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Investigation into the role of the truncated denitrification chain in *Rhizobium sullae* strain HCNT1

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Abstract

Most denitrifying bacteria reduce nitrate to the inert gases nitrous oxide or nitrogen. A remarkable exception to this is *Rhizobium sullae* strain HCNT1, which catalyses only a single step in the denitrification pathway, the reduction of nitrite to the reactive molecule nitric oxide. Further study demonstrated that HCNT1 does not encode the genes for NO reductase. Prolonged incubation of HCNT1 under anoxic conditions revealed that the cells had reduced culturability but not viability when nitrite was present. This may indicate an adaptation to anoxic conditions to provide resistance to environmental stresses. A closely related strain of *R. sullae*, strain CC1335, unable to denitrify, was found to lose culturability but not viability irrespective of the presence of nitrite. When the gene for nitrite reductase was mobilized into CC1335, this increased culturability with or without nitrite. These results indicate that the presence of nitrite reductase can influence the long-term survival of *R. sullae* strains and may provide an explanation as to why HCNT1 possesses this unusual truncation of its denitrification electron transport chain.

Rhizobia are soil bacteria typically able to symbiotically interact with legume plants to produce nitrogen-fixing root nodules. While all rhizobia were once placed under the same genus, Rhizobium, nowadays the classification of rhizobia using molecular analysis has revealed a more complex relationship among strains. Several genera have been described and accepted (i.e. Rhizobium, Allorhizobium, Azorhizobium, Mesorhizobium, Sinorhizobium and Bradyrhizobium) with many species in each genus. However, within the same species, it is common to observe different strains with quite different physiological and biochemical profiles. While some traits are common among all rhizobia, selected traits such as denitrification seem to be randomly distributed among genera and species. Moreover, many species are complete denitrifiers (strains of Bradyrhizobium japonicum) [1] while some are only partial nitrogen oxide reducers (strains of Rhizobium sullae) [2]. While the evolutionary advantage deriving from the complete denitrification pathways may be easily explained, the advantage gained from expressing only a fragment of such a metabolic property has not been completely clarified.

An exceptional example of fragmentation of the denitrification pathway is given by *R. sullae*, formerly *Rhizobium* 'hedysari', a nitrogen-fixing bacterium that induces symbiotic nodule formation on the legume *Hedysarum coronarium* [3–6]. Some isolates belonging to this species have been shown to encode a copper-containing nitrite reductase [2,7].

complete denitrification.

The role of nitrite reductase in *R. sullae* has yet to be elucidated. These bacteria convert stable molecular nitrogen into combined forms via nitrogenase during intranodular nitrogen fixation, and at the same time they convert combined nitrogen back into gaseous molecules that are lost into the atmosphere. The most obvious advantage expected is

that during free life, even in the absence of oxygen, they can

Nitrite reductase reduces nitrite to nitric oxide (NO). Nitrite

reductase is encoded by nirK, which is closely related to

nitrite reductases in true denitrifiers. Expression of nirK is

atypical in that it does not require the presence of a nitrogen

oxide, but only requires a decrease in oxygen concentration

(below 16.5% air saturation) [2]. Reduction of nitrite by the

HCNT1 strain results in the cessation of growth. This growth

inhibition is likely due to the accumulation of toxic levels

of NO [8]. Inhibition by NO was demonstrated by measuring

NO accumulation and by the observation that inactivation of

nirK eliminated the phenotypic traits associated with NO

accumulation but did not cause other obvious phenotypic

changes [8]. These results indicate that there is no NO reductase activity in the cells, and it was also confirmed by

a PCR-based approach using specific primers to detect the

presence of norB, yielding no amplification product. There is

no nitrate reductase activity since there is no O2 uptake in-

hibition if nitrate is added to the medium. No evidence

consistent with the presence of N2O reductase, such as

growth on N2O, was found as well. R. sullae strain HCNT1

is therefore an exceptional bacterium due to the radical

truncation of its denitrification electron transport chain,

having only one of the four terminal reductases required for

Key words: bacteria, denitrification, electron transport chain, HCNT1, nitric oxide, *Rhizobium*

Abbreviations used: CFU, colony forming units; VBNC, viable-but-not-culturable.

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survive by anaerobic respiration of nitrite, but this hypothesis is unsatisfactory because strain HCNT1 cannot grow as a denitrifier. In other words, no proton translocation occurs during the reduction of nitrite to NO. Moreover, since Nir activity will inhibit oxygen respiration as long as nitrite is present due to the binding of NO to terminal oxidases, nitrite reduction also inhibits the only other means by which cells can conserve energy. Once the available nitrite has been reduced, O₂ consumption will resume [2]. Therefore there is no obvious bioenergetic benefit as a consequence of nitrite respiration.

Since nitrite reductase expression only occurs under microoxic conditions, it is possible that the enzyme plays some role within the root nodule, which is a low-oxygen environment. For instance, it is well known that nitrite may be toxic to nitrogenase and may bind to leghaemoglobin. Thus nitrite reduction in HCNT1 may be as a nitrite detoxification strategy during intranodular life [9]. This role for Nir is only valid if the unreactive intermediate N2O is the end-product of this reduction. The lack of Nor means that detoxification leads to conversion of nitrite into the even more reactive NO. Since a more toxic compound is produced, the nitrite detoxification hypothesis seems unlikely [10]. It has also been observed that strains of the same species that lack Nir (e.g. strain CC1335) can nodulate and fix nitrogen at the same level [3]. Comparisons of nodulation efficiency, plant growth and nitrogen fixation have not revealed any significant differences between wild-type and nitrite reductase-deficient strains under any of the conditions tested so far. However, this should be further investigated because this strain was found to gradually lose nodulation ability under laboratory conditions. Taken together, these results do not identify any obvious role for the truncated denitrification chain in R. sullae.

The presence and expression of nitrite reductase has been also investigated as a strategy to reduce the energy content in the bacterial cell in order to induce dormancy. Some evidence has been provided suggesting a link between nitrite reductase activity and the viability and culturability of the cells. In response to a number of environmental stresses, many bacterial species, including Vibrio vulnificus, Sinorhizobium meliloti, Micrococcus luteus, Escherichia coli and Helicobacter pylori, enter the VBNC (viable-but-notculturable) status [11]. In this metabolic state, they lose their ability to grow on media that usually sustain them and undergo such physiological and morphological changes as increased resistance to several physical and chemical factors, and changes in protein and lipid content. The use of specific fluorescent dyes such as Syto 9, CTC (5-cyano-2,3-di-4tolyl-tetrazolium chloride), Acridine Orange and propidium iodide has made possible a more accurate evaluation of the viability and the metabolic state of microbes [12]. Experiments performed with S. meliloti 41, a rhizobium nodulating Medicago sativa, showed that it enters VBNC status in liquid microcosms when O2 is depleted from the atmosphere of the incubation mixture [13,14]. Plasmid-borne, firefly-derived, luciferase gene (luc) was inserted and stably inherited in S. meliloti 41 (pRP4-luc) as a reporter gene. The strain obtained, S. meliloti 41 pRP4-luc and its parental strain, served as a model system for VBNC experiments both in vitro and, thanks to the marker gene inserted, also in soil samples and in the plant system. This strain has been found to recover its viability under certain conditions, but only at a given ratio to the number of metabolically active cells ([14] and M. Basaglia, S. Povolo and S. Casella, unpublished work). R. sullae strain HCNT1 enters the same VBNC status when oxygen is limiting, but only when nitrite is present and Nir is expressed allowing for production of NO [13]. The hypothesis that expression of nirK by HCNT1 may induce the VBNC status has been investigated through a comparison of S. meliloti and R. sullae in order to verify the possible connection of nirK with the VBNC status. It was found that nitrite reductase activity may reduce energy content but it was unclear whether this was an indirect consequence of the generation of nitric oxide or a desired result that would prolong cell viability under certain conditions. While the energy content of S. meliloti decreased under anoxic conditions, leading the strain to the VBNC status, HCNT1 only reduced its internal energy under anoxic conditions when nitrite was present. NO does not accumulate at lethal levels because differential staining of the cells during oxygen uptake experiments in the presence of nitrite revealed that they were still alive, although the CFU (colony forming units) number had dramatically decreased [13]. An explanation for this result is that NO produced by nitrite reduction induced VBNC status, making the cells more stress-resistant. Such a metabolic state confers to the cells the ability to withstand stresses, including anoxic conditions, antibiotic effects or nutrient depletion. When suitable environmental conditions reoccur, it has been demonstrated that some VBNC bacterial populations, including S. meliloti, can recover their culturability [14,15].

To learn more about the role of Nir in R. sullae, we examined the VBNC status of CC1335, which does not possess nirK. Prolonged incubation of CC1335 under anaerobic conditions resulted in a significant decrease in CFU but DAPI (4,6-diamidino-2-phenylindole) staining indicates that the cells are still alive. Therefore, unlike HCNT1, CC1335 can enter VBNC without Nir activity. In order to provide support for the hypothesis that expression of nirK is favourable because it induces the VBNC state, nirK from HCNT1 was mobilized into CC1335, a strain of R. sullae that lacks nirK, and the resulting phenotype was studied. The presence of nirK in CC1335 resulted in a phenotype similar to that of HCNT1 under anoxic incubation: there is no anaerobic growth, but the number of cells with the ability to form a colony does not decrease significantly for an extended time. However, CC1335 wild-type does not behave like HCAT2 (the Nirdeficient strain of HCNT1). CC1335 rapidly reduces its internal energy and the number of cells capable of forming a colony upon re-incubation under aerobic conditions. This suggests that strain CC1335 does not need Nir to reduce its internal energy (culturability) under anoxic conditions. The difference between these strains is intriguing and suggests that HCNT1 has the ability to survive for long periods without loss of ability to form CFU, but also that the presence of Nir leads to a reduction in the internal energy to VBNC levels, making the strain more resistant to a variety of stresses.

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