

Genetic structure of *Juniperus turbinata* in Algeria. Implications in conservation.

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INTRODUCTION

J. Turbinata Guss. is a species from the Mediterranean and Macaronesian regions that very often is located in isolated populations that correspond to environments in which soil and climatic conditions are unfavorable, such as coastal dune formations, lito soils, cold moors or windy areas (Fig 1, Fig 2). *J. turbinata* is of great interest from the point of view of conservation since this species can be found in habitats given priority in the European Directive 92/43 EEC.

In this work, as partial result of a global study on this species, we present results on the genetic variability of 6 Algerian populations as well as on the distribution of the genetic diversity using AFLP (Amplified Fragment Length Polymorphism) molecular markers.

MATERIAL AND METHODS

109 individuals belonging to 6 populations were collected covering the whole range of *J. turbinata* (Fig 4) in Algeria. The study of genetic variability and genetic structure of populations was carried out with three selected AFLP primers

Amplification products were analyzed with an automated sequencer. Data sizing and scoring were done with Genemapper software (Fig 3). Genetic diversity parameters were calculated with AFLPSurv 1.0 and MVSP 3.2. A bayesian model-based analysis was performed to infer the genetic structure of populations with Structure 2.2. DeltaK was used to infer the number of clusters in which the individuals were included.

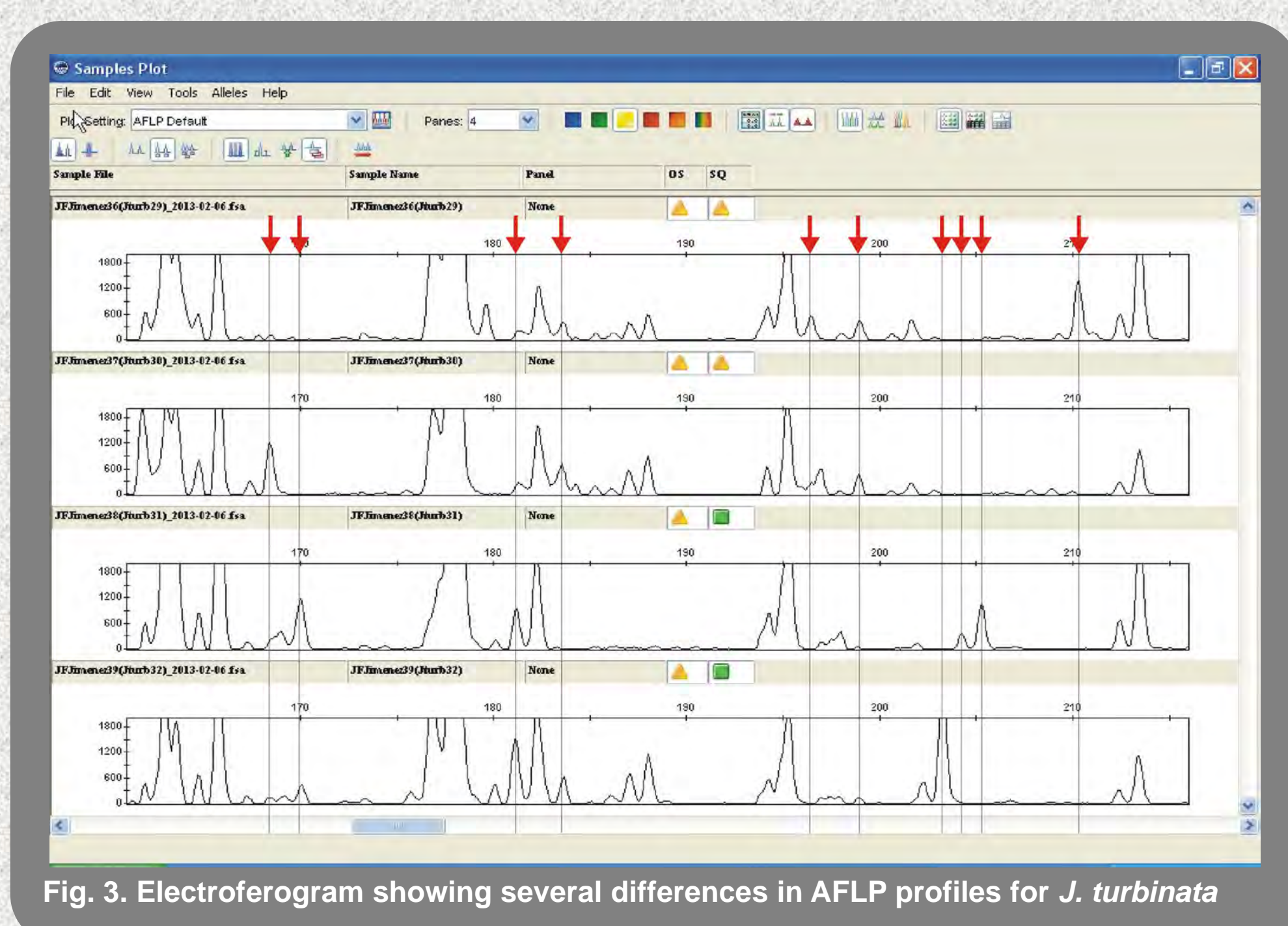


Fig. 3. Electroferogram showing several differences in AFLP profiles for *J. turbinata*

DISCUSSION

AFLP shows high genetic diversity in *J. turbinata*. In deed, our data shows higher genetic diversity values than other studies that used other kind of molecular markers.

Fst values suggest that populations of Algeria are in process of differentiation. The reduction and isolation of populations could be the main cause for this differentiation.

The genetic structure of populations do not follow a clear geographic pattern. Palaeobiogeographical processes (geological rearrangement of mediterranean terranes during Miocene) could explain the present pattern of distribuion of genetic variation. The analysis of populations from Balearic islands or Sardinia could help to solve this issue.



Fig. 1. Population of *J. turbinata* from the North of Algeria.



Fig. 2. *J. turbinata* from Mecheria (pop 1).

RESULTS

A total of 634 AFLP fragments were scored with 3 primer combinations, being polymorphic 610 (96.2%) of them.

Genetic diversity was high in every population, and a moderate genetic differentiation between populations was observed (Fig 4).

PCoA (Fig 5) and bayesian inference (Fig 4) suggest that genetic variation is distributed in two main groups, the first one includes the populations of Stidia, Beni-Saf and La Calle, and the second one groups Mecheria, Cherchell and Amés populations.

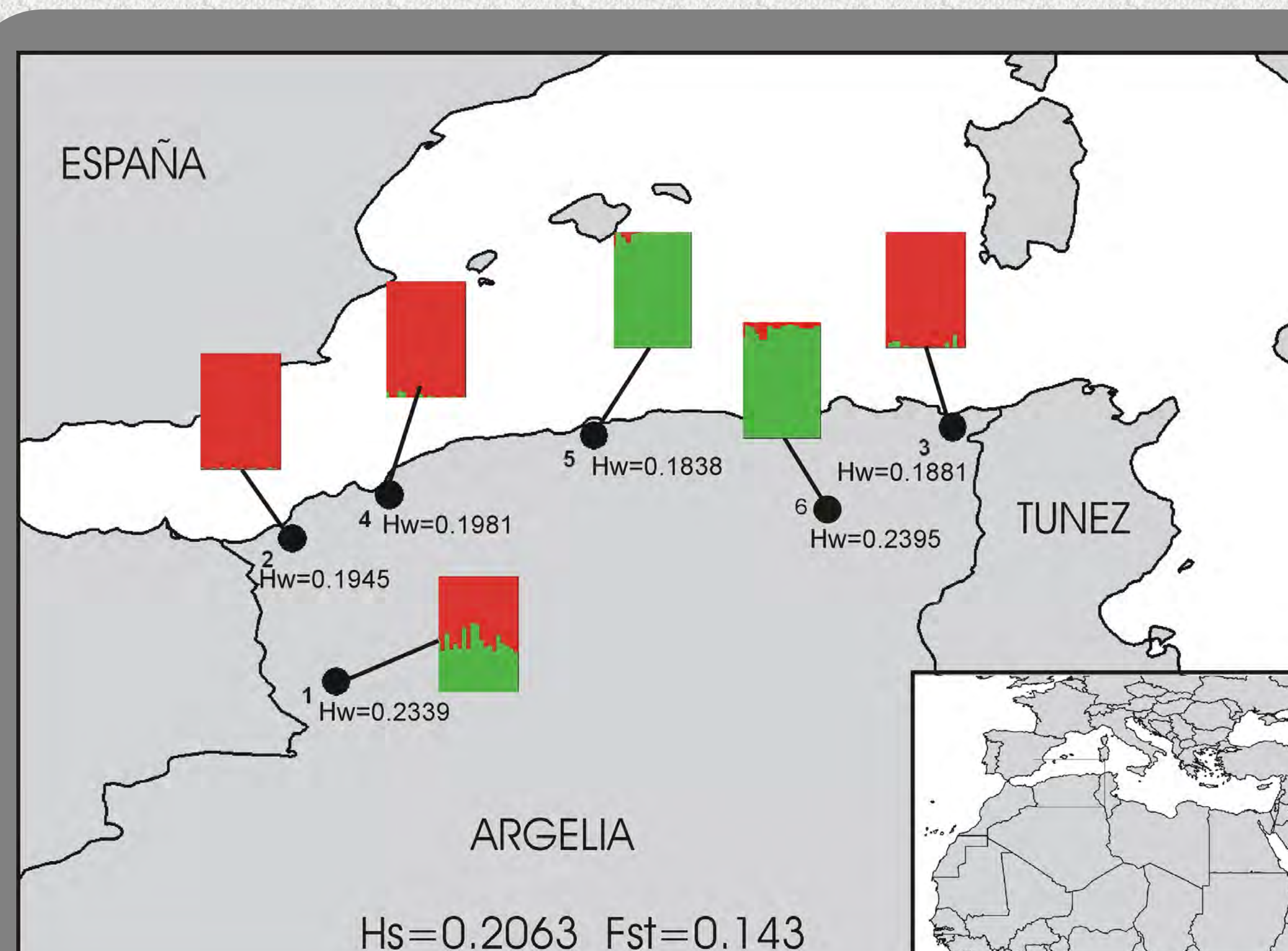


Fig. 4. Sampled populations of *J. turbinata*. Coloured polygons represent the proportion of membership of individuals to one or other group inferred with Structure 2.2. Hw, genetic diversity. Hs= Total Genetic diversity. Fst, Wright fixation index. Populations: 1. Mecheria, 2. Beni Saf, 3. La Calle, 4. Stidia, 5. Cherchell, 6. Amés.

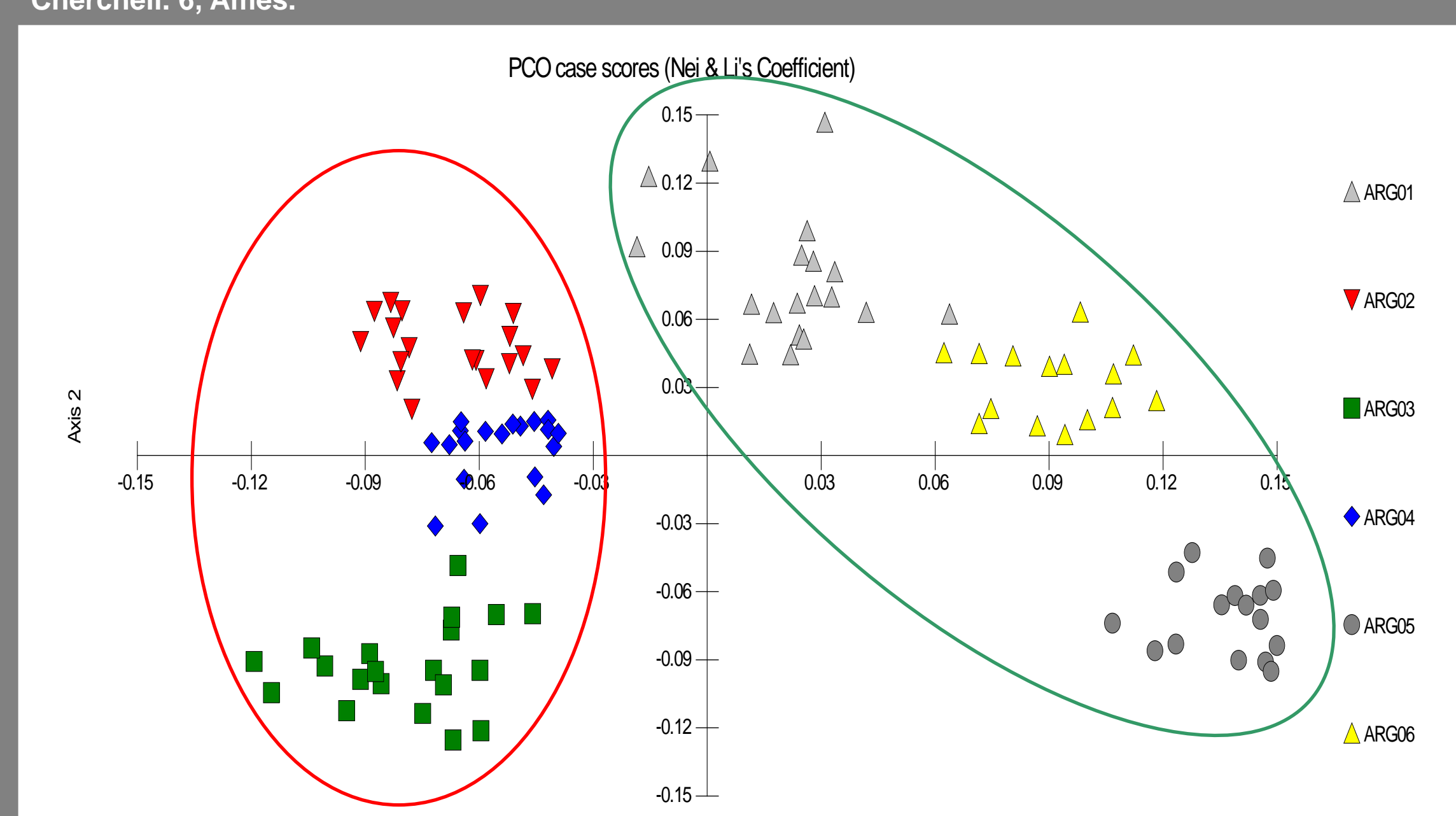


Fig. 5. PCoA plot showing the genetic relationships among 6 populations of *J. turbinata* from Algeria.