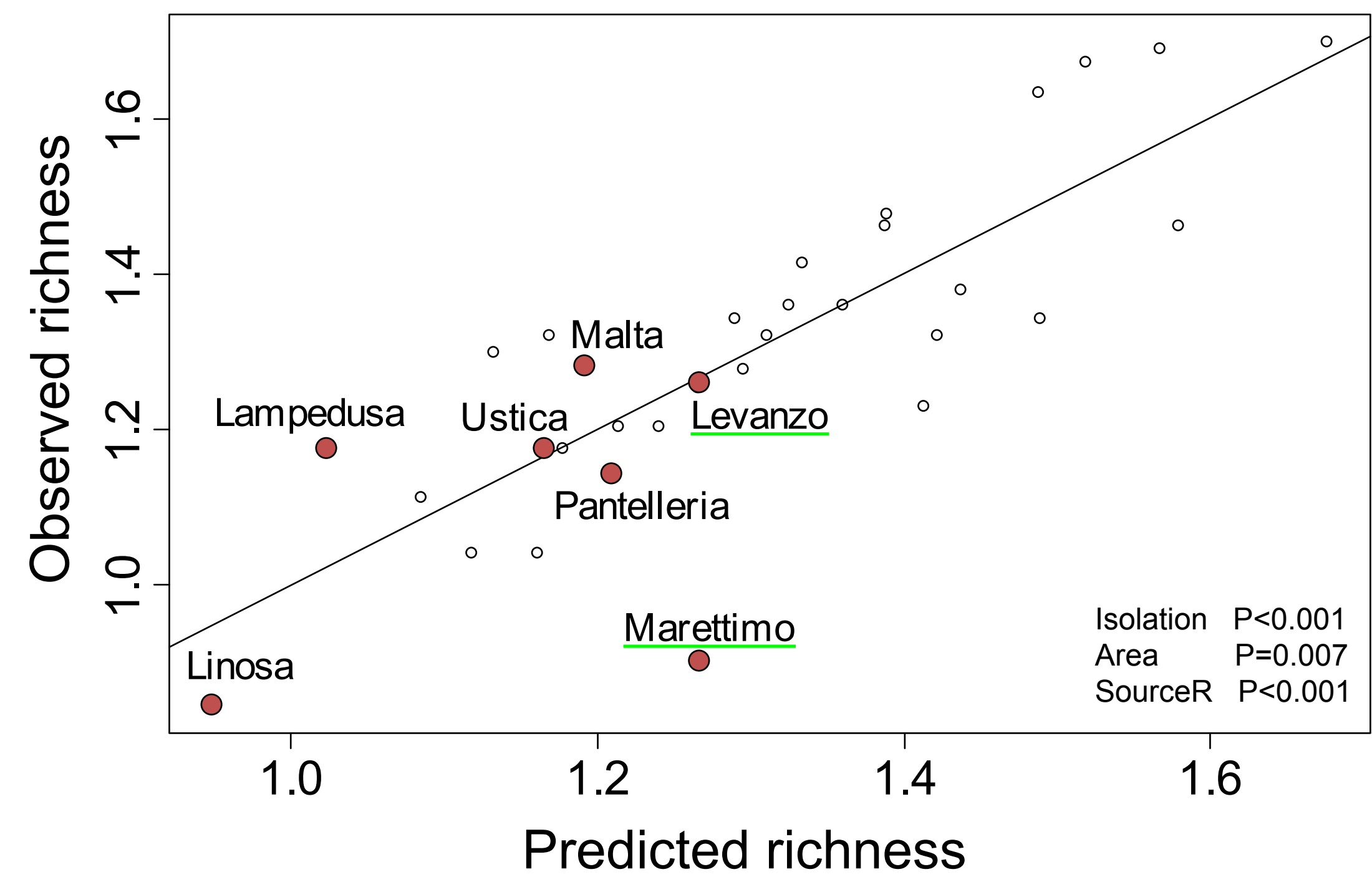


# Biodiversity loss in the Maltese islands hits relictual species

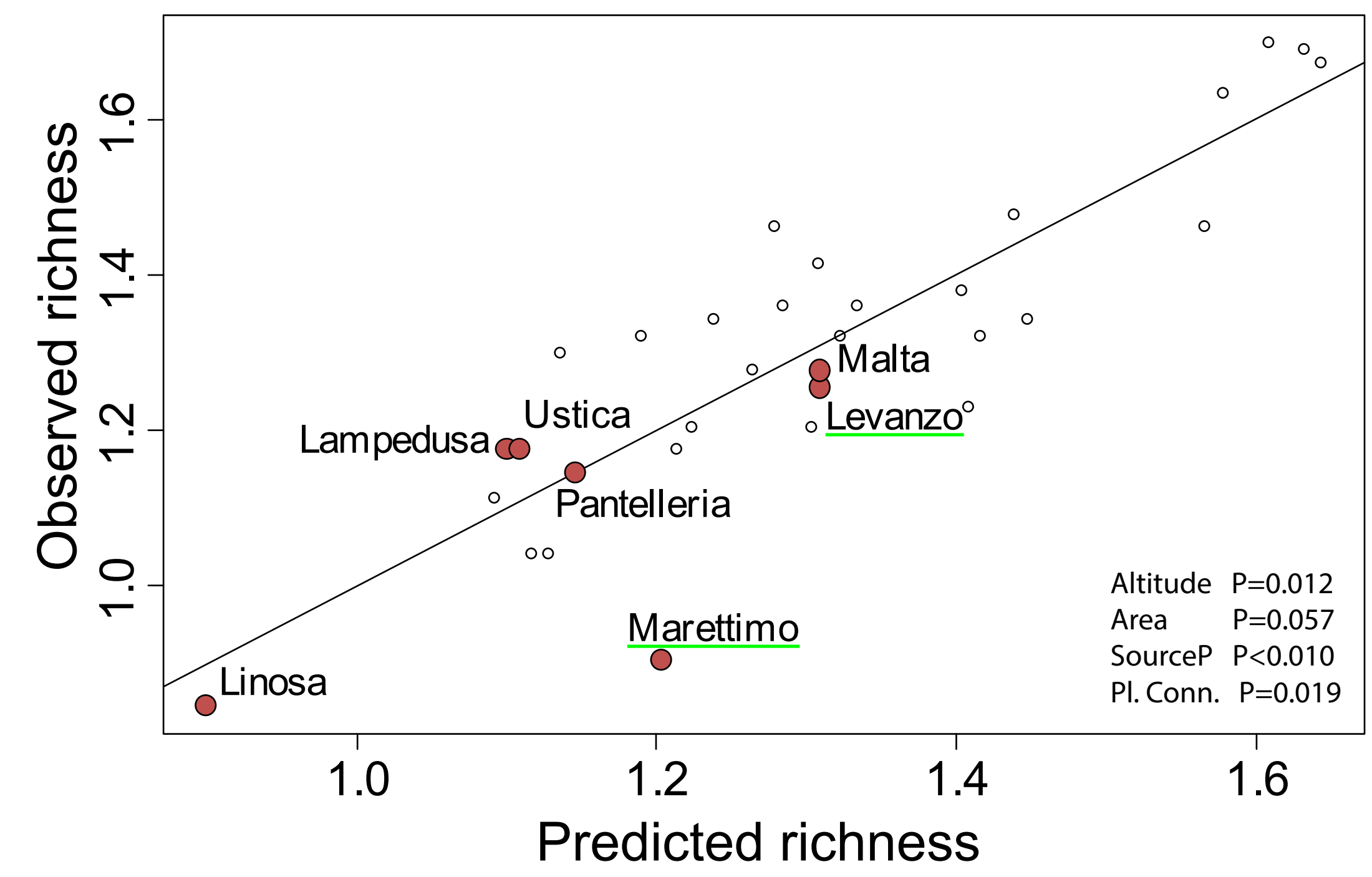
Raluca Vodă<sup>1,2</sup>, Leonardo Dapporto<sup>3</sup>, Vlad Dincă<sup>1,4</sup>, Tim Shreeve<sup>3</sup>, Mourad Khaldi<sup>5</sup>,  
Ghania Barech<sup>5</sup>, Khellaf Rebbas<sup>5</sup>, Paul Sammut, Roger Vila<sup>1</sup>

We studied the butterfly communities occurring on the islands of the Sicilian channel and compared their genetics and faunal structures with those of communities from adjacent mainland and Sicily. The aim was to identify current and historical factors shaping the distribution of butterflies in an area which represents a main faunistic suture zone in the Western Mediterranean basin. We used a multidisciplinary approach, based on a GLM to identify current and historical determinants of species richness, we studied the nestedness structure of the island communities to recognize the species characterizing the faunas of each island, and finally we analysed the cytochrome oxidase I of the species occurring on Malta, Gozo, Lampedusa, Pantelleria, Levanzo, Marettimo, Ustica, Sicily and the near mainland: Southern Italy, Tunisia and Algeria. The results were integrated in order to describe the biogeographic patterns displayed by the butterflies occurring on these islands and to identify the species that demand urgent conservation efforts.

## 1. Butterfly richness in Western Mediterranean islands

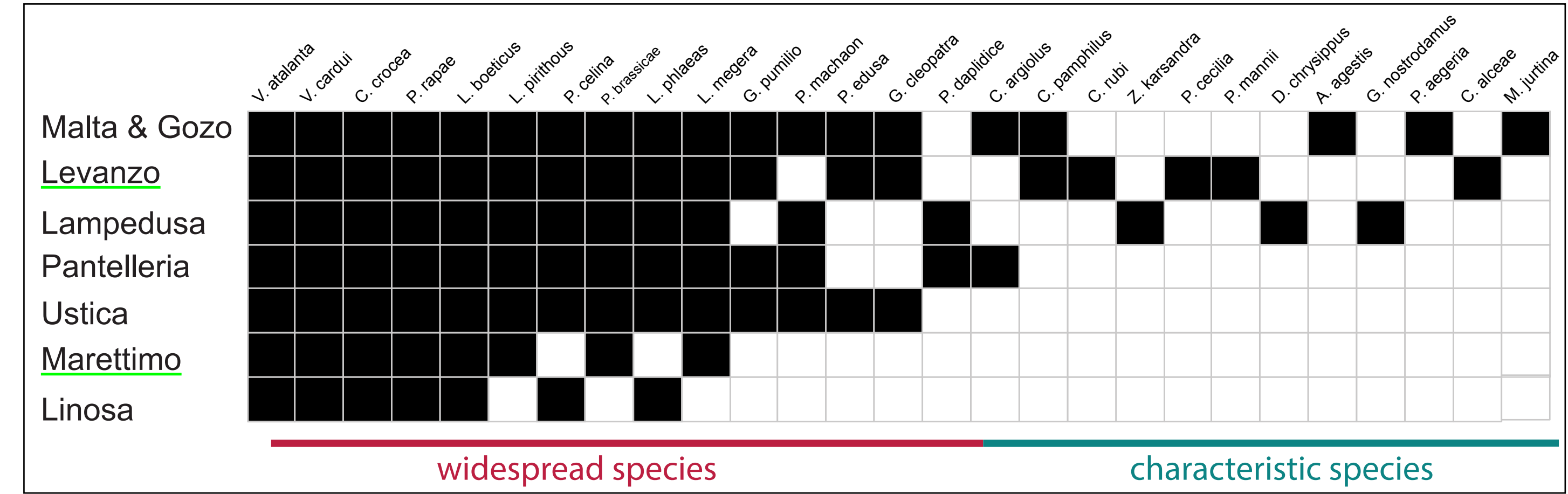


**A.** Generalized Linear Model (AIC selection) of the butterfly species richness in the Western Mediterranean islands, based on mean temperature, mean precipitation, altitude, isolation, area and source richness. Only the last three variables entered in the model with significant effects. Marked in red are the islands from the studied area. Malta and Lampedusa are richer in species than expected, with residuals of +4 and +5. Pantelleria and Linosa have two species less than expected, while Marettimo appears very poor in species (-10).



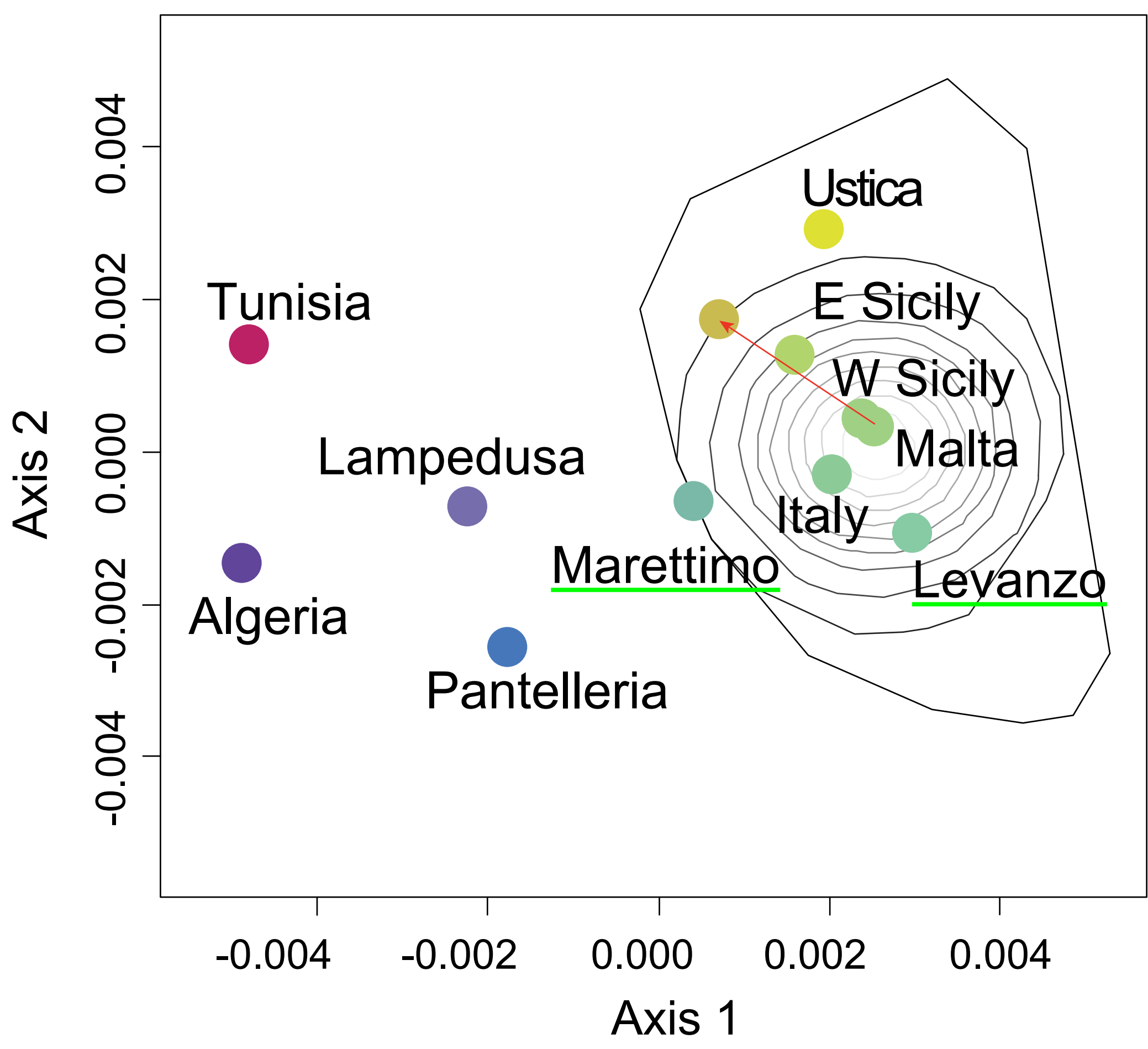
**B.** Generalized Linear Model for the same islands and predictors as in fig. 1A, with the addition of the Pleistocene connection as a factor variable, which had a significant effect in the model. The Maltese islands are almost perfectly modelled, suggesting that the four residual species from the previous model have been acquired during the Pleistocene connection with Sicily. Lampedusa is predicted to host three more species than expected, while Marettimo and Linosa maintained negative residuals (-8 and -1).

## 2. Nestedness structure of the butterfly fauna



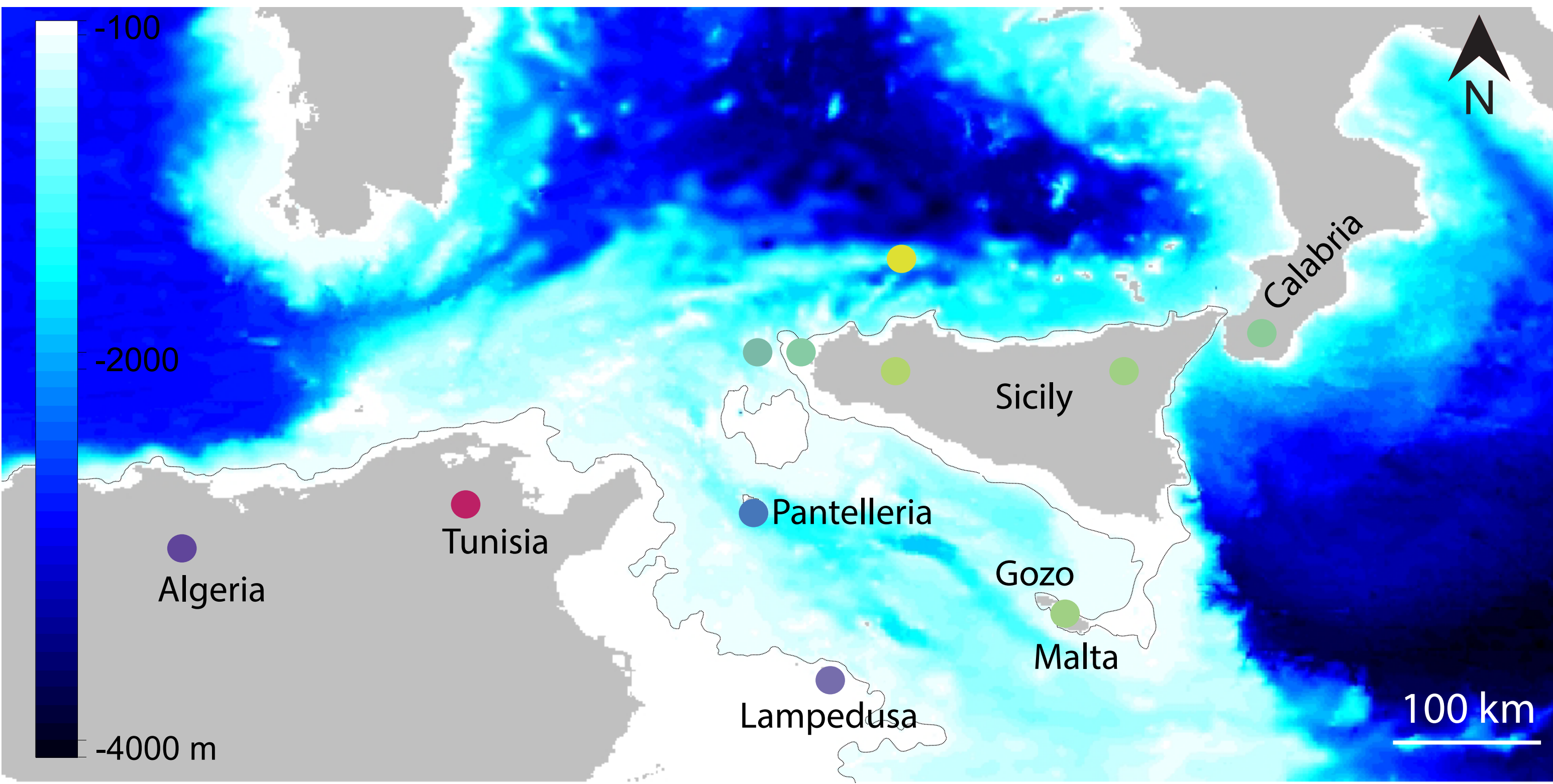
Representation of the nestedness structure (NODF algorithm) in the studied islands. The rows represent the islands, ordered from the poorest (down) to the richest (up), Malta and Gozo being the richest and Linosa the poorest. The columns represent the species occurring on the studied islands, ordered from the most frequent (left) to the most uncommon (right). We marked the species occurring in just one or two islands as “characteristic species”. In Malta and Gozo the four characteristic species are the best candidates to have colonized them during the Pleistocene (*C. pamphilus*, *A. agestis*, *P. aegeria*, *M. jurtina*). They occur in all mainland areas (North Africa, Sicily-Italy) but show high geographic variation in mt-DNA. Some characteristic species in Levanzo are also found in Europe and Africa (*C. pamphilus*, *P. cecilia*), but some only occur on mainland Sicily-Italy (*P. manni*, *C. alceae*). Lampedusa is characterized by highly vagrant species with no genetic diversification, most of them belonging to North Africa (*P. daplidice*, *Z. karsandra*, *D. chrysippus*), while *G. nostradamus* is widespread but without genetic diversification. All the other islands have no characteristic species.

## 3. PCoA of the mean genetic p-distances of all species



We computed 25 matrices of mean genetic distances among the studied areas for all the 25 studied species and obtained a final dissimilarity matrix among areas based on mean genetic distance among all species. Using this matrix we applied a PCoA and projected the results in the RGB space. The first axis accounts for the main genetic variation among continental areas (N Africa vs. Sicily-Italy) and the second one for variations inside each main area. Levanzo, Ustica, but mostly Maltese islands are genetically more similar to Sicily-Italy. Marettimo, Pantelleria and Lampedusa have a more intermediate position, which is most likely due to the lack of the widespread species that show high genetic divergence between continents: *C. pamphilus*, *P. aegeria*, *A. agestis*, *M. jurtina*. Intriguingly, these species are the ones characteristic to the Maltese islands, but also experiencing there the strongest decline. When we removed these species from the Maltese community and recalculated the PCoA, the islands were highly displaced toward the centre, becoming very similar to Marettimo (red arrow). The lines represent 10% displacement quantiles of all the different combination of removals of four species from the Maltese islands.

## 4. Conclusions



The butterfly communities of the studied islands displayed different ecological and historical fingerprints. The effect of the Pleistocene paleogeography is most evident in the Maltese islands. In particular, the GLM suggests that Malta and Gozo host around four species acquired during the Pleistocene connection and the nested structure of communities suggests that these species are the ones not occurring on other islands of similar size in the studied region. The genetic structure of the species from Malta and Gozo show a very high similarity with the Sicilian populations, supporting the hypothesis that these islands were colonized from Sicily during the last glacial maximum when a land bridge existed. Precisely these populations are the ones currently experiencing strong decline and in some cases are already extinct from one or both Maltese islands, a phenomenon that is apparently not affecting the rest of the taxa. Because these species are presumably weak dispersers over water, they are unlikely to recolonize the Maltese islands after extinction and they should be considered as priority species for conservation.

We conclude that current extinction processes apparently caused by anthropogenic factors are rapidly erasing Pleistocene biogeographic signatures that confer idiosyncrasy to islands, leaving only undifferentiated communities, mainly composed by highly dispersive generalist species.