighboring tree of populations



Pond : Spatial structure with isolation by distance
River : Few clones but with stochastic spatial pattern



Ponds :
Different MLGs from year to year (seeds)
After biomanipulation new MLGs and clonal spread within first year

River sites :
One or two abundant MLGs in each river site
Similar MLGs from year to year
Few very common clones along river (clonal dispersal)

Conclusions

Our results highlighted substantial demographic and genetic variation between the two sampled years, illustrating a decrease in genotypic diversity for some river and pond populations. From a spatial point of view, our findings revealed the possibility of clonal propagule dispersal over several kilometres along the river. Thus, few multilocus genotypes were present along a major part of the river and revealed the impact of vegetative reproduction (i.e. allowing an individual to export its own genotype). On the contrary, *Potamogeton pectinatus* populations of ponds contained a higher amount of multilocus genotypes, indicating the importance of conditions that promote sexual reproduction through seeds (i.e. producing new genotypes). Moreover, the genotypic diversity decreased along the river from upstream to downstream, in contradiction with previous empirical observations and theoretical expectations in that type of habitat. Higher levels of diversity are indeed expected in downstream parts because of the potential accumulation of various genotypes from upstream locations.

* Present address :
Laboratoire de Génétique et Evolution des Populations Végétales,
UMR CNRS 8016, FR CNRS 1818, Université de Lille, Lille 1
F-59655 Villeneuve d'Ascq Cedex, France



IWOIB

Instituut ter bevordering van het Wetenschappelijk Onderzoek en de Innovatie van Brussel

Research funded by the IRIB (Institute for the promotion of Scientific Research and Innovation in Brussels), action 'Research in Brussels 2007' with a postdoc grant for Stéphane Féart

