Supplementary Information

Figures

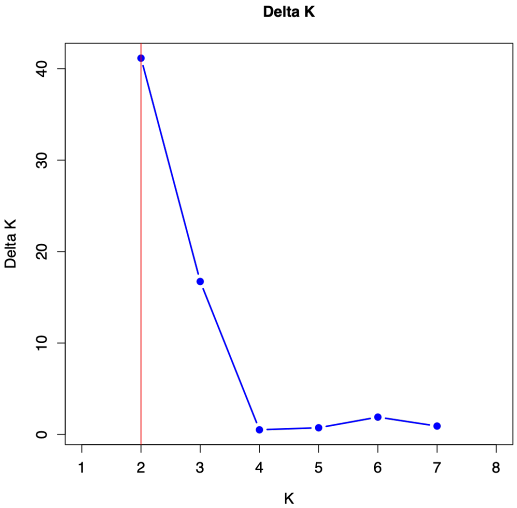

Figure S1. Number of genetic clusters inferred with the Evanno method from the Structure results, based on DeltaK for the total dataset which includes the three major populations (Italy, Algeria and Canary Islands) of *O. patens s.l.*

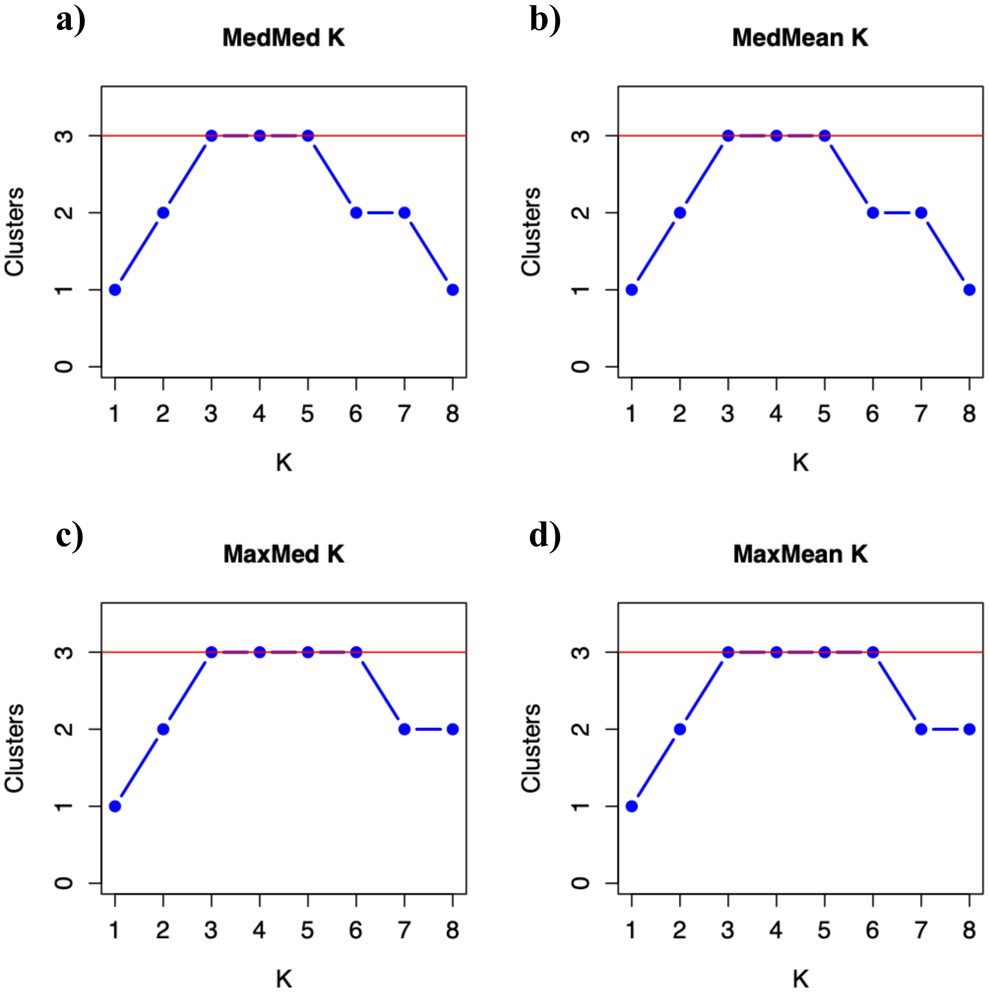

Figure S2. Number of genetic clusters inferred with the estimators MedMedK (a), MedMeanK (b), MaxMedK (c) and MaxMeanK (d) from the Structure results, for the total dataset including the three major populations (Italy, Algeria and Canary Islands) of *O. patens s.l.*

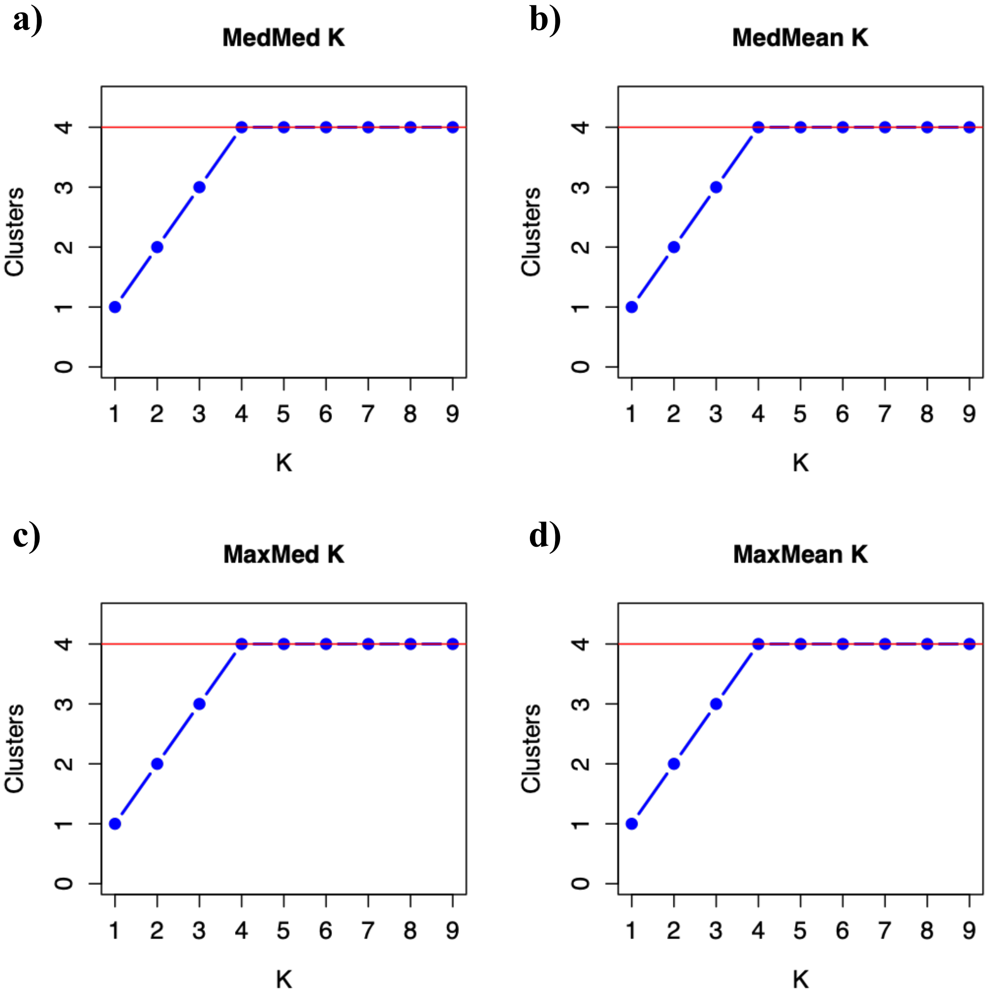

Figure S3. Number of genetic clusters inferred with the estimators MedMedK (a), MedMeanK (b), MaxMedK (c) and MaxMeanK (d) from the Structure results, for the dataset that includes the *O. patens* populations from Italy and Algeria.

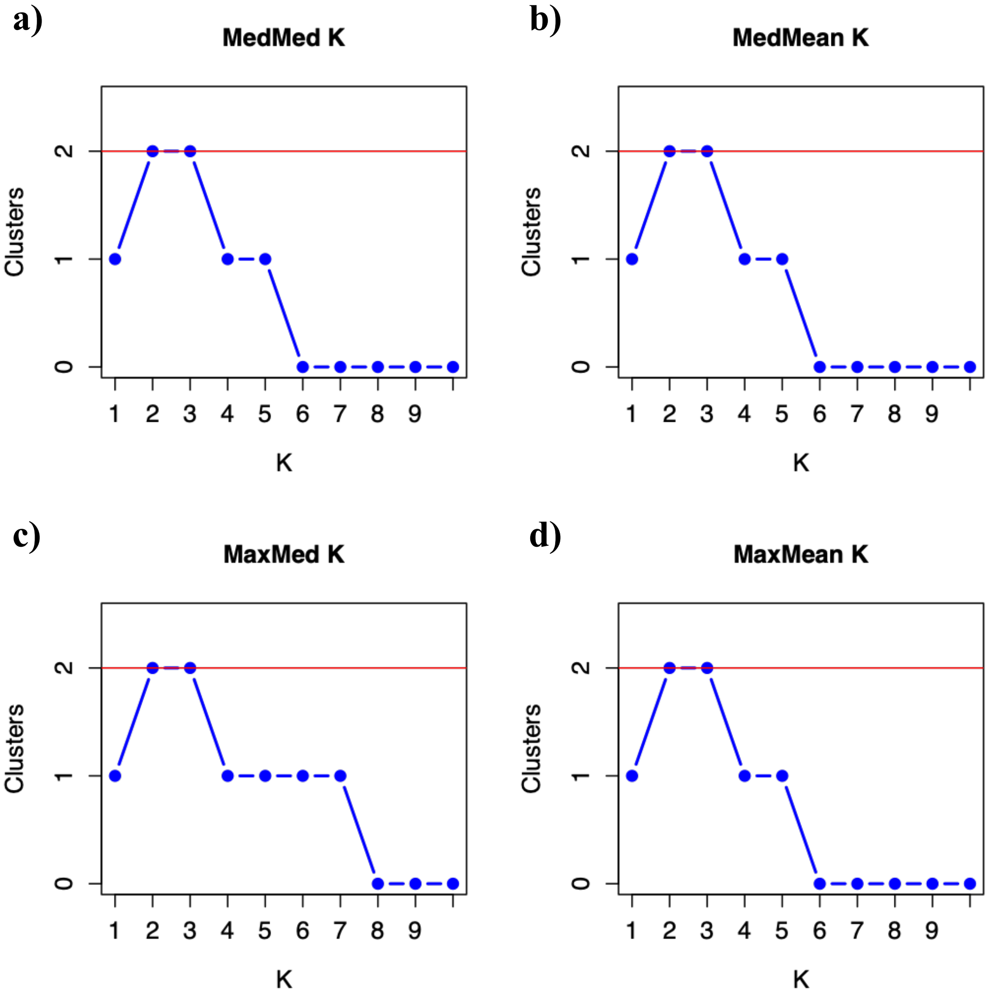

Figure S4. Number of genetic clusters inferred with the estimators MedMedK (a), MedMeanK (b), MaxMedK (c) and MaxMeanK (d) from the Structure results, for the dataset that includes the Algerian samples of *O. patens*.

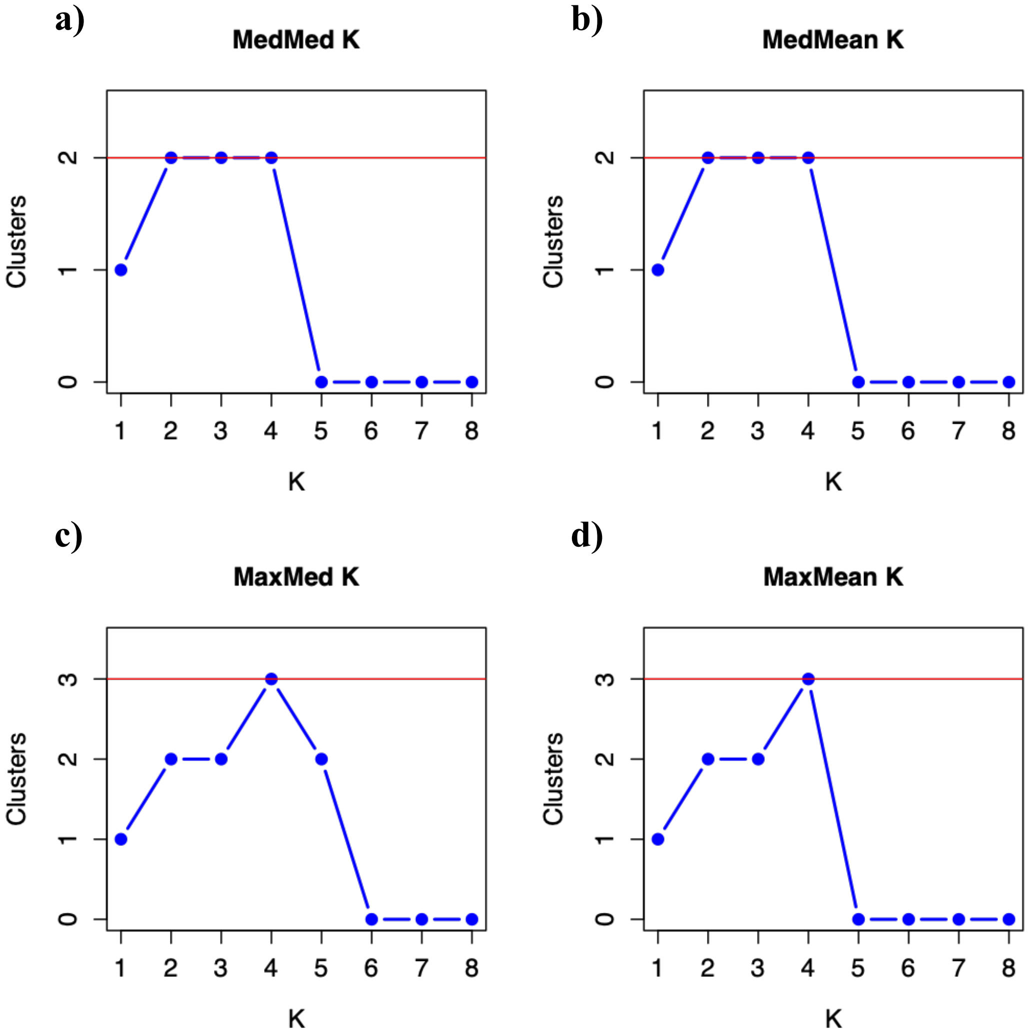

Figure S5. Number of genetic clusters inferred with the estimators MedMedK (a), MedMeanK (b), MaxMedK (c) and MaxMeanK (d) from the Structure results, for the dataset that includes the Italian samples of *O. patens*.

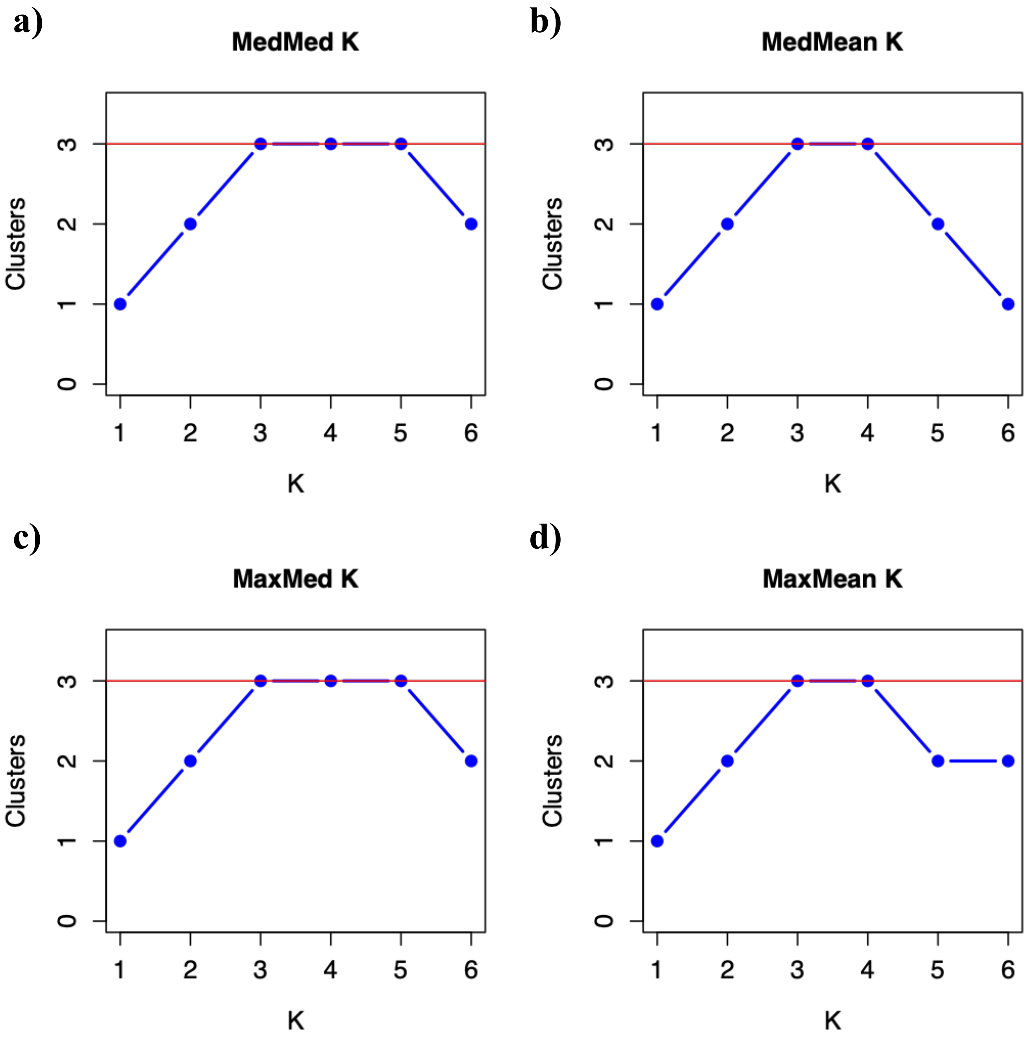

Figure S6. Number of genetic clusters inferred with the estimators MedMedK (a), MedMeanK (b), MaxMedK (c) and MaxMeanK (d) from the Structure results, for the dataset that includes only the populations of *O. canariensis* (Canary Islands).