



# FORAMS

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**Abstract** (max 2600 characters including space)

**Assessing the effect of chromium pollution on benthic foraminiferal community: morphological vs. environmental metabarcoding approaches**

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The purpose of this experimental study is to assess the impact of different concentrations of chromium (Cr) through time on the diversity of cultured benthic foraminifera combining two morphological approaches for the identification of living specimens that are Rose Bengal (RB) staining and CellTracker Green (CTG) labelling as well as environmental DNA and RNA metabarcoding. Seven tanks/aquaria with different concentrations of Cr in water, namely 100 ppt, 1 ppb, 10 ppb, 100 ppb, 1 ppm and 10 ppm plus the control were used. A mesocosm was extracted from each tank at pre-established time (1 week, 2 weeks, 4 weeks 6 weeks and 8 weeks). Morphological analyses produced 6 datasets based on staining techniques (RB vs. CTG) and the considered sediments' fractions (>125  $\mu\text{m}$ , 63-125  $\mu\text{m}$  and >63  $\mu\text{m}$ ) and several foraminiferal parameters (i.e., S, H' and Fisher  $\alpha$  index). On the basis of the correlation analyses, no significant correlations among diversity indexes calculated for RB and Cr concentrations in water and sediment were found. On the contrary, significant negative correlation values were observed between

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diversity indexes from the CTG datasets and Cr concentrations in sediment. Molecular analyses produced 6 datasets (Filter 1, 10 and 100 for both eDNA and eRNA). In all datasets generated from the eRNA but not with eDNA analyses, the diversity decreased with increasing Cr concentrations. Environmental DNA/RNA metabarcoding show evidence that Cr pollution has detrimental effects on benthic foraminifera. Compared to morphological approach, the metabarcoding offers several advantages, such as wider range of analyzed foraminiferal taxa among which some may be potential key indicators of Cr pollution. This study further supports foraminiferal metabarcoding as a complementary and/or alternative method to standard biomonitoring program based on the morphological identification of species communities.