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deterministic (Clements, 1916) versus the stochastic views (Gleason, 1926). Although both approaches have received much attention, species assembly theory has grown mainly based on observational studies due to the difficulty of manipulating entire communities. In this study, we designed a novel field experiment in a semi-arid Iberian gypsum system lasting four consecutive years, to evaluate the relative contribution of both stochastic events (here represented by the arrival of seeds) and biotic (represented by the presence of *Macrochloa tenacissima* perennial tussocks and biological soil crust) and abiotic (yearly rainfall) environmental filtering to the assembly of the annual-plant dominated communities. Our field experiment was performed on paired plots (i.e., seed free soil vs. homogenised natural soil with the complete seed bank) testing the effects of tussocks vs. BSC vs. open areas on plant assemblages. Results demonstrated that, in years without water stress, stochastic processes were more active than deterministic processes. Although the latter affected cover and taxonomic diversity in assemblages, they did not clearly select for species on the basis of their functional traits. Furthermore, the role played by the presence of BSCs in the community assembly should be highlighted, as their presence substantially accelerated the reconstitution of major plant community features.

P.1178 Tracing 30 years of genetic diversity changes along pollution gradients in brown algae: A pool-sequencing approach

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Studying the temporal evolution of genetic diversity is crucial for predicting adaptive potential and mitigating future ecological changes, particularly in ecosystem engineer species like the brown algae *Fucus vesiculosus*. This alga serves as a foundational species

in the North Atlantic coastal environments, making its genetic health vital for the entire ecosystem. In this study we analyzed samples of *F. vesiculosus* from an environmental specimen bank to investigate changes in genetic diversity over a 30-year period across a pollution gradient. Specifically, we examined samples from five populations of *F. vesiculosus* (~50 thalli per population) collected in 1990, 2005 and 2021 in the North Atlantic Ocean (Galicia, NW Spain), assessing genetic variation and their pollutant concentrations. Levels of the latter in *F. vesiculosus* tissues ranged from 0.31 to 2.4 mg kg⁻¹ for Cd, from 0.22 to 6.5 mg kg⁻¹ for Pb and from 7.2 to 372.5 µg kg⁻¹ for Hg during the 30-year period. We hypothesize that populations in polluted areas have could experienced a loss in genetic diversity as a result of chronic pollutant exposure, and that populations from areas that varied from polluted to unpolluted have not recovered genetic variability yet. The ongoing pool-sequencing analysis will allow us evaluate the impact of anthropogenic activities on genetic variability. Loss of genetic diversity can limit adaptive potential, which is particularly relevant in the context of global change and in this specie given its essential roles in coastal ecosystems. By elucidating temporal patterns of genetic diversity, we gain valuable insights into the mechanisms driving evolutionary processes. This study highlights the broader implications of utilizing environmental specimen banks to understand genetic temporal patterns to offer valuable contributions to ecological and evolutionary research under a reliable and cost-effective method.

P.1179 Mercury concentration declines in brown algae along the North Eastern Atlantic Coast: Three decades of observations

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CERTIFICATE OF PRESENTATION

On behalf of the Organizing Committee, I am glad to inform you
that the Abstract

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(1) Carme Pacín Salvador

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and mycology from all over the world.

Madrid, July 30th 2024



Marcial Escudero

*GENERAL SECRETARY OF THE ORGANIZING COMMITTEE
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