SUPPLEMENTARY MATERIAL

On the Methods: Pollen Rarefaction

In Zoñar and Gádor pollen diversity was quantified by estimating the richness of fossil assemblages (number of taxa present) using rarefaction analysis, implemented with the program ANALYTIC RAREFACTION 1.3 (available in http://www.uga.edu/strata/software/Software.html).

Pollen richness of a sample generally increases with the increasing number of pollen grains counted per sample (N) (Odgaard, 1999). Therefore, to compare richness between different samples is needed to reduce them to a common size (n) (Hurlbert, 1971). E(Tn) is the expected number of pollen types in a sample of n individuals randomly selected from a collection that contains N individuals and T pollen types. This can be calculated from the formula (Hurlbert, 1971, Heck et al., 1975):

$$E(T_n) = \sum_{i=1}^{T} 1 - \left[\left(\begin{array}{c} N - N_i \\ n \end{array} \right) \right]$$

Where E(Tn) is the standardized number of pollen types in a sample, T is the number of pollen types originally in a sample, Ni is the number of grains of the pollen type i in a sample, N is the pollen sum in a sample ($=\Sigma$ Ni), and n is the number chosen for standardization ($n \le N$).

While, the variance of the expected number of pollen types in a random sample of n individuals is:

$$\operatorname{var}(T_n) = \begin{pmatrix} N \\ n \end{pmatrix}^{-1} \left[\sum_{i=1}^T \begin{pmatrix} N - N_i \\ n \end{pmatrix} \left(1 - \frac{\begin{pmatrix} N - N_i \\ n \end{pmatrix}}{\begin{pmatrix} N \\ n \end{pmatrix}} \right) + 2 \sum_{j=1}^T \sum_{j=i+1}^T \begin{pmatrix} N - N_i - N_j \\ n \end{pmatrix} - \frac{\begin{pmatrix} N - N_i \\ n \end{pmatrix} \begin{pmatrix} N - N_j \\ n \end{pmatrix}}{\begin{pmatrix} N \\ n \end{pmatrix}} \right] \right]$$

Confidence intervals were defined with p=0.05.

Rarefaction uses a strategy of random selection without replacement, typically selecting a sample of the same size as the smallest count from the entire sequence. The sample-standardized data produced by rarefaction can then be used to compare the diversity of datasets that originally differed in sample size (Birks and Line, 1992, Foote, 1992). In order to apply rarefaction analysis we need to bear in mind that (Birks and Line, 1992):

- Pollen count of every sample (N) must be statistically suitable and representative.
- Rarefaction analysis only considers number of taxa, not the identity of the taxa.
- To compare pollen spectra it is necessary similar taxonomic effort.
- The count routine of the samples must be random.

This analysis was carried out in every palynological sample of Gádor and Zoñar, being n=203 in Zoñar and 216 in Gádor. The rarefaction analyses conducted in this study include terrestrial pollen types (trees, shrubs and herbs), without considering spores and other fossil remains.

Those rarefaction values above or below the confidence intervals were considered as significant biodiversity changes and are discussed on the text.