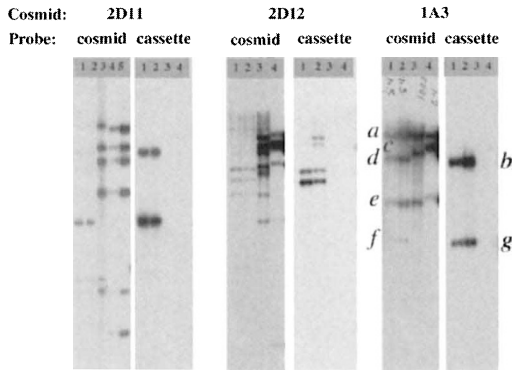

FIG. 2 GTA-mediated deletions in *R. capsulatus*. Each panel contains the following DNA samples restricted with *Eco*RV: lanes 1, 2, total DNA from two independent transductants; lane 3, total DNA from wild-type *R. capsulatus*; lane 4 (and 5 in the first panel), cosmid DNA. For each pair of panels, the hybridization probes were the total cosmid (left) or the antibiotic-resistance cassette (right), which contains a single *Eco*RV site. Discrepancies between fragment sizes in lanes 3 and 4 are due to vector sequences attached to *Rhodobacter* DNA in lane 4. For cosmids 2D11 and 2D12, most of the DNA present in the cosmids has been deleted from the transductants. For cosmid 1A3, fragments *a* (20 kb) and *e* (2 kb) cannot be deleted. Fragment *c* (11.5 kb) is disrupted by the cassette in the transductants, yielding fragments *d* and *f*; these fragments correspond in the right-hand panel to fragments *b* and *g*, which hybridize with the cassette probe, confirming the location of the disruption. The sum of the sizes of fragments *d* and *f* is 11–12 kb. Because the cassette size is 2 kb, the deletion in these transductants is only 1–2 kb. Fragment *c* is close to one end of cosmid 1A3. We believe that the recombination event creating these deletions began in the region of fragment *c* flanking the cassette and that the second crossover occurred in a region of partial homology located nearby, rather than at the far end of the cosmid where homology with the GTA-carried DNA is perfect.

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OLIVER REPLIES — Kumar and colleagues demonstrate that techniques now exist in a wide range of organisms which will permit the systematic analysis of gene function. Such an analysis is most meaningful in organisms such as *Saccharomyces cerevisiae*, whose genome has been completely sequenced, and it is encouraging to learn that an international effort to sequence the *Rhodobacter capsulatus* genome has begun.

The techniques outlined by Kumar *et al.* for *R. capsulatus* have quite exact analogues in other systems. In *S. cerevisiae*, the complete genome sequence, together with the organism's high efficiency and accuracy of mitotic recombination, is being exploited in a gene replacement strategy involving the polymerase chain reaction (PCR)[1], and resulting in the efficient deletion of individual open reading frames (ORFs).

Following the successes of our European Yeast Genome Sequencing Network[2], we have formed another scientific network (EUROFAN) committed to elucidating the function of novel yeast genes. In EUROFAN, we are exploiting a gene-by-gene deletion strategy, using PCR-mediated replacement and (as with *R. capsulatus*) Gm^r as a replacement marker[3,4]. Some laboratories are also performing more extensive chromosomal deletions using a combinatorial approach[5], which we term "mass murder".

A parallel European network is working on functional analysis in the Gram-positive bacterium *Bacillus subtilis*. This group is exploiting the operon organization common for bacterial genes by using a single plasmid insertion event to (simultaneously) disrupt an ORF, create a *lacZ* fusion with the upstream ORF, and place the downstream ORF under the control of a regulatable promoter (S. D. Ehrlich, personal communication).

As with more conventional approaches to defining gene function, different model organisms will be used for the systematic analysis of particular biological systems. Thus, *R. capsulatus* may be used for an exhaustive genetic analysis of nitrogen fixation or photosynthesis, while *S. cerevisiae* may be used to study functions that are peculiar to eukaryotes and thus not accessible to experimentation with a bacterium.

Within a given organism, it will be important to construct strains which have an improved potential for elucidating the function of novel genes in particular areas of biological activity[6]. More generally, there is a need to develop global approaches to the analysis of gene function, such that data from these model organisms can be exploited rapidly for analysing species that are less genetically malleable, but which have great biological, medical, agricultural or industrial interest. In particular, it will be important to develop strategies to permit the 'functional mapping' of the genomes of such species onto those of the model organisms.

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Contamination of drinking water

SIR — Until now, the availability of organic carbon has been considered the key factor controlling microbial regrowth in drinking-water networks[1,2]. This availability is considered to be a potentially serious problem, especially in boreal regions (northern Europe, Russia and North America) where surface water, and sometimes ground waters, contain high amounts of organic matter[3]. Natural organic matter acts as a substrate for microbial growth and, when water is used for public supply, disinfectants such as chlorine, hypochlorite and ozone are used. In addition to killing microorganisms, these oxidizing agents break down large organic compounds to smaller ones[4,5]. These compounds can be easily decomposed, further increasing microbial growth in the distribution system and thus impairing water quality. Because of this, considerable effort and resources have been deployed to remove the organic contaminants from drinking water. In the United States, for example, current annual expenditure exceeds 5 billion dollars[6].

Finnish drinking waters contain high concentrations of organic carbon (75–640 $\mu g\ C\ l^{-1}$) easily available to microorganisms. But because the available organic carbon correlates negatively with microbial growth, we investigated the possibility that other factors regulate this growth. In experiments with ground and surface waters, addition of phosphate alone to water increases microbial growth (the number of culturable bacteria) to the same extent as does a mixture of added inorganic nutrients (see figure).

The concentration of phosphate needed to enhance microbial growth is extremely low. When we added phosphate ranging from zero to 50 $\mu g\ l^{-1}$ to the processed drinking water supplying five waterworks (three with surface water and two with ground water), we found a hyperbolic relationship between $[PO_4\text{-}P]$ and microbial growth, with a half-saturation value of only 2–3 $\mu g\ PO_4\text{-}P\ l^{-1}$. Investigation of samples from four distribution

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