Corso di Dottorato di Ricerca in Scienze della Vita e dell’Ambiente - Ciclo XL

Integrated eDNA-based approaches for biodiversity analysis (DiverSea)

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INTRODUCTION

Marine biodiversity is fundamental for the structure and functioning of ocean ecosystems and for providing a broad range of ecosystem services that support humans on local, regional, and global scales. While traditional methods are based on morphological identification and observation surveys, innovative methods include the use of molecular approaches. In particular, the use of the environmental DNA (eDNA) metabarcoding enhances the capability to simultaneously capture a wide range of biological components.

OBJECTIVES

Task 1.

Mapping and assessing marine biodiversity.

Task 2.

Integration of traditional and innovative methodologies to enhance knowledge of marine biodiversity.

Task 3.

Identification of gaps, constraints, and potential limits of eDNA technique.

METODOLOGIES

Study areas: four areas along the Adriatic coasts (Gabicce Mare, Falconara Marittima, Conero Riviera and Torre Guaceto) have been identified.

Sampling activities: Samples of seawater and benthic substrates are collected biannually in four areas along the Adriatic coasts (Italy) in different habitats and environmental conditions (e.g., impacted and non-impacted areas). Transect analysis, image acquisition and use of drones.

Laboratory and field experiments: to investigate the persistence of eDNA signals over temporal and spatial scales, as a function of selected Adriatic model species and their associated abundance and biomass.

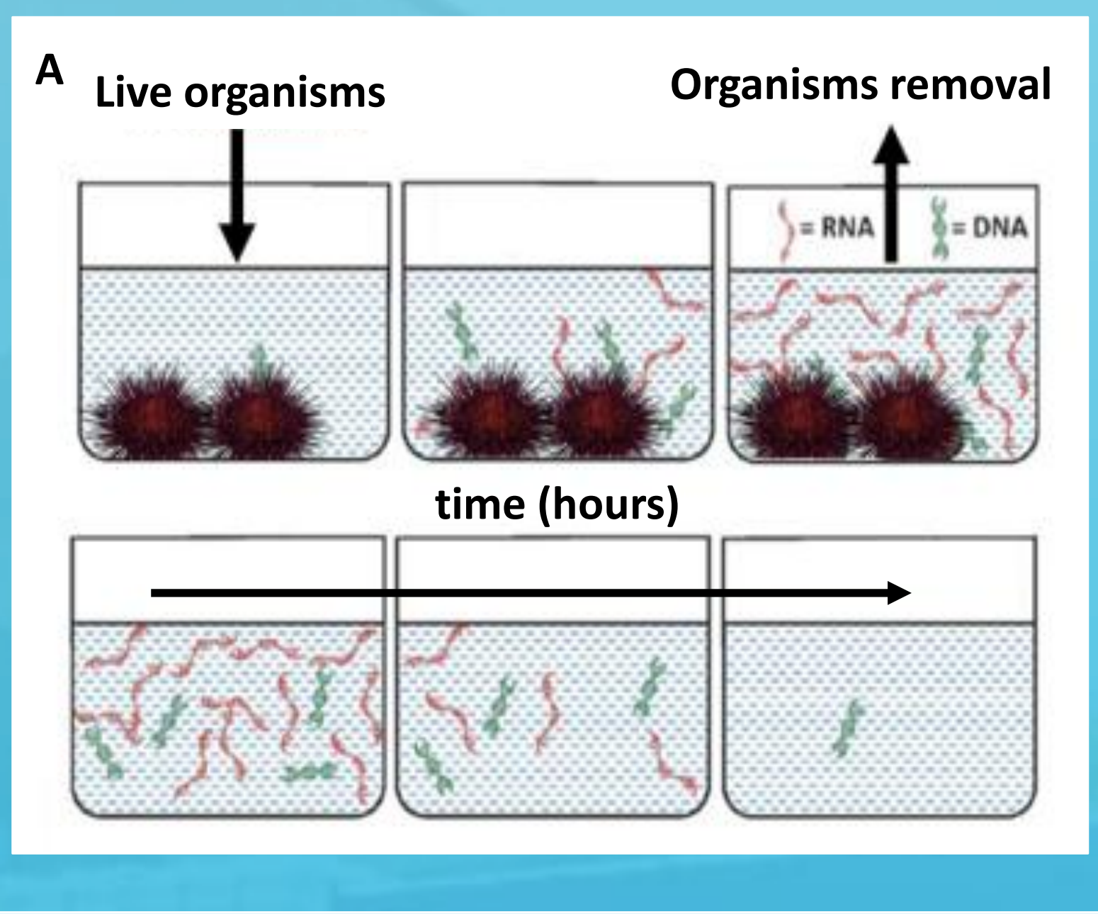
Laboratory analysis: Sorting and morphological identification of meio- and macro-fauna samples. Metabarcoding and bioinformatics.

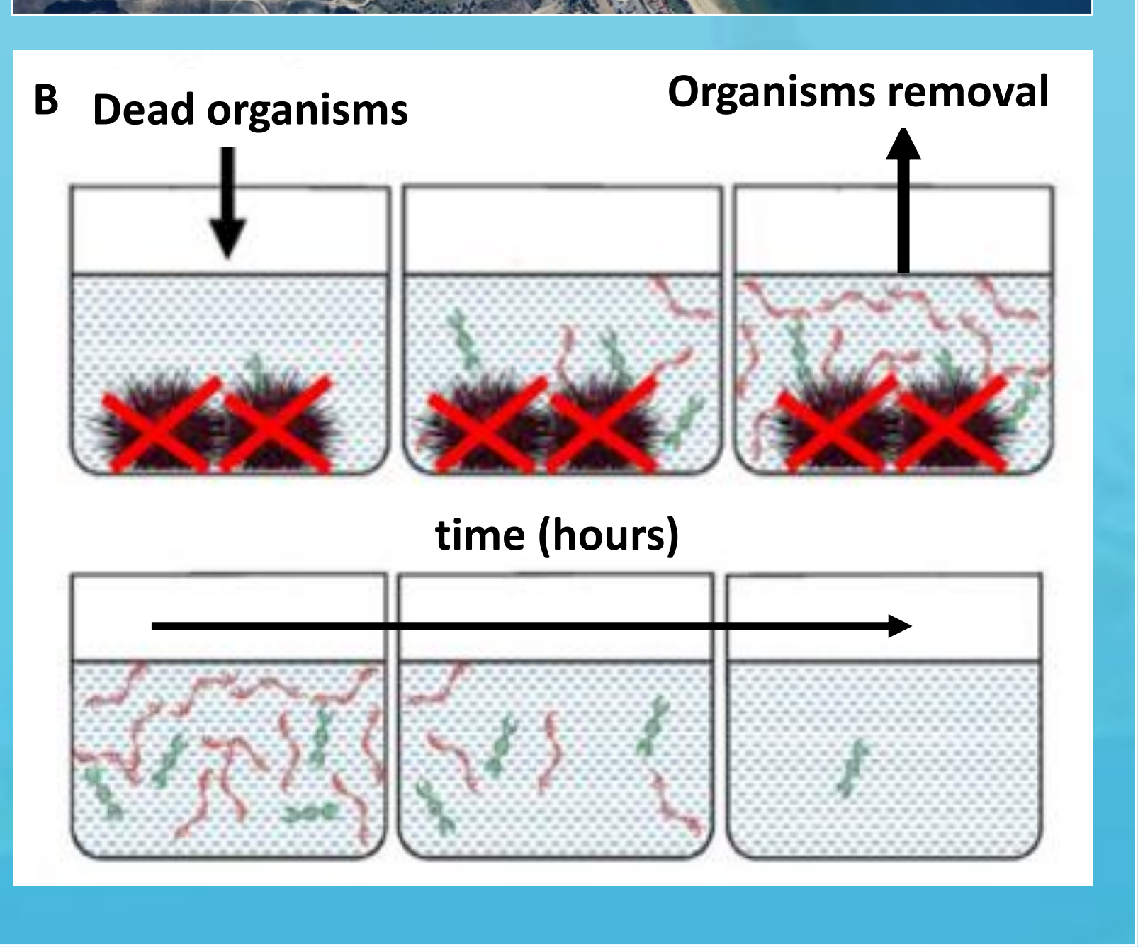
Gabicce Mare

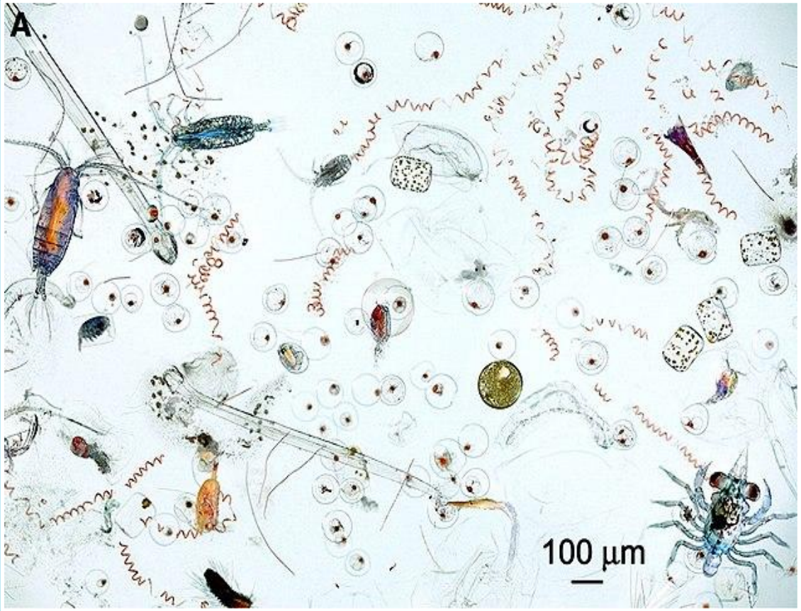
Conero Riviera

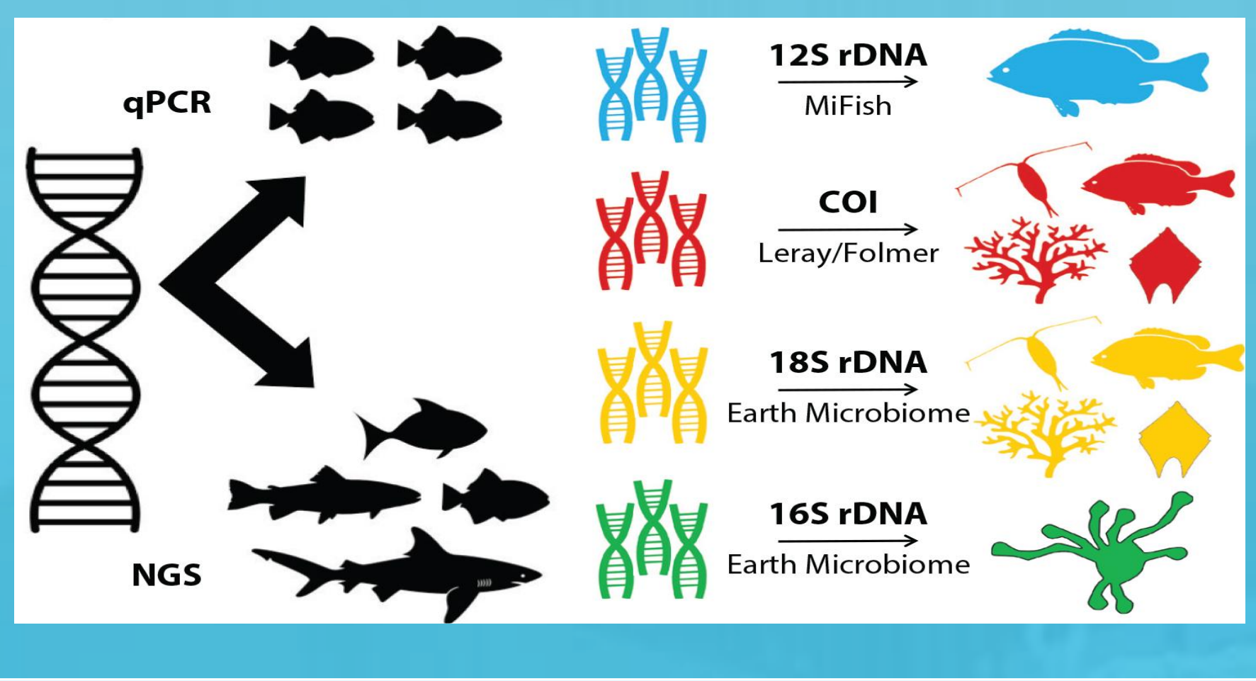
Torre Guaceto

Falconara Marittima

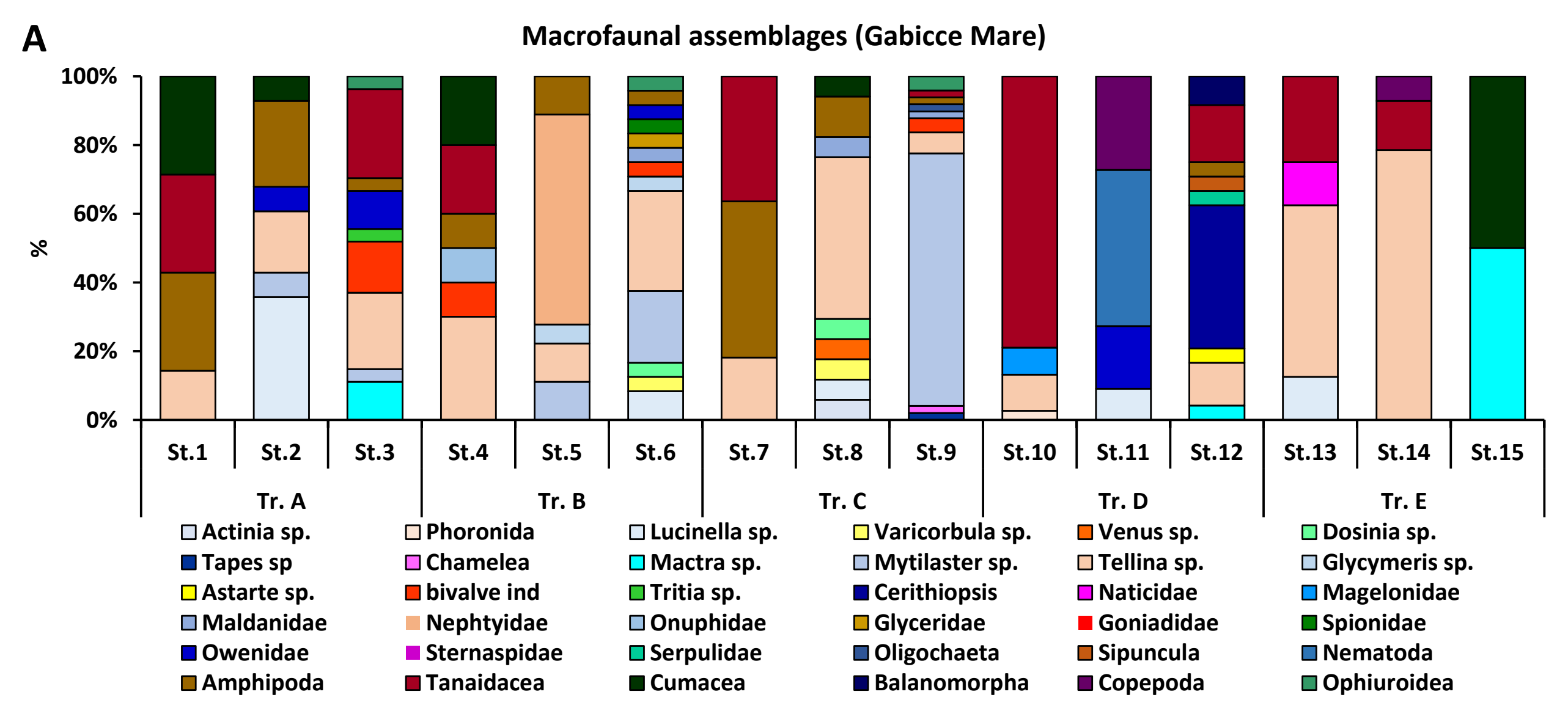


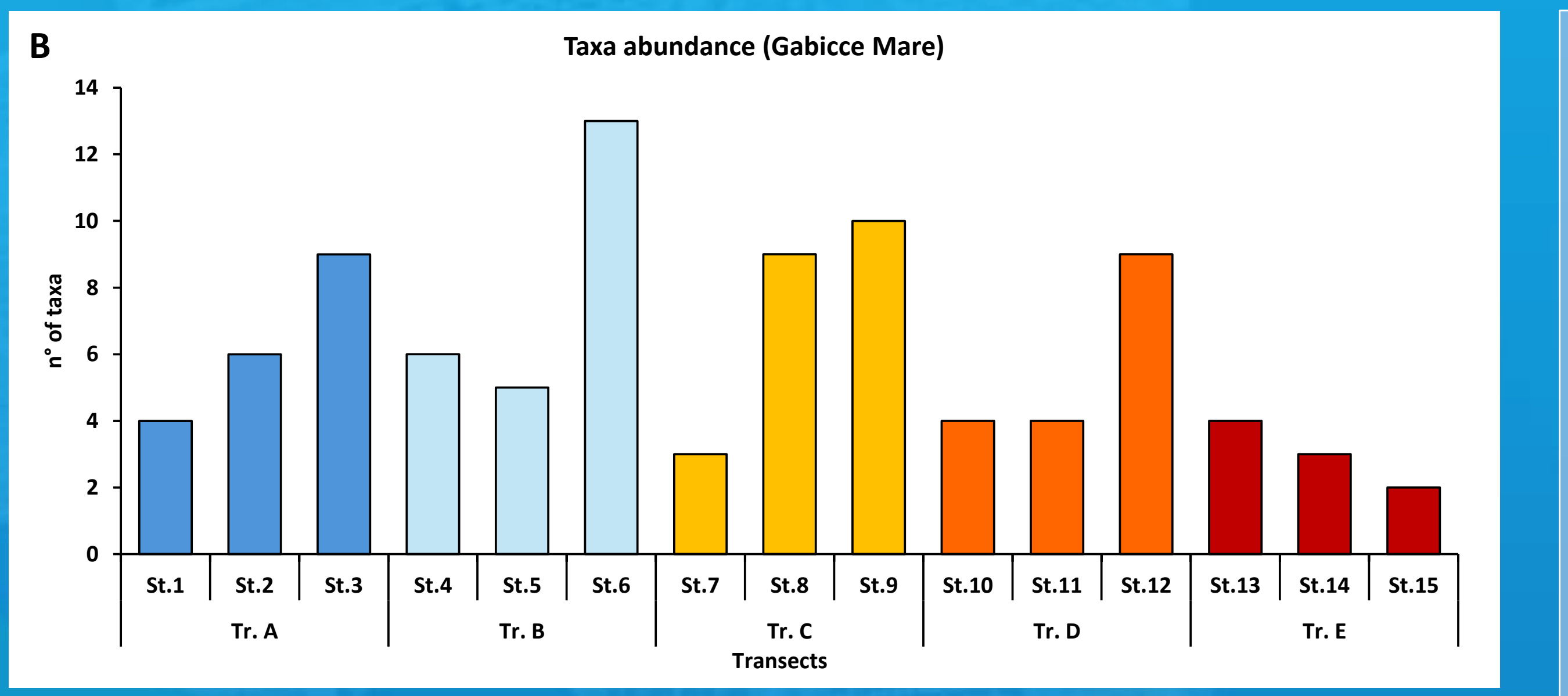


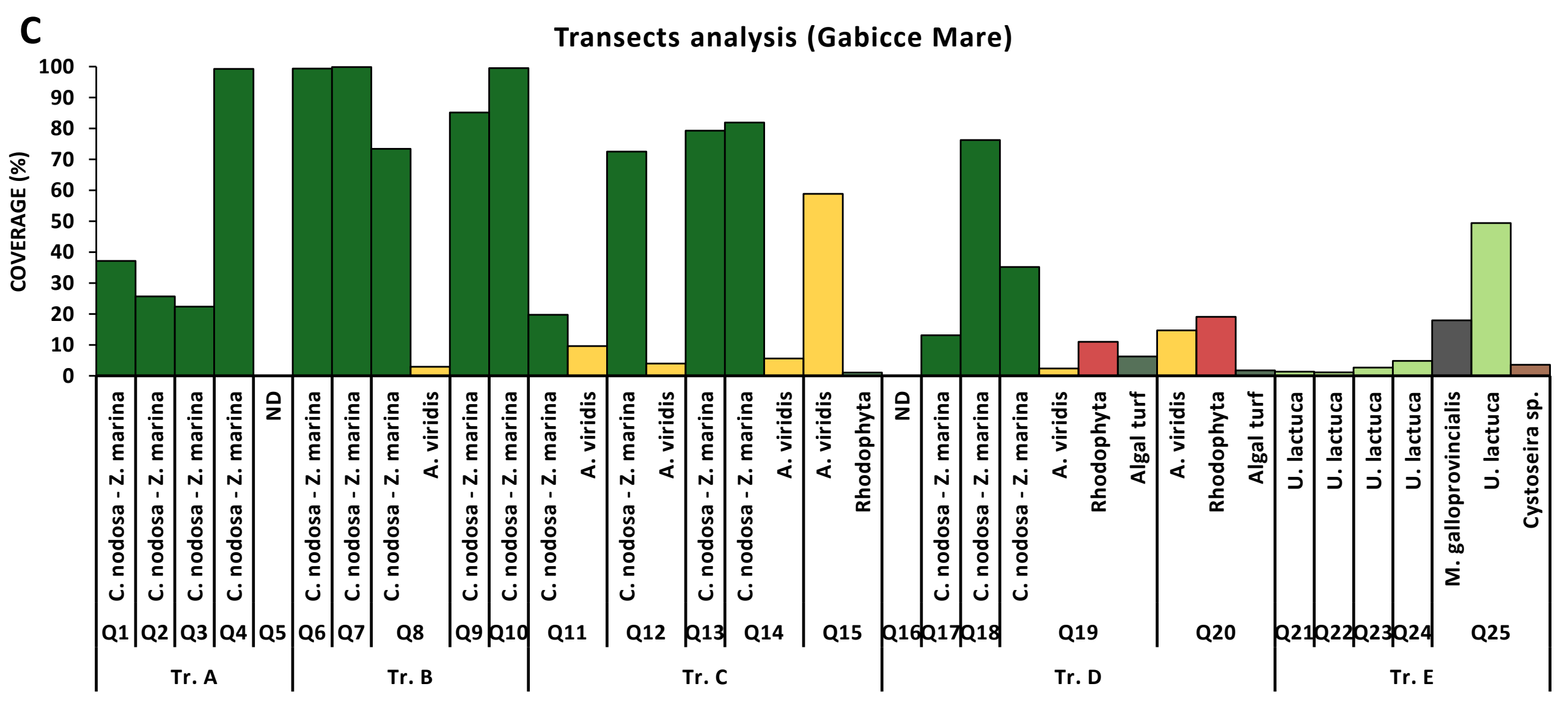


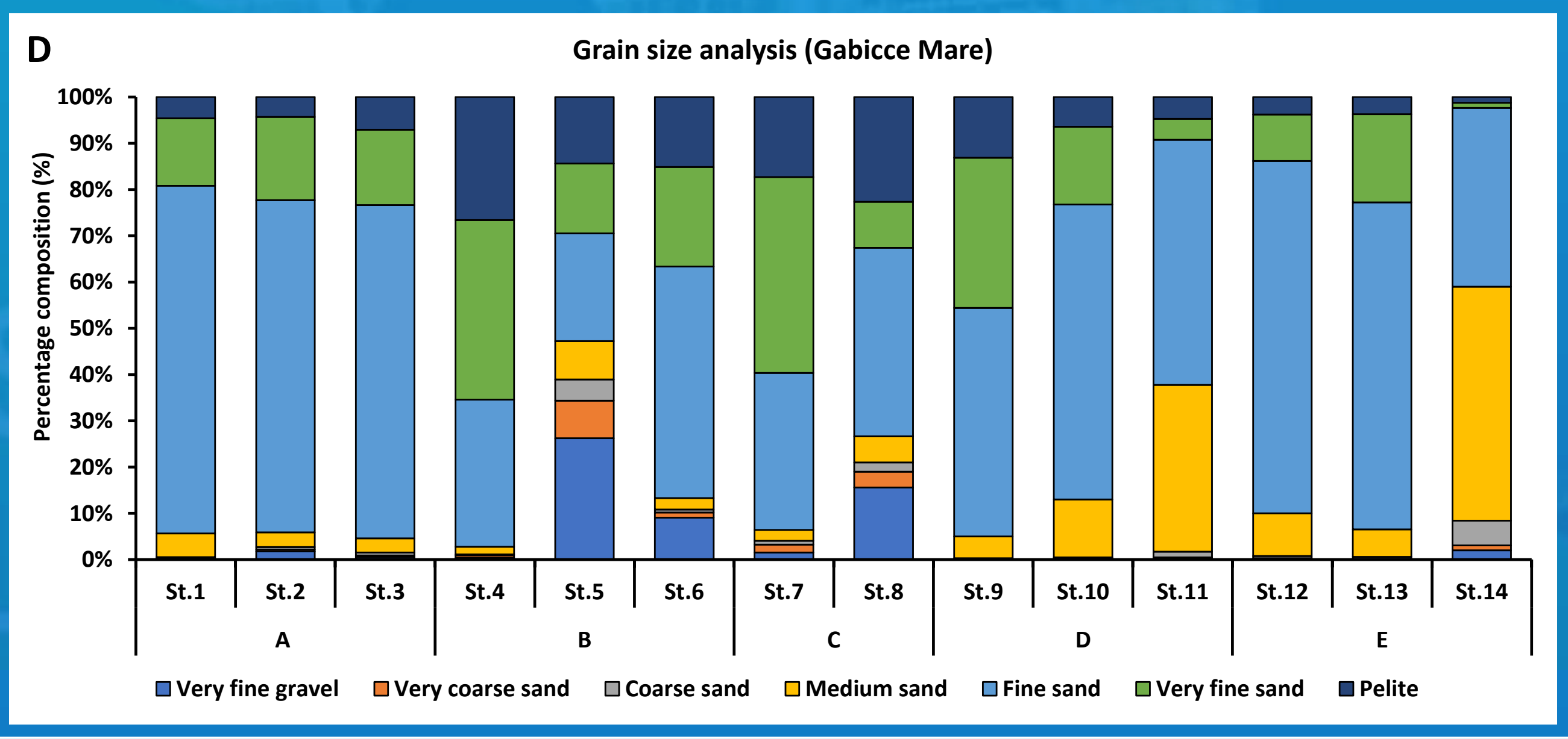


PRELIMINARY RESULTS









The data show a macrofaunal composition and abundance among transects (Fig. A and B), with higher taxonomic diversity in central stations (particularly St.6 and St.9). The structure of macrofaunal communities differs significantly between transects, following an impact gradient due to human pressure. These findings align with a higher abundance of *C. nodosa* and *Z. marina* (Fig. C and D).

REFERENCES