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ence on the distribution of species. Data on the distribution of IAS in Anaga have been correlated with the bioclimatic belts and occupied vegetation belts and a new concept called Bioclimatic Invasibility is proposed to define the susceptibility of invasion of homogeneous bioclimatic zones based on thermoclimatic and ombroclimatic factors. The habitats with the greatest susceptibility to invasion are also determined at the level of Climactic Domain (Association) or Climactic Territory (Alliance). Bioindicative IAS of habitat invasion have been defined. The variation in the distribution of these species across bioclimatic parameters will serve to observe and predict trends of increasing temperatures and climate change in the Canary Islands. It is considered that knowledge about IAS populations and their chorology is very relevant to be able to establish a diachronic monitoring study in the evergreen cloud-forest of the Anaga Rural Park.

## P.1554 Exploring floral trait adaptation to ornitophily and entomophily: A genomic examination of two Macaronesian endemics

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Across the Macaronesian islands, several lineages independently adapted their flower structures to bird pollination. In contrast with the genetic basis of adaptation to entomophilous pollination, this convergent adaptation of floral traits to interacting with non-specialist birds remains largely unexplored. Using comparative, functional and evolutionary genomics in three species of Malvaceae with contrasting pollination syndromes and a shared phylogenetic history, the Canarian endemics ornitophilous *Navaea phoenicea* and entomophilous *Malva canariensis*, and its mediterranean sister entomophilous *Malva wigandii*, we performed genome and transcriptome sequencing, assembly, annotation and analysis of gene sequence and expression to explore the genomic mechanisms by which pollinator shifts exert natural selection on floral traits. Genome sequencing with Illumina and PacBio reconstructed *de novo* draft assemblies highly frag-

mented but complete at gene space. Further, we assembled high coverage Illumina floral transcriptome data across five pre- and anthetic flower developmental stages. The results show that for most gene families involved in morphological, anatomical, biochemical and physiological traits examined, the gene content, sequence evolution and gene expression profiles are similar between ornitophilous and entomophilous species, yet, several candidate genes show unique features associated to each pollination syndrome, in each of the steps of advertisement, mechanical interaction and reward to pollinators, that eventually determine the fitness of pollination. In brief, the gene expression of entomophilous species is directed to produce a pale blue petal pigmentation and an epidermal surface mainly composed of sinuous cells, while *N. phoenicea* produces a salmon-like color pigment suite, and its transcriptional regulation of sinuous cell differentiation is also almost absent, leading petal epidermal surface be mainly composed of tabular cells. The higher expression of transcription factors related to floral nectary inception results in a bigger floral nectary area, and the higher production of parenchymatic carbohydrate biosynthesis machinery results in a higher outcome of secreted nectar.

## P.1555 Resolving cryptogenic species within the Compositae across the Canary Islands using a generalized demographic-based approach

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