Targeted gene-replacement mutagenesis of
*dcrA*, encoding an oxygen sensor of the
sulfate-reducing bacterium *Desulfovibrio vulgaris* Hildenborough

Rongdian Fu† and Gerrit Voordouw

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A gene-replacement mutagenesis method has been developed for the
anaerobic, sulfate-reducing bacterium *Desulfovibrio vulgaris* Hildenborough
and used to delete *dcrA*, encoding a potential oxygen or redox sensor with
homology to the methyl-accepting chemotaxis proteins. A suicide plasmid,
containing a *cat*-marked *dcrA* allele and a counter-selectable *sacB* marker was
transferred from *Escherichia coli* S17-1 to *D. vulgaris* by conjugation. Following
plasmid integration the desired *dcrA* deletion mutant (*D. vulgaris* F100) was
obtained in media containing sucrose and chloramphenicol. Southern blot
screening was required to distinguish *D. vulgaris* F100 from strains in which
the *sacB* marker was inactivated by transposition of an endogenous IS
element. No anaerotactic deficiency has so far been detected in *D. vulgaris*
F100, which was found to be more resistant to inactivation by oxygen than the
wild-type. Increased transcription of the *rbo-rub* operon, located immediately
downstream from *dcrA*, was demonstrated by Northern blotting and may be
the cause of this unusual phenotype, in view of the recent discovery that Rbo
can complement the deleterious effects of superoxide dismutase deficiency in
*E. coli*.

**Keywords:** gene replacement, oxygen sensor, aerotaxis, superoxide dismutase,
*Desulfovibrio*

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**INTRODUCTION**

Anaerobic, sulfate-reducing bacteria such as those of the
genus *Desulfobulbus* are gradient organisms that position
themselves in niches with optimal chemical
parameters in soils and aquatic sediments. In sediments
these parameters (e.g. the concentrations of oxygen and
sulfide) vary over modest distances (0 to 20 cm) in the
direction perpendicular to the water–sediment interface
(Lillebaek, 1995). Steeper gradients and, as a consequence,
narrower distributions of bacteria were demonstrated in a 4 mm thick, photosynthetic biofilm,
in which sulfate-reducing bacteria were present. The
zone occupied by the bacteria shifted towards the base
when surface oxygen concentrations increased during
illumination (Ramsing et al., 1993), indicating bacterial
motility in response to light-induced changes in the
oxygen concentration gradient.

We have shown that *D. vulgaris* Hildenborough has at
least one chemoreceptor (*DcrA*) that serves as a sensor
of the oxygen concentration or redox potential of its
surroundings (Fu et al., 1994). Although its function in
chemotaxis remains to be demonstrated, DcrA has the
structural design of the methyl-accepting chemotaxis
proteins (MCPs) found in the *Enterobacteriaceae*, with
an N-terminal, periplasmic, sensing domain and a C-
terminal, cytoplasmic, signalling domain. The sensing
domain contains a c-type haem and the degree of methyl-
labelling of the signalling domain was found to be
influenced by addition of oxygen (decreased labelling)
and of the reductant dithionite (increased labelling).
Thus DcrA and the 15 other members of the *D. vulgaris*
chemoreceptor family (Deckers & Voordouw, 1994)
may help the organism to find its optimal ecological
niche.

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Elucidation of the function of DcrA requires a genetic approach in which the phenotypic change of a targeted gene replacement mutant is assessed relative to the wild-type. Unfortunately, the genetics of the sulfate-reducing bacteria have lagged far behind their physiological and biochemical characterization (Wall, 1993). Conjugal transfer of broad-host-range plasmids belonging to incompatibility group IncQ is presently the only gene transfer method available for *D. vulgaris* (Argyle et al., 1992; Powell et al., 1989; van den Berg et al., 1989). Attempts to use conjugation of suicide plasmids for construction of specific gene mutants of *D. vulgaris* were unsuccessful (van den Berg et al., 1989; van Dongen et al., 1994). The intriguing biochemical properties of DcrA provided a strong incentive to revisit the problem and plasmids used in this study are listed in Table 1. Bacterial strains, plasmids and growth conditions. Bacteria and plasmids used in this study are listed in Table 1. *Escherichia coli* strains were grown at 37 °C in tryptone/yeast extract (TY) medium or on TY agar plates with antibiotics as required (Voordouw et al., 1989). Liquid cultures of *D. vulgaris* were grown in medium C (Postgate, 1984) at 35 °C in an anaerobic hood (Forma Scientific) containing a gas mixture of 5% (v/v) H_2, 10% (v/v) CO_2 and 85% (v/v) N_2. Strains used for chemotactic studies were first grown on a medium C swarm plate (0.1%, w/v, agar) to select motile cells and then grown in liquid medium C or in TY medium overnight before use. Plating and colony purification of *D. vulgaris* was done by spreading diluted liquid cultures (containing approx. 50 c.f.u.) on medium E plates (Postgate, 1984), containing appropriate antibiotics, at 35 °C in the same gas atmosphere. *D. vulgaris* strains were stored as liquid cultures in medium B (Postgate, 1984) at 4 °C.

Mating of *D. vulgaris* with *E. coli* S17-1 was done on a medium E plate supplemented with 1.5 g KNO_3 L^-1 to allow growth of *E. coli* in the anaerobic hood (Powell et al., 1989). Integrant selection was on a medium E plate containing chloramphenicol (Cm; 10 μg ml^-1) and kanamycin (Km; 50 μg ml^-1). These concentrations of antibiotics were used throughout in both liquid cultures and plating media unless otherwise stated. Medium C or medium E containing Cm and sucrose (2.5 to 10%, w/v) were used for enrichment and selection of gene replacement mutants.

**Integration plasmid construction.** Plasmid pDr1 was cut with *Hind*III and *Bam*HI, and ligated after end-filling to remove these sites (Fig. 1). The resulting plasmid was cut with *Pst*I and *Mlu*I, and ligated with a *Bam*HI linker after end-

**Table 1. Bacterial strains and plasmids**

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant genotype and/or phenotype</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Desulfotiribio vulgaris</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hildenborough</td>
<td>NCIMB 8303; wild-type, Km^R^ Cm^R^ Suc^R^</td>
<td>Postgate (1984)</td>
</tr>
<tr>
<td>F1</td>
<td>With pADcrA2CTB integrated into the chromosome; Km^R^ Cm^R^ Suc^R^</td>
<td>This study</td>
</tr>
<tr>
<td>F1SR</td>
<td>All F1 derivatives with sacB gene mutated; Km^R^ Cm^R^ Suc^R^</td>
<td>This study</td>
</tr>
<tr>
<td>F100</td>
<td>dcrA gene replaced with a cat gene cassette from pUC19Cm; Km^R^ Cm^R^ Suc^R^</td>
<td>This study</td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TG2</td>
<td>Δ(lac–pro) supE thi hsdM hsdR recA F' (traD36 proAB lacZAM151::Tn7) in the chromosome; mobilizer strain</td>
<td>Sambrook et al. (1989)</td>
</tr>
<tr>
<td>S17-1</td>
<td>thi pro hsdR recA with RP4–2[Tc::Mu,Km::Tn7] in the chromosome;</td>
<td>Simon et al. (1983)</td>
</tr>
<tr>
<td>Plasmid</td>
<td></td>
<td></td>
</tr>
<tr>
<td>pADcr1</td>
<td>pUC8 containing the dcrA gene on a 3.4 kb Avar–EcoRI fragment; Ap^R^</td>
<td>Dolla et al. (1992)</td>
</tr>
<tr>
<td>pJK9Avac1</td>
<td>pUC8 containing the 5' end of the dcrA gene on a 1.4 kb Avar–EcoRI fragment; Ap^R^</td>
<td>Dolla et al. (1992)</td>
</tr>
<tr>
<td>pMOB2</td>
<td>Containing an oriT–sacBR cassette on a 4.8 kb NotI fragment; Km^R^</td>
<td>Schweizer (1992)</td>
</tr>
<tr>
<td>pNOT19</td>
<td>pUC19 with 10 bp NdeI–NotI adaptor in NdeI site; Ap^R^</td>
<td>Schweizer (1992)</td>
</tr>
<tr>
<td>pSUP104</td>
<td>Broad-host-range vector; Cm^R^</td>
<td>Priever et al. (1985)</td>
</tr>
<tr>
<td>pUC19</td>
<td>Cloning vector, pMB1 origin of replication; Ap^R^</td>
<td>Yanisch-Perron et al. (1985)</td>
</tr>
<tr>
<td>pUC19Cm</td>
<td>pUC19 containing in its <em>Bam</em>HI site a 1.4 kb SacII–TthIII fragment from pSUP104, carrying the cat gene; Ap^R^ Cm^R^</td>
<td>This study</td>
</tr>
<tr>
<td>pADcrA2</td>
<td>A derivative of pDr1, containing the flanking regions of the dcrA gene of which the PstI–MluI fragment has been replaced with a <em>Bam</em>HI linker; Ap^R^</td>
<td>This study</td>
</tr>
<tr>
<td>pADcrA2Cm</td>
<td>pADcrA2 with a cat gene inserted at the <em>Bam</em>HI site; Ap^R^, Cm^R^</td>
<td>This study</td>
</tr>
<tr>
<td>pADcrA2N</td>
<td>pADcrA2 with the NdeI site changed to NotI; Ap^R^</td>
<td>This study</td>
</tr>
<tr>
<td>pADcrA2CmN</td>
<td>pADcrA2N with a cat gene inserted at the <em>Bam</em>HI site; Ap^R^, Cm^R^</td>
<td>This study</td>
</tr>
<tr>
<td>pADcrA2CTB</td>
<td>A mobilizable derivative of pADcrA2CmN containing an oriT–sacBR cassette from pMOB2 in the NotI site; Ap^R^ Cm^R^ Suc^R^</td>
<td>This study</td>
</tr>
</tbody>
</table>
Deletion mutagenesis of *dcrA*

Deletion mutagenesis of *dcrA* pDcr1 1kb I I E Nd pADcrA2 LI Y A" (from pUCl9Cm) E Nd pADcrA2Crn bla down

Change the Ndel site to Not I site pADcrA2CmN P,H (from pMOB2)

**Fig. 1.** Construction of integration plasmids pADcrA2Cm and pADcrA2CTB. The thin line indicates DNA from pUC vector; bla, gene for β-lactamase; ori, pMB1 origin of replication (functional in *E. coli* only). The hatched boxes indicate DNA of the target gene region of *D. vulgaris*: 'up' and 'down', DNA upstream and downstream from the *dcrA* gene. The cat gene from pUC19Cm is indicated, as well as the NotI cartridge from pMOB2 containing the origin for conjugal transfer (oriT) and the counter-selectable gene sacB from *B. subtilis*. Relevant restriction sites are: B, BarnHI; E, EcoRI; H, HindIII; M, MluI; Nd, Ndel; No, Nott; P, PstI; Pv, Pvull; X, XbaI.

repair to form pADcrA2 (Fig. 1). A 1.4 kb BamHI fragment from pUC19Cm was then ligated to the BamHI site of pADcrA2 to form pADcrA2Cm. This plasmid was used directly, or after linearization with Ndel, for transformation of *D. vulgaris* by electroporation. For construction of the integration plasmid pADcrA2CTB, pADcrA2 was cut with PvuII, and the 2.4 kb vector fragment replaced with the equivalent PvuII fragment of pNOT19 to generate pADcrA2N. The BamHI fragment from pUC19Cm was next inserted to form pADcrA2CmN, followed by insertion of the 4.8 kb NotI cassette to give pADcrA2CTB (Fig. 1). After confirmation that the inserted sacB was functional in an *E. coli* strain containing this plasmid, it was used for conjugal transfer from *E. coli* S17-1 to *D. vulgaris*.

**Transformation of D. vulgaris by electroporation.** Plasmids pADcrA2Cm, pSUP104 prepared from *E. coli*, and pSUP104 prepared from *D. vulgaris* were used for transformation of *D. vulgaris* by electroporation as described by Rousset et al. (1991). A 100 ml culture of *D. vulgaris*, grown in medium C to OD^600_0.4, was suspended in a final volume of 200 µl. A 35 µl aliquot of this cell preparation and 3 µl DNA (1–2 µg) were transferred into an electroporation cuvette (Bio-Rad), and subjected to electric pulses (2.5 kV, 25 mF and 400–1000 Ω) in a Gene Pulse (Bio-Rad); 1 ml SOC buffer (Dower et al., 1988) was added to the cuvette immediately and the cell mixtures were allowed to recover at 37°C for 1 h. Aliquots of 200 µl were then plated onto medium E plates containing Cm. The plates were incubated for 3 to 7 d. TE buffer (10 mM Tris/ HCl, pH 7.4, 1 mM EDTA) replaced the DNA sample in negative controls.

**Conjugal transfer and selection for plasmid integration.** *E. coli* mobilizer strain S17-1 transformants were used as the donor for conjugal transfer of the integration plasmid pADcrA2CTB (Fig. 2, pA) into recipient *D. vulgaris* using a filter mating method adapted from Powell et al. (1989). Plasmid pSUP104 was similarly transferred to determine the conjugation efficiency. Overnight cultures of *D. vulgaris* in medium C (1 ml) and *E. coli* donor cells (0.2 ml) were mixed in a 1.5 ml microfuge tube under anaerobic conditions. After centrifugation the cell mixture was resuspended in 20 µl medium C, and spread onto a membrane filter (Millipore-MF, 0.22 µm; diameter 25 mm) placed on a medium E/nitrate mating plate. Following anaerobic incubation for 1 d the filter was transferred to a microfuge tube and the cells resuspended in 1 ml medium C. Aliquots of 10 µl, approx. 10^6 *D. vulgaris* cells, for transfer of pADcrA2CTB; 20 µl 10^-4 dilution for transfer of pSUP104) were plated onto medium E plates containing Km and Cm. These were incubated for 5 to 7 d and the Cm^- colonies that emerged were restreaked and analysed by Southern hybridization to verify and map plasmid integration.

**Sucrose sensitivity assays.** Aliquots (1 ml) of fresh, saturated cultures of colony-purified integrants were inoculated
Fig. 2. Strategy used for gene-replacement mutagenesis of dcrA in D. vulgaris Hildenborough through conjugation. Maps of the suicide integration plasmid pΔDcra2CTB (pΔ), and the dcrA target gene region in D. vulgaris wild-type (wt), the plasmid integrant D. vulgaris F1 (F1), and the desired gene-replacing second recombination product D. vulgaris F100 (F100) are shown with symbols for genes the same as in Fig. 1. The same restriction sites are indicated as in Fig. 1, as well as A, Accl and AvaI. The DNA regions used as probes in Figs 3, 5 and 6 (thick lines beneath the wt and F1 map), and the sizes of the relevant Act fragments, are also indicated. The homologous recombinations (+) are indicated as: 1, plasmid integrative recombination; 2, gene-replacing, second recombination; 3, reversing, abortive recombination.

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áganoerobically into screw-capped glass tubes (external diameter 13 mm) containing 5 ml medium C with Cm. Two tubes were inoculated for each culture and growth was monitored with a Klett meter. After 3 h, 0.67 ml w't're inoculated for each culture and growth was monitored of both tubes was then monitored regularly for 2 d.

Selection and enrichment of deletion mutants. Liquid enrichment of CmR SucR cells was done by inoculating 5 to 10 μl of the integrant culture into 5 ml medium C with Cm and sucrose (2.5–10%, w/v) and growing anaerobically for 7 to 9 d until saturation. Chromosomal DNA was prepared from these cultures and analysed by Southern blotting. Cultures containing the desired dcrA deletion were next subjected to colony purification on medium E plates with Cm, and DNAs obtained from liquid cultures of isolated colonies were again screened by Southern blot analysis.

Southern blot analysis. Chromosomal DNA of D. vulgaris was isolated by a mini-preparation protocol adapted from Marmur (1961), using 1-5 to 5 ml cultures. For verification of plasmid integration, undigested chromosomal DNA was run on an agarose gel and blotted onto a Hybond-N nylon membrane (Amersham). The blot was probed with 32P-labelled cat gene DNA, obtained as a 1-4 kb fragment from plasmid pUC19Cm. This targets the region indicated for the integrant strain F1 in Fig. 2 (F1, cat). For the integration mapping and identification of the gene-replacing second recombination, chromosomal DNA was digested to completion with Accl or EcoRI before agarose gel electrophoresis and blotting. The blots were analysed by hybridization with 32P-labelled DNA probes of the dcrA gene flanking regions: the AvaI-KpnI region upstream from the dcrA gene and the MluI–EcoRI region downstream from the dcrA gene (Fig. 2, F1, wt, ‘up’ and ‘down’), obtained as 0.58 kb BamHI–KpnI and 0.9 kb BamHI–EcoRI fragments from plasmids pJK9Aval and pΔDcra2, respectively. The blots were then stripped of these probes, and re-probed with 32P-labelled dcrA gene (Fig. 2, wt, dcrA), obtained as a 2.0 kb KpnI–MluI fragment from plasmid pΔcra1, to confirm the absence of dcrA. In addition, a 32P-labelled sacB gene (Fig. 2, F1, sacB), obtained as a 2.4 kb XbaI fragment from pMOB2, was used as a probe for analysing deletion and insertion mutations of the sacB gene. All the above Southern hybridizations were performed under highly stringent conditions as described elsewhere (Sambrook et al., 1989).

Growth properties and stability of the D. vulgaris F100 strain. The ΔdcrA strain, D. vulgaris F100, and the wild-type were grown separately in medium C in screw-capped tubes and their growth curves were determined by measuring the change in cell density with time using a Klett meter. For assessment of competitiveness under anaerobic conditions the F100 strain was co-cultured with the wild-type in medium C without Cm. Following mixing, a 5% inoculum was used and allowed to grow for 1–2 d before the next transfer. Chromosomal DNAs were prepared from a portion of the initial mixture of the two strains and from each of the subsequent co-cultures. The chromosomal DNAs were restricted with EcoRI, and the
digests were analysed by agarose gel electrophoresis and Southern blot hybridization with the downstream region probe to assess changes in the ratio of F100 to wild-type DNA. For assaying the differential stability under aerobic conditions, fresh cultures of F100 and wild-type were mixed at a ratio of 1:1 or 1:2 (v/v), and 1 ml of these mixtures was diluted immediately with 50 ml medium C, which was prepared aerobically and contained resazurin (0.5 mg l-1) as redox indicator. The diluted cell mixtures were then incubated aerobically in 50 ml Erlenmeyer flasks at 37 °C with vigorous shaking for up to 6 h. Aliquots of 1.5 ml were taken at different times and moved immediately into the anaerobic hood. To each of these samples, 30 to 60 pl 115 mM Na2S2O3 solution was added until the light blue colour disappeared. The samples were then re-grown anaerobically at 35 °C to saturation. Chromosomal DNAs were prepared from each of the re-grown samples to determine the ratio of the two strains by Southern blot analysis.

**Determination of the anaerotactic phenotype.** The anaerotactic behaviour of *D. vulgaris* F100 and wild-type was assessed by micro chamber and capillary tube assays. The micro chamber was made of a glass microscope slide and a coverslip (60 x 25 mm, 0.17 mm thick) separated with two narrow strips of a coverslip as spacers between them and sealed with nail-polishing solution along the longer axis to form a rectangular flattened chamber with two open ends. Motile cell samples in medium C or TY medium were transferred out of the anaerobic hood in capped microfuge tubes before use. About 100 pl of the anaerobic preparation of motile cells was transferred into the micro chamber with a pipette to form a continuous liquid phase along the chamber with a liquid–air interface at both ends. The aerotactic behaviour of motile cells near the liquid–air interface was then examined under a Nikon Labophot light microscope with dark-field illumination.

The capillary tube assay was used to examine the effect of changing the gas phase on cell migration near the medium–gas interface. Micro-measuring capillary tubes (20 pl capacity, 100 mm long; Fisher, catalogue no. 21-164-2D) were autoclaved before use. Two capillary tubes were filled anaerobically with a 5 cm long column of a motile cell preparation of *D. vulgaris* wild-type or F100 by the capillary effect and sealed at the medium phase end with Plasticine (Canada Games Company). Both tubes were then moved out of the anaerobic hood and exposed to air to allow anaerotactic banding of the cells. The tubes were then lined up and loosely connected to a rubber tubing leading to the gas cylinders (either nitrogen or oxygen; Fig. 7a). A gas humidifier containing water was added to the gas line to prevent sample evaporation. Anaerotactic behaviour was examined either visually or with the Nikon Labophot light microscope, which had a narrow slit light stop inserted into the light path to alter the illumination for better visualization of bacteria in the round-shaped capillary tubes.

**Northern blot analysis.** The effect of deletion of the *dcrA* gene on transcription of the *rbo-rub* operon was investigated by Northern blot assays. *D. vulgaris* wild-type and F100 were grown in 12 ml medium C overnight. Aliquots of 2 ml of these cultures were transferred to 12 culture tubes, which were moved out of the anaerobic hood. One sample of each strain was used immediately for total RNA preparation. The others were exposed to oxygen by shaking in air at 300 r.p.m. Total RNA was extracted from each sample with a rapid isolation protocol (Reddy & Gilman, 1990). The total RNA preparations were analysed by Northern hybridization (Brown, 1990). Following electrophoresis the gel was stained with ethidium bromide and photographed to ascertain equality of RNA loading from the intensities of the bands for 23S, 16S and 5S rRNA. The RNA was then transferred to a Hybond-N membrane and hybridized with the 32P-labelled insert of plasmid pRbol (Brumlik & Voordouw, 1989).

Following washing the blot was exposed to the phosphor-imaging plate of a Fuji BAS1000 Bioluminizing Analyzer for quantification of *rbo-rub* mRNA.

**RESULTS**

**Electroporation of *D. vulgaris***

Electroporation of *D. vulgaris* with circular or linearized pADcrA2Cm failed to give CmR transformants. Electroporation of the broad-host-range vector pSUP104 isolated from *E. coli* also failed to give CmR transformants, although they could be readily obtained by conjugation (van den Berg et al., 1989; this work, Table 2). The results indicated either that *D. vulgaris* is not readily transfected by electroporation or that a restriction barrier prevents the establishment of foreign DNA. In order to distinguish between these two possibilities, we isolated native pSUP104 from a *D. vulgaris* transconjugant. Electroporation of this native pSUP104 gave approximately 102 transformants per µg DNA, while no transformants were obtained upon electroporation of *E. coli* pSUP104 under the same conditions. This result suggested that a restriction/methylation system in *D. vulgaris* prevents the establishment of foreign DNA transferred by electroporation. We therefore resorted to the conjugal transfer approach in which the DNA being transferred is not as susceptible to host restriction (Schweizer, 1992).

**Conjugal transfer and integration of a suicide plasmid**

Plasmid pADcrA2CTB was transferred by conjugation from *E. coli* S17-1 to *D. vulgaris*. A positive control (matting with *E. coli* S17-1[pSUP104]), and a negative control (matting with nontransformed *E. coli* S17-1) were also done. Following spreading of the mating mixtures onto medium E plates containing Km and Cm, pSUP104 transconjugants appeared after 3 d while pADcrA2CTB integrants (*D. vulgaris* F1) were obtained at a frequency of 1 x 10-6 per recipient after 4–5 d anaerobic growth (Table 2). Two colonies appeared in plates spread with the negative control mating mixture. Integration of the suicide plasmid was verified by hybridization of the cat gene probe to the undigested chromosomal DNA (data not shown). Chromosomal DNAs from two of the integrants were further analysed. Digestion with AccI and hybridization with the flanking region probes gave 0-9 and 1-1 kb fragments for *D. vulgaris* wild-type (Fig. 3, lane 2). In the two integrants the 1-1 kb fragment was missing and three new hybridization bands appeared (Fig. 3, lane 3: 1-3, 2-2 and 4-5 kb), indicating that these two integrants were identical, with integration of pADcrA2CTB through the downstream region of *dcrA* as illustrated in Fig. 2(1).
Table 2. Results of conjugal transfer and selection of integrants

<table>
<thead>
<tr>
<th>Plasmid for transfer</th>
<th>Growth time* (d)</th>
<th>Apparent conjugal transfer frequency (no. of transconjugants per recipient cell)</th>
<th>Apparent integration frequency (no. of integrants per recipient cell)</th>
<th>Integration frequency† (no. of integrants per transconjugant cell)</th>
</tr>
</thead>
<tbody>
<tr>
<td>pSUP104</td>
<td>3</td>
<td>2.3 x 10^{-4}</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>pαDcrA2CTB</td>
<td>4-5</td>
<td>ND</td>
<td>1.1 x 10^{-7}</td>
<td>4.7 x 10^{-6}</td>
</tr>
</tbody>
</table>

ND, Not determined; NA, not applicable.

* Time required for appearance of CmR colonies on plates containing 10 μg Cm ml^{-1}.

† Estimated by dividing the number of integrants per recipient cell of pADcrA2CTB by the number of transconjugants per recipient cell of pSUP104.

‡ Result is the mean of four experiments.

This integrant, D. vulgaris F1, was used for further manipulation.

Effect of sucrose and Cm on the growth of D. vulgaris F1

Cm up to 10 μg ml^{-1} had no severe effects on growth of F1. However, in the presence of both sucrose and chloramphenicol the cell density decreased significantly after one generation (Fig. 4), indicating the occurrence of cell lysis. Addition of sucrose to wild-type D. vulgaris samples had no such effect. These results indicated that the sacB gene was expressed in D. vulgaris F1 and that its product, levansucrase, was toxic to D. vulgaris in the presence of sucrose, as has been demonstrated in E. coli (Steinmetz et al., 1983), allowing sacB to be used as a counter-selectable marker to select for the rare, gene-replacing, second recombination (Fig. 2, 0).

Use of 10 μg Cm ml^{-1} in both liquid and agar media was found to be the appropriate concentration to select D. vulgaris F1 from the wild-type. D. vulgaris F1 grew and maintained high plating efficiency, while the wild-type did not grow provided that a cell density of no more than 10^5 cells cm^{-2} was used for plating and that no
more than \(10^7\) cells ml\(^{-1}\) (1% inoculum) was used for liquid culture. Hence, Cm at 10 \(\mu\)g ml\(^{-1}\) and a limited volume of inoculum were used in combination with sucrose in the next step to select for conversion of \(D. vulgaris\) F1 to the gene replacement mutant F100 and against conversion to wild-type resulting from plasmid excision.

**Sucrose and Cm enrichment of the gene-replacing second recombination**

\(D. vulgaris\) F1 was first grown to saturation in liquid medium C containing Cm to allow more recombination events to happen (Fig. 2, (2)) prior to selection of the desired \(D. vulgaris\) F100. Small inocula (0.1 to 0.2%, v/v) in medium C with Cm and sucrose were then grown to saturation in 7 d. Genotypic changes in the population were identified by Southern blot analysis. Deletion of \(dcrA\) was expected to change the AccI fragment size, hybridizing with the ‘up’ probe, from 0.9 and 4.5 kb in F1 to 0.95 kb in F100 (Fig. 2) and a variable fraction of this F100-specific band was found after the enrichment (Fig. 3, lanes 4 to 12). The rest of the population showed mainly enrichment of the desired gene-replacing F1 control (Fig. 3a, lanes 4, 6, 9 and 11). The remainder had the same restriction pattern as the wild-type. Sucrose concentrations of 2.5, 5 and 10% (w/v) were all found to be effective in enrichment of the desired gene-replacing second recombination.

After plating one of the enriched cultures on a medium E plate containing Cm, 117 colonies were obtained. From this plate 30 colonies were randomly selected and grown to saturation in medium C with Cm. Southern blot analysis of their chromosomal DNAs with the \(dcrA\) flanking region probes indicated 14 of these to have the restriction pattern expected for the \(dcrA\) gene deletion strain \(D. vulgaris\) F100 (Fig. 5a, lanes 3, 5, 7, 8 and 10). The remainder had the same restriction pattern as the \(D. vulgaris\) F1 control (Fig. 5a, lanes 4, 6, 9 and 11). Deletion of the \(dcrA\) gene was proven unambiguously by stripping the blot shown in Fig. 5(a) of the flanking region probes and re-hybridizing with a \(dcrA\) probe (Fig. 5b). \(D. vulgaris\) F100 clearly lacks the \(dcrA\) gene (Fig. 5b, lanes 3, 5, 7, 8 and 10) which is present in the wild-type (Fig. 5b, lane 1). \(D. vulgaris\) F1 (lane 2), and the remaining Cm\(^R\) Suc\(^R\) strains denoted \(D. vulgaris\) F1SR (Fig. 5b, lanes 4, 6, 9 and 11). The \(\Delta dcrA\) strain \(D. vulgaris\) F100 is cat-gene marked (Cm\(^R\)) but was stable without Cm selection.

**Inactivation of \(sacB\) by an IS element**

The possibility that the \(D. vulgaris\) F1SR strains harboured a modified \(sacB\) gene was investigated by stripping and re-probing the blots with the \(sacB\) gene probe. While, as expected, none of the 14 \(\Delta dcrA\) strains (\(D. vulgaris\) F100) showed hybridization to the \(sacB\) probe (Fig. 5c, lanes 3, 5, 7, 8 and 10), all of the 16 \(D. vulgaris\) F1SR strains showed the hybridization, as did their parent \(D. vulgaris\) F1, indicating that none of these became sucrose-resistant by plasmid excision. Among these 16 \(D. vulgaris\) F1SR strains, 10 gave a 3.1 kb \(sacB\)-hybridizing AccI fragment (Fig. 5c, lanes 4 and 6) as did the parent F1 (lane 2), while six of them displayed two AccI fragments with a combined size of 4-3 kb (Fig. 5c, lanes 9 and 11), indicating an insertion of a 1.2 kb DNA element with one AccI site (Fig. 5d). Cloning and sequencing of the modified \(sacB\) gene from one of these \(D. vulgaris\) F1SR strains has indicated that the 1.2 kb fragment is a novel IS element of \(D. vulgaris\) (unpublished).
Changes in oxygen sensitivity of D. vulgaris F100 vs wild-type

The growth curve of the F100 strain was identical to that of the wild-type (data not shown), confirming that dcrA is not essential for growth under anaerobic conditions. This was also shown in three differential growth experiments in which the wild-type and F100 were co-cultured. The chromosomal DNA ratio of F100 to wild-type remained the same after five sequential subcultures in 7 d, approximately 2.5 generations (Fig. 6a, b), indicating that F100 was as competitive as the wild-type under anaerobic growth conditions without Cm selection.

To allow the determination of small differences in oxygen sensitivity, a mixture of the two strains was aerated to ensure that both strains received identical aeration treatment. Survival of wild-type vs F100 was determined by restoring anaerobic conditions and by regrowing the diluted samples to saturation before the genomic DNA ratio of the two strains was determined by Southern blot analysis. As shown in Fig. 6(c, d), exposure of a wild-type–F100 mixture to oxygenated medium C resulted in a significant decrease of the ratio of recovered wild-type to F100 cells after 5 h. The same results were obtained with different initial mixing ratios. Even when twice as many wild-type as F100 cells were used, the ratio of recovered wild-type to F100 cells decreased (Fig. 6d), indicating that the dcrA deletion strain F100 is more resistant to inactivation by aeration than the wild-type.

Anaerotaxis behaviour

Anaerotactic movement of D. vulgaris, defined as movement away from a liquid–air interface, was first observed by Johnson et al. (1995), who suggested that positive aerotaxis (movement towards a liquid–air interface) may also be present, causing the cells to concentrate at an optimal, low oxygen concentration. Motile cells of D. vulgaris near the medium–air interface of the microchamber also moved towards the inner area, leaving a clear zone and forming a dense band of cells (not shown). This banding effect was observed for both D. vulgaris wild-type and F100. To confirm that this behaviour was due to anaerotaxis, capillary assays were conducted. When a capillary filled anaerobically with a motile cell preparation was opened to the air, the banding appeared within 20 min about 2 mm away from the liquid–air interface. The position shifted further away from the interface with time. No banding was observed in control capillaries which were protected from exposure to air, either by keeping them inside the anaerobic hood or by sealing them anaerobically with petroleum jelly before transfer. These results indicate that band formation was air-dependent. In capillary...
assays with a gas shift the open ends of capillaries were perfused with pure nitrogen or pure oxygen (Fig. 7a). The changes in banding position from the meniscus were visually recorded with a ruler. Cell bands of both D. vulgaris wild-type and FlOO strains, formed by exposure to air, shifted further away from the meniscus when oxygen was perfused into the capillaries (Fig. 7b, capillaries 2 and 4) while they remained unchanged in the nitrogen control samples (Fig. 7b, capillaries 1 and 3). When oxygen was later introduced into the nitrogen control samples, the bands moved again further away from the meniscus (Fig. 7b, capillaries 1 and 3).

**Northern blot analysis**

Recent work by Pianzzola *et al.* (1996) has shown that the product of the rbo gene, which is present in an operon together with the gene for rubredoxin (rub) immediately downstream from dcrA, can complement the deleterious effects of sod deficiency in E. coli. In order to assess whether the increased oxygen resistance of D. vulgaris FlOO is due to altered rbo gene expression, we compared levels of rbo-rub mRNA. The major species of rbo-rub mRNA detected had a length of 700 nt in both D. vulgaris wild-type and FlOO, in good agreement with the size reported before (Brumlik & Voordouw, 1989). A minor species of larger size (approx. 3000 nt) was also present. The 700 nt transcript was expressed at a fivefold higher level in D. vulgaris FlOO compared to the wild-type under anaerobic conditions (Fig. 8, lanes 2 and 1; the same result was obtained in two experiments). Exposure to air for 5 or 30 min had no effect on the transcription level of the rbo-rub operon in D. vulgaris FlOO, while a 50% increase was recorded for the wild-type (Fig. 8, lanes 3 to 6).

**DISCUSSION**

Prior to this work, only Rousset *et al.* (1991) had succeeded in using marker-exchange mutagenesis in *Desulfovibrio*, for construction of a [NiFe] hydrogenase gene deletion mutant of *D. fructosovorans*. These authors used electroporation to deliver the non-replicating plasmid and penicillin enrichment for selection of the gene-replacing double recombination. The probable presence of a restriction/modification system, as documented here, prevented use of this approach for D. vulgaris Hildenborough. Attempts to electroporate plasmids into *D. desulfuricans* were also unsuccessful (Wall *et al.*, 1993). This may also be due to a restriction problem; for example *D. desulfuricans* strain Norway harboura the restriction endonuclease DdeI (Sznyter
The conjugal transfer method with sacB counter-selection used here is less affected by host restriction (Schweizer, 1992) and does not require a specific phenotype of the target gene for selection. The physiological function of other genes from *D. vulgaris* Hildenborough which have been cloned and sequenced (Voordouw, 1995) can now, in principle, be tested with this approach.

Use of the * Bacillus subtilis* sacB gene as a counter-selectable marker for gene-replacement mutagenesis has been successful in many other Gram-negative bacteria (Cai & Wolk, 1990; Kamoun *et al.*, 1992; Quandt & Hynes, 1993; Ried & Collmer, 1987; Schweizer, 1992; Schweizer & Hoang, 1995). The sacB gene encodes levansucrase, which is toxic to the host in the presence of sucrose (Steinmetz *et al.*, 1983; Gay *et al.*, 1985). The occurrence of spontaneous sacB mutations has also been demonstrated in other systems (Cai & Wolk, 1990; Kamiga *et al.*, 1991) and necessitates additional screening either by monitoring the loss of an antibiotic resistance marker or, as we have done, by Southern blotting. We found a high frequency of sacB mutations (50% of all CmR SucR colonies), of which 40% were due to insertional inactivation by an endogenous IS element. The development of an efficient selection system was essential for the success of our method, because conjugal-transfer-based gene replacement requires two homologous recombination events that take place at low frequency, usually between $10^{-9}$ and $10^{-4}$ (Blomfield *et al.*, 1991; Kamiga *et al.*, 1991). Unfortunately, *Desulfovibrio* spp. have a high level of endogenous resistance to many antibiotics and many of the commonly used antibiotic resistance genes do not perform well in these bacteria (van Dongen *et al.*, 1994). The CmR marker is the only reliable marker found so far for selection in *D. vulgaris* Hildenborough provided that selection of plasmid integrants is done at a Cm concentration of $10 \mu g \text{ ml}^{-1}$. At lower concentrations of Cm, for example 5 $\mu g \text{ ml}^{-1}$ (van den Berg *et al.*, 1989), colonies develop that lack the cat gene. Use of a recipient cell density in excess of $10^9$ cells cm$^{-2}$ also caused wild-type cells to develop into colonies. These observations are consistent with the fact that Cm is only bacteriostatic and can be detoxified by cat-minus anaerobes through a ferredoxin- or NADH-dependent reduction of its aryl nitro group (Argyle *et al.*, 1992; Staudenbauer & Dabbert, 1993). This problem may be aggravated when Km selection against the *E. coli* donor cells containing the cat gene on a multicopy plasmid is inefficient.

The deletion of the dcrA gene does not affect growth of *D. vulgaris* under anaerobic conditions (*Fig. 6a, b*). The earlier finding, that the degree of methyl labelling of DcrA's signal transduction domain decreased in response to oxygen (Fu *et al.*, 1994), led to the hypothesis that DcrA allows *D. vulgaris* to recognize oxygen as a chemotactic repellent, i.e. repellents also decrease the degree of methyl labelling of MCPs in the *Enterobacteriaceae* (MacNab, 1987). This hypothesis would be confirmed if deletion of DcrA were to abolish the anaerotactic response (the fleeing from oxygen).

Measurement of the effect of oxygen on *D. vulgaris* chemotaxis is complicated by the fact that oxygen may have pleiotropic effects. Oxygen can react directly with the sulfide formed by sulfate respiration, creating novel gradients, and some sulfate-reducing bacteria, including *D. vulgaris*, have been reported to use oxygen as the terminal electron acceptor (Dilling & Cypionka, 1990). With these reservations in mind, the data indicate that the dcrA mutant retains the anaerotactic phenotype (*Fig. 7b*). This observation rules out DcrA as the sole determining factor in *D. vulgaris* anaerotaxis. Recent work on a novel aerotaxis receptor in *E. coli* has shown that its deletion abolished aerotaxis only after a second gene was also deleted (B. L. Taylor, personal communication). Anaerotaxis of *D. vulgaris* may similarly be determined by multiple genes from the large dcr gene family (Deckers & Voordouw, 1994).

The possibility that DcrA serves as a sensor in other cellular processes should also be considered. It is of great interest in this respect that the gene for the oxygen or redox potential sensor DcrA is followed immediately by the gene for Rbo. The transcriptional start of the rbo-rub operon is located only 300 bp downstream from the 3' end of the dcrA gene and the operon is transcribed in the same direction (Brumlik & Voordouw, 1989; Della *et al.*, 1992). A role for Rbo in repair and/or prevention of oxidative damage can be inferred from the work of Pianzola *et al.* (1996), who cloned a DNA fragment from the sulfate-reducing bacterium *Desulfococcus baarsii* by functional complementation of an *E. coli* strain can only grow anaerobically due to mutations in the sodA, sodB and recA genes. The cloned fragment was found to contain the rbo gene, which restored the capacity of aerobic growth. The rbo gene from *D. vulgaris*, cloned by Brumlik & Voordouw (1989), also complemented *E. coli* sod deficiency (Pianzola *et al.*, 1996). The rbo gene with which rbo forms an operon in both *Desulfocaldus baarsii* and *D. vulgaris* is not required for the complementation in *E. coli*. The Northern blot data indicated that under anaerobic conditions *D. vulgaris* F100 overexpresses rbo-rub mRNA about fivefold relative to the wild-type. This could explain the increased oxygen survival of *D. vulgaris* F100. An intriguing possibility is that DcrA is involved in regulation of the expression of the rbo-rub operon through a mechanism that represses transcription under anaerobic conditions and allows increased transcription under conditions of oxidative stress. Transcription levels rise somewhat in wild-type cells upon oxygenation (*Fig. 8*) but do not reach the level found in *D. vulgaris* F100, irrespective of aeration. This may mean that the oxidative stress signal that leads to full induction of rbo transcription is not mere aeration and is currently not known. Elucidation of the role and regulatory interactions of the dcrA-rbo-rub region in *Desulfovibrio* spp. thus requires more experimentation. The mutagenesis method described here will be a help in future work that focuses on determining the physiological role of Rbo by deletion of its gene from *D. vulgaris*. 1824
ACKNOWLEDGEMENTS

We thank H. P. Schweizer for providing plasmids pMOB2 and pNOT19, B. L. Taylor and coworkers for discussions on aerotaxis assays, and D. Touati for communicating her findings and for establishing that D. vulgaris rbo complements superoxide dismutase deficiency of E. coli. We thank Ms M. Jiang for technical assistance in Northern blot hybridization experiments. This work was supported by a grant from the Natural Science and Engineering Research Council of Canada (NSERC) to G.V.; R.F. was the recipient of a Full-time Postgraduate Studentship award from the Alberta Heritage Foundation for Medical Research.

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Received 11 October 1996; revised 11 December 1996; accepted 20 December 1996.