

Clonal variability of the common reed, *Phragmites australis* (Cav.) Trin. ex Steudel

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Phragmites australis (Cav.) Trin ex Steudel is a cosmopolitan big grass species, present in a wide climate range and potentially of great economic and ecological value. *P. australis* is a typical competitor; thanks to its efficient carbon assimilation metabolism and agamic spread by rhizomes, it can constitute virtually monospecific stands that often dominate wetland ecosystems.



Some of the largest *P. australis* dominated ecosystems occur in Europe where there is a long tradition of reed-based economical activities, such as roofing, fencing, insulation and thatching material, cardboard and paper manufacturing.



In recent years the exploitation of *P. australis* in the context of sustainable economic development has given rise to considerable interest. Wetlands dominated by *P. australis* have a great economic value for tourism (bird-watching and hunting).

The practices of planting reed stands along rivers to protect the banks from erosion and the use of reeds in phytodepuration systems (natural and constructed wetlands) are spreading from Northern Europe to all over Europe. Also the use of reeds as energy crops is exploited at an experimental scale.

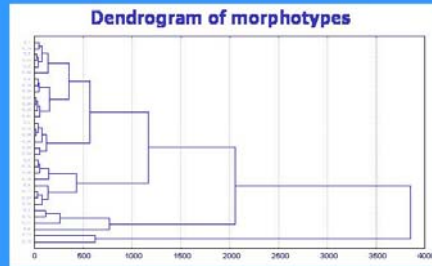


In this context, researches on the morphological and genetical variability of *P. australis* are important to identify suitable local clones and/or ecotypes to be implemented in various environmental applications.



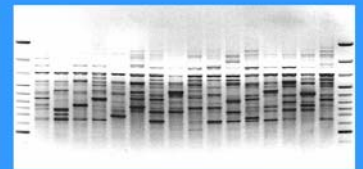
This study investigates into the morphological and genetical variability of eight *P. australis* populations growing in eight wetlands of the Bologna Po Plain.

The morphological analysis was carried out on the basis of some biometric characters measured on samples of 100 shoots, collected in each of the eight sites. Cluster analysis by complete linkage on the Euclidean distance matrix identified 33 different morphotypes in the eight populations, four of which were exclusive of three different populations, while the others were common to all the eight populations.



Samples of each morphotype were then fingerprinted by two primers, by means of RAPD technique (Random Amplified Polymorphic DNA) and their genetic similarities were evaluated according to Nei and Li (1979) coefficient.

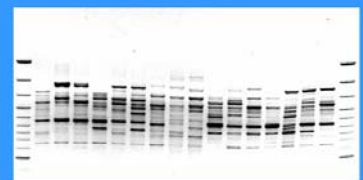
The genetic investigations revealed the presence of a certain number of very similar genotypes inside each population and a weak relationship between the identified morphotypes and the fingerprinted clones. The genetic distances were higher among the clones of the eight populations than inside each population, but it was not possible to sharply characterize the genetic pools of each population.



Po Plain clones – primer M13

From left to right:
Pos. 1 and 18: gene rule
Pos. 2-3: samples from "Vale Le Tombe" (1)
Pos. 4-5: samples from "Vale Erroliera" (2)
Pos. 6-7: samples from "Vale La Comune" (3)
Pos. 8-9: samples from "Vale La Boscon" (4)
Pos. 10-11: samples from "Casa Boschetti" (5)
Pos. 12-13: samples from "Vale Fracassata" (6)
Pos. 14: sample from "Vale Beroglio" (7)
Pos. 15-16: samples from "Oasi Quadrona" (8)
Pos. 17: sample from Belgium, used as outgroup

The study of the clonal variability was then extended to a wider context by comparing the Po Plain clones with the clones of Mediterranean and Centre-European populations surrounding the Po Plain.

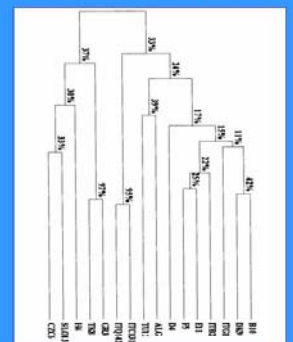


Mediterranean and Centre-European clones – primer M13

From left to right:
Pos. 1 and 18: gene rule
Pos. 2: ALG = Algeria
Pos. 3: E11 = Spain
Pos. 4: FS = France
Pos. 5: B10 = Belgium
Pos. 6: T112 = Tunisia
Pos. 7: ITG1 = Italy Gergona
Pos. 8: ITB2 = Italy Bergamo
Pos. 9: ITG21 = Italy "Vale Comune" (3)
Pos. 10: ITG140 = Italy "Oasi Quadrona" (8)
Pos. 11: D40 Germany
Pos. 12: D49 = Denmark
Pos. 13: SLO19 = Slovenia
Pos. 14: C26 = Czechoslovakia
Pos. 15: H4 = Hungary
Pos. 16: G2 = Greece
Pos. 17: T12 = Turkey

A larger genetic variability was appreciated when the Po Plain clones were compared with the Mediterranean and Centre-European clones. It was possible to differentiate the Po Plain clones from the other ones. The compared clones revealed the presence of two genetic groups: South and Western clones, including clones from Tunisia, Algeria, Spain, France, Belgium, Germany and Denmark to which the Po Plain genotypes were more similar to, and East Europe clones with *P. australis* samples from Turkey, Greece, Slovenia, Hungary and Czechoslovakia.

Dendrogram and bootstrap analysis of Mediterranean and Centre-European clones – primers M13, GACA4



The genetic approach detected a higher variability than revealed by the morphological parameters in the eight Po Plain populations of *P. australis*. The variability increases and is more evident when the investigations are extended to a wider scale, such as the European context. *P. australis* population variability is thus worthy of further study in order to identify clones of environmental interest and particularly applicable to phytodepuration, biomass production, ecological engineering.