Multilevel analysis of the bacterial diversity along the environmental gradient Río de la Plata–South Atlantic Ocean

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Supplement 1.

Fig. S1. Phylogenetic relationships of 16S rRNA gene sequences from Río de la Plata bacterioplankton for (A) Actinobacteria, (B) Deltaproteobacteria, and (C) Acidobacteria. GenBank accession numbers are given for 1 representative per unique sequence type. Numbers in parenthesis indicate the number of identical sequences retrieved per phylotype. Clones are named according to their origin: riverine (ARTE3), frontal zone (ARTE5), marine water surface (ARTE9), and marine sediment (ARTE9Sed). Horizontal bar below each tree: 10% of estimated sequence divergence.
Fig. S2. Redundancy analysis triplot representing the variation in catalyzed reporter deposition-fluorescence \textit{in situ} hybridization (CARD-FISH) abundance data as a function of environmental and spatial parameters. Longitude and latitude coordinates were converted into Euclidean distances in km, where the largest dimension becomes $x$ and the second, perpendicular dimension becomes $y$. Ordination plot represents 62\% of the biological variation and 82\% of the taxa-environment relationships. Constrained ordination was overall significant (trace = 0.753, $F$-ratio = 2.44, $p = 0.020$) as determined by 1000 permutations of the data. S3 = Stn 3, S5 = Stn 5, etc.; sed = sediment; surf = surface; 4 m = 4 m depth, 5 m = 5 m depth, etc.; ROS537, CF319a, etc. were the probes used in CARD-FISH.