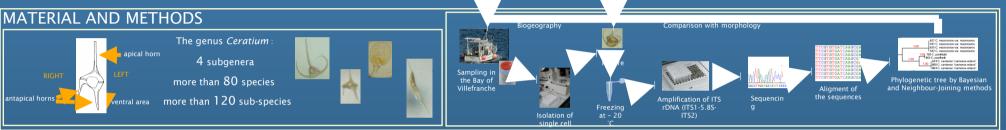
Genetic variability and molecular phylogeny of the genus *Ceratium* (phytoplanktonic dinoflagellate) from Ligurian Sea inferred from single-cell analysis of ITS rDNA sequences

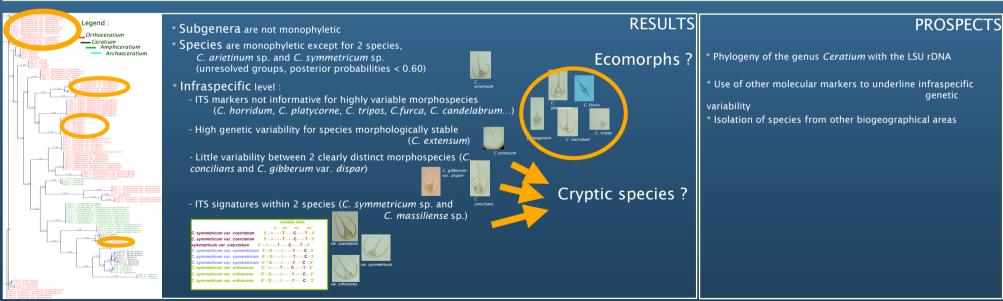
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Since a few decade, classical morphological identification of phytoplankton species is questioned because of the unexpected genetic diversity (1). To date, molecular biology helps to complete morphological information or to find subtle differences that define species more accuretly. Moreover, comparative analysis of portions of the ribosomal gene has underlined genetic populations that were correlated with specific biogeographical areas, for example, tropical, subtropical and intermediate for the 3 genetic types of the planktonic foraminifer *Orbulina universa* (2) or correlated with specific ecological niches like for the 4 genetic types of the unicellular green algae *Ostreococcus tauri* that occupy different niches mainly depending on light and nutrient conditions (3). In this context, my present work compares ITS rDNA sequences of 30 species of the genus *Ceratium*, a dinoflagellate easily identifiable and isolable thanks to its size, very diverse and largely distributed, present all the year and found in an abondant scientific literature since the end of the XIX th century. Its study, completed by studies of other functional groups, could allow to better understand the mechanisms influencing diversity as well as the functioning of aquatic ecosystems.





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