Magroviruses and marine group II euryarchaeota co-adaptation to low salinity environment in the Pearl River Estuary

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Marine group II (MG II) Euryarchaeota are the most abundant heterotrophic planktonic archaea in the ocean and play important roles in global carbon cycle [1-2]. One unique feature of MGII is their sensitivity to freshwater invasion, with the cell abundance of MGII decreasing significantly below 15 per mil salinity. Metagenome data from Pearl River estuary (PRE) showed that a unique group, called MGII-PR is adapted in the low salinity environment. However, mechanisms underlying this adaptive physiology are not delineated. Here we applied a novel culture-independent, high-throughput sequencing approach to examine the role that MGII-specific viruses (magroviruses) play in the organisms' adaptation to low salinity. A total of 124 putative magroviral genomes were obtained from 15 PRE metagenomes. Five subclasses were identified based on phylogeny of the conservative DNA polymerase B gene. Examination of the relative abundance of magroviral genomes in the metagenomes showed that some lineages were specifically detected to the low salinity environment, indicating that they may predominately infect the MGII-PR group, thus possibly representing a newly evolved clade of magroviruses adapted to the low salinity. These magroviral contigs also encoded a number of heavy metal resistance protein CzcA, which may assist MGII's adaptation toward heavy mental contamination in the estuarine environment. This work provides insight into the role of magroviruses play in MGII's expansion in the estuarine environments characterized by salinity variation.

[1] Zhang (2015) *Frontiers in Microbiology*. **6,** 1108; [2] Rinke (2018) *ISME J.* **13,** 663-675