PLANT BIOGEOGRAPHY IN THE WESTERN MEDITERRANEAN BASIN: NEW INSIGHTS FROM PHYLOGEOGRAPHICAL STUDIES

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Species diversity is unevenly distributed across the globe, with some concentrations of taxa within few relatively restricted biodiversity hotspots. In a conservation perspective, these areas associate high levels of species richness and endemism with high losses of "pristine" vegetation due to increased human population density (Myers et al., 2000). With the growing number of threatened species, much attention has been focused on the taxonomic level (i.e. species richness and endemism) within these biodiversity hotspots to identify priority areas for conservation. However, there are two other important components of biodiversity: functional diversity and evolutionary diversity.

With the exponential increase of molecular tools, it is now largely admitted that the conservation of evolutionary processes sustaining biodiversity needs to be acknowledged as a priority task in the face of global change. Here, we aim to explore how a multidisciplinary approach centered on phylogeography can be used not only to infer the origin, dynamics and persistence of current patterns of biodiversity, but also to discuss the role of conservation biogeography and population genetics in biodiversity management, especially in the Western Mediterranean Basin.

The Mediterranean region is an outstanding biogeographical crossroad which results from a complex history and highly heterogeneous environmental factors. Within the Palearctic, the Mediterranean has been considered as one of the 34 global biodiversity hotspots, since it encompasses 20% of the world's total floristic richness in only 2% of the world's surface (Médail & Quézel, 1997; Blondel & Médail, 2009). More recently, the multiplication of biological models genetically studied in the

Mediterranean has conducted to define this region as a key hotspot of plant evolutionary history where genetic lineages of different Tertiary origins were shaped by the Quaternary glacial and interglacial cycles (Comes, 2004; Médail & Diadema, 2009). In this context, a new great challenge in the Mediterranean consists in taking into account the processes underlying the spatial and temporal dimensions of genetic variation at several spatial scales, in order to define key areas for biodiversity conservation in a changing world.

A review of the literature aimed firstly at identifying congruent phylogeographical patterns for plants in the Mediterranean, focusing on the delimitation of glacial refugia (Médail & Diadema, 2009). Refugia have played an unsuspected role in shaping modern biodiversity in temperate regions, and especially around the Mediterranean. Response of plants and vegetation to natural change in climate and their survival in spatiallyrestricted refugia provide thus important insights to predict the effects of future climate change on biodiversity patterns. Of the 52 refugia defined, they were generally distributed either in low-altitude areas, notably moist sites, in deep gorges with continued moisture availability, and at midaltitude. Half of these "phylogeographical refugia" are largely associated with the ten regional hotspots of taxonomic diversity, being mainly situated in mountains and islands (Médail & Quézel, 1997; Médail & Diadema, 2009). They represent thus climatically stable areas characterized by the cumulative effects of complex historical and environmental factors that have occurred since the Tertiary and not only during the Last Glacial Maximum (ca 21,000 years BP.). To precise the location of these refugia, and more generally key evolutionary areas, we have to consider the high specificity of the Mediterranean mosaic of ecosystems by confronting the relative importance of historical and modern drivers on the biodiversity patterns (species richness, endemism, range size of species, and genetic variability) for different groups of species.

At the interface between the Temperate, Alpine and Mediterranean bioclimatic regions, the Maritime and Ligurian hotspot in the south-western Alps is a relevant regional biodiversity hotspot with contrasted topography and historical biogeography (Médail & Diadema, 2006; Casazza et al., 2008). In the framework of a new french-italian program (BIODIVAM), we investigate the fundamental relationships between population processes and regional patterns of diversity and biogeography for flora and fauna. We are analyzing some key insights of a comparative phylogeography recently undertaken at the regional spatial scale, in order to identify patterns of genetic structure, migrations routes and genetic discontinuities. Another objective consists in evaluating spatial congruences with patterns of endemism and plant diversity established in south-western Alps. The taxonomic and evolutionary diversities will be then compared to the existing protected areas to evaluate the efficiency of the current network and to propose orientations for future improvements.

However, evolution does not stop to hotspot areas! To promote more sustainable strategies of conservation, we have chosen to better understand the evolutionary history of Mediterranean representative plants at different spatial scales through an integrative phylogeography approach. This road to statistical phylogeography implies thus to draw together information from genetics to ecology and paleontology, to understand the processes underlying the spatial and temporal dimensions of genetic variation. Here, we explore in parallel to Mediterranean biogeography, how a multidisciplinary approach integrating molecular and fossil data with species distribution modeling can be used to infer the effects of past climate change on the distribution and genetic diversity of plants.

Outside a biodiversity hotspot (S-E France) and despite its narrow distribution (*ca.* 145 km²), *Arenaria provincialis* (Caryophyllaceae) harbours a high level of nucleotidic variation within chloroplast DNA loci, supporting its persistence during the whole Pleistocene period (Pouget et al., in revision). Genetic, ecological and abundance data even emphasize the relevance of phylogeography to address the central-marginal hypothesis (Eckert et al., 2008) for Mediterranean endemic plants. The historical and ecological distinctiveness of populations can be used to define evolutionary significant units (Youssef et al., 2011; Pouget et al., in rev.).

At a wider spatial scale, we provide a particular focus related to our recent findings about the phylogeography of the genus *Myrtus* (Myrtaceae), one of the few cases of circum-Mediterranean plant to have been studied at the scale of its whole distribution (Migliore et al., 2012). The Tertiary genus *Myrtus* bears witness to the evolutionary response of the flora to successive environmental changes, such as the Messinian salinity crisis, the onset of the Mediterranean climate, and the Quaternary climatic oscillations, including European glacial and interglacial periods and even Saharan arid and humid ones. Our comprehensive sampling of the populations of *Myrtus communis* in the Mediterranean and the central-Saharan endemic *M. nivellei* was analyzed using a multimarker approach to depict the historical biogeography of this genus through molecular dating and ancestral area reconstructions. A striking ability to persist locally in various climatic refugia is therefore associated to migration capacities to reach new areas over time (Migliore et al., in revision).

Thus, the combination of spatial phylogeography and taxonomic diversity appears as a powerful test of assemblage-scale responses to

environmental changes, and thereby provides a means for critical assessment of the scenarios produced by modeling of species' distributions under paleoclimates. This provides also some robust predictions of future biogeographical processes related to global change.

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