

Four PCR primers necessary for the detection of periplasmic nitrate reductase genes in all groups of Proteobacteria and in environmental DNA

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Abstract

Generic primers are available for detecting bacterial genes required for almost every reaction of the biological nitrogen cycle, the one notable exception being *napA* (gene for the molybdoprotein of the periplasmic nitrate reductase) encoding periplasmic nitrate reductases. Using an iterative approach, we report the first successful design of three forward oligonucleotide primers and one reverse primer that, in three separate PCRs, can amplify *napA* DNA from all five groups of Proteobacteria. All 140 *napA* sequences currently listed in the NCBI (National Center for Biotechnology Information) database are predicted to be amplified by one or more of these primer pairs. We demonstrate that two pairs of these primers also amplify PCR products of the predicted sizes from DNA isolated from human faeces, confirming their ability to direct the amplification of *napA* fragments from mixed populations. Analysis of the resulting amplicons by high-throughput sequencing will enable a good estimate to be made of both the range and relative abundance of nitrate-reducing bacteria in any community, subject only to any unavoidable bias inherent in a PCR approach to molecular characterization of a highly diverse target.

The missing link in our ability to detect nitrogen cycle genes in community DNA

The availability of oxygen, phosphate, sulfate and reduced carbon compounds are major determinants of the balance between beneficial and detrimental chemical changes in soils, sediments and water. However, the productivity of many ecosystems, especially soils, is limited by biologically available nitrogen. Micro-organisms, especially bacteria, are critical in determining the balance between nitrification, denitrification, nitrate assimilation, anammox, nitrogen fixation and the reduction of nitrate to ammonia. The range of species involved in these processes is extremely diverse. Many groups of bacteria synthesize multiple enzymes for each reaction. Nevertheless, considerable progress has been achieved in developing oligonucleotide PCR primers to detect, amplify and quantify the capacity of any given community to catalyse each process. A notable exception to this generalization is the current inability to detect the complete range of genes encoding periplasmic nitrate reductases from Gram-negative bacteria.

Three types of bacterial nitrate reductase have generally been recognized, though detailed analysis of their subcellular location and associated electron transfer components justifies more detailed subdivisions. Assimilatory nitrate reductases located in the cytoplasm catalyse the first step in nitrate reduction to ammonia, which is then used for amino acid biosynthesis. During anaerobic growth, respiratory

nitrate reductases typified by the NarGHI (membrane-associated, energy-conserving nitrate reductase) complexes from *Escherichia coli* and *Paracoccus denitrificans* are associated with the cytoplasmic membrane where they conserve energy released during nitrate reduction as proton motive force [1,2]. Although the active site of most NarG proteins is located in the cytoplasm, exceptions to this have recently been recognized, creating a further subdivision of nitrate reductase, typified by Nar from various Archaea (reviewed in [3]). The third group, the periplasmic nitrate reductases, are biochemically and genetically distinct from the other groups. They fulfil diverse roles: the maintenance of redox balance during growth on reduced carbon sources [4–10]; maintenance of redox balance during photosynthetic growth [11]; scavenging low concentrations of nitrate [12]; or nitrate respiration in the first stage of denitrification or nitrate reduction to ammonia [5,13,14].

Due to their diverse roles, there is much greater sequence variation in *napA* genes encoding the periplasmic nitrate reductases than those of the assimilatory and membrane-associated nitrate reductases. Consequently, oligonucleotide primers designed for detecting *napA* from some groups of bacteria are unsuitable for detecting *napA* in other groups. Based on very limited sequence data available at the time, primers were designed that successfully amplified *napA* sequences from DNA isolated from soils, but the range of bacteria detected was limited [15]. Conversely, primers that amplified *napA* from the δ -proteobacterium *Desulfovibrio desulfuricans* strain 27774 would not recognize *napA* from *E. coli* or *P. denitrificans* [16]. The Phillipot group subsequently redesigned primers suitable for detecting a

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wider range of α -, β - and γ -proteobacteria and have used them to estimate the balance between different groups of nitrate-reducing bacteria in community DNA from 18 different environments [17,18]. However, none of the primers currently available are suitable for detecting all known *napA* sequences represented in the DNA sequence databases. This review describes a strategy to overcome this limitation, its successful application and its limitations.

A standardized PCR protocol to detect periplasmic nitrate gene products

The PCR protocol was developed using as templates chromosomal DNA isolated from *E. coli* K-12, *D. desulfuricans* 27774, *Campylobacter jejuni*, *Haemophilus influenzae*, *Habella chejuensis*, *Wolinella succinogenes*, *Campylobacter lari*, *Campylobacter hominis*, *Campylobacter curvus*, *Campylobacter concisus*, *Bortetella bronchiseptica*, *Bradyrhizobium japonicum* and *Paracoccus pantotrophus*. DNA sequences of species that were known to contain the *napA* gene were downloaded from the NCBI (National Center for Biotechnology Information) database. They were aligned with the ClustalX tool and displayed by the BoxShade tool in order to detect conserved regions. Degenerate primers were designed based on these alignments and produced by Alta Biosciences.

After many preliminary experiments that included trials with hot start, touchdown and gradient PCR, a standardized touchdown protocol was developed that included a 5 min denaturation step at 95°C followed by 32 touchdown cycles in which the annealing temperature was decreased by 0.5°C per cycle from 55°C down to 39°C. Samples were held at the annealing temperature for 1 min. In each subsequent cycle, the sample was denatured for 30 s at 95°C and extended for 150 s at 72°C. The amount of product was amplified in 30 steps in which the denaturation and extension steps were exactly as in the touchdown cycles, but primers were annealed for 1 min at 39°C. After a final 10 min extension step at 72°C the sample was stored at 4°C. Products were checked by electrophoresis in a 100 ml 1% agarose gel.

Limited applicability of previously described primers

In preliminary experiments, various primers described in the literature or developed in-house were tested for their ability to direct the synthesis of a limited range of *napA* target genes. The design of primers V16 and V17 was based on the known sequences of *napA* genes from a limited number of bacteria that included *E. coli* and *P. denitrificans* [15] (Figure 1). The ability of these primers to recognize these templates, but not *napA* from *D. desulfuricans* strain 27774, was confirmed. Similar results were obtained with related primers described by Bru et al. [17]. Conversely, primers DdV16 and DdV67, which were used in the determination of the sequence of

D. desulfuricans nap operon [16], were unable to recognize *E. coli* or *P. denitrificans* templates.

Design of primers that recognize both *D. desulfuricans* and *E. coli napA* templates

We then attempted to design universal primers that would amplify *napA* DNA from all groups of proteobacteria by comparing the sequences of highly divergent *napA* genes from 3 α -, 3 β -, 6 γ -, 2 δ - and 4 ϵ -proteobacteria (Figure 1). Although very few regions of sequence identity were found, two primers resulting from this analysis, 1173b and R2, were predicted to amplify *napA* fragments from both *E. coli* and *D. desulfuricans*. This prediction was confirmed. However, none of the primer combinations available recognized *napA* genes in *C. jejuni* or *C. lari*.

Design of primers that recognize *napA* templates from all groups of proteobacteria

Further analysis revealed that this limited range of sequences could be split into two subgroups within which were more regions of sequence similarity. Two pairs of degenerate primers based on these regions of similarity were designed. Primers SF1173d and SR2294 successfully amplified the expected *napA* fragments of both *E. coli* and *D. desulfuricans* DNA, but failed to recognize *C. jejuni* DNA (Figures 1 and 2 and Table 1). Primers LF716 and LR1837 amplified *napA* fragments from both *E. coli* and *C. jejuni* DNA, but not from *D. desulfuricans* DNA. When primer SF1173d was combined with LR1837, the expected 0.5 kb fragments were generated, but no product was obtained with *D. desulfuricans* DNA as template (Figure 2). The primer pair LF716 and SR2294 generated the expected 1.5 and 1.8 kb products with *E. coli* and *C. jejuni* DNA templates (Figure 2). However, not every expected product was generated, and some templates directed the synthesis of more than one product.

The sequence analysis was then extended to all 140 *napA* sequences from 70 bacterial species in the NCBI database in February 2010. Each of the four primers was checked against the database sequences to determine whether there was a mismatch in the last six bases at the 3'-end of each primer sequence that might prevent effective amplification of the required fragment (Table 1). This analysis revealed only three sequences, those from *Geobacter lovleyi*, *C. lari* and *C. hominis*, that failed to meet the stringent criteria set with the forward primers SF1173d and LF716. One of the reverse primers, SR2294, was predicted to recognize every *napA* sequence in the database, and was therefore potentially truly generic. Furthermore, this primer allowed problems predicted when using primer LR1837 to be avoided (Table 1).

In a final attempt to design a universal forward primer, alignments were first generated for all five subdivisions of proteobacteria, with a further alignment of sequences that posed the greatest problems. This resulted in the design of

Figure 1 | Oligonucleotide primers used to detect *napA* genes in all groups of proteobacteria

The top five segments of the Figure show the sequences of five of the primers used to develop the generic protocol for the detection of *napA* in various groups of proteobacteria above the typical sequences they were designed to recognize. The lower diagrams show where within the *napA* genes of *Escherichia coli*, *D. desulfuricans* and *C. jejuni* the various primers mentioned in the text are predicted to bind.

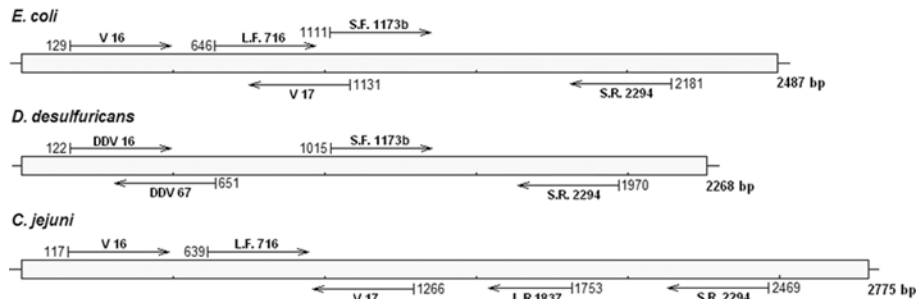
Primer OF640: GGNKCHAAAYATGGC
C. hominis 620 TTACCTGGGGTGC~~AAATATGGCTGAAATG~~ 648
G. lovleyi 608 TCCTCTGGGGGGCC~~AACATGGCAGAGGCC~~ 636

Primer LF716: GCNGARATGCACCC
D. desulfuricans 626 CATCCGAGGCGCATCCC~~GTGCTTTTTTCGC~~ 654
C. jejuni 638 TGGCTGAAATGCACCC~~AATCCTTTGGTCA~~ 666

Primer SF1173b: GTATGGNNTNAACC
E. coli 1105 TACTGGACGATGGGCTTCA~~ACCAGCATA~~C 1133
D. desulfuricans 1009 CTCTGGTGTATGGGCATCA~~ACCAGCGTGT~~ 1037

Primer LR1837: TTWCCRTADGCWCCC
P. marina 1773 ATGGGGAGCTTATGGTAA~~CGCTGAAAGAA~~ 1801
C. jejuni 1725 ATGGGGTGCCTTATGGTAA~~TGCTGAAAGAA~~ 1753

Primer SR2294: GWR TGCCARTGNTC
C. jejuni 2448 GGTTTTAGAGCATTGGCATA~~GTGGA~~ACTA 2476
D. desulfuricans 1947 CGTTATCGACCACTGGCATA~~CGGCA~~ACCA 1975

**Table 1 | Overview of *napA* sequences that might not be amplified using each of the four primers**

| Class/primer | LF716 | LR1837 | SF1173d | SR2294 |
|---|---|--|---|--------|
| α -Proteobacteria (eight sequences) | - | <i>B. japonicum</i> , <i>Rhodobacterales</i> <i>bacterium</i> , <i>Sinorhizium</i> <i>meliloti</i> , <i>Agrobacterium</i> <i>tumefaciens</i> , <i>Rhodospirillum centrum</i> , <i>Pseudovibrio</i> sp. | <i>Pseudovibrio</i> sp. | - |
| β -Proteobacteria (11 sequences) | <i>Candidatus</i> , 'Accumulibacter phosphatis' clade, <i>Cupriavidus taiwanensis</i> , <i>Burkholderia xenovorans</i> | - | - | - |
| γ -Proteobacteria (34 sequences) | <i>Aggregatibacter</i> <i>actinomycetem</i> , <i>Colwellia psychrerythraea</i> | <i>Aeromonas salmonicida</i> , <i>Shigella sonnei</i> | <i>Haemophilus ducreyi</i> , <i>Haemophilus somnus</i> , <i>Vibrio parahaemolyticus</i> , <i>H. chejuensis</i> | - |
| δ -Proteobacteria (four sequences) | <i>G. lovleyi</i> , <i>D. desulfuricans</i> | - | <i>G. lovleyi</i> | - |
| ϵ -Proteobacteria (13 sequences) | <i>C. lari</i> , <i>C. hominis</i> , <i>Nautilia</i> <i>profundicola</i> | <i>Campylobacter fetus</i> , <i>C.</i> <i>hominis</i> , <i>Sulfospirillum</i> <i>deleyianum</i> , <i>Arcobacter</i> <i>butzleri</i> | <i>C. jejuni</i> , <i>C. lari</i> , <i>C. hominis</i> , <i>W. succinogenes</i> , <i>Heliobacter hepaticus</i> , <i>Arcobacter butzleri</i> | - |

are used with community DNA as a template, multiple PCR products were obtained from most samples. Nevertheless, as discussed below, these PCRs can now be combined with high-throughput DNA sequencing that is increasingly widely available to determine the diversity of *napA* sequences in any bacterial community.

High-throughput DNA sequencing avoids a requirement for highly specific primers

Before the availability of high-throughput DNA sequencing, analysis of the variety of species capable of catalysing major environmental changes required the cloning and sequencing of individual PCR products one at a time, a process that was both time consuming and extremely expensive. Consequently, it was essential to design oligonucleotide primers that were not only sufficiently degenerate to capture all of the relevant target genes in community DNA but also sufficiently specific to avoid the generation of PCR products irrelevant to the investigation. The ability to generate up to 10^6 DNA sequences in a single experiment, for example using Roche 454 DNA sequencing technology, renders the second problem largely irrelevant because species that represent less than 0.1 % of the population can be detected even in a mixture of relevant and irrelevant amplicons [19]. Primer design can now focus on ensuring the amplification of the widest range of target sequences. This has enabled us to resolve a major outstanding problem in determining the range of nitrate reducing bacteria in complex communities by designing for the first time a set of primers that have been shown to recognize all of the *napA* genes currently known to occur. For each sample to be analysed, three PCRs involving different forward primers but the same reverse primer are essential. Note, however, that different bar codes could be added to each of the three forward primers and the resulting PCR products could then be mixed to decrease the costs associated with sequencing products from multiple samples. In another study, we have validated this approach by determining the range of sulfate-reducing bacteria represented in the same faecal DNA samples used in the work described in the present paper (W. Jia and J.A. Cole, unpublished work). By using 15 different barcoded sequencing primers and splitting the Roche 454 sequencing plate into four segments using gaskets, up to 60 samples can be analysed in a single DNA sequencing experiment. Typically, this will generate 150000 useful sequences per segment, or on average 10000 sequences per barcoded product.

Even with the more relaxed objectives of the work described in the present paper, the design of universal primers to detect the wide variety of periplasmic nitrate reductase genes was a challenging task, solved by an iterative approach. The three forward primers LF716, SF1173d and OF640, in combination with the reverse primer SR2294, have either been shown or are predicted to recognize all currently known *napA* sequences not only from DNA from single strains of the complete range of Proteobacteria but also from DNA

isolated from the faeces of patients with three different gastric diseases. Amplicons of the correct size were also obtained with primer pairs in which there was at least one mismatch in the last six bases, suggesting that the current primers might also recognize targets for which they were not designed. If necessary, further refinements can be made to these primers as additional *napA* sequences resulting from metagenomic studies are added to the databases.

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