



21st Evolutionary Biology Meeting at Marseilles

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Analysis of genetic structure of common reed in Italy and some implications on reed die-back syndrome.

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The aims of this study were to explore the genetic diversity of five natural populations of *Phragmites australis* in Italy, and to analyse the evolutionary dynamics and possible relations with the common reed die-back syndrome (RDBS). In recent decades, many cases of common reed retreat have been recorded in central and Mediterranean Europe, and although it is conjectured that low genetic variability can contribute to reed decline, this aspect remains neglected. The combined analysis on the trnT-trnL/ rbcL-psaI regions of cpDNA and a AFLP fingerprinting approach highlights unexpected complexity of the genetic structure between and within populations of *P. australis* from Italy in terms of (1) haplotype occurrence and (2) genetic variability. The broad complexity in the genetic structure might be due in the first instance to repeated introductions and stabilisation of diverse haplotypes at the population level. In this light, migratory routes of waterfowls such as ducks, might represent a key factor in long-distance dispersal of this *taxon*. Once stabilised, variable environmental conditions and exposure to different stress factors, occasionally exhibited in wet habitats, might have contributed to promote outbreeding leading to a higher genetic differentiation at intra-population level and a reduction of genetic distances among populations. The large amount of genetic variation within the populations might thus be derived from external factors. For instance, phenomena such as eutrophication, mechanical damages or grazing by animals, presence of heavy metals in the sediment and/or water combined with water regulation and permanent flooding, or even phenomena such as allelopathy or phytotoxic effects by biotic components, might play a crucial role in the population dynamics of common reed. Our study shows the occurrence of four different haplotypes (M; M1; J and K) in central Italy. Nevertheless, the haplotypic diversity only represents a small portion of the total intra-genetic diversity of populations, which instead, seems to be more influenced by the quality and concentration of the heavy metals in the sediments/soil. Even if neither a positive relationship among sediment heavy metals abundance and rates of clumping (a RDBS strong trait) nor among high genetic diversity and clumping have been showed, our study points out the existence of similar fingerprinting-profile for stands affected by RDBS (flooded with presence of clumping). Finally we observe outlier loci positively related with the decrease of the diameter (another clear RDBS trait), indicating a selection of genomic region of DNA for plants under RDBS. This last aspect suggests future and further insights by means of different investigation technics (e.g. new generation sequencing approach).