

A disastrous Changjiang River flood changed prokaryotic picoplankton assemblage in the surface East China Sea

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Abstract

In the summer of 2010, a disastrous floods occurred in the Changjiang River basin and subsequently resulted in a decline in salinity from 33 to 31 in the surface East China Sea (ECS). In this study, we investigated whether this unique hydrography shape prokaryotic picoplankton assemblage by pyrosequencing 16S rRNA genes (V6 to V9 region) in the samples collected from the surface ECS in the non-flooding summer 2009 and the flooding summer 2010. Based on a 3% distance threshold, a total of 4290 OTUs in 2009 and 8851 OTUs in 2010 were identified. While *Synchococcus* were the dominant picoplankton over the ECS in both summers, the increase of diversity (e.g. Shannon index from 2 to 4) and richness (e.g. Chao1 index from 1111 to 6137 at station19) in 2010 was observed. Our results suggested that the flood transiently changed the assemblage of prokaryotic picoplankton.