

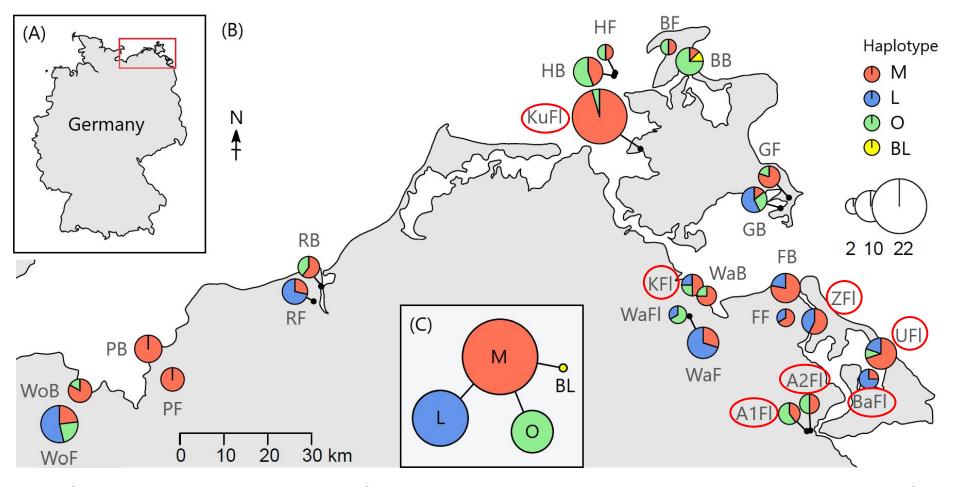




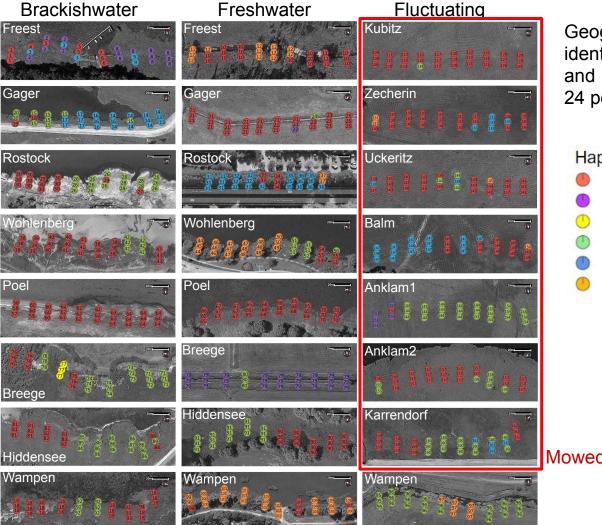


POPULATION GENETIC STRUCTURE OF COMMON REED (PHRAGMITES AUSTRALIS) IN MECKLENBURG-WESTERN POMERANIA (GERMANY)





Map of sampling region (A), sampling sites of *P. australis* with haplotype distribution (B) and the haplotype network (C) 2

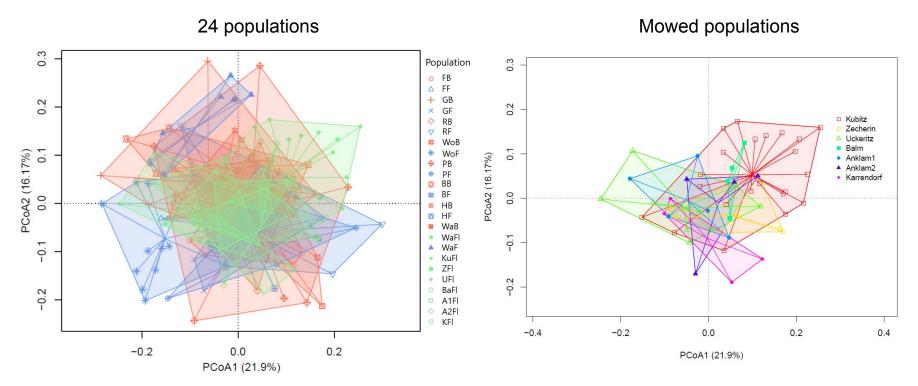


Geographical arrangement of identified haplotypes (colours) and genotypes (numbers) for 24 populations of *P. australis*.

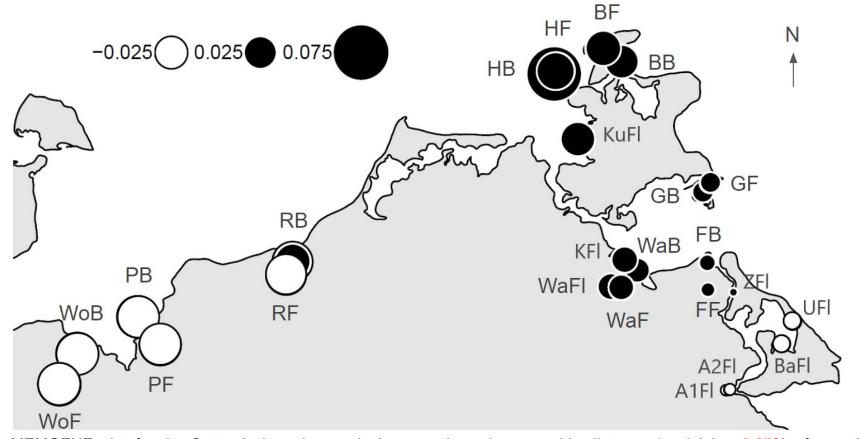
Haplotypes:



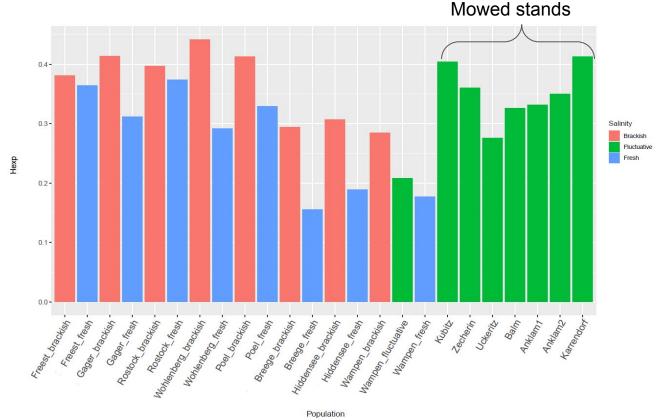
Mowed stands



Principal coordinate analysis for all (left) and commercial (right) populations

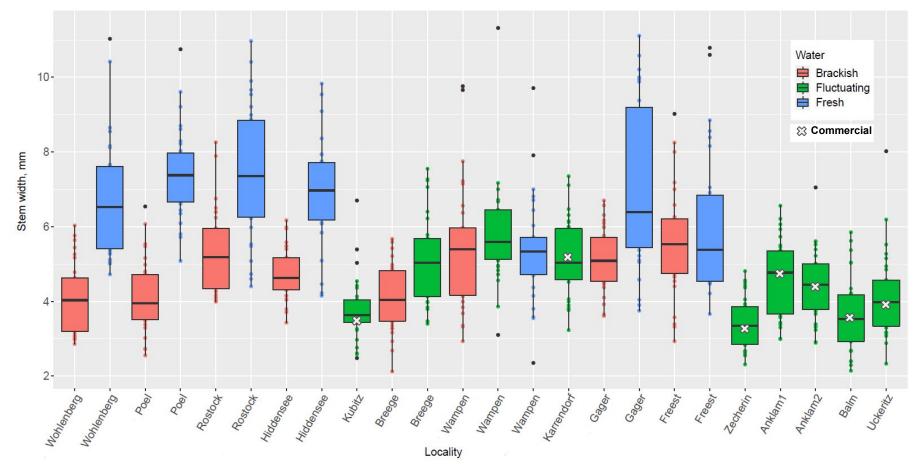


MEMGENE plot for the first axis based on pairwise genetic and geographic distance (explaining 3.27% of genetic variation) for 164 samples from 24 populations of *P. australis*. The size and the color of the circle represent genetic similarity between individuals along the first MEM variable axis

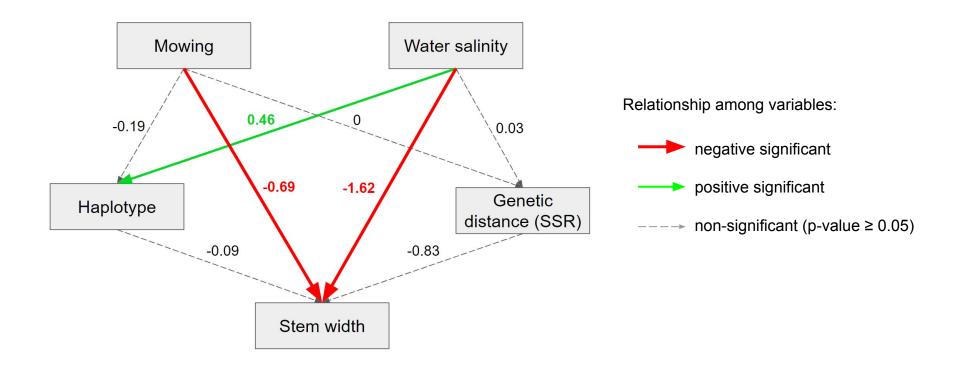


Barplot for expected heterozygosity (Hexp) of 24 populations of *P. australis*

Populations from brackish stands have higher (p-value <0.05) allelic diversity!



Comparison of stem width of P. australis in 24 localities (from west to east), n=30 in each



Path diagram for structural equation modelling exploring the effects of disturbance (by mowing and water salinity) and genetics (haplotype and genetic distance) on stem width. Numbers are the standardized coefficients showing the magnitudes of the relationships between variables.

Summary:

- Reeds in MW have high level of genetic diversity and low level of genetic differentiation
- 2) Populations freely interbreed; both pollen and seeds spread over long distances
- 3) Individuals intensively grow clonaly, but don't spread far by rhizome
- 4) Regularly mowed stand don't show a tendency to have the lower genetic diversity
- 5) Reeds from brackish stands have thinner and shorter stems, and their populations have higher allelic diversity.