KATHOLIEKE UNIVERSITEIT LEUVEN

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No evidence for loss of genetic variation after 50 years of population declines in the riparian species Saxifraga granulata

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Introduction

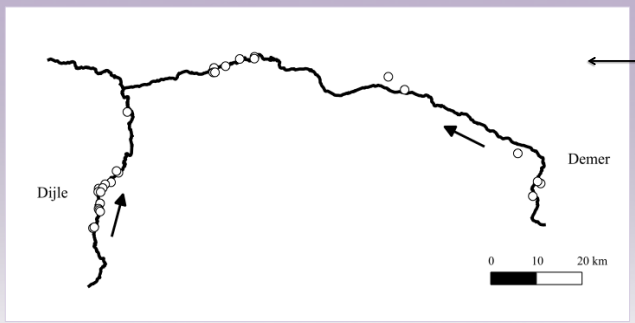
Habitat loss and fragmentation have caused populations of many plant species to become smaller and more isolated during the last century. Riparian plant species (growing near rivers) can ensure exchange of genetic material via the water (e.g. through seed dispersal) and maintain high population genetic diversity structured along the river.

The aim of this study was to unravel the effect of population decline on gene flow and population genetic structure in the riparian grassland species *Saxifraga granulata*.

Aims

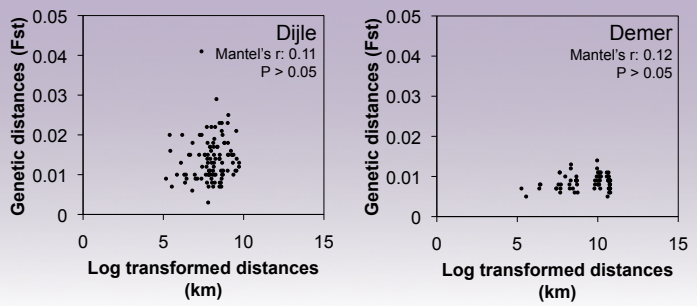
- Investigate the population genetic structure along two river systems (Dijle and Demer)
- Investigate patterns of genetic diversity and test 'the unidirectional flow hypothesis' (i.e. accumulation of allelic diversity downstream)
- Asses patterns of gene-flow

Population differentiation



F_{ST} Dijle: 0.07, Demer: 0.02, all: 0.05 ($P < 0.001$)

Isolation-by-distance



Unidirectional flow hypothesis

Downstream accumulation of genetic diversity was not significantly related to the position of populations along the river (Dijle: $F_{1,13} = 0.068$, Demer: $F_{1,11} = 1.56$; $P > 0.05$)

Discussion

Over 50 years ago, populations of *S. granulata* were well connected within semi-natural grasslands situated along the Dijle and Demer rivers, however, nowadays most populations have become smaller and more isolated.

In the current study we found that the river systems did not significantly affect the population genetic structure of the riparian species *S. granulata* and we found no evidence for the 'unidirectional flow hypothesis'. Population differentiation within both river systems was very low, suggesting high gene flow and limited genetic drift. Ramets of *S. granulata* have a short lifespan, but genets can become very old and can maintain high genetic diversity within populations. Thus, clonality has probably limited the genetic impoverishment of populations after habitat deterioration.