HIGHER TAXA SURROGATES OF MARINE BIVALVIA (MOLLUSCA) AND POLYCHAETA (ANNELIDA) DIVERSITY IN THE EASTERN MEDITERRANEAN (GREEK WATERS)

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Abstract
Higher-taxon richness as a surrogate for species was used to estimate the species richness of marine bivalvia and polychaeta in the Greek waters of the Eastern Mediterranean. In both these classes, significant and positive relationships between generic and species richness were found. Family richness is also strongly related to the number of species. This suggests that identification to the family level may be sufficient in many routine surveys. At the generic or family level, this surrogate method may be a valuable tool for locating and designing representative systems of protected areas for the well-documented zoobenthic communities that occur in Greek waters.
Keywords: Biodiversity, Bivalves, Polychaeta

Introduction
The assessment of biodiversity usually relies on a proxy, such as species richness or diversity [1]. However, the use of lower taxonomic resolution has also proved promising in environmental monitoring and impact studies [2-3]. A series of studies have demonstrated good congruence between species richness patterns and higher-taxon richness, indicating that this approach could be a promising tool in conservation biology for the rapid estimation of species richness [4-5]. In the present study 753 species of marine polychaeta and 308 bivalvia were considered and using regression techniques were tested for whether higher taxons are a good surrogate for species diversity.

Materials and Methods
According to the comprehensive checklist of Simboura and Nicolaidou (2001) [6], 753 benthic polychaete species have been recorded in Greek waters. Data 308 species of bivalvia [7] were used. The data were aggregated to higher taxonomic levels and correlations were made between species richness, genus and family richness. Four models (linear, polynomial of power 2, polynomial of power 3 and exponential) were fitted so as to be able to investigate the predictive power of higher order diversity on species richness. The best-fitting model was chosen on the basis of the highest correlation coefficient values. The univariate method applied was that of linear regression (Pearson and Spearman correlation coefficients). Correlations were used to relate the number of species to the number of genera and families in the two datasets.

Results and Discussion
All relationships between species, genus and family were significant for both taxa studied ($P < 0.001$) (Tab1).
These correlations show that it is possible to use higher taxa as a surrogate for species in surveys of richness. Cross taxon correlations of the richness at the different taxonomic levels were positive and strong (Tab 2). The analyses performed in the present study showed that generic and family levels could be used as a reasonable surrogate for species richness in eastern marine bivalvia and polychaeta. Surrogacy can be seen both as a preliminary approach, in cases when it is not possible to quickly identify all for conservation purposes, or as an end in itself, in regions where most species are unknown, or when insufficient resources are available to further pursue the identification process [8].

Tab. 1. Correlation coefficients for the regression between species, family and genera richness for the bivalvia and polychaeta fauna

	Linear	Polynomial of power 2	Polynomial of power 3	Exponential
Species vs. family				
Bivalvia	0.939	0.973	0.974	0.967
Polychaeta	0.877	0.950	0.998	0.978
Species vs. genera				
Bivalvia	0.961	0.970	0.9734	0.982
Polychaeta	0.965	0.966	0.977	0.992
All correlations are significant at p < 0.001 level				

Tab. 2. Cross taxon correlations (Pearson and Spearman coefficients) for different taxonomic levels

	Polychaeta					
	Pearson			Spearman		
	Species	Genera	Families	Species	Genera	Families
Bivalvia						
Species	0.974	0.952	0.920	0.991	0.991	0.900
Genera	0.966	0.953	0.947	0.964	0.964	0.991
Families	0.929	0.906	0.913	0.891	0.891	0.954
All correlations are significant at a = 0.001 level						

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