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Abstracts

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Habitat and island area and isolation as drivers of community assembly in an archipelago

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Islands represent one of the most attractive study models in biogeographical and ecological research, and are often considered as natural laboratories. In fact, islands are well defined ecosystems that permit to clearly model most of the variables controlling the diversity and composition of the local biotas. The advent of large plot databases offers new possibilities for investigating assembly patterns in plant communities in such ecosystems. Aim of this paper is to investigate the spatial scaling patterns in the plant communities of the Tuscan archipelago, one of the most thoroughly investigated areas of the Mediterranean basin in terms of vascular flora and having been subject to intense vegetation sampling. The specific hypotheses that we wish to test are: 1) Habitat area predicts species richness within island as island area predicts total species richness; 2) habitat type and extent are more important than island identity in controlling species composition.

The Tuscan archipelago is composed of 7 major islands, one “fossil” island connected to the continent by 2 sand strips, and several smaller islets. During the Pleistocene part of the archipelago was connected to the Italian Peninsula due to the repeated variations of sea level. We assembled a database including all the vegetation relevés (hereafter referred as plots), sampled in various periods. We geo-localised all the plots for which it was possible to have spatial information and we classified all the habitat types of the plots according to EUNIS classification. We then used island and habitat Species-Area Relationships (ISAR and HSAR), and beta diversity to quantify their role in controlling the changes in turnover and replacement for native and alien species.

The assembly of the database resulted in as much as 23,657 occurrences of 867 plant species in 1,563 plots concerning 17 EUNIS habitat types. Despite the methodological limitations due to the lack of a specific sampling design, the size of the data base is enormous and quite well balanced in terms of number of plots per island and habitat type. The analyses of ISAR and HSAR highlighted the major role of habitat area in controlling species richness patterns within island and community composition, even if the island identity signal was also clear as predicted by island biogeography theories.