detected the presence of two biogeographic regions, a) one, to north of 5°–6° LS of warm waters (Transition zone of the Panamanian province) and b) to south of 5° LS of cold temperate waters (Peruvian province). Through the thousands of years, the evolutionary changes that the coast of Southeastern Pacific underwent could help to explain much better the current distribution that displays the seaweed. This work represents the first step to understand the factors that govern the distribution of the marine flora in Peru.

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ANALYSIS OF MACROALGAL DIVERSITY DIFFERENCES AMONG TIDAL POOLS: IMPLEMENTATION OF THE HYPOTHETICO-DEDUCTIVE METHOD

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Tidal pools are extensive patchy habitats present on coasts all over the world, with marked differences compared with other coastal habitats. During low tide they function as an archipelago of subtidal protective niches inside the eulittoral zone, out of the influence of waves or currents, and without suffering the extreme environmental conditions of the emersion. Up to now, the studies focusing on the processes that control the biodiversity of tidal pools have been performed within the scientific inductive method, trying to explain the influence of certain factors (biotic and abiotic) on the diversity of organisms colonizing the pools. The aim of the present study is approaching the study of macroalgal specific diversity in tidal pools using the hypothetico-deductive method, testing the suitability of different classical biodiversity hypotheses to explain the differences in alpha diversity among tidal pools from Tarifa Island (Southern Spain). With this study we distinguished the characteristics of the pools that mainly control macroalgal alpha diversity differences among pools. Thirty four tidal pools were analyzed, and for each one 14 descriptive variables were registered as well as the whole containing macroalgal flora. In order to analyze the suitability of eight diversity hypotheses, univariant and multivariant statistical analyses were performed, based on linear and logistic regressions between pool variables and macroalgal alpha diversity values. The biodiversity hypotheses that best explain the differences in alpha diversity among tidal pools were the climatic severity hypothesis (Richerson & Lum, 1980), the colonization-extinction equilibrium hypothesis (McArthur & Wilson, 1967) and the predation hypothesis (Paine, 1966).

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PHYLOGENY OF THE *LAURENCIA* COMPLEX (RHODOPHYTA) FROM THE ATLANTIC BASED ON *rbc*L, *rbc*L-S AND *cox*1

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The first sequences for species of the *Laurencia* complex using the 5′ region of mitochondrial cytochrome c oxidase subunit I gene (*cox*1, 710 pb) were obtained from 46 taxa of *Laurencia* and *Palisada*. The results were compared with *rbc*L/*rbc*L-S data and with the combination of the three markers (*rbc*L, *rbc*L-S and *cox*1) from the same set of species. In *cox*1 analyses, 146 sites were parsimoniously informative in 665 positions, whereas in *rbc*L/*rbc*L-S, 305 sites were parsimoniously informative in 1564 positions. For the combined analyses, 451 sites were parsimoniously informative in 2229 positions. In *cox*1, the interspecific divergence ranged from 5.5 to 13.6% (36 to 90 bp) and the intraspecific divergence from 0 to 5.1% (0 to 29 bp). In *rbc*L, the interspecific divergence varied from 1.9 to 6.2% (27 to 89 bp) and the intraspecific divergence from 0 to 1% (0 to 14 bp). The trees topology found in separate analyses of *rbc*L/*rbc*L-S and in combined analyses was similar, forming two monophyletic groups represented by *Palisada* and *Laurencia*. However, the combination of the three markers improved the support for most of the established relationships and presented better topology definition. In the cox1 tree, three groups were formed: the *Palisada* clade, the *Laurencia* clade and a third group formed by two unidentified species of *Laurencia*. The relationships within *Laurencia sensu stricto* clade were best determined with the *rbc*L rather than with *cox*1, however the later proved to be efficient to identify and delimitate the specific taxonomic categories, corroborating its use for barcoding. Partially supported by CNPq, Fapesp, Capes (Brazil), Ministry of Education and Sciences (Spain) and PROMEP (Mexico).