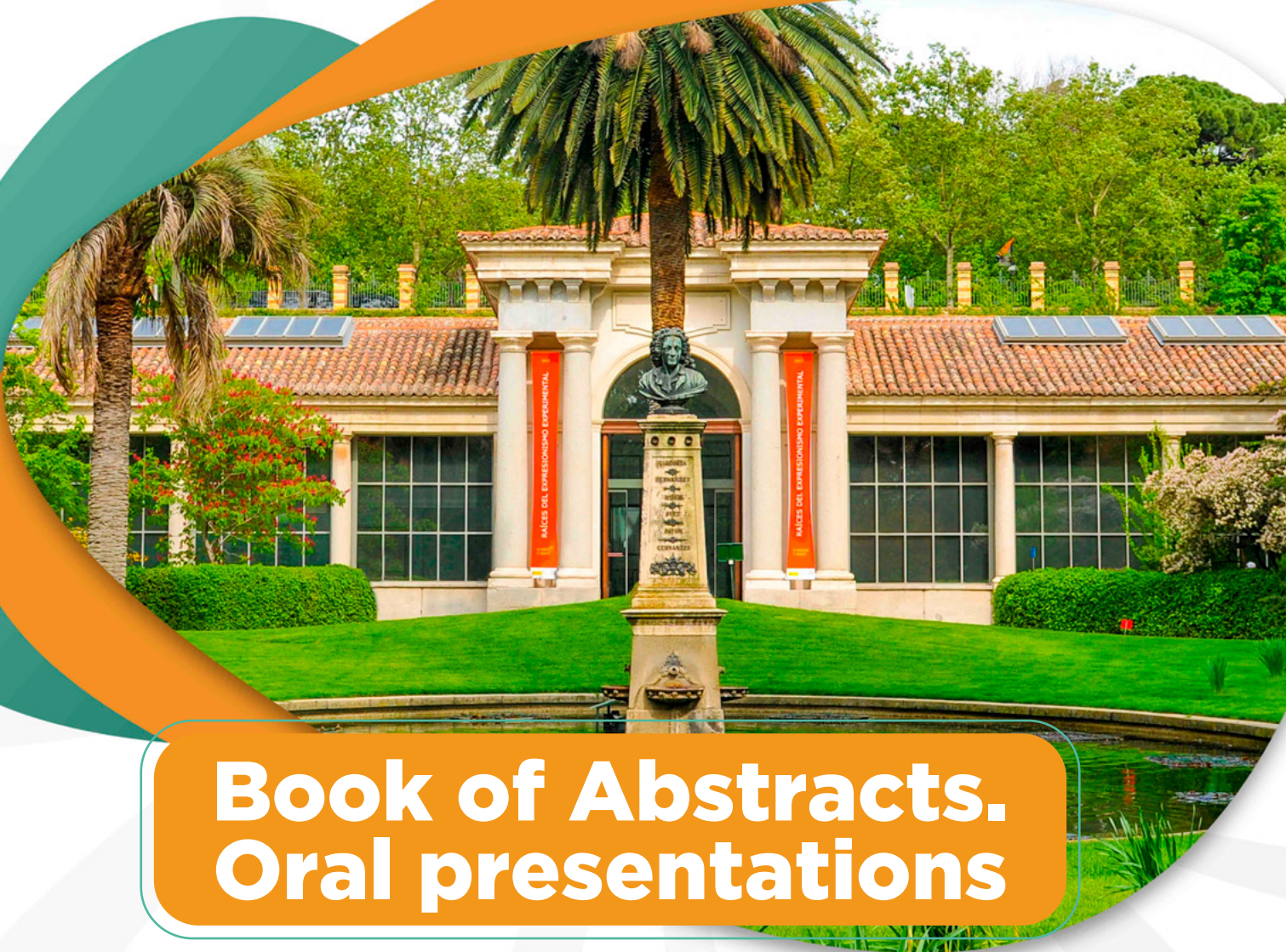




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of distribution changes under climate change. Likewise, the close contact with the managers of the different natural areas is essential for the transferability of the results.

S.85.5 A review of the reproductive biology of endemic Azorean taxa

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The Azorean archipelago is located in the North Atlantic Ocean between 36°55'–39°43'N and 25°00'–31°15'W and is composed of a total of nine volcanic islands divided by three groups. Positioned as the northernmost segment of the Macaronesian biogeographic region, it is considered a hotspot of biodiversity due to the elevated number of endemic species and a significant number of endangered species present. The flora of Azores faces significant threats, primarily stemming from human settlement. The clearing of native vegetation for cereal crops and pasture, along with the introduction of numerous crops, forage, forest, ornamental, and hedgerow plant species, poses a substantial risk. Therefore, it is imperative to prioritize conservation efforts and to implement protective measures to preserve the unique flora of Azores. One approach for *in* and *ex situ* conservation is the combined study of reproductive biology and the genetic characterization of natural populations. There is a considerable lack of information regarding the reproductive biology of the Azorean endemic flora, therefore recent Interreg projects MacFlor (MAC/4.6d/190) and MacFlor 2 (MAC2/4.6d/386) have aimed to improve the knowledge of this particular subject. During the above-mentioned projects, seven endemic Azorean taxa were reviewed: *Hypericum foliosum* Aiton; *Picconia azorica* (Tutin) Knobl.; *Veronica dabneyi* Hochst. ex Seub.; *Frangula azorica* Grubov; *Myosotis azorica* H.C.Watson; *Viburnum treleasei* Gand. and *Laurus azorica* (Seub.) Franco.

New data was collected about micro-morphological elements of the flower, phylogenetic relationships, seasonal and floral phenology, palynology, fruit and seed characterization and reproductive success. It was estimated (by ratio Pollen/Ovule) that the target species have xenogamy as their preferable breeding system, which implies that they favour outcrossing as their main reproductive strategy.

S.85.6 Reconstructing the historical biogeography of an (almost) lost ecosystem: Evolutionary genomics of the Canarian cedar, *Juniperus cedrus*

Jairo Patiño¹, Javier Morente-López¹, Agustín Naranjo-Cigala², Abraham Araña-Padilla¹, Guillermo Sicilia-Pasos^{1,3}, Javier Martín-Carbajal¹, David P. Padilla¹, Yurena Arjona^{1,3}, Manuel Nogales¹

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The extinction of unique species and the disappearance of various types of vegetation have been recurring phenomena on oceanic islands since human colonization. However, the extent of both prehistoric and colonial anthropic impact, as well as their consequences, remains a subject of debate in many island systems. In this context, the study of historical demography through genetic information preserved by current populations offers a unique opportunity to understand how humans have transformed island ecosystems. Our study leverages recent advances in massive high-throughput DNA sequencing (ddRADseq) and population genomic analyses to address the case of *Juniperus cedrus* Webb & Berthel. in the oceanic archipelago of the Canary Islands. It has been suggested that the Canarian cedar was the primary structuring species of a vegetation type that has now practically vanished due to anthropogenic pressure. Consequently, the Canarian cedar, endemic to the islands of Tenerife, La Palma, La Gomera, and Gran Canaria, is classified as nationally and internationally threatened. Herein,

cific hybrids. Plant genomics can untangle evolutionary history as well as complex histories of hybridization on islands. Genomic evidence is presented that hybridization has occurred in the *Commidendrum/Melanodendron* clade due to recent conservation efforts due to planting species in proximity. Furthermore, there is genomic evidence that hybridization events may be ancient, with the species forming a syngameon, so raising the genetic effective population sizes (N_e) of species. A syngameon is here defined as: “a group of otherwise distinct species interconnected by limited gene exchange, i.e., the most inclusive interbreeding evolutionary unit” (Suarez-Gonzalez et al., “Adaptive introgression: a plant perspective” *Biology Letters* 2017). Such hybridization events are postulated to be a continual source of background ‘evolutionary rescue’ of species from any small population size impacts over geological time, a phenomenon of particular importance and impact on islands. Genomic studies are an essential tool for the study of plant evolution on islands, and for endemic plant conservation.

S.137.6 Phylogenomics of the hyperdiverse Asteraceae family in an oceanic archipelago: unveiling insights into the mechanisms of evolution

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Invasive species pose a significant threat to biodiversity, particularly on oceanic islands. The native biota of oceanic islands is both fragile and unique, rendering these ecological systems especially susceptible to biological invasions and

other anthropogenic disturbances. Despite this recognition, the mechanisms driving the success of invasive species remain uncertain. Charles Darwin proposed two competing hypotheses, collectively known as Darwin’s Naturalization Conundrum (DNC), to predict a species’ invasive potential. The first hypothesis, termed the “Pre-adaptation Hypothesis,” posits that species closely related to the native community are more likely to invade successfully. This is attributed to their possession of similar life-history traits that pre-adapt them to establish and thrive under the local environmental conditions (environmental filtering). Conversely, the “Naturalization Hypothesis” suggests that species distantly related to native species can exploit empty ecological niches, avoiding competitive exclusion and thus exhibiting a higher potential for invasion (biotic filtering). Herein, we present the findings of a long-term project, **ASTERALIEN**, focused on testing the DNC within the Compositae family across the Canary Islands. We explored the DNC by examining two dimensions of relatedness between species: phylogenetic and functional distance. Utilizing a comprehensive phylogenomic approach to infer a super-tree encompassing all genera and a majority of species in the archipelago, we assessed the phylogenetic relatedness between alien and native species. This super-tree is constructed using hybrid capture-based target enrichment of the angiosperm-wide 353 and the Asteraceae family-specific 1061 probe sets for approximately 300 species. The integration of measured functional traits of all species collected in the field allow us to estimate functional distances between these two (naive vs. exotic) distinct functional groupings. By integrating both phylogenomic and functional approaches at unprecedented resolution, our study explicitly evaluates the mechanisms of evolution and invasion in alien species on oceanic islands within the framework of the DNC.

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