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aceae as ingroups and two genera of Elatinaceae as outgroups. Pollen grain, plant habit, and chromosome number traits were retrieved from different sources of the literature, scored and coded into six traits and mapped into the most recent generic molecular phylogeny of Malpighiaceae using maximum likelihood criteria. The patterns of pollen grain evolution evidenced by our results showed that all pollen traits showed a strong correlation with the evolution of different habits and chromosome numbers in Malpighiaceae. Pollen grain axis mean values steadily increased in all phylogenetic clades, from the oldest (80 Mya) to the earliest (10 Mya) groups arising throughout the geological time. Our results evidence that even though the pollen traits of Malpighiaceae are somewhat homogeneous for the four largest lianescent clades (Hiraeoid, Malpighioid, Tetrapteroid, and Stigmaphylloid) with larger chromosome numbers, a greater variability in pollen traits was recorded in the six early diverging, shrubby to tree lineages of this family showing smaller chromosome numbers. Additionally, all pollen traits studied showed a great taxonomic potential in circumscribing most of the ten molecular phylogenetic clades resolved in this family and will be properly and widely tested in future studies by us.

P.0168 A field study of the molecular response of brown macroalgae to heavy metal exposure: an (epi) genetic approach

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Our understanding of the relative contribution of genetic and epigenetic mechanisms to organismal response to stress is largely biased towards specific taxonomic groups (e.g., seed plants) and environmental stresses (e.g., drought, salinity). Here, we investigated the molecular basis of the response of the brown macroalgae *Fucus vesiculosus* to heavy metal (HM) exposure. This species can accumulate and tolerate high concentrations of HMs, yet the molecular mechanisms underlying

the response are poorly understood. We reciprocally transplanted living thalli of *F. vesiculosus* between two polluted (P) and two unpolluted (UP) sites on the Galician coast for 90 days. We determined initial (before transplantation) and final (after transplantation) concentrations of HMs in the thalli and characterized their genetic (single nucleotide polymorphisms) and epigenetic (cytosine DNA methylation) variability using epigenotyping by sequencing (epiGBS). Distance based redundancy analyses of genetic, epigenetic and phenotypic pairwise distance matrices showed that: **(i)** all populations differed in their HM content profiles before transplantation (origin explained 98% of the variation in phenotypic distances). After transplantation, they clustered by exposure site regardless of origin (exposure explained 60% of the variation in phenotypic distances); **(ii)** all populations were genetically differentiated; **(iii)** epigenetic differentiation was not significant before transplantation and, when accounting for genotype effects, it was not significant either after transplantation; **(v)** macroalgae from UP sites transplanted within and outside their origin sites showed a higher proportion of individual cytosine methylation changes than those from P sites. Albeit we could not find a consistent epigenetic response to transplantation, potentially due to the environmental differences across all study sites, we found differences in the amount of point methylation changes between macroalgae originated from P and UP sites. Hence, although genetic mechanisms seem to prevail, we cannot completely rule out a potential contribution of epigenetic mechanisms to macroalgal response to HMs.

P.0169 Taxonomic exploration of diatoms in saline wetlands of the Ebro Basin, NE Spain, integrating conventional and molecular approaches

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Saline wetlands, renowned for their uniqueness in the Iberian Peninsula and very scarce in Europe, represent