



TITLE Is viral metagenomics missing something?: A tale of Single-Virus Genomics

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It is well known that cultivation techniques inefficiently capture naturally occurring viral diversity in nature. To circumvent these limitations, past and current efforts based on metagenomics have significantly and unquestionably broadened our knowledge on viral genomics in marine ecosystems. However, even with expeditions such as *Tara Oceans*, the available reference viral genomes – cultivated and uncultivated – fail to recruit most viral metagenomic reads. Thus, there is agreement that much viral diversity remains to be discovered in the oceans. Recently, single-cell genomics has emerged as a powerful strategy to disentangle the genetic information of many abundant and ecologically significant prokaryotes in marine and other environments. In this study, we will show the results on the implementation and optimization of cutting-edge techniques based on single-cell genomics to uncultured marine viral assemblages from epi- meso- and bathypelagic samples collected in the Mediterranean Sea and South Atlantic. Our single-virus genomics data has enabled the discovery of some of the likely most abundant and ecologically relevant viral species at the global scale, such as vSAG 37-F6, which were overlooked by current methodologies. Finally, we will discuss why the genomes of these viral species have not been assembled by metagenomics. Our data point that microdiversity matters for metagenomic assembly.