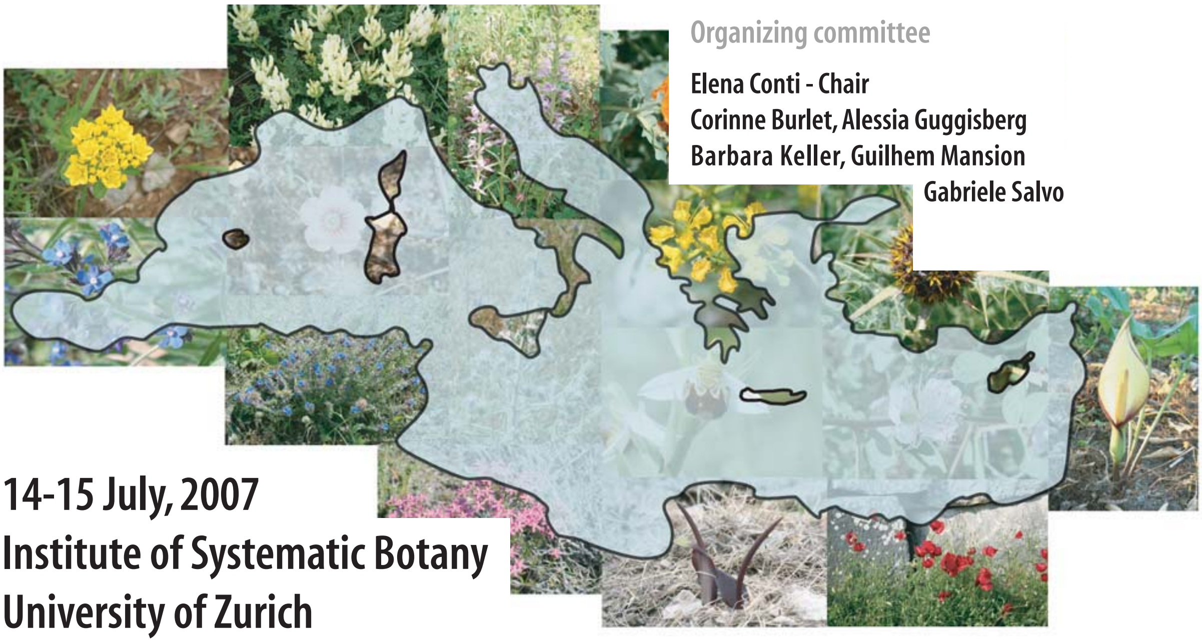
Origin and Evolution of Biota in Mediterranean Climate Zones

an Integrative Vision



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14-15 July, 2007
Institute of Systematic Botany
University of Zurich

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Aim of the conference

Understanding the biotic and abiotic processes that contribute to high species numbers in biodiversity 'hot spots' is one of the major tasks of biology. The exceptional biological richness of the five mediterranean climate zones of the earth - the Mediterranean basin, South Africa, Australia, Chile and California - makes them an ideal case study to investigate the evolutionary and ecological dynamics that generate elevated species numbers. By focusing on the Mediterranean basin, the conference will synthesize the current state of knowledge on the origin of mediterranean biota, while charting a map for pushing the frontier of conceptual and methodological advances in biodiversity studies. The goal of the conference is to clarify the history of biotic assembly in mediterranean climate zones by integrating evidence across multiple disciplines, including evolutionary biology, systematics, ecology, paleontology, paleoclimatology, and paleogeology.

The conference is aimed at scholars from various biodiversity disciplines at different stages of their careers, from beginning Ph.D. students to established scholars.

Marmaris, Turkey, June 2005 (Photo: G. Mansion)

Organization committee

Prof. Elena Conti **Chair**	
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Alessia Guggisberg **Poster sessions** **Dinners** **Field trip**	
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Program

Sat., July 14	TOPIC	SPEAKER	TITLE
9:00-9:20	**Introductory remarks**		
9:20-9:55	Plenary Speaker	Donoghue	Phylogenetic Biogeography: Past, Present, and Future
9:55-10:20	Methods	Cheddadi	Past climate changes in the Mediterranean and potential impacts on some plant species
10:20-10:45	Methods	Rosenbaum	Geological history of the Mediterranean basin
10:45-11:05	**Coffee Break**		
11:05-11:30	Methods	Ree	Stochastic models of geographic range evolution and likelihood-based inference of ancestral ranges
11:30-11:55	Methods	Sanmartin	The promise of Bayesian inference for Mediterranean historical biogeography
12:20-13:45	**Lunch Break**		
13:45-14:10	Methods	Magallon	Paleobiology in aid of molecular clocks
14:10-14:35	Macroevol	Conti	Dating the origin of plants endemic to the Corso-Sardinian microplate: a window on the biogeography of the western Mediterranean Basin
14:35-15:00	Macroevol	Medail	Importance of historical biogeography in shaping plant diversity in the Mediterranean basin
15:00-15:25	Macroevol	Oberprieler	The temporal, spatial, and ecological differentiation of Compositae-Anthemidae in the Circum-Mediterranean area
15:25-15:45	**Coffee Break**		
15:45-16:10	Macroevol	Vargas	Reconstructing micro- and macroevolution in snapdragons (*Antirrhinum* and relatives)
16:10-16:35	Macroevol	Linder	Evolution of the Cape flora of Southern Africa, and the influence of the mediterranean-type climate
16:35-17:00	Microevol	Comes	Plant evolution in the Aegean region
17:00-17:25	**Discussion**		
17:25-19:00	**Aperitif & Posters**		
20:00-23:00	**Dinner: Uetliberg**		

Sun., July 15	**TOPIC**	**SPEAKER**	**TITLE**
9:00- 9:20	**Introductory remarks**		
9:20-9:55	Plenary Speaker	Thompson	The dynamics of plant populations in the Mediterranean mosaic landscape: Ongoing adaptation and response to contemporary changes
9:55-10:20	Microevol	Fady	Biodiversity at gene level in Mediterranean conifers
10:20-10:45	Microevol	Kadereit	Determinants of phylogenetic structure in Mediterranean coastal plants
10:45-11:05	**Coffee Break**		
11:05-11:30	Microevol	Nieto Feliner	Species distribution modeling matches phylogeographic patterns in the Atlantic-Mediterranean disjunct *Armeria pungens*
11:30-11:55	Microevol	Rossello	Plant evolution in a continental archipelago: The Balearic islands
11:55-12:20	Microevol	Stuessy	Microevolutionary patterns in *Hypochaeris* of the western Mediterranean
12:20-13:45	**Lunch Break**		
13:45-14:10	Microevol	Wilson	Environmentally-mediated reproductive variation in a nearshore European Pipefish species
14:10-14:35	Ecology	Arroyo	Sex polymorphism in Mediterranean plants: insights from heterostyly and floral biology
14:35-15:00	Ecology	Cozzolino	Pollination strategies, reproductive isolation and speciation processes in Mediterranean orchids
15:00-15:25	Ecology	Verdu	Evolution of plant traits under Mediterranean fire-prone environments
15:25-15:45	**Coffee Break**		
15:45-16:10	Ecology	Lamont	Plant adaptations in mediterranean Australia
16:10-16:35	Ecology	Medel	Evolutionary ecology of mutualistic animal-plant relationships in mediterranean ecosystems
16:35-17:00	Ecology	Ackerly	Climate and the California flora: Past, Present and Future
17:00-17:25	**Discussion**		
17:25-19:00	**Aperitif & Posters**		

MAIN SESSION

PHYLOGENETIC BIOGEOGRAPHY: PAST, PRESENT, AND FUTURE

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Vicariance biogeography rightly focused attention on deriving generalities across clades, but it limited itself to obtaining area relationships from tree topologies. Although it produced a dense literature, few genuinely new biogeographic insights emerged. Fortunately, attention has recently shifted to incorporating other sources of relevant information, such as the timing of divergence events, and toward the development expandable model-based inference methods. At the same time, renewed attention to several major biogeographic problems, such the movement of biotas around the Northern and Southern Hemispheres, is yielding fresh perspectives, and the historical assembly of Mediterranean biotas can now be seen in a new light. The future for phylogenetic biogeography is exceptionally bright: methods will be extended to incorporate additional sources of evidence as well as uncertainties, phylogenies will be integrated with niche-modeling approaches, new problems will be addressed (such as species richness gradients), and the need for biogeographic knowledge will increase dramatically, especially in relation to global change.

PAST CLIMATE CHANGES IN MOROCCO AND POTENTIAL IMPACTS ON SOME PLANT SPECIES

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During the past 20 thousand years, climate has oscillated from a global glacial era to a warmer and more humid period than the present. Unlike Europe, climate changes during that time span are very poorly documented in Northern Africa. Thus, we know very little about the impact of past climates on the vegetation and particularly on some nowadays endagered species such as Cedar. We have collected new fossil records from a few sites located in the Middle Atlas, Morroco. The pollen content and other proxies allowed us to reconstruct a few climate variables and the history of a few species among which cedar. These data indicate that cedar survived during the last glacial period in refugia which are located in the Middle Atlas. The reconstructed temperature changes indicate that cedar has reacted to both strong dryness and warming which may allow us to expect that it might survive to the expected future climate change. However, the model simulations we have performed show that its distribution will be different from the modern one and its range will be much more reduced by 2100.

GEOLOGICAL HISTORY OF THE MEDITERRANEAN BASIN

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The Mediterranean Basin is positioned between Africa and Eurasia, which are two tectonic plates that have been moving towards each other since the Cretaceous (ca. 120 Myr ago). During most of the Mesozoic era (245-65 Myr ago), the regional geology was dominated by marine sedimentation within the Mesozoic Neotethys Ocean and in its peripheral shallow marine basins. Progressive consumption of the Neotethys Ocean since the Cretaceous involved subduction and collisional processes and resulted in the development of the Alpine belt. Currently, the only remnants of the Neotethys Ocean floor are the Levant, Herodotus and Ionian Basins in the eastern Mediterranean. In contrast, all the basins in the western Mediterranean, as well as the Aegean Sea, have been developed since the Oligocene (ca. 30 Myr ago) by stretching of the thick continental crust, thus destroying large parts of the earlier Alpine belt. The tectonic evolution of the western Mediterranean, therefore, was dominated by extension tectonics that was active simultaneously with the far-field convergence of Africa with respect to Eurasia. During this process, relatively small continental blocks, such as Corsica, Sardinia and Calabria, were rifted off from their original positions, and were subsequently subjected to large horizontal displacements.

STOCHASTIC MODELS OF RANGE EVOLUTION FOR HISTORICAL INFERENCE AND BIOGEOGRAPHIC HYPOTHESIS TESTING

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An important line of inquiry in historical biogeography concerns past geographic ranges of species and clades, and the sequence of biogeographic events connecting phylogenetic ancestors to descendants. Stochastic models of the processes that cause ranges to evolve, namely dispersal (range expansion) and local extinction (range contraction), may be used to infer the past on phylogenetic trees, in a manner analogous to models used to infer ancestral character states. A recently developed example of this is the dispersal-extinction-cladogenesis (DEC) model, that allows maximum-likelihood estimation of dispersal and local extinction rates, as well as comparison of likelihoods of distinct ancestral range inheritance scenarios at cladogenesis events. Unlike previous parsimony-based methods, the DEC model allows external information about geological history to be incorporated into biogeographic hypothesis testing. Using an example of island biogeography, I show how general models that allow unrestricted ranges and dispersal between areas may be refined to better fit the data.

THE PROMISE OF BAYESIAN INFERENCE FOR MEDITERRANEAN HISTORICAL BIOGEOGRAPHY

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Despite its growing popularity in phylogenetics, Bayesian inference has rarely been used in biogeographic research. Bayesian approaches, however, offer many advantages. Unlike parsimony methods, they use branch length information and an explicit evolutionary model to estimate the probability of alternative states and can thus accommodate the uncertainty associated to ancestral area reconstruction. In contrast to maximum likelihood, they can also accommodate phylogenetic uncertainty in topology and branch lengths through stochastic sampling from the posterior probability distribution of the phylogeny. Phylogenetic uncertainty is likely to be a serious source of error in many biogeographic studies, for which support and resolution for phylogenetic relationships is often low at basal nodes. By integrating out other parameters in the model (trees and molecular substitution variables), we can obtain marginal probability distributions for the parameters in the biogeographic model such as extinction and dispersal rates. This can be of particular importance in area biogeography, in which inferences on biogeographic history are drawn from multiple groups evolving on different trees. Finally, Bayesian model comparison allows biogeographic inference to be placed within a quantitative hypothesis-testing framework. Here I review recent methodological advances to adapt the Bayesian approach to biogeographic inference and its promising application to Mediterranean biogeography.

PALEOBIOLOGY IN AID OF MOLECULAR CLOCKS

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Accurate knowledge about timing of speciation is crucial for a correct understanding of the origin and diversification of geographically circumscribed biotas. Relaxed molecular clocks represent a viable alternative to estimate speciation times. The need to incorporate independent information to extricate rate and time in the branches of a tree has been formally recognized, and there is an increasing appreciation of the relevance of fossil information as an auxiliary in molecular dating. Fossil-derived bounds on the ages of nodes have been shown to buffer extensive variation derived from different data, estimation procedures and rate smoothing. Nevertheless, molecular clocks have not benefited from paleobiological perspectives that could lead to methodological and conceptual improvements. More realistic divergence time estimates may be achieved by introducing calibration and constraints as confidence intervals likely to contain the true time of origin of a clade, derived from observed stratigraphic ranges and density of fossil preservation. The plausibility of missing fossil histories implied by molecular clock dates that substantially predate first fossil occurrences may be tested considering the number of lineages at the onset a clade´s diversification, its preservation and extinction rates. Finally, paleobiology may provide parameters to model rate change over macroevoutionary time.

DATING THE ORIGIN OF PLANT ENDEMICS TO THE CORSO-SARDINIAN PLATE: A WINDOW ON THE BIOGEOGRAPHY OF THE WESTERN MEDITERRANEAN BASIN

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Despite the remarkable species-richness of the Mediterranean flora, relatively few studies have investigated the temporal and spatial origins of this extraordinary diversity. Within the Mediterranean basin, the islands of Corsica and Sardinia have been identified as one of the areas with the highest endemism, hence they play a key role for understanding the evolution of Mediterranean diversity. Furthermore, the well-known geologic history of the Corso-Sardinian microplate, marked by the Late Oligocene split from northeastern Spain and southern France, and proposed land bridges with central Italy in the Miocene and northwestern Italy in the Pleistocene, provides the necessary framework to investigate the relative contribution of land connections and over-water dispersal to the assembly of their endemic flora. In our study, we investigate the origins of a selected group of Corso-Sardinian endemics in Rutaceae, Araceae, and Boraginaceae through a combination of phylogenetic analysis, molecular dating, and ancestral area reconstruction. After a review of the geologic history of the Corso-Sardinian microplate, I will integrate results from the mentioned lines of evidence to elucidate the origin and likely migration routes of *Ruta corsica*, three endemics in Araceae, and eight endemics in Boraginaceae.

IMPORTANCE OF HISTORICAL BIOGEOGRAPHY IN SHAPING PLANT DIVERSITY IN THE MEDITERRANEAN BASIN

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Recent phylogeographical studies indicate that some major palaeogeographical events and glacial-interglacial cycles have had a previously unsuspected role in shaping modern biodiversity in temperate regions. The Mediterranean Basin hotspot represents a major biogeographical crossroads, and the conservation of this unique biodiversity is recognised as a world-scale priority. The identification and description of glacial refugia is critical for an optimal evolutive conservation of this highly threatened ecoregion. We present here an analysis of the scientific literature in order to identify refugia in the Mediterranean region, based upon intraspecific phylogeographical studies of plant species. 50 refugia are identified, and with a shared total of 24 refugia, the role played by the three major peninsulas is confirmed. Also, we emphasize the importance of other areas that have previously been attributed a lesser role. These refugia are strictly coincident with the major plant endemism areas and the regional biodiversity hotspots, which are mainly situated on islands and mountains. They represent generally "phylogeograpical hotspots", i.e. significant reservoirs of unique genetic diversity for preserving the future of evolutionary processes of Mediterranean species. Through the persistence of plants, these refugia could also play a crucial role in mitigating the putative mass extinction of plant species linked to climate changes.

THE TEMPORAL, SPATIAL, AND ECOLOGICAL DIFFERENTIATION OF CIRCUM-MEDITERRANEAN COMPOSITAE-ANTHEMIDEAE

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A combination of dispersal-vicariance analysis (DIVA) and molecular clock dating of a calibrated, rate-smoothed maximum-likelihood tree based on sequence information from the internal transcribed spacer region of the ribosomal repeat (nrDNA ITS) was used to reconstruct the biogeographical history of the Circum-Mediterranean clade of Compositae-Anthemideae. The reconstructions suggest that the ancestor of this clade diverged from the basal African lineages in the late Early Miocene (18 Myr) and that recurrent dispersal/vicariance events during the Middle and Late Miocene (16-11 Myr) both between the eastern and western Mediterranean regions and (in the latter region) between the northern and southern Peri-Tethys platforms caused the further diversification of the clade. We used over 3000 geo-referenced herbarium specimens of the species used in the phylogenetic analysis and global climate data to reconstruct potential climate range overlaps among representative clades through a GIS-based approach implying a ´genetic algorithm of rule-set prediction´ (GARP). Niche comparisons among 14 clades revealed values between 5% and 68% of potential climate range overlap. No significant correlations between the age or the mode (sympatric vs. allopatric speciation) of dichotomies in the tree and the niche overlap of the resulting sister-clades were detected. For the circum-Mediterranean genus *Anthemis,* more detailed analyses comprising c. 130 of its 193 species are provided. A phylogenetic analysis of the polyploidy complex of the genus *Leucanthemum* sheds further light on glacial refugia in the Mediterranean.

RECONSTRUCTING MACRO- AND MICROEVOLUTION IN SNAPDRAGONS (*ANTIRRHINUM* AND RELATIVES)

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The snapdragons (tribe Antirrhineae: 30 genera, c. 300 species) are the subject of a study at the genus, species and population levels. Developmental genetics have shed light on major phenotype changes supporting macroevolutionary patterns in *Linaria* and *Mohavea*. Allopolyploidization at deep nodes has been also inferred by phylogenetic reconstructions of plastid and nuclear markers, indicating a different evolutionary mechanism in the macroevolutionary process. At the species level, new sequencing (*matK*, *trnS-G*, ITS) and AFLP fingerprint data reveal that hybridization has been responsible for complex relationships between the 21 species of *Antirrhinum*, even though considerable isolation by geography is easily interpreted. A population study in a particular species (*Antirrhinum charidemi*) reveals that pollinators (bees) of personate flowers drive divergence in new morphotypes. Life traits and territorial bees may be responsible for a structured population distribution of this narrow-endemic. Although there are self-incompatible *Antirrhinum* species, we interpret that recent isolation (onset of the Mediterranean climate) by geography and the effect of territorial bees are responsible for speciation patterns. The body of knowledge accumulated to date leads us to hypothesize that both macro- and microevolutionary processes have been involved in differentiation of snapdragons.

EVOLUTION OF THE CAPE FLORA OF SOUTHERN AFRICA, AND THE INFLUENCE OF THE MEDITERRANEAN TYPE CLIMATE

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The Cape flora, centered on the southern tip of Africa, includes some 7’000 species, of which the majority belongs to 30 very species-rich clades. The structure of the vegetation and the summer-dry climate of the Cape are reminiscent of that of the Mediterranean basin, and as a result this it is regarded as a Mediterranean Type Ecosystem. I will consider three aspects of the evolution of this flora: the origin of the typical sclerophyllous, evergreen leaves; the origination of the clades of this flora; and the evolution of the modern species diversity. The role that the climate might have played is confounded by the fragmentary knowledge of the palaeoclimates of the region. However, it seems that both the origins of the older clades, as well as the typical morphological attributes of these clades, might be more related to the oligotrophic soils. The climate may have played a much larger role in the evolution of the modern diversity of these regions, possibly because members of these Cape clades can tolerate summer drought, and also exploit the more open vegetation and regular fires resulting from this seasonal climate.

PLANT EVOLUTION IN THE AEGEAN REGION

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The *Nigella arvensis* complex (Ranunculaceae) comprises twelve annual taxa in the Aegean region. While all species are self-compatible, most taxa are mainly cross-fertilized, and occur throughout mainland Greece/Turkey and the larger Aegean islands (Rhodes, Crete). However, two small-flowered species are selfers, one widespread in the Cylades/Crete (*N. doerfleri*) and the other restricted to western Crete and Kythira (*N. stricta*). Molecular clock data (ITS sequences) imply a monophyletic origin of the complex in the Late Tertiary/Pleistocene, and testify to its recent and rapid radiation as evidenced by survival analysis. Among characteristics studied so far, those that seem most likely to have increased speciation rate seem to be the opportunity for allopatry within an archipelago and the shift from outcrossing to selfing. Moreover, a survey of amplified fragment length polymorphisms (AFLPs) across the *N. arvensis* complex indicates that the evolution of selfing in the complex was mainly associated with colonization events, as predicted under the reproductive assurance hypothesis. Together, these observations suggest that plant diversification in the Aegean may owe more to geographical contingency and the evolution of reproductive isolation (due to selfing) than to ecological diversification, calling into question the notion that ecological divergence is the major force driving evolutionary radiation.

THE DYNAMICS OF PLANT POPULATIONS IN THE MEDITERRANEAN MOSAIC LANDSCAPE: ONGOING ADAPTATION AND RESPONSE TO CONTEMPORARY CHANGES

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Plant biodiversity in the Mediterranean Basin is characterised by two major features: first, on a biogeographic scale many species have narrow endemic distributions; second, at the local landscape scale species distributions occur in a highly heterogeneous ecological setting. In this context my talk will have three main components. First and foremost, I illustrate how biological traits have evolved and are showing ongoing adaptation to both highly localised spatial variation in ecological conditions and the configuration of their populations in the mosaic landscape. Secondly, I discuss how the Mediterranean mosaic landscape is changing rapidly, the causes of such changes and their implications in terms of the response of plant populations to new selection pressures and dispersal possibilities. Finally, I reflect briefly on the need for both (a) new fundamental research to identify the role of population variability in species persistence as human activities become the dominant force shaping Mediterranean plant population ecology and evolution and (b) faster and more effective transmission and input of this scientific knowledge into decision-making and conservation policy for the endemic Mediterranean flora.

BIODIVERSITY AT GENE LEVEL IN MEDITERRANEAN CONIFERS

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Biodiversity is commonly assessed at species level to monitor the spatial structure of richness and endemism, both worldwide and in specific biomes, and to understand how particularly rich regions came to emerge as the result of macro-evolutionary processes. The same type of investigations can be done using genetic diversity, where patterns of within and among population gene diversity can be plotted against past and current environmental variables to assess how past ecological processes have shaped the evolutionary structure of populations. In this talk, I will present how gene diversity at neutral markers is structured in the Mediterranean, using published data on four conifer genera commonly found in the northern hemisphere, *Abies*, *Cedrus*, *Cupressus* and *Pinus*. Species from these four genera had higher genetic diversity than non-Mediterranean conifer species worldwide, indicating that the Mediterranean is not only a hotspot of species biodiversity, but also a hotspot of genetic biodiversity. Genetic diversity in the Mediterranean was spatially structured, higher in the Eastern than in the Western Mediterranean, suggesting different micro-evolutionary patterns at the two ends of the Mediterranean. A possible cause for this pattern is the last Quaternary ice age, drastically harsher in the western than in the eastern Mediterranean. Such conditions are likely to modify available ecological niches, with the advent of small-sized refugia in the western Mediterranean, and demographic bottlenecks leading to genetic drift and loss of genetic diversity within populations. Genetic diversity was also found to be bioclimatically structured, with low elevation thermophilous conifers displaying less genetic diversity than mesophilous or mountain conifers. Again, this pattern could be explained by a more severely shrinking ecological niche during the ice ages for thermophilous than for mesophilous and mountain conifers. These results show that Quaternary refugial zones were probably very different in size and shape across the Mediterranean, depending on species ecological requirements and spatial distribution. Finally, the extent to which human activities may have obscured these natural micro-evolutionary processes is discussed.

DETERMINANTS OF PHYLOGENETIC STRUCTURE IN MEDITERRANEAN COASTAL PLANTS

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We investigated the genetic structure of two coastal flowering plant species (*Cakile maritima*, *Eryngium maritimum*) across four sea straits (Skagerrak, Strait of Gibraltar, Dardanelles, Bosporus) using AFLP variation. By investigating two species of different dispersability across sea straits of greatly different history and with different modern sea currents, we try to disentangle the relative significance and interplay of historical and modern abiotic and modern biological factors on genetic structure. No phylogeographic structure was found across the Skagerrak (*C. maritima* only). This we attribute to the young age of this strait. Strong genetic differentiation was observed across the Strait of Gibraltar (both species), the Bosporus (both species) and the Dardanelles (*C. maritima* only). Differentiation across the Strait of Gibraltar is postulated to be the result of a modern barrier to gene flow. Differentiation across the Bosporus and the Dardanelles is postulated to be the result of the repeated closure of these straits during Quaternary glacials. Differences in genetic differentiation across the Dardanelles and the Bosporus (with lower amounts of genetic differentiation across the Dardanelles than across the Bosporus) are attributed to the earlier postglacial opening of the former. This last hypothesis is further explored in a simulation study.

SPECIES DISTRIBUTION MODELLING MATCHES PHYLOGEOGRAPHIC PATTERNS IN THE ATLANTIC-MEDITERRANEAN DISJUNCT *ARMERIA PUNGENS*

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An AFLP study using two restriction enzyme combinations (EcoRI/MseI and KpnI/MseI) was conducted to explore the causes for the West Iberian-Corso/Sardinian disjunction of the coastal sand-dune species *Armeria pungens* (Plumbaginaceae). The genetic groups revealed by Bayesian, AMOVA and genetic distance analyses of the AFLP data did not match the main geographic disjunction. Instead, Corso-Sardinian populations were found to be genetically closer to southwest Portuguese than to those from the Gulf of Cadiz (the closest geographically), a pattern that is adequately explained by eastwards long-distance dispersal (LDD). To understand the causes for this LDD, a bioclimatic envelope modeling analysis was performed aiming to characterize the current locations where *A. pungens* grow. The results match the genetic structure inferred from AFLP data since similarities between climatic parameters in the Portuguese and Corso-Sardinian sites are much stronger that either one with those in the Gulf of Cadiz. This approach emphasizes the importance of the ecological requirements (ecological biogeography) in the success of establishment after LDD events as compared to that of stochastic events leading to dispersal. Further, these results are congruent with an unpublished plastid DNA sequences data.

PLANT EVOLUTION IN A CONTINENTAL ARCHIPELAGO: THE BALEARIC ISLANDS

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The Balearic Islands show one of the most diverse floras of the Mediterranean basin, both in terms of richness, with about 1500 native species in 4992 km^2, and singularity, with about 121 restricted endemic taxa of which 100 show non-apomictic reproduction. In this talk we will summarize the patterns and processes of diversification which have occurred on the endemic Balearic flora. Specifically, we will focus on the (i) strong phylogeographical signal present in several narrowly distributed endemic species (e.g. *Naufraga balearica*, *Crepis triasii*, *Senecio rodriguezii*), (ii) the intraspecific karyological variation that accounts for about 10% of the whole endemic flora and includes within-individual polymorphisms related to euploid changes involving somatic segregation or endopolyploidy, the presence of supernumerary (B) chromosomes, and karyological variation in species showing holocentric chromosomes, (iii) the origin of the autochthonous polyploidy in Balearic endemics, accounting for at least 26.2% of the endemic polyploid flora and contrasting with the low estimates of polyploid evolution reported from oceanic archipelagos, and (iv) the role of homoploid hybridization in shaping species boundaries in several noteworthy polymorphic groups (e.g. *Limonium*, *Helichrysum*, *Lotus*).

MICROEVOLUTIONARY PATTERNS IN *HYPOCHAERIS* (ASTERACEAE, LACTUCEAE) OF THE WESTERN MEDITERRANEAN

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Hypochaeris consists of approximately 50 species distributed in Europe, the Mediterranean region, Asia, and South America. In the Western Mediterranean there are several species that have undergone different evolutionary processes, resulting in patterns illustrative of this part of the world: (1) populational divergence relating to the Strait of Gibraltar as seen in *H. radicata* and *H. salzmanniana*; (2) genetic diversity in central Morocco in *H. angustifolia* and *H. arachnoidea*; (3) long-distance dispersal from northwestern Africa to the New World of ancestors similar to *H. angustifolia*, followed by dramatic adaptive radiation; and (4) historical introduction from Spain to colonies in South America as reflected by populations of *H. radicata* and *H. glabra*. DNA sequence variation, especially ITS, has helped reveal relationships among sections of the genus worldwide. AFLP markers have been used to hypothesize relationships among closely related taxa, especially those recently evolved in South America, as well as in the Western Mediterranean. Results indicate that the populational divergence in *H. salzmanniana* has been too recent for impact from the closing and reopening of the Strait of Gibraltar. The Middle Atlas in Morocco appears to have been a center for the origin of higher levels of genetic variation, followed by patterns of migration, especially northward, as seen within and among populations of *H. angustifolia* and *H. leontodontoides*. Morocco has also been the source of a progenitor to the New World, followed by explosive continental adaptive radiation during the past approximately one million years. Human intervention during the past 500 years has resulted in introduction of *H. radicata* from southern Spain, near Huelva, to other countries of the former Spanish colonies in the New World.

ENVIRONMENTALLY-MEDIATED REPRODUCTIVE VARIATION IN A NEARSHORE EUROPEAN PIPEFISH SPECIES

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Historical climate oscillations have strongly influenced organismal distribution and ecology, and accelerated rates of contemporary climate change appear to explain recent phenological shifts in a diversity of plant and animal groups. While it is difficult to accurately forecast the outcome of future temperature increases on organismal life history, predictive frameworks may be derived from the analysis of how species have responded to past fluctuations in climate. Both North American and European species of *Syngnathus* pipefish show a strong signature of Pleistocene glaciation, with high genetic diversity in southern populations in California and the Mediterranean and reduced diversity in the north, consistent with post-glacial recolonization. While patterns of genetic diversity in both species are consistent with the actions of glacial activity, morphological and reproductive characters exhibit a mosaic pattern of variation that is highly correlated with local environmental conditions. Ongoing work in our lab aims to determine whether high levels of morphological and life history variation found in this group reflect phenotypic plasticity shared by all populations and/or genetic adaptation to local environmental conditions. High levels of phenotypic plasticity likely increase a species' ability to persist through periods of rapid climate change.

SEX POLYMORPHISM IN MEDITERRANEAN PLANTS: INSIGHTS FROM HETEROSTYLY AND FLORAL BIOLOGY

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Stylar polymorphisms are a useful system for studying the mechanisms underlying the maintenance of genetic and phenotypic diversity in flowering plants. Among these, heterostyly is the most common and has generated a bulk of both theoretical and empirical studies on its functional and evolutionary significance. I review available evidence about Mediterranean plants, mostly *Narcissus* species, which is throwing much light in testing competing hypotheses on the evolution of heterostyly. It is shown that particular pollinators play a crucial role in promoting reciprocal positioning of anthers and stigmas for enhancing male and female plant fitness. Contrary to most of formerly studied heterostylous groups, some of the intermediate evolutionary stages are abundant in the Mediterranean with ample variation, both across species and populations. This has permitted detailed exploration of the mechanisms promoting, maintaining and eliminating style polymorphism. Studies at both macro- and microevolutionary levels have shown that style polymorphism is evolutionarily and ecologically labile. Also, shifts between stages are governed by contingent combinations of pollinator types, perianth morphology, plant population structure, flowering season and lineage ancestry. The high spatio-temporal variability of these factors in Mediterranean regions may play a role in the shifting nature of this polymorphism.

POLLINATION STRATEGIES, REPRODUCTIVE ISOLATION AND SPECIATION PROCESSES IN MEDITERRANEAN ORCHIDS

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The means by which new species arise such as the mechanisms that contribute to reproductive isolation remain a fundamental problem in evolutionary biology. Orchid flowers are often highly specialised to attract and fit their pollinators, and many orchid-pollinator relationships are species-specific. This has traditionally led to the general view that speciation processes and integrity of orchid species are achieved by the specializations of the pollinator attraction and visitation rather then by intrinsic genetic barriers. Consequently, the rule of post-mating barriers in promoting orchid speciation has been often under-estimated. However, several Mediterranean food-deceptive orchids, occur in sympatry, have overlapping flowering phenologies and habitat preferences, and share the same pollinators as revealed by molecular analyses of orchid pollinaria found on insects. Karyotype analyses showed that these orchids, with a weak pollinator specificity, display strong chromosomal differences, suggesting that postzygotic reproductive barriers mediated by karyotype divergence have played a key role in the maintenance of their species boundaries. In contrast, sexually deceptive *Ophrys* species display a specialized pollination strategy and largely rely on pre-mating reproductive barriers. The marked difference in types and strength of reproductive barriers in deceptive orchid with different pollination strategies directly affect the rate and the evolutionary consequences of hybridization and species diversification.

EVOLUTION OF PLANT TRAITS UNDER MEDITERRANEAN FIRE-PRONE ENVIRONMENTS

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In the Mediterranean Basin, the tropical climate occurring during the Tertiary period changed to a drier (Mediterranean) climate in the Quaternary. Such climatic change was associated to a fire regime change and produced a random extinction of Tertiary (sclerophyllous, fleshy-fruited) taxa and a differential diversification of Quaternary (non-sclerophyllous, dry-fruited) taxa. In the current flora, the two groups of plants cope with fire by different strategies: Tertiary taxa resprout after fire (i.e. resprouters) while Quaternary taxa die after fire but their seeds germinate (i.e. seeders). In fact, the ability to resprout (R) is negatively correlated with the ability to germinate after fire (P), and phylogenetic analyses show that R preceded P and the state of R affected the probability of change in P. This result supports the biogeographical history of the Mediterranean Basin flora where most of lineages already resprouted after a disturbance during the Tertiary, making it improbable that an additional costly persistence strategy would evolve under the Quaternary climatic conditions. Although fire has been hypothesized to trigger the evolutionary and diversification rates of seeders, neither genetic nor phylogenetic evidences support this hypothesis. At community scale, fire filters the species by favouring the seeders, producing a phylogenetic clustering given the narrow taxonomic distribution of P in the Mediterranean plants (mainly Cistaceae, Lamiaceae and Fabaceae)

PLANT ADAPTATIONS IN THE AUSTRALIAN MEDITERRANEAN FLORA

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The Australian Mediterranean flora has its origins in Gondwana from genetic stock already well represented in the Eocene-Miocene but isolated since the Pliocene. Environmental factors thought to have exerted selective pressure on plant life since the end of the Tertiary include nutrient-impoverished soils, fire, summer drought and heat, reliability of winter rains, bouts of cold, efficient vertebrate herbivores (kangaroos), florivores and granivores (emus, cockatoos), and nectarivorous birds. No other region contains so many species (up to 30% of perennial floras) that store their seeds in the crown of the plant (serotiny). Predispositions include families with woody dehiscent fruits or cones, wind-dispersed seeds, highly combustible foliage and infructescences, low fecundity, frequent fire, limited opportunity for interfire recruitment and reliable rain. Seed release is cued to fire that simultaneously creates optimal conditions for recruitment. Fire stimulates rapid vegetative recovery in more than half of all perennials, and flowering in some - most notably grasstrees. Exaptation to drought or herbivory are incomplete explanations of these fire-cued responses. 60% of species store their seeds in the soil (55% of which are woody shrubs), with heat (hard seeds) or smoke (leathery seeds) inducing winter germination. No other Mediterranean flora is more spinescent. Secondary compounds are effective deterrents of herbivory in seedlings and young foliage (phenolics, fluoracetate) and bird-pollinated flowers (cyanide). Granivorous birds (cockatoos) may have had a profound effect on plant architecture and production of woody fruits in the flora.

EVOLUTIONARY ECOLOGY OF MUTUALISTIC ANIMAL-PLANT RELATIONSHIPS IN MEDITERRANEAN ECOSYSTEMS

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Studies performed in the last 20 years have revealed that mutualistic interactions represent an appropriate ecological setting to extract useful generalizations about the intensity, direction and form of selection acting on natural populations. While animal-plant mutualistic relationships have captured the attention of evolutionary ecologists in Mediterranean ecosystems, there is a conspicuous lack of integration regarding the role of natural selection in molding the phenotypic evolution of contemporaneous flora. In this work, I will analyze pollinator-mediated selection coefficients from studies performed in California, Spain, and Chile in an attempt to understand the extent to which natural selection has shaped the adaptive diversification of the flower phenotype and the relative role of historical processes in Mediterranean floral evolution. In spite of the conspicuous asymmetry in the number of studies performed in the different regions, historical and climatic processes seem to be more important than adaptive processes in accounting for flower diversification in Mediterranean ecosystems. This effect is further illustrated in the Chilean biota where increasing aridity, habitat shifts and probably pollinator extinctions led to a notorious depauperate pollinator fauna, anachronic flower characters, and idiosyncratic mismatches between floral morphology and current pollination.

CLIMATE AND THE CALIFORNIA FLORA: PAST, PRESENT AND FUTURE

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The diversification, evolution and ecology of the California flora have been profoundly shaped by the development of the mediterranean-type climate over the past 10-20 MY. The native flora of the California Floristic Province, with over 5000 plant taxa, assembled from lineages originating from temperate, arid and subtropical zones. Among extant taxa, the disparity of ecological traits such as seed size and specific leaf area reflects these diverse origins. Among evergreen woody shrubs, there is evidence that more dramatic adaptive shifts in leaf form occurred among lineages derived from temperate ancestors, compared to those derived from the subtropics. Evolutionary radiations within the native flora are responsible for a significant fraction of the extant diversity. These radiations include adaptive divergence in ecological traits that contribute to both local (alpha) and regional (beta) diversity. Climate change may threaten the survival of many native plant taxa, in particular those of interior regions and high elevations. Areas of steep topographic relief in coastal and interior moutain ranges provide critical climatic diversity where many threatened species are predicted to persist. The effects of climate change in California, and other regions with mediterranean-type climate, highlight the importance of changing precipitation as well as rising temperature.

POSTER SESSION

P1. DISCORDANCE BETWEEN VENTRAL COLOR AND MTDNA HAPLOTYPE IN THE WATER FROG *RANA (RIDIBUNDA) CARALITANA*

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The water frog form *caralitana* was first defined as a new subspecies based on orange colored maculation on ventral part by Arikan (1988) from the Lake District of southwestern Turkey. For many years ventral color has been used as a diagnostic character. Ventral color for 188 individuals collected from 30 localities was scored into one of three categories, based on the amount of orange or grey/brown spots. We mapped the distribution of each category and tested whether there is spatial correlation between mtDNA haplotype and ventral color of sampled individuals at the regional level. Furthermore, we analyzed relationships between ventral color and altitude. The distribution of orange ventral color exhibits a complex clinal variation especially in western Lake District where different colored individuals are seen syntopically. In other regions, there are abrupt changes presumably due to geographic barriers such as mountains. Our results indicate that neither mtDNA haplotype nor altitude shows significant correlation with ventral color. In certain regions, individuals with *caralitana* specific haplotype have ventral maculation patterns of non-*caralitana* or vice versa. This is probably due to introgression among *caralitana* and non-*caralitana* water frog maternal lineages, and is supported by the presence of orange-brown color, an intermediate character between different forms, in transition zones.

P2. REGENERATION AND FINE-SCALE SPATIAL GENETIC STRUCTURE IN THE MEDITERRANEAN ENDEMIC *ECHINOSPARTUM ALGIBICUM* TALAVERA & APARICIO.

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Restricted seed dispersal is one of the most often claimed explanations for the presence of significant spatial genetic structure (SGS) within populations. Further, it is expected that recent colonized populations exhibit higher SGS than old-established populations. *Echinospartum algibicum* (Leguminosae), a Mediterranean woody endemism from S Spain, is characterized by a limited seed dispersal mechanism. The only known population is split in two plots; one was leaved unmanaged and no signs of regeneration have been observed since 1994 (disturbed plot), whereas the other plot was fenced to prevent plants from the grazing of cattle (undisturbed plot). AFLP analysis was carried out to compare SGS in both plots and to infer patterns of regeneration of the species. The results of the spatial autocorrelation analysis for all individuals showed a clear monotonic trend, with significant positive and negative values of genetic autocorrelation occurring at small and large spatial scales, respectively. However, contrary to our expectation lower SGS and genetic relatedness between individuals were detected in the undisturbed plot. We claimed to a relatively high seed movement through secondary dispersion by ants and water, promoting the overlapping of seed shadows, as the most likely explanation for the observed results.

P3. ABANDONED AGRICULTURAL LAND IN PERI-URBAN MEDITERRANEAN AREAS. CRITERA FOR SELECTING BIODIVERSITY-SUPPORTIVE LAND-USE

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Abandonment of agricultural land characterizes many Mediterranean countries, and is regarded detrimental to biodiversity. Abandonment of cultivation is often considered and tackled in peripheral areas, although in many places (e.g., Israel) it is observed in fringes of cities, where farmers relinquish agriculture in favor of urban jobs. Our objective was to identify a biodiversity-supportive land-use for abandoned agricultural lands, which is suitable specifically to peri-urban conditions. We identified the special criteria, which apply when selecting a land-use for the urban fringe. In addition to the benefits to biotic and a-biotic resources, which is a relevant criterion everywhere, biodiversity-supportive land-uses in vicinity of cities should also: (1) satisfy urban dwellers' preferences for landscape amenities, especially when urban inhabitants are asked to financially support landscape upkeep; (2) be easy to convert back into agriculture, in the event of food crises in the cities; and (3) be "visible" in the metropolitan landscape, demarcating the land as belonging to someone and cared for, and thus deter unwanted urban activities (e.g., illegal construction). We compared three traditional Mediterranean land-uses: grazing, agro-forestry and olive-groves, and concluded that olive groves best satisfy the special considerations of the peri-urban context, as detailed above.

P4. PHYLOGENETIC RELATIONSHIPS AND REPRODUCTIVE BIOLOGY OF *HYPOCHAERIS* SECT. *SERIOLA* (ASTERACEAE, LACTUCEAE) IN THE MEDITERRANEAN BASIN WITH EMPHASIS ON *H. LEONTODONTOIDES,* AN ENDEMIC SPECIES TO MIDDLE AND HIGH ATLAS (MOROCCO)

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The genus *Hypochaeris* L. (Asteraceae, Lactuceae) contains c. 60 species distributed in two main areas, the Mediterranean Basin (15 species) and South America (c. 45 species). *Hypochaeris* sect. *Seriola* has five taxa: *H. leontodontoides* (endemic to the Middle and High Atlas, Morocco), *H. achyrophorus* (circunmediterranean), *H. saldensis* (endemic to Algeria), *H. rutea* (endemic to the Betic Cordillera, Spain), and *H. laevigata* (which occurs in the Centre of the Mediterranean Basin and North West Africa). Except for *H. achyrophorus*, which is annual, all species are

perennial herbs, woody at the base and rupicolous. In this study we investigated phylogeographical patterns in *H. leontodontoides* and phylogenetic relationships between all the taxa in sect. *Seriola*. We also assessed the self-incompatibility mechanism and the reproductive success in the wild. All species in this sect. are mainly self-incompatible and present quite high reproductive success levels in the wild. With AFLP's markers we found that *H. leontodontoides* is the basal species of sect. *Seriola* and *H. achyrophorus* the sister species of *H. laevigata* and *H. rutea*. This result is congruent with Tremetsberger et al. (2005), a previous study with nuclear rDNA sequences (ITS 1, ITS 2, 5.8 rDNA).

P5. INSIGHTS INTO HISTORICAL RANGE DYNAMICS FROM THE SPATIAL PATTERNS OF GENETIC VARIATION IN *ELYTROPAPPUS RHINOCEROTIS* (ASTERACEAE: GNAPHALIEAE) IN THE CAPE PROVINCES OF SOUTH AFRICA

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We surveyed spatial genetic structure in a widespread Cape shrub using ISSR PCR and noncoding chloroplast DNA sequences in order to examine potential signals of past history. Inter-SSR variation is very unevenly distributed across the range, with geographic distance being a poor predictor of genetic distance. Although a low number of chloroplast haplotypes was detected, these also show significant spatial structuring that is not consistent with current distributions, and indicate a historical disjunction between the western and eastern parts of the range. Populations from the arid northwest have lower genetic diversity for both types of markers. The exception to this pattern is the Kamiesberg massif, possibly due to amelioration of aridity with altitude. Spatial genetic patterns are less consistent elsewhere in the range. To the extent that our data reflect historical patterns, they are consistent with a scenario in which recent climatic perturbations were either of greater amplitude or of more consistent direction in the northwest, while in the south and east shifts were of smaller magnitude and more frequent, or may have oscillated between favourable/unfavourable conditions with no consistent directionality.

P6. FLORAL VISITORS OF TWO SYMPATRIC MEDITERRANEAN *ARISTOLOCHIA* SPECIES: DO THEY COMPETE FOR POLLINATORS?

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Aristolochia baetica and *A. paucinervis* are two Mediterranean species that commonly appear in South-Western Spain. Both species share the same mechanism of trap pollination and overlap their flowering periods. Thus, when cohabiting, they may share pollinators and competition could occur between them, causing reductions in the fitness of one or both species. In this study, flower visitors of both *Aristolochia* species were monitored and analysed, in order to evaluate their efficiency as pollinators and to elucidate whether both species share pollinators. *Aristolochia baetica* and *A. paucinervis* attracted a great variety of floral visitors, included several orders of insects, mostly

dipteran. However, only a few families were effective pollinators, carrying pollen loads on their thoraces. The main pollinators of *A. baetica* were drosophilids, which visit almost exclusively this species. However, the main pollinators of *A. paucinervis* were phorids, which were also attracted by *A. baetica* flowers. When both species share the same habitat, competition for pollinators seems to lower the number of visits to *A. paucinervis* flowers, which may negatively affect its reproductive success.

P7. PHYLOGENETIC RELATIONSHIPS IN *Santolina* L. (COMPOSITAE: ANTHEMIDEAE) BASED ON NONCODING CHLOROPLAST SEQUENCES.

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We have sequenced a 1000 bp region of the chloroplast DNA that contains trnL intron and the intergenic spacers trnT-trnL and trnL-trnF for 25 taxa of the genus *Santolina* L. The results of phylogenetic analysis reveal that *Santolina* L. forms a monophyletic clade, with high bootstrap support. The genus was divided into two sister clades which are congruent with morphological characters: one grouping the *S. rosmarinifolia* L. complex, the other grouping the *S. chamaecyparisus* L. complex. Sequence variation within each of these clades is very low, and the relationships between the species are poorly resolved, indicating that the morphological variability observed within each of the different geographical areas may be a result of recent diversification processes.

P8. PREDATION AND REPRODUCTIVE SUCCESS IN THE MONOSPECIFIC GENERA *EROPHACA BAETICA* SUBSP *BAETICA* (FABACEAE) ALONG ITS DISTRIBUTION

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Insect predation is often an important factor determining final plant reproductive success. The aim of this work is to assess reproductive success (measured as fruit set, seed set and preemergent reproductive success) in 17 populations of *Erophaca baetica* (L.) Boiss., a perennial species which lives in temperate forest in the West Mediterranean Basin (South Iberian Peninsula, Morocco and Algeria) and East Mediterranean Basin (Cyprus, Greece, Turkey and Lebanon). In populations where the major insect predator (caterpillar of *Tomares ballus*, Lycaenidae: Lepidoptera) is absent reproductive success reaches up to 35%, whereas it is as low as 1% in other populations where this butterfly species is present.

P9. PHYLOGENY AND EVOLUTION OF SERPENTINOPHYTISM IN CIRCUMMEDITERRANEAN LITHOSPERMEAE (BORAGINACEAE): A WINDOW FROM ITS AND MATK DNA SEQUENCES

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Tribe Lithospermeae DC. (Boraginaceae) includes 24 genera and c. 415 species in America, Europe, Asia and Africa. Our present knowledge of this group is mostly based on a series of papers by I.M. Johnston published about a half century ago. In the Euro-Mediterranean region it is represented by 16-18 genera, but uncertainties still exist on the relationships and even circumscription of some genera, e.g. *Lithospermum* s.l., *Moltkia, Arnebia, Macrotomia, Podonosma* and others. As in other Boraginaceae groups, this is due to the difficult interpretation of shared characters as phylogenetically informative homologies or as simple analogies. Here we present the results of the first study on the phylogeny of circummediterranean Lithospermeae, based on ITS and matK DNA sequences obtained from members of 18 genera. Using members of Echiochileae as outgroup, we confirm the monophyly of the group and suggest some relationships which were not hypothesized before, especially concerning the Balkan monotypic genera *Halacsya* and *Paramoltkia*, both obligate serpentinophytes. Mapping the aptitude of the taxa to grow on ultramaphic soils, either obligatedly or facultatively, we suggest that serpentinophytism may have originated at least three times in different lineages of Lithospermeae, e.g. the *Onosma*, the *Halacsya-Paramoltkia* and the *Echium-Pontechium* clade.

P10. GENETIC DIVERSITY IN THE RARE, ENDEMIC SPECIES *PRIMULA APENNINA* WIDMER, DETECTED BY INTER-SIMPLE SEQUENCE REPEAT (ISSR).

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Primula apennina Widmer (Primulaceae) is an endangered rhizomatous herb endemic to the North Apennines. Its range is a narrow corridor of approximately 45 km x 5 km between Parma and Reggio Emilia provinces, where *P. apennina* grows on the mountain tops, mostly in north-facing ledges and sandstone crevices at 1,500-1,800 m. ISSR (inter-simple sequence repeat) polymorphism was investigated in six natural populations of *P. apennina*. The first primers used identified pronounced levels of genetic variability both at population level and at species level, probably resulting from recent (Pleistocene) speciation and/or outcrossing favoured by floral heteromorphism. A moderate level of genetic differentiation among populations was detected and attributed to both habitat fragmentation and limited gene flow through pollen or seeds (isolation-by-distance). This pattern of differentiation was corroborated by the finding of a positive correlation between inter-plant spatial and genetic distances. Current results point out that the species still maintains relatively high levels of genetic diversity in spite of its extremely small geographic range. Additional studies, evaluating the extent of clonality, would be especially helpful in determining the role of vegetative reproduction on the genetic structure within single populations.

P11. AFLP FINGERPRINTING OF *ANCHUSA* (BORAGINACEAE) IN THE CORSO-SARDINIAN SYSTEM: PATTERNS OF GENETIC DIFFERENTIATION IN AN INSULAR ENDEMIC GROUP THREATENED WITH EXTINCTION

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Anchusa L. is one of the major genera of tribe Boragineae, with ca. 30 species in the Mediterranean and Middle East. The Corso-Sardinian system is a major centre of diversity and endemism for this genus, with seven allopatric taxa occurring in either coastal or mountain habitats of the two islands. Here we use AFLP fingerprinting to analyse the patterns and extent of genetic differentiation in *Anchusa* endemic to Sardinia and Corsica, using a sample covering the entire taxonomic and geographic range of the group. We also estimate levels of genetic diversity at the population and taxon level, in relation to the distribution and habitat of the species. Preliminary data indicate no clear relationships between genetic distances and geographic or habitat differentiation, suggesting that random genetic drift may have played a key role in the divergence of these small populations. Mean levels of intrapopulation genetic diversity are higher in montane than in littoral taxa, and reach lowest values in the psammophytic *Anchusa crispa* ssp. *maritima, A. sardoa* and *A. littorea*, which are seriously threatened with extinction. Stochastic events of habitat reduction followed by genetic bottlenecks may have caused such genetic impoverishment, also combined with high incidence of inbreeding.

P12. POLYPLOIDY, ANEUPLOIDY, AND CHROMOSOME NUMBER EVOLUTION OF ARUM AND ITS ALLIES (AREAE, ARACEAE)

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Chromosome numbers (CN) have been reported for 700 (20%) of the species of Araceae, representing 99% of the 105 genera. In the relatively derived Areae clade (150 spp.), CNs are available for 40% of the species. We analyzed their distribution on a new chloroplast phylogeny that includes 76 Areae from all seven genera. Most core Areae (60 spp., 21 seq., 32 counted) have CNs based on $x = 14$: *Helicodiceros* (4*x*), *Eminium* (2*x*), *Dracunculus* (2*x*)*, Arum* (2*x*, 4*x*, 6*x*). *Biarum* (21 spp., 9 seq., 10 counted) instead has CNs based on of $x = 11$ and/or 13 (plus derived higher polyploid numbers combined with aneuploidy). The "*Sauromatum*" clade of *Typhonium* (9 spp. seq., 5 counted), sister to the core Areae, has CNs based on $x = 13$ with diploids and tetraploids present. A yet unplaced Indian genus, *Theriophonum* (5 spp., 2 seq., 4 counted), is based on $x = 8$, with diploids, triploids and tetraploids. The newly revealed SE Asian core *Typhonium* clade (31 spp. seq., 6 counted) includes three species (*T. jinpingense, T. baoshanense, T. tubispathum*) with established CNs of $2n = 10$, the lowest in Araceae. Those species are embedded among species with $2n = 16$ ($x = 8$), 18/36 ($x = 9$), 26/52 ($x = 13$), 40 ($x = 5$ or 8). In an isolated Australian *Typhonium* clade (4 spp. seq., 2 counted), CNs of 110 and 160 have been reported in *T. eliosurum* and *T. brownii,* indicating multiple rounds of polyploidization. These ranges of diploid and basic CNs suggest that polyploidy and aneuploidy have played an important role in the evolution of Areae in creating reproductive barriers between ancestral species and their derivatives. In the Mediterranean

core Areae alone, polyploidy occurred at least 5 times. Chromosome sizes in the species with $2n = 10$ in comparison with related groups suggest that they result from CN reduction (possibly via fusions and other rearrangements, such as translocations).

P13. HOMEOTIC ORCHID MUTANTS, HOPELESS CASES OR HOPEFUL MONSTERS?

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How novelties or changes in body plans originate during evolution is still controversial among biologists. The Modern Synthesis, explains how gradual processes by natural selection can be responsible for micro- and even macro-evolution. Homeotic mutants, however, that are able to establish stable populations in a natural environment, so-called “hopeful monsters”, prove that a saltational mode of character change is a potential alternative mechanism for speciation. In the homeotic mutant *Coelogyne leungiana* (Orchidaceae), the second perianth whorl of the flower has changed organ identity compared to the wildtype *C. fimbriata:* petals and lip are sepal-like. This morphological change is caused by a different expression of MADS-box B class genes involved in floral development. The same B gene lineages (PI- and AP3) are expressed in sepals of *C. fimbriata* and the sepaloid petals and labellum of *C. leungiana.* Homeotic mutants of *Ophrys* and *Dactylorrhiza* are observed in the mediterranean area, most of these seem hopeless cases, unable to pass their phenotype on to their offspring. Several homeotic mutants of *Nigritella* are known that successfully established new lineages, though. Morphological transitions attributable to homeosis may therefore be a more common driver of speciation than generally assumed.

P14. THE ORIGIN, EVOLUTION, AND DIVERSIFICATION OF THE AFRICAN DISJUNCT GENUS *ANDROCYMBIUM* (COLCHICACEAE)

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The genus *Androcymbium* includes 57 species distributed in the Mediterranean climate regions of Africa. We present the first molecular phylogeographic analysis of the genus which includes species from all of its five distribution areas (North Africa, the Horn of Africa, Namibia, Western South Africa, and Eastern South Africa). We used sequence data from six chloroplast, and one nuclear region, and phylogeographic reconstructions were performed both by parsimony and Bayesian inference methods. Time estimations using a Bayesian approach, suggest a middle Miocene (12.8±1.5 my) origin of the genus, and a late Miocene (9.4±1.7 my) start of diversification in the summer-dry area of western South Africa – southern part of Namibia, the Benguela current perhaps being an important triggering factor. Three northwards dispersion events have been suggested in

Androcymbium: the first, dated at the end of Miocene (6,2±2.0 my), gave rise to the genus *Colchicum*. The second and the third took place in the mid Pliocene and were simultaneous (3,5±1,5 my), one from eastern South Africa producing the only species found in the Horn of Africa, and the other from Namibia to the Mediterranean Basin. The formation of several late Miocene – Pliocene arid tracks in the east of Africa is of a great importance in explaining these northwards dispersions of *Androcymbium*.

P15. PHYLOGENETIC ANALYSIS BASED ON THE LOW-COPY GENE *CES*A1B REVEALS UNSUSPECTED ALLOPOLYPLOID SPECIATION EVENTS WITHIN THE *MALVA* ALLIANCE (MALVACEAE)

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Phylogenetic relationships among the genera *Lavatera*, *Malva* and *Althaea* remain obscure despite previous work with the ITS, *psb*A-*trn*H and *trn*L-*trn*F sequences. As a result of radiation and reticulation, tree branches are either short or unresolved at critical points. To overcome this problem, we amplified a region of 900-1050 base pairs comprising the first five exons of the cellulose synthase 1b gene (*ces*A1b) and their four spanning introns. The total dataset included 1268 characters, 730 corresponding to introns and 538 to exons. Most sequences grouped into three paralogs, which could be identified in a tree topology. From 351 sequences analysed, most (197) correspond to paralog 1 (P1), while the remaining fall within paralogs 2 (P2, 98 sequences) and 3 (P3, 56). These three paralogs differ in sequence length, exon sequence and intron structure. Hybrid speciation is inferred to have occurred at least four times: once in the *Malvalthaea* lineage and twice within the "Malvoid group", affecting the Mediterranean *L. mauritanica* and probably also the *L. assurgentiflora* aggregate. In addition, a previously unsuspected hybrid speciation event affecting *Malva alcea* is revealed. This species appears to be an allopolyploid derivative of *M. moschata* and the Euro-Asiatic *L. thuringiaca*.

P16. THE MOLECULAR PHYLOGENY OF *LITHODORA* GRISEB. (BORAGINACEAE): IMPLICATIONS FOR THE EVOLUTION OF STYLAR POLYMORPHISMS

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Lithodora (Boraginaceae) traditionally consists of 12 taxa distributed around the Mediterranean basin. Ongoing research is revealing that this genus is an excellent study systems as to test models for the evolution of heterostyly. Phylogenetic analysis of ITS, *matk and* $trnL_{UAA}$ is inferred for this genus. The study included 11 ingroup as well as 7 outgroup taxa belonging to tribes Lithospermeae, Echieae and Cynoglosseae. Parsimony analysis and Bayesian inference resolve both with high resolution that, as currently considered, *Lithodora* is not a monophyletic group. Two clades are well

differentiated in the nuclear, plastid and combined cladograms. Moreover, clade *L. prostrata*, formed by *L. diffusa*, *L. prostrata*, *L. moroccana*, *L. rosmarinifolia*, *L. nitida* and *L. oleifolia,* is more related to genus *Lithospermum* than to clade *L. fruticosa.* The later, composed of *L. hispidula*, *L. zahnii* and *L. fruticosa* appears also to be related to other genera (*Cerinthe*) rather than to species in clade *L. prostrata*. We use the available resolved phylogenetic relationships as to a preliminary account for the current contending hypotheses on the evolution of heterostyly.

P17. REPRODUCTIVE BIOLOGY OF NAVAEA PHOENICEA (MALVACEAE): A CANARIAN ORNITHOPHILOUS PALAEOENDEMIC SHRUB

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Navaea phoenicea is a palaeoendemic shrub from Tenerife (Canary Islands, Spain). Previous works have recorded flower visits by generalist passerines, and linked them with floral traits such as the orange corolla and hexose-rich nectar. It has been suggested that this is an ancestral adaptation to pollination by extinct true pollinator birds that involve a group of species known as the Macaronesian ornithophilous element. We present preliminary results of an ongoing reproductive biology study where we assess: 1) relative contribution of autogamy and allogamy to seed production, 2) flower phenology, 3) flower visitors, 4) P/O ratio and 5) patterns in nectar production. In *Navaea*, delayed selfing is better explained through selection for outcrossing rather than a mean to ensure seed production in case of outcrossing failure. This hypothesis is based mainly on the early dissemination of available pollen. Further, results show that autogamy represents a negligible contribution to seed set, which is mainly due to outcrossing. This is performed by birds rather than insects, as they are the main flower visitors and the most effective ones. Nectar presents the characteristic low sugar concentration as well as large volumes production of bird pollinated flowers along different stages of anthesis.

P18. MATING PATTERNS AND CONESPECIFIC NEIGHBOURHOOD COMPOSITION OF *MYRTUS COMMUNIS* IN LOWLAND MEDITERRANEAN FORESTS

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Plant mating system is determinant for progeny performance (through inbreeding depression) and for the genetic structure of the populations. Although, mating system is usually considered as a species attribute, variability in the outcrossing rates has been documented under different conespecific densities or between years. Generally, the higher the density the higher the outcrossing rates, although the clumping of individuals may lead to biparental inbreeding. In this study, we investigated the mating patterns of the myrtle *Myrtus communis* (an insect pollinated and vertebrate dispersed shrub) assessing the outcrossing rates and the biparental inbreeding at individual level. We developed a “conespecific neighbourhood index” (*Cn*) on the basis of both local density and distance to the nearest flowering myrtle, and made 4 *Cn* groups (from HIGH to LOW). We performed allozyme analysis of progeny-arrays to estimate the mating parameters using the software MLTR (v.3.0). Outcrossing rates were low and decreased significantly from "HIGH" to "LOW" *Cn* groups (from 0.43 to 0.26). However, the highest levels of biparental inbreeding were detected in the "Medium" *Cn* groups. The results highlight the importance of the conespecific neighbourhood at local-scale for the genetic composition (and consequently for the fitness) of the progenies.

P19. ALLOPATRIC DIVERGENCE AND SECONDARY CONTACT OBSERVED IN *EUPHORBIA SPINOSA* L.

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We reconstruct the phylogeographic history of strongly diverged chloroplast DNA haplotypes in the *Euphorbia spinosa*. We show the partition in two groups, each with an independent phylogeographic history during the Quaternary period. Our data showed that geographical structure of chloroplast haplotypes divides this species into two distinct parts: southern France and western Italy and southern Italy and the Balkan. The phylogeny obtained with nrDNA sequences corresponded enough with that based on chloroplast data. This structure seems to be associated mainly with the migration history and indicates that two putative refugia contributed significantly to the recolonization processes. Then, we hypothesize the presence of two main migration routes during the interglacial periods. According to this hypothesis, central Italy represents the confluence of migration routes radiating from separate refugia. Moreover, a range-overlap of two clade is stretched from southern Ligurian to the Tuscany. The nuclear data suggest that this secondary contact resulted in hybridization between the allopatrically diverged groups. The absence of monophyly in the intermediate group in the ITS tree indicate several cycles of range contraction, isolation and range expansions leading to repeated hybridization events. We hypothesize that concerted evolution has not yet completely homogenized ITS sequences, indicating more recent hybridization.

P20. DISENTANGLING RETICULATE EVOLUTION: EXAMPLES FROM *PRIMULA*

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Speciation via hybridisation is a widespread phenomenon in plant evolution, but traditional phylogenetic studies often fail to detect it. Indeed, hybrid taxa may show an incongruent placement in phylogenies generated from differently inherited markers, but directional homogenisation of nuclear repeat types may render their identification impossible. Given these challenges, studies on reticulation must integrate additional sources of evidence (e.g. infra-specific polymorphisms, genomic *in situ* hybridisation [GISH]) and analytical approaches (e.g. principal component analysis [PCoA], investigation of diagnostic sites). *Primula* sect. *Aleuritia* (*Aleuritia*) represents an ideal case study to investigate reticulation. *Aleuritia* displays variation in ploidy levels from diploidy to

14-ploidy, while morphological, caryological and distributional data suggest a hybrid origin for most polyploids. Sequences from chloroplast and nuclear ribosomal DNA (nrDNA) loci were analysed to reconstruct the respective phylogenies. Furthermore, extensive cloning of the nrDNA marker was performed to identify the progenitors of hypothesised allopolyploids via PCoA, while the tracing of diagnostic nucleotide positions in the nrDNA matrix permitted the detection of recombinant clones. Lastly, GISH allowed the confirmation of an intersectional hybrid. Overall, the results support many cases of reticulation and highlight the need for diverse experimental and analytical approaches in the study of reticulate evolution.

P21. *ANTIRRHINUM SICULUM* MILLER PHYLOGEOGRAPHY AND BAYESIAN ANALYSIS THROUGH CPSSR

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Antirrhinum siculum Miller is a perennial herb growing in old walls and monuments. The species range is wide within *Antirrhinum* genus, with populations spanning from Southern Europe to Israel, North Africa and several Mediterranean islands. It is considered as genetically isolated from the other species of *Antirrhinum* being the only self-compatible species. Previous data on the genetic variability of the species show that it has the lowest levels of variability within the genus, contrasting with the high levels of other species of similar range. Present research aims to study patterns of differentiation among populations through six chloroplast microsatellites (cpSSR). Six universal primer pairs (ccmp2, ccmp3, ccmp4, ccmp6, ccmp7 and ccmp10) designed for angiosperms were selected for amplification and yielded products sequenced to check for presence of microsatellite regions as well as different size variants. Haplotypes were defined as distinct combinations of size variants at the polymorphic cpSSRs and a statistical parsimony network was built with the software TCS 1.18. A posterior distribution of partitions of the sampled populations into panmictic groups was obtained through Bayesian analysis performed with BAPS 3.2 software, and AMOVA partition of genetic variability was analyzed with Arlequin 3.0. Fragment sizes ranged from 68 to 193bp. Two out of six studied loci showed variability and five haplotypes had been found, two of them being more frequent, one exclusive of a single population and two rare ones. The Bayesian analysis shows that populations are arranged into three groups not corresponding to geographical position. AMOVA analysis performed following results of Bayesian analysis showed that 94.5% of variation is found among groups while only 51% of the variation is due to among groups when considering the geographical distribution of populations.

P22. EARLY POST FIRE ESTABLISHMENT OF ANNUAL PLANT SPECIES IN RELATION TO FIRE REGIME: A FUNCTIONAL GROUP APPROACH

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A hierarchical approach was applied for the classification of Mediterranean plant taxa into functional groups in relation to their long-term post-fire patterns of performance. Species were

grouped according to their growth form, regeneration mode, persistence and dispersal. Other specific competitive advantages such as N-fixation ability were also explored, resulting in the identification of 29 different functional groups. Annuals are known to poses a key-role during the first few post fire years. Due to the increased establishment of annual species after fire, Mediterranean plant communities show their maximum species richness in the first few years after the fire event. Six different functional groups of annuals have been identified in the current classification. In the present study, the effect of fire severity, fire interval and distance from unburned patches on the relative richness of the different annual functional groups has been investigated by means of direct gradient analysis (CCA). Data derived from three different fire events, where stands of different fire characteristics had been sampled during the first post-fire year. The strongest relations have been revealed between taxa forming a permanent soil seed bank and high fire severity and between anemochorous taxa and short distance from unburned stands.

P23. PATTERNS OF GENETIC DIVERSITY IN SEEDER AND RESPROUTER POPULATIONS OF THE CAPE FYNBOS SPECIES *ERICA COCCINEA* L. (ERICACEAE)

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With *ca*. 700 species and a high level of endemism, the genus *Erica* represents the epitome of plant biodiversity in the South African Cape *fynbos*. Both species diversity and endemism are markedly associated with the *seeder* habit. PV Wells (1969: *Evolution* 23, 264–267) highlighted a tight relation between the fire-sensitive, fire-recruiter (i.e. *seeder*) life-history and species diversity in two woody genera from the Californian chaparral, and suggested that post-fire regeneration mode influences speciation rates in fire-recruiting woody plants. In this contribution, we present a microevolutionary approach aimed to explore Wells's hypothesis. Specifically, we have carried out a comparative study of genetic diversity between five seeder and four resprouter populations of the Cape fynbos species *Erica coccinea*, by using AFLP markers, in order to ascertain whether population (genetic) differentiation is associated to the seeder habit in this species. After obtaining pairwise F_{ST} values for every population pair and analyzing them using standard statistics for characterizing population differentiation patterns, we have detected significantly lower genetic divergence between resprouter populations than between seeder ones. These results encourage us to suggest that population (genetic) differentiation is linked to the seeder life-form in *Erica coccinea*, which seems to agree with Wells's hypothesis.

P24. NATURALISED ALIEN PLANT TAXA OF GREECE: ORIGIN AND HABITAT

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Greece is a Mediterranean country hosting a high number of plant taxa (approx. 6.500 species and subspecies) and is influenced by human activity for millennia. A survey of the alien plants of the country was undertaken as part of a European project aiming at Delivering an Alien Species Inventory for Europe (DAISIE). For this purpose, a thorough investigation of the existing literature was made. Information derived was compiled in a database with all the alien plants. The data collected concern taxonomy, status, life and growth form, habitat, origin, distribution etc. The current contribution reports on the naturalized alien plant taxa only (198 out of 325 alien taxa). The majority of them belong to the families of Gramineae, Amaranthaceae, Compositae and Leguminosae. Their origin is mainly South or Northamerican, Southwestern European or African but a large number of them are of indeterminate origin. The habitats which usually host these plants are either disturbed or man-made, such as cultivations, road sides, fallow lands and waste deposits. It is notable that only a limited number of alien plants intrude natural habitats. The latter is an evidence of the resistance of the Mediterranean environments to the introduction of new plant taxa.

P25. SIZE MATTERS – INFLUENCE OF MEDITERRANEAN CLIMATE ON BODY SIZE EVOLUTION IN BEES?

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Body size in female bees is correlated with foraging range and time of daily and seasonal activity, with larger species being active earlier and having a larger foraging range. The goal of this study was to compare the variation in body size among bee species with different seasonal activity in mediterranean western South Africa and NE Greece, regions that show remarkable differences in air temperature during the flowering season. In contradiction to theoretical expectations our results show that bees were smaller in winter / spring than later in the year. We hypothesize that a combination of harsh climatic conditions in both regions early in the year and mass floral displays (surplus of pollen / nectar) especially in western South Africa select for smaller body size in bees. This combination of environmental factors is typical for these mediterranean ecosystems and is supposed to select for higher foraging efficiency thus promoting smaller foraging ranges (reduced flight distance / duration) and favouring body size reduction. Small bees also need less resources for reproduction and would have a selective advantage. Decreased flower availability later in the year force bees to increase their foraging range leading to selection for larger body size.

P26. DEVELOPMENT OF ISSRS (INTER SIMPLE SEQUENCE REPEAT) TO DETECT HYBRIDIZATION IN *CENTAUREA HORRIDA* AND *C. FILIFORMIS* (ASTERACEAE)

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Centaurea horrida Badarò and *C. filiformis* Viviani (Asteraceae) are morphologically distinguishable endemic species, whose habitat is restricted to Northern Sardinia. On the Tavolara

Island, where a partial overlap occurs, many individuals showing morphological traits common to both species have been found and have been studied either for morphological and genetic traits. The morphological analysis was carried out by examining the variability of capitula and leaves. To perform genetic analysis, the ISSR (Inter-Simple Sequence Repeat) technique was applied on both *C. horrida* and *C. filiformis*. By means of nine ISSR primers we amplified the genomic DNA extracted from 23 samples of *C. horrida*, seven of *C. filiformis* and 13 of the intermediate forms.
Eight out of nine ISSR primers tested gave positive results, in terms of repeatability of amplification and band resolution. We found a number of polymorphic bands from 7 to 2, in the range of 380-1500 bp. The number of bands specific to *C. horrida* and *C. filiformis* was 16 and 9 respectively. The morphologically hybrid plants displayed bands from both putative parents. Our results support the utility of ISSR markers for addressing questions of population genetics and taxonomic differentiation also in these endangered, endemic plant species.

P27. EVIDENCE OF INTENSIVE HYBRIDIZATION WITHIN THE MEDITERRANEAN GENUS *CENTAURIUM* (GENTIANACEAE)

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The remarkable species-richness of the Mediterranean flora results from the relative contribution, in space and time, of geological processes (e.g. plate fragmentation), stochastic events (e.g. chance dispersal), and biotic interactions (e.g. hybridization), which altogether shape the distribution and genetic make-up of plant communities. Here, we used DNA sequence data of both nuclear (internal transcribed spacers, ITS) and chloroplast (*trn*L intron and *trn*L-*trn*F spacer) regions, along with extensive chromosome counts, to infer the speciation patterns associated with the diversification of *Centaurium* (Gentianaceae), a Mediterranean genus comprising ca. 27 annual or biennial species/subspecies. The importance of reticulation and polyploidization in the evolution of *Centaurium* was evidenced by strongly incongruent topologies, and the presence of diploid to hexaploid taxa in each clade. Among the different causes of incongruence, hybridization was favored over lineage sorting or paralogy, for numerous additive polymorphic sites were detected in the ITS dataset. Based on our molecular and cytological evidence, we further examined the origin of several diploid-polyploid complexes. Overall, allopolyploidy, associated or not with introgression, appears to be the main evolutionary trend in *Centaurium*, and only a few autopolyploid taxa have been detected so far.

P28. INVASIONS OF THE MEDITERRANEAN BASIN BY THE ARACEAE: INTEGRATIVE PHYLOGENY-BASED EVIDENCE

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The relative contribution of geological and stochastic processes to the composition of contemporary Mediterranean biotas remains largely unknown. Here, we used phylogenetic analyses of sequences from six chloroplast DNA markers, Bayesian dating methods, and ancestral area reconstructions, in combination with paleogeographic, paleoclimatic, and ecological evidence, to elucidate the time frame and biogeographic events associated with the diversification of Araceae in the Mediterranean basin. We focused on the origin of four species, *Ambrosina bassii*, *Biarum dispar*, *Helicodiceros muscivorus*, *Arum pictum*, subendemic or endemic to Corsica, Sardinia, and the Balearic Archipelago. These islands were part of the Hercynian belt, a continuous geological entity located in the Iberian microplate, until its fragmentation in the Early Oligocene. The results support two main invasions of the Mediterranean basin by the Araceae, one from an area connecting North America and Eurasia in the Late Cretaceous and one from the Anatolian microplate in western Asia during the Late Eocene, thus confirming the proposed heterogeneous origins of the Mediterranean flora. A recurrent theme emerging from our analyses is that land connections and interruptions, caused by repeated cycles of marine transgressions-regressions between the Tethys and Paratethys, favored geodispersalist expansion of biotic ranges from western Asia into the western Mediterranean basin and subsequent allopatric speciation at different points in time from the Late Eocene to the Late Oligocene. In the light of these geological processes, the origin of the Hercynian endemics is discussed.

P29. *CARDAMINE MARITIMA* AND RELATED TAXA IN THE MEDITERRANEAN

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The broadly conceived species *Cardamine maritima* and several related taxa occurring in the Central and Eastern Mediterranean are in the focus of the present study. AFLP and morphological data have been gathered to address the following questions: (1) is there any support for the currently recognized or previously described taxa? (2) what are the genetic and morphological variation patterns within and among these taxa? (3) can we trace the impact of glaciation events in their variation and distributional patterns? Clear differentiation among the currently recognized *C.*

maritima, *C. montellucii* and *C. graeca* was found, and in addition, recognition of a few other taxa can be supported: *C. fialae, C. serbica*, and *C. rupestris* restricted in their distributions to Western Balkan mountain ranges. Also, two or three taxa can be recognized within what was considered previously as *C. maritima* s. str. The evidence presented here, supported also by DNA sequences, suggest a rapid radiation within the *C. maritima* lineage that most probably predated glaciation events. Apparently, these taxa were not influenced by the large-scale latitudinal shifts due to climatic changes, but rather, they experienced small-scale altitudinal distributional shifts and remained localized within small mountain ranges.

P30. MOLECULAR EVIDENCE FOR MULTIPLE HYBRIDIZATION EVENTS AND TWO DIFFERENT PATERNAL SPECIES INVOLVED IN THE ORIGIN OF *NARCISSUS XPEREZLARAE* (AMARYLLIDACEAE)

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Polyploid hybridization is an important process in plant evolution but determining the parental species of a hybrid is often difficult. *Narcissus* x*perezlarae* Font Quer was proposed to be the result of interspecific hybridization between *N. cavanillesii* and *N. serotinus*, based on morphological characters and cytological observations. While the first putative progenitor is endemic to SW Iberia and N Africa, the second is widespread along the Mediterranean Basin. The hybrid has a disjunct occurrence (SW Iberian Peninsula / Valencia in E Spain). Thus, we investigated the hybrid origin of *N.* x*perezlarae* using cpDNA (*ndh*F, *mat*K), mDNA (*cob*) and nrDNA (ITS) sequences. Results confirmed the hybrid origin of this taxon and identified *N. cavanillesii* as the maternal species involved in all the hybrid populations even those in which it is currently absent. *Narcissus serotinus* ($2n$=10) was determined as the paternal progenitor for SW Iberian populations. For E Iberian hybrid populations, available data indicate that either *N. serotinus* ($2n$=30) or *N. elegans* ($2n$=20) could have acted as the paternal progenitor. These data, together with demographic patterns suggest that *N.* x*perezlarae* is the result of multiple hybridization events that involve one maternal and two paternal species, which have different evolutionary outcomes.

P31. GENETIC DIVERSITY AND PHYLOGEOGRAPHICAL STRUCTURE OF THE CORSO-SARDINIAN ENDEMIC *MERCURIALIS CORSICA* COSSON (EUPHORBIACEAE)

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Endemic to Corsica and Sardinia, *Mercurialis corsica* Cosson (Euphorbiaceae) consists at present of 20 populations scattered all around Corsica, whereas 70 populations were previously reported. This rare and dioecious shrub occurs along a wide ecological range and it is characterized by an important variability of the demographic structure. For conservation purpose we are going to study several ecological and biological variables, and we have chosen here to examine the neutral genetic structure in relation with population viability. The first caryological counts exhibit an important variation of the chromosome number (2n = 66, 68, 69) which may indicate a certain degree of divergence between populations. Therefore, we conduct a genetic diversity study at the level of the whole distribution range of the species to explore possible phylogeographic pattern induced by palaeogeographical or historical events, or linked to the complex physiography of these tyrrhenian islands. AFLP markers, rDNA-ITS and non coding cpDNA sequences were used to reveal the genetic diversity of 13 populations in Corsica and 2 in Sardinia. We discuss the first results in order to determine the influence of historical processes on the genetic diversity of the species and the consequences linked to persistence of this threatened plant.

P32. GENERIC DELINEATION, PHYLOGENY AND SUBTRIBAL AFFINITIES OF *PHAGNALON* AND *ALIELLA* (ASTERACEAE, GNAPHALIEAE)

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Phagnalon Cass. comprises about 40 taxa and is distributed throughout the Macaronesian Region, the Mediterranean Basin, the Irano-Turanian and Saharo-Arabian Regions and North East Tropical Africa. The generic delimitation of *Phagnalon* and its subtribal position have been controversial. Firstly, it was placed between *Athrixiinae-Gnaphaliinae*. Later on, it was included in the *basal group complex* by Anderberg, unassigned to any subtribe. Finally, it has been placed in subtribe *Relhaniinae* together with *Anisothrix*, *Pentatrichia* and *Athrixia* in the latest phylogenetic study of the *Gnaphalieae*. The main goals are to verify the monophyly of *Phagnalon* and *Aliella*; to elucidate the sister group of *Phagnalon* and its relationship with other genera of the *Relhaniinae*; and to resolve the phylogenetic position of *Ph. pygmaeum*, *Ph. quartinianum*, *Ph. phagnaloides* and *Ph. carolipaui*. We have carried out a combined analysis of the nrDNA and plastid spacers ETS, ITS, *ycf*3-*trn*S and *trn*T-*trn*L. Results indicate that the sister group of *Phagnalon* are *Anisothrix* and *Pentatrichia*; *Phagnalon* and *Aliella* form a monophyletic group; the phylogenetic position of *Ph. carolipaui* is unresolved; *Ph. quartinianum* is merged within the Mediterranean-Macaronesian taxa; *Ph. phagnaloides* is nested with taxa from Ethiopia and Yemen; *Ph. pygmaeum* is related to the western and central Asia taxa. Correlations of our results with morphologic characters and phytogeographical patterns are discussed.

P33. PHYLOGENETIC RELATIONSHIP, POPULATION STRUCTURE, AND REPRODUCTIVE BIOLOGY OF *HYPOCHAERIS ANGUSTIFOLIA* (LITARD & MAIRE) MAIRE (ASTERACEAE, LACTUCEAE), AN ENDEMIC SPECIE TO MOROCCO.

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The genus *Hypochaeris* has a disjunct distribution, with ca. 15 species in the Mediterranean region, Europe and Asia, and more than 40 species in South America. *H. angustifolia* is an endemic species to North Africa (Middle and High Atlas, Morocco). This species is the most probable ancestor of the American taxa of this genus. The American species of the genus *Hypochaeris* show a wide diversity of compatibility systems and we aimed to know the importance, in the speciation of this genus, of the breeding system of *H. angustifolia*. In the glasshouse of the university of Seville we sowed field-collected seeds and grew seedlings transplanted from the field, with a total of eight studied populations; the reproductive success in the wild was also assessed. Finally, in order to know the population structure of *H. angustifolia*, 286 plants of ten populations covering the total distribution range of this species in Morocco were analysed using the AFLPs technique (“Amplified Fragment Length Polymorphism”).

P34. THE MEDITERRANEAN SPECIES OF LICHENS AT NORTH-WESTERN PART OF THE BLACK SEA COAST

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The crucial question at the study of lichen flora of any territory is establishment of regularity of distribution of species that is conducting of analysis of types of area. In lichen flora of north-western part of the Black sea coast the species of lichens belonged to the holarctic type of area prevail. However, there is the element of species with the Mediterranean (in the wide sense) type of area. These are the species which mainly grow on silicate rocks, some of them meet also on outcrop of limestones. Among the species of lichens belonged to the Mediterranean type of area there are: *Caloplaca coronata* (Krempelh. ex Körber) J. Steiner, *Caloplaca inconnexa* (Nyl.) Zahlbr. and *Caloplaca limonia* Nimis & Poelt (Nimis, 1993, 1995). Besides, there is sufficiently large group of

lichens which it is possible to attribute to Submediterranean type of area. The Submediterranean type of area include species which spread from south part of Central Europe to the low mountains of Mediterranean. Among this type of area are *Caloplaca aractina* (Fr.) Häyrén, *Caloplaca marmorata* (Bagl.) Jatta, *Dirina stenhammari* (Fr.) Poelt & Follm., *Lecanographa grumulosa* (Dufour) Egea & Torrente and others. The most part of species, with the Mediterranean (in the wide sense) type of area was find out on an island Zmiiniy, which being the remain of mountains of North Dobrudzha in theory could be component part of connection of mountains of North Dobrudzha with the Crimean peninsula, that is confirmed by some geological data. It is possible that the migration of the east mediterranean species of lichens from the Balkan peninsula through such continental connection could be carried out including the north-western part of the Black sea coast.

P35. EVOLUTIONARY PATTERNS WITHIN *HYPOCHAERIS* L. SECT. *HYPOCHAERIS* (ASTERACEAE, LACTUCEAE)

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Integrative models are necessary to understand the general patterns affecting the evolution of specific groups. In this work we approach this problem using *Hypochaeris* L. sect. *Hypochaeris* as a model system. This section comprises four species: *H. glabra*, *H. radicata*, *H. salzmanniana* and *H. arachnoidea*, all of them native to the Mediterranean area (two endemic and two world-wide introduced). *H. glabra* has $2n = 10$ chromosomes, whereas the others have $2n = 8$. *H. arachnoidea* and *H. radicata* are self-incompatible, whereas *H. glabra* is self-compatible and *H. salzmanniana* has self-compatible, self-incompatible and mixed populations. The phylogenetic relationships and the population structure of these species, as well as of the hybrids between them, were assessed with the AFLPs method.

P36. BUTTERFLY DIVERSITY IN PENTADACTYLOS FORESTS OF CYPRUS

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We used butterflies as an indicator group to identify the habitats for biodiversity conservation in the island of Cyprus. A total of 1602 butterflies and 23 species were recorded during this research. To understand the relative importance of local characteristics for Pentadactylos mountains butterflies, transects counts were used to assess the abundance and butterfly diversity in two different forest types. We observed highly significant effects of forest type on abundance of butterflies. For example, number of butterflies was significantly higher in old forest than young forest ($p=0.0008$). Also, the abundance of endemic butterflies was highest at old forest habitats. The survival of the majority of endemic butterflies in Cyprus may depend on conservation of old forests and their understorey plants.

P37. MEDITERRANEAN DIVERSIFICATIONS IN TRIBE SENECIONEAE (ASTERACEAE)

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Tribe Senecioneae (Asteraceae) contains approximately 150 genera and 3000 species and is well represented in all five mediterranean regions of the World. To determine whether the origin of mediterranean climates has been an important factor in its diversification, we are examining lineages of Senecioneae using phylogenetic and biogeographic techniques. A phylogeny of the tribe reveals that lineages occuring in mediterranean-climates are present in various parts of the tree, but are concentrated in subtribes Othonninae and Senecioninae. *Senecio* is the only genus in the tribe present in all five mediterranean areas, and in general, species in mediterranean climate zones are found in relatively few clades that also include species from neighbouring geographical areas. A pilot study focussing on central Chile showed that most Chilean *Senecio* species are found in two major clades, both of which contain mediterranean species. One of these clades most likely originated in southern Chile. The other clade is composed of species growing in various parts of southern Andean South America. Relationships are poorly resolved within this latter clade due to limited ITS and ETS variation. This is in sharp contrast to wide morphological variation in this clade, and perhaps indicates recent adaptive radiation in central Chile.

P38. PHYLOGEOGRAPHY OF MEDITERRANEAN SHRUB *CISTUS LADANIFER* L. BASED ON CHLOROPLAST MICROSATELLITES

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Sixteen populations of *Cistus ladanifer* L. from the Iberian Peninsula and Northern Morocco were analysed with six chloroplast microsatellites (cpSSR) in order to determine the phylogeographic structure of this plant species. Two cpSSRs resulted polymorphic producing eight haplotypes. A haplotype network was constructed with TCS program. This network showed that a haplotype shared by moroccan and southern-spanish populations was the outgroup. From this haplotype three different lineages were originated: 4 haplotypes exclusive to Iberian Peninsula, 2 haplotypes exclusive to Northern Morocco and a haplotype exclusive to Southern Spain serpentine outcrops populations. Genetic differentiation among populations was relatively low: Rst (0,645) is not significantly higher than Gst (0,542) thus indicating the absence of a phylogeographic structure.

Spatial Analysis of Molecular Variance (SAMOVA) defined four groups of populations (Fst: 64,55): the first one comprised the Moroccan and the southernmost Spanish populations; the second included populations growing in Baetic serpentines; while the other two groups included the remaining Iberian populations. These results seem to suggest that *Cistus ladanifer* colonysed the Iberian Peninsula from its original area in the Baetic-Riffain arc

P39. DISTRIBUTION AND ABUNDANCE OF ENDEMIC SPECIES *DEGENIA VELEBITICA* (DEGEN) HAYEK (BRASSICACEAE)

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The area of occupancy and estimation number of individuals of threatened and narrow endemic species *Degenia velebitica* (Degen) Hayek (Velebit, Croatia) were measured. The area of occupancy was defined on all known localities by defining the edges of areal by using GPS devices and elaboration by GIS tools. Abundance (density) was estimated according to the full counting of individual plants on 38 standard plots each with surface of 25 m^2, and with approximation to the total area of occupancy. The results show that *D. velebitica* is present on total area of 4.8 ha with the estimated 37 000 individuals. Locality on Velika Kapela with two sub-localities occupy the largest area (44 600 m^2) and have the highest estimated number of individuals (24 175), but with the lowest abundance (0.53/m^2). Small and spatially close localities on South Velebit occupy area of 2 790 m^2, they are second according to the estimated number of plants (6 897), but with higher abundance (≤4.36/m^2). Locality on Central Velebit is the smallest in area, but with utmost density (5.33/m^2). On the locus classicus, Plana, the species was not found. A trend to gorse with natural potential vegetation was detected on all localities. Results should serve as a background for tracking population trends and for conservation action plans developing.

P40. MOLECULAR DATING AND RECONSTRUCTION OF THE BIOGEOGRAPHICAL HISTORY OF CAMPANULA AND RELATED GENERA

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Campanula L. is a sub-cosmopolitan genus with 350-500 species in the Northern Hemisphere, mainly distributed in Eurasia, and poorly represented in North America and Africa. A large concentration of Campanula species is found in the Eastern Mediterranean and the Caucasus. This genus inhabits a wide range of habitats. We use here molecular phylogeny based on plastid markers rbcL and trnL-F to estimate split and diversification ages, and to reconstruct the ancestral areas of distribution of Campanula and related genera. Two molecular dating methods were applied, the Penalized Likelihood approach and the Bayesian Relaxed Molecular Clock. Biogeographical

history was reconstructed by means of the dispersal-vicariance approach. The results suggest an Early Miocene origin for the genus Campanula, a Mid-Miocene divergence of the two main clades (Campanula s. str. and Rapunculus), a Mid-Late Miocene radiation in the Eastern Mediterranean and Caucasus regions of the Campanula s. str. clade, and a Late Miocene diversification of distinct groups within Rapunculus clade. At least two different arrivals at North America are suggested by the results, first at the end of the Miocene and secondly in the Mid Pliocene.

P41. PHYLOGENY OF *RUTA* (RUTACEAE): IMPLICATIONS FOR BIOGEOGRAPHIC PATTERNS IN THE MEDITERRANEAN BASIN

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In its current circumscription *Ruta* includes 8 species of perennial shrubs: four species have a peri-Mediterranean distribution (*R.chalepensis*, *R.graveolens*, *R.angustifolia*, and *R.montana*), and four species are island endemics (*R.corsica* is endemic to the Corso-Sardinian microplate; and *R.pinnata*, *R.oreojasme*, and *R.microcarpa* are endemic to the Canary Islands). The Mediterranean basin, with its complex but well-known history of microplate movements and climatic oscillations, provides the geological backdrop for the diversification of *Ruta*. Phylogenetic analyses of three chloroplast DNA regions (*mat*K, *rpl*16, and *trn*LF) support the monophyly of *Ruta*. Within *Ruta*, the monophyly of the species endemic to the Canary Islands indicates a single origin of the lineage, followed by diversification within the archipelago. Furthermore, the relative temporal order of splitting within this clade is congruent with the order of island formation in the Canarian archipelago.Within *R.corsica,* the populations from Corsica and Sardinia, respectively, form two well-supported clades. This result confirms recent morphological and karyological work that identified the populations of the two islands as two species, and suggests that the Strait of Bonifacio, separating the two islands, acted as a barrier to gene flow.

P42. UNUSUAL STYLAR POLYMORPHISM IN SOUTHERN MOROCCAN *NARCISSUS BROUSSONETTI*

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Narcissus has been a key genus to test evolutionary hypothesis of the evolution of heterostyly, since it includes many of the proposed transitional stages. One of theme, style dimorphism with different levels of reciprocity, is very common in the genus, whereas heterostyly is only represented in two species. Here we describe an unusual style polymorphism in *Narcissus broussonetti*, which is not completely reciprocal but presents a high degree of herkogamy, both in L- and S- morph flowers. We report flower morphometrics on several populations of this southern Moroccan endemic species, and preliminary results on breeding systems and its phylogenetic relationships, which permit a first approach to assess the evolutionary significance of this novel polymorphism.

P43. PHYLOGEOGRAPHIC PATTERN OF *Artemisia eriantha* (Asteraceae) IN THE EUROPEAN ALPINE SYSTEM.

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The southern portion of the European alpine system comprises mountain ranges that are situated in, or border on, areas with Mediterranean climate: Pyrenees, Alps, Apennines, Carpathians, Dinaric mountains and Balkans. The historical biogeography of plants endemic to the southern part of the European alpine system remains largely unexplored. We studied the phylogeographic pattern of *Artemisia eriantha*, an alpine plant highly disjunctly distributed mainly throughout the southern European mountain ranges. We applied AFLP fingerprinting and DNA sequencing of plastid markers covering the entire range of the species. In the neighbour joining analysis of AFLP phenotypes two main supported branches were formed: southern Balkans populations and those from the western Pyrenees. The Pyrenees, the Alps and the Balkans were the ranges with the highest number of private fragments. The distribution of the nine chloroplast haplotypes found showed a more pronounced geographical structuring. The most common haplotype predominated in the Alps and Pyrenees and the greatest haplotype diversity was found in the Pyrenees and the Balkans.The large-scale phylogeographic pattern observed suggested that, in spite of being an alpine species, *A. eriantha* had a ‘‘classical’’ pattern of Pleistocene refugia: Iberian Peninsula, Italy, SW Alps and the Balkans.

P44. MOLECULAR PHYLOGENETICS OF *JASIONE* (CAMPANULACEAE), BASED ON THREE CHLOROPLASTS REGIONS.

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Jasione is a genus with unclear phylogenetic relationships, a wide ecological range and mostly diversified around the Mediterranean Basin. Our work presents the results of sequence analyses from three plastid regions, *ndh*F, *trn*L-F, and *psb*A-*trn*H, analysing 1,8 Kb for a total sampling of 47 described taxa. The obtained topologies show several well defined groups: 1) A clade from North Africa and South Iberia, ecologically and morphologically diversified, sister to rest of the group. Its nucleotide divergence and relative position from remaining *Jasione* would support the previously described subgenus *Phyteumopsis*; and 2) the core *Jasione* lineage encompassing several lineages which includes the mainly Balkan-Anatolian (gr. *J. supina*) and another clade including the mainly Iberian *J. crispa* group, the *J. montana* group and the African "*J. crispa*" group. The analysis suggests an African (or Betic-Rifean) origin for the genus, yet migration between northern and southern parts of the Mediterranean seems to have occurred several times along different

lineages. Our topology reveals that two southern European clades, the Iberian *J. crispa* group and the *J. supina* group have experienced a recent radiation, the former one involving changes in ploidy level.

P45. CAN A PLANT TAXON'S DISTRIBUTION BE VIEWED AS A SPATIAL REFLECTION OF THE HABITAT TYPES IT OCCUPIES? *TEUCRIUM* L. IN THE EAST AEGEAN ARCHIPELAGO (GREECE)

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The present work is part of an ongoing PhD thesis of the first author about the range of Labiatae taxa on Chios Island in relation to their occurrence in other East Aegean Archipelago islands. Among the 27 genera of the family grown on Chios, *Teucrium* L. is represented by four taxa, which exhibit different distribution patterns on the island. These patterns seem to be related to the number of habitat types (as defined in the Interpretation Manual of EU Habitats, 2003) occupied by each taxon. *T. capitatum* (sect. *Polium*) and *T. divaricatum* (sect. *Chamaedrys*) are common throughout Chios and both occur in ten habitat types. *T. scordium* subsp. *scordioides* (sect. *Scordium*) is found only in N-NW Chios and occurs in four habitat types. *T. brevifolium* (sect. *Teucrium*) is found in the SW coasts of the island and restricted in one habitat type. Regarding the presence of each taxon in the whole archipelago, *T. capitatum* is found on 14 islands, *T. divaricatum* on 13, *T. scordium* subsp. *scordioides* on five and *T. brevifolium* on eight. The question arising is: Does the distribution of *Teucrium* taxa in the East Aegean Archipelago depend on the presence of different habitat types on each island?

P46. TWO CYNOGLOSSUM TAXA IN SOUTHERN ITALY - PALEOGEOGRAPHICAL BACKGROUND OF THEIR SPECIATION

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Despite the close morphological and ecological similarity and relatively short distance of occurrence of *Cynoglossum nebrodense* Guss. (growing in northern Sicily) and *Cynoglossum montis-pollini* Sutorý in prep. (growing on Monte Pollino in southern Apennines) their tertiary origin is not excluded. We can assume according to Rosenbaum´s et al (2002), detailed work concentrated on western Mediterranean, that Sicily and Apennines were connected directly until Messinian (6 Ma) when they disconnected and about in late Pliocene (2 Ma) were Calabria and Peloritanian land (NW part of Sicily) inserted between them. The time of disconnection allowed to evolve a new distinct taxon in southern Apennines.

P47. PATTERNS OF FRUIT PRODUCTION IN THE HETEROCARPIC ANNUAL *RUMEX BUCEPHALOPHORUS* SUBSP.*GALLICUS* (STEINH.) RECH. FIL.

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Heterocarpy is a reproductive strategy, typical of plants from unpredictable changing habitats, which can leads to diversity in dispersability, germination behaviour, and offspring size. *Rumex bucephalophorus* subsp. *gallicus* is an annual plant from the W Mediterranean, producing three types of fruits. The first to be produced are "Basal fruits", which come from female flowers located at the plant basis, and show geocarpy at maturity. The two other types come from hermaphrodite flowers produced on long racemes. "Short fruits" show a short and thick pedicel, remain on the plant until senescence and are not dispersed individually. "Long fruits" show long, broad and flat pedicels and are wind dispersed. The three fruit types differed in weight, "Basal fruits" being the heaviest ones and "Long fruits" the slightest ones. The number of fruits per node increased along the raceme and a definite pattern of fruit distribution appeared. "Short fruits" were more abundant at the lower portion of the raceme while "Long fruits" predominated at the apical portion. The weight of "Short fruits" decreased along the raceme while that of "Long fruits" remained constant. Results of fruit production and distribution in two populations are discussed in relation to their ecological roles in dispersal.

P48. ECOLOGICAL PATTERNS IN THE FLORA OF THE BALEARIC ISLANDS (W. MEDITERRANEAN)

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Previous phylogenetically-controlled studies have attributed the differences in species richness among angiosperm families to the effects of traits such as pollination mode, growth form, or seed dispersal mode. Here we analyze the flora of the Balearic Islands (Western Mediterranean) with the main goal of testing for differences in reproductive and non-reproductive characteristics between genera with endemic species and genera without endemics. By means of GLMM models, we tested whether breeding system (hermaphrodite, monoecy, dioecy), pollination mode (biotic/abiotic), type of reward (pollen, nectar, both, none) and seed dispersal mode (biotic/abiotic) were associated to the occurrence of endemism within a genus. Family nested within order was introduced as random variable in models to control for taxonomic bias. We also evaluated the association between presence of endemic species in genera and habitat type, life-form, and bioclimatic distribution. We used the 529 genera of gymnosperms and angiosperms catalogued from the Balearics. Pollination mode was the only reproductive trait associated to endemism occurrence within genera (18.7% of biotically pollinated genera have endemic species vs 3.5% of abiotically pollinated genera). Incidence of endemism was more likely in rocky sites than elsewhere, and in woodlands/shrublands than in moist (coastal, ponds and riparian) areas. The drier thermomediterranean bioclimatic stage showed the lowest proportion of endemics (7.6%), regardless of pollination mode, as this was evenly distributed across bioclimatic stages. Chamephytes showed significantly higher percentage of endemics (35.6%) than the other life forms which did not differ among them. The incidence of

biotic pollination varied among life forms, but the higher occurrence of endemism in chamephyte genera cannot be explained by a greater level of biotic pollination.

P49. KNOWLEDGE OF THE MEDITERRANEAN BIOGEOGRAPHY IN NORTH AFRICA: RECENT CONTRIBUTION OF GENETICS AND PHYLOGEOGRAPHY

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The revival of botany and other taxonomical studies in North Africa is gradually appearing and follows the passion of the European countries bordering the Mediterranean these last decades. The best studied country is currently Morocco, while Algeria, Libya and to a lesser extent Tunisia are not much concerned with this renewed interest. The biogeographic bonds between Morocco and the Iberian Peninsula are being analyzed in the light of recent works on phylogenetics and phylogeography. Great gaps remain with regard to the flora of Algeria and Tunisia and their particular bonds with the Italian peninsula and the Tyrrhenian flora. The origin of high endemism, great diversity and refuge function of the hotspot "Kabylies-Numidia-Kroumiria" in particular, was not treated yet. A short synthesis on the contribution of modern molecular methods to the knowledge and comprehension of North African flora and fauna is presented, concerning Morocco primarily. Some new published or still unpublished results concerning the vascular flora or invertebrate fauna of Algeria will be presented, in a biogeographical context of the western Mediterranean. An assessment of the prospects opened by this new investigation field will be carried out.

P50. MOLECULAR PHYLOGENY AND BIOGEOGRAPHIC PATTERNS OF *CARDUNCELLUS-CARTHAMUS* COMPLEX (CARDUEAE-CENTAUREINAE): COMBINED ANALYSIS OF PLASTID AND NUCLEAR DNA SEQUENCES

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The Mediterranean *Carduncellus-Carthamus* complex (Cardueae-Centaureinae) is formed by ca. 50 species. The generic delimitation of this complex has been extremely controversial. We have revised generic delineation and biogeographic patterns using a combined analysis of one plastid region and two nuclear-ribosomal spacers. Our results confirm the existence of two lineages in *Carduncellus-Carthamus:* one formed by annual species with an eastern Mediterranean distribution that include only the genus *Carthamus* (the hybrid species of this genus have a more extended distribution), and a second lineage formed by perennial species distributed in the western Mediterranean that include the genera *Carduncellus, Phonus,* and *Femeniasia*. In *Carduncellus* there are two sister clades, the first one formed mainly by Iberian-Balearic endemics and the second one formed by species from North Africa and other taxa of wider distribution. Our results show total congruence with the delimitation of the complex based on morphology, karyology and biogeography: the complex is formed by four genera, *Carduncellus*, *Carthamus*, *Femeniasia*, and *Phonus*. The copiose evidence that supports this generic division confirms that a recent proposal of re-including all the species in a single genus *Carthamus* is unsubstantiated.

P51. PHYLOGEOGRAPHY OF THE MEDITERRANEAN CUCURBITACEAE

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The only native clade of Cucurbitaceae occurring in the Mediterranean/western Eurasian region comprises *Bryonia* (12 species) and *Ecballium* (1 species); it is sister to the Australian *Austrobryonia* (4 species). To infer species boundaries in this morphologically almost unresolved group we sequenced 136 geo-referenced accessions for chloroplast (1858 nt) and nuclear regions (468 nt). Chloroplast haplotypes split into 12 entities that in turn form six clusters (Canary Islands, Eastern Mediterranean, Western Mediterranean, Central Europe, Near East, Central Asia), with the greatest diversity in Central Asia. The low haplotype diversity in the two species north of the Alps suggests a recolonization after the last permafrost. Source populations appear to have been in the Near East and the Mediterranean. *Bryonia verrucosa* from the Canary Islands is sister to all others, with a family-wide strict molecular clock suggesting an age of 8 my for this split and of 5 my for the rapid radiation of all remaining haplotypes. The divergence from *Ecballium* is at least 41 my old. The nuclear tree does not contradict the chloroplast tree, but several clades comprise species sharing common haplotype pools, with one nc haplotype being found far from its expected clade. Most species are diploid or tetraploid. The sole hexaploid, *B. cretica*, contains several nc haplotypes, with one apparently coming from *B. dioica*. Taken together, these data point to a role of hybridization and chloroplast capture in the evolution of *Bryonia*.

P52. THE *TRIGLOCHIN BULBOSA* COMPLEX (JUNCAGINACEAE) IN THE MEDITERRANEAN BASIN

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In the Mediterranean basin the genus *Triglochin* (Juncaginaceae) is represented by the following species: *T. maritima*, *T. palustris*, *T. bulbosa* ssp. *barrelieri* and *T. bulbosa* ssp. *laxiflora*. The latter two bulbiferous taxa are variously treated as subspecies of *T. bulbosa*, which was originally described from South Africa, or considered separate species (*T. barrelieri* and *T. laxiflora*). The identification of these two taxa is based on small differences in fruit morphology and on their divergent flowering time. Whereas *T. bulbosa* ssp. *barrelieri* is spring-flowering, *T. bulbosa* ssp. *laxiflora* is autumn-flowering. Phylogenetic relationships between the two taxa and their relationship to the South African *T. bulbosa* complex have never been investigated. In this study plant material of different geographical origin was analysed using molecular markers (e.g., ITS). First results suggest that: (1) Material of *T. bulbosa* ssp. *barrelieri* and ssp. *laxiflora* form well-supported clades. (2) Within ssp. *barrelieri* a geographical pattern can be identified. (3) Subspecies *laxiflora* is more closely related to the South African taxa of the complex than to ssp. *barrelieri*. We conclude that *T. bulbosa* ssp. *barrelieri* and ssp. *laxiflora* should be treated at specific rank, and that the South African taxa may have originated from the Mediterranean region.

P53. PHYLOCLIMATIC MODELLING CAN ESTIMATE ANCESTRAL AREAS

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Ancestral area selection is traditionally based on geographic patterns analyzed alongside phylogenetic data. The approach assumes consistent climate and will only select areas from within present day distributions. The combination of observed distribution and inferred climate preferences have been used to determine the potential distribution of species in the past, present and future. The heritability of environmental niches, based on climate preferences, has been demonstrated, and ancestral niches have been reconstructed using phylogenetic techniques. These techniques can be combined to estimate ancestral areas. Ancestral area selection via environmental preference differs from traditional methods, as areas which are outside the current observed distribution can be selected if they are environmentally suitable. We present an example using the carnivorous plants *Drosera* (Droseraceae). We reconstruct the climatic preferences of lineages to model ancestral environmental niches. These ancestral niches are explored to determine the limits of distribution within contemporaneous palaeo-climate scenarios suggested by a temporally calibrated phylogeny. The patterns of palaeo-climate support a restricted Southern Australian distribution that offers a more plausible explanation of the current centre of diversity in South-Western Australia than do models based only on present day climates.