Ubiquitous microbial communities in river sediments actively govern organic matter decomposition, nutrient recycling, and remediation of toxic compounds. In this study, prokaryotic diversity in two major rivers in central Thailand, the Chao Phraya (CP) and the Tha Chin (TC) distributary was investigated. Significant differences in sediment physicochemical properties, particularly silt content, were noted between the two rivers. Tagged 16S rRNA sequencing on a 454 platform showed that the sediment microbiomes were dominated by *Gammaproteobacteria* and sulfur/sulfate reducing *Deltaproteobacteria*, represented by orders *Desulfobacteriales* and *Desulfluromonadales* together with organic degraders *Betaproteobacteria* (orders *Burkholderiales* and *Rhodocyclales*) together with the co-existence of *Bacteroidetes* predominated by *Sphingobacteriales*. Enrichment of specific bacterial orders was found in the clayey CP and silt-rich TC sediments, including various genera with known metabolic capability on decomposition of organic matter and xenobiotic compounds. The data represent one of the pioneered works revealing heterogeneity of bacteria in river sediments in the tropics.

Analysis of bacterial diversity by tagged 16S rRNA sequencing revealed enrichment of specific taxa in CP and TC rivers.