SPATIAL CONGRUENCE BETWEEN FISH BIODIVERSITY HOTSPOTS, HUMAN IMPACT AND THE NETWORK OF MARINE PROTECTED AREAS AT THE MEDITERRANEAN SCALE

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Abstract

The biodiversity of the Mediterranean Sea is exceptional relative to its water volume. This hotspot of biodiversity and endemism is facing ever increasing human-induced threats and marine protected areas (MPAs) have been extensively established. Rather surprisingly, no attention has been paid to how well the actual network of MPAs spatially matches with the hotspots of biodiversity and how much these hotspots are spatially congruent with human pressures. Here we used spatially explicit data to provide a first global assessment of these congruencies. We show that the global network of Mediterranean MPAs is spatially congruent with fish richness and fish endemic richness hotspots while the highest human pressures spatially matches with hotspots of fish endemic richness but not with hotspots of fish richness.

Keywords: Biodiversity, Conservation, Fishes, Marine Parks

We used the database compiled by Ben Rais Lasram (2009) which includes the geographical distribution areas of all known fish species in the Mediterranean Sea, i.e. 619 species among which 81 are endemic and 120 are exotic. These distributions areas were compiled from the FNAM atlas (Fishes of the Northern Atlantic and Mediterranean) (Whitehead et al. 1986) and digitized using a Geographical Information System software (ArcView3.3 by ESRI). These areas correspond to those of adult stages since they are based on observations and samples and may ignore spawning areas and larvae migration paths.

The digitized polygons were overlaid to a regular grid with a total of 27078 cells covering the whole Mediterranean basin (0.1° latitude x 0.1° longitude). For each cell, species richness was estimated as the sum of the species co-occurring. We excluded exotic species because they are not included in conservation strategies. Migratory, large pelagic species as well as those occurring beyond the continental shelf were also excluded from the analysis because coastal reserves do not provide any benefit for them. Indeed, Mediterranean reserves are often small (e.g. 0.003 km2 for Temuli/Sagone marine cave), and pelagic and migratory species undergo high fishing pressure out of the reserve limits. Species exhibiting a distribution area fraction up to 40% on the continental shelf were considered as coastal and thus included in the analysis. Thus, the final database includes the distribution areas of 345 species.

Even if Marine Protected Areas (MPAs) are not only devoted to fish diversity, since they care much about habitat diversity, recent studies point out their positive effects on fish density and biomass even outside reserve boundaries. Reserves locations were digitized using the Geographical Information System software and compiled from the MedPan data as well as from maps, polygons and GPS coordinates provided by persons in charge of the Mediterranean reserves. Digitizing was carried assuming that even if a small part of a cell belongs to a reserve, the whole species occurring in that cell potentially benefit from the reserve effect. Since the 100 Mediterranean reserves (the Pelagos sanctuary being excluded) are strictly coastal, we only considered the continental shelf because deep-sea ecosystem conservation would require particular strategies. We thus extracted a set of 8186 cells corresponding to the limit of 200m water depth from the 27078 cells constituting the whole Mediterranean Sea dataset.

Each of the 8186 grid cells contained the following information: (i) MPA network with reserve presence (coded 1) or absence (coded 0) (Res), (ii) fish species richness excluding migratory and large pelagic fish and species usually inhabiting beyond the continental shelf (Rich), (iii) endemic fish species richness (End); and (iv) the human-induced pressure values (Press). So, the database consisted of a 8186 rows (grid cells) x four columns (three variables and the reserve network) matrix.

We implemented two different methods that are commonly used to assess spatial congruence: correlations and overlap between hotspots. First, we calculated coefficient of correlations between all pairs of variables. Significance levels were calculated using Dutilleul's degrees of freedom (a correction for spatial autocorrelation), as implemented in the program 'Modttest'. This correction was necessary because spatial autocorrelation in both of the variables under consideration can greatly inflate Type-I statistical error rates. Second, we tested for congruence between the three variables and the reserve network by measuring the extent of spatial overlap between hotspots. To this aim we needed to identify hotspots for human impact and for biodiversity (fish richness and fish endemic richness). Since MPAs are present in 390 cells which roughly represents 5% of the total number of cells on the continental shelf we defined hotspots as the 5% of grid cells with the highest values with respect to species richness, endemism or threat, respectively. When two or several cells had the same number of species they were all included in hotspots. Thus the 5% highest values of each variable were replaced by 1 and other values by 0. So, the new data matrix consisted of 1 and 0 and showed 519, 412, 410 and 390 cell grids with 1 for *Rich*, *End*, *Press* and *Res*, respectively. Then we computed the proportional overlap, as a measure of area shared between two entities expressed as a percentage of the one with the smallest area (number of cells). To this aim, all pairs of columns were considered successively (6 unique combinations) and the observed number of overlaps O_o (i.e. the number of cells for which we had a couple of 1: congruence of hotspots) was counted.

The fish richness pattern exhibits a decreasing gradient from west to east, the Alboran Sea being a hotspot of richness. The endemic species gradient is more pronounced latitudinally, i.e. from north to south: the northern side exhibits a greater richness and the Adriatic appears as a hotspot of endemism with a maximum of 45 species per cell. We observe that fish richness and fish endemic richness hotspots are not congruent at all (0 observed overlap) and significantly less than expected by chance (26.1 cells with overlap). Fish richness and fish endemic richness hotspots are significantly more congruent than expected by chance with the MPA network. Fish richness hotspots are significantly less congruent with human pressure hotspots while fish endemic richness hotspots are significantly more congruent with human pressure hotspots. Finally the MPA network is spatially independent from the hotspots of human pressure. Nevertheless MPAs are not the only tool to sustain fish biodiversity and conservation in the Mediterranean may also deal with fishery management and habitat protection.

References

1 - Lasram F.B.R., Guilhaumon F. & Mouillot D., 2009. Fish diversity patterns in the Mediterranean Sea: Deviations from a mid-domain model. *Marine Ecology Progress Series*. 376: 253–267.