Report.

This is a methodological study raising with the question of how to deal with turbid waters in eDNA studies, using the turbid coastal lagoons in California for this case study. While the authors report and document important methodological issues and solutions, I feel that the current paper feels short and that many of the aspects that I list hereafter should be considered for a careful and thorough revision that could take two different formats (see below)

1- It is difficult to compare the three treatments as it mixes different questions. The first question is comparing habitats, i.e., water versus sediments. Nested within the water habitat is the methodological question used in the current title, i.e. to freeze or to scoop.
2- It is obvious that microbial communities are totally different in the water column and sediments. This is also the case when considering the invertebrates, which were not studied in detail here, but certainly have been recovered in the metazoans (CO1) PCR products. In addition to the habitat specific communities, the sediments are also the receptacle for particles sedimenting from the water column. Indeed, one would not expect living pelagic fishes in the sediment, but you can anticipate eDNA from pelagic fishes in the sediment occurring diluted within the eDNA from the sediment communities.
3- The turbid waters of the lagoons in addition to the difficulties in filtering and associated methodological questions also raise another important issue when the turbidity is related to sediment resuspension. In that case the water column will also include eDNA from the sediment community mixed with the eDNA from the autogenic community in the water column.

To my opinion for this paper two different options exist, i.e.

i) A very short focused paper (e.g. a Note) that I would restrict on the question of recovering the eDNA from fishes in these turbid coastal lagoons, i.e. the main question how to treat the water sample (freeze or scoop) and if alternatively, by using their role as a receptacle for particles from the water column, can sediment samples be an alternative approach for addressing this question?
ii) A more in-depth analysis of the eDNA in the different compartments (water versus sediments) with the methodological issue (freeze or scoop for the water samples) as a secondary question, taking into account the points 1, 2, 3 mentioned above. The current paper falls short for this approach and the presentation of the questions is not clear. However, the comparison of the pelagic and sediment Bacteria and Archaea communities in sediments and water column makes a lot of sense. In this case I would also expect you to present data on the invertebrate communities and also on microbial eukaryotes in general. In addition, if you choose this option, I would suggest that you consider a different title for this study.

I thank you for carefully considering my comments and look forward to a revised version.