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The genetic polymorphisms and the morphological variations by which the natural populations of taxa belonging to the polytypic molluscan genus Albinaria differ among themselves in the islands of the Aegean archipelago and the adjacent continental lands of eastern Greece hav been investigated in order to uncover the patterns of these differences and thus eventually attribute them either to historical (paleogeographical, anthropogenic or due to "recent" dispersion accidents) and/or ecological causes. An electrophoretic study of 27 genetic markers was carried out in 31 Albinaria populations belonging to 15 different species and several



subspecies (their number varying according to the opinion of different subspecies (their number varying according to the opinion of different silands, 8 Crete and the Gavdos island and 5 the eastern Greece including the Antikythira island. From the data gathered the between oppulations genetic distances were estimated using Sourdis distances instances, the application of the Neighbour Joining Method on these distances provided the most reliable dendrogram, depicted above. This tree is in good accordance in general with the accepted taove. This tree is in good accordance in general with the accepted taove. This tree is in good accordance in general with the accepted taove. This tree is an good accordance in general with the accepted taove. This tree is an good accordance in general with the accepted taove. This tree is in good accordance in general with the accepted taove. This tree is an good accordance in general with the accepted taove. This tree is an good accordance in general with the accepted taove. The features of this tree are not easily understood as produced by historic acuses. One possibility is that the topology of the tree uncovers the featoponnesus through Crete with Asia Minor; another possibility is that the structure is due to more recent migrational events between nearby lands separated by sea barriers, events extremely rare but not fipcosible occurrence. On the contrary the study of 18 quantitative and 10 qualitative characters regarding the external morphology of the shell in 20 of the pipculations examined electrophoretical, does not provide a clear picture, when all characters are only used shows a definite resemblance to the genetic (electrophoretic) tree mentioned earlier. Simulations of which are used in the taxonowy, have a distribution governed also painly by the same historical factors. On the contrary the subset on the totality of the morphological characters, some painlitative characters, responsible for the patchiness displayed by the sthe sheed on the totality of the morphologica

Qualitative character



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116

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