

Erratum

In L. Riemann and A. Winding, "Community Dynamics of Free-living and Particle-associated Bacterial Assemblages during a Freshwater Phytoplankton Bloom," *Microb Ecol* 42:274-285 (DOI: 10.1007/s00248-001-0018-8), a substandard version of Figure 1 appeared on page 278. The publisher wishes to apologize to the authors of the article, the readers, and the editors of the journal for this mistake. Below is the correct figure.

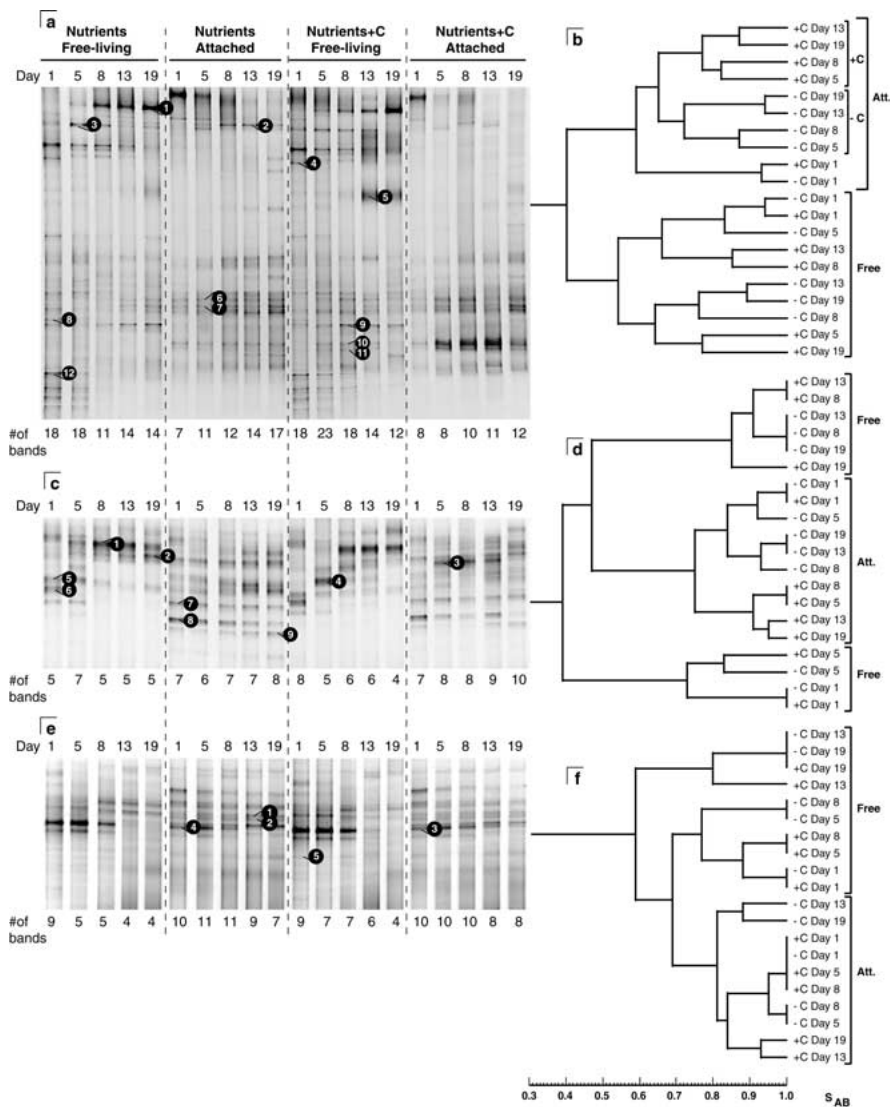


Fig. 1. Bacterial community composition profiles during the course of the phytoplankton bloom analyzed by DGGE of PCR amplified 16S rDNA using primers specific for Bacteria (a), Cytophaga-Flavobacterium (c), and α -Proteobacteria (e). The vertical denaturant gradients applied were 33–53%, 35–54%, and 33–60%, respectively. Excised and sequenced bands are numbered to the right of the lane. The relationships of excised band sequences to other sequences in the GenBank database are indicated in Table 3. Similarity analyses of the DGGE banding patterns are visualized as dendrograms (b, d, and f) to the right of each gel. The number of bands used in similarity analysis is indicated at the base of the dendrograms. +C and –C refer to with and without added carbon (glucose).