

TITLE: NEARLY IDENTICAL 16S RRNA SEQUENCES RECOVERED FROM LAKES IN NORTH AMERICA AND EUROPE INDICATE THE EXISTENCE OF CLADES OF GLOBALLY DISTRIBUTED FRESHWATER BACTERIA

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Abstract: We compared bacterial 16S ribosomal RNA gene sequences recovered from Lake Loosdrecht, the Netherlands, to reported sequences from lakes in Alaska and New York State. In each of the three lake systems, which differ in pH and trophic state, some sequence types were found without related sequences (sequence identity <90%) in the data sets from the other two systems. Two sequences in the Actinomycetes and Verrucomicrobia radiations were more closely related to sequences from the New York: lakes data set than to any other sequence in the global databases. However, the most striking similarities were found in the subdivisions alpha and beta of the Proteobacteria. In these subdivisions three different clusters of highly related bacteria were identified (97-100% sequence identity) that were represented in all three lake regions. The clusters contained no members other than freshwater bacteria. One cluster falls within a monophyletic aquatic supergroup that apparently diverged early in evolution into an exclusive freshwater cluster and an exclusive marine cluster, the so-called SAR11 cluster. The detection of these three bacterial clades in lakes distinguished by geographic distance as well as physical and chemical diversity suggests that these organisms are dispersed globally and that they possess unique functional capabilities enabling successful competition in a wide range of freshwater environments.