

## Eukaryotic nitrate and nitrite transporters

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**Abstract.** Nitrate transport is the key step controlling the amount of nitrate incorporated by the cells and subsequent of storage, reduction or export. Molecular, genetic and biochemical approaches to the study of eukaryotic nitrate/nitrite transporters allow an initial understanding of this step, which is much more complex and structured than previously suspected. At the plasma membrane level, two gene families, *Nrt1* and *Nrt2*, account for high- and low-affinity nitrate transporters. Functionality of NRT1

from *Arabidopsis* and NRT2 proteins from *Aspergillus* and *Chlamydomonas* has been demonstrated. However, redundancy of these systems makes it difficult to assign particular physiological roles to each. Data on genes involved in the regulation of nitrate transport and reduction are still scarce. Information on nitrite transporters to the chloroplast is biased by the belief that in vivo nitrous acid diffuses freely to this organelle. The recent progress on these aspects is discussed in this review.

**Key words.** Nitrate transporter; nitrite transporter; chlorate; *Nrt1*; *Nrt2*; chloroplast nitrite transport.

### Introduction to eukaryotic nitrate/nitrite transporters

In photosynthetic eukaryotes, nitrate assimilation involves two membrane barriers: the plasma membrane, which delimits the cytosolic reduction of nitrate to nitrite, and the envelope of the chloroplast, where nitrite reduction to ammonium occurs [1]. In addition to its role as an essential nutrient, nitrate acts in plants as a signal molecule involved in root morphogenesis [2], shoot:root balance [3] and carbon metabolism adaptations [4], and in arresting the gametogenesis program in *Chlamydomonas reinhardtii* [5]. Although many aspects have still to be learnt about how nitrate is sensed and how the signal transduction mechanisms for nitrate-regulated genes operate, there exists a certain consensus that the nitrate transport (NT) step is key in controlling the efficiency of nitrogen assimilation.

Intensive efforts have been addressed to identifying and characterizing of nitrate transporters and reviewed recently [6–8]. The present review will focus on the functional characteristics of the plasmalemma nitrate/nitrite transporters in eukaryotes and nitrite transport to the chloroplast.

Nitrate entry through the plasmalemma requires active transport systems, which are proton coupled and depend on a proton motive force generated by the H<sup>+</sup>-ATPase [9, 10]. NT systems can be classified on the basis of physiological data (substrate affinity or induction) and gene sequence analysis [9, 11]. The physiological data show the existence of distinct NT systems: constitutive high-affinity (cHANT), inducible high-affinity (iHANT), constitutive low-affinity (cLANT) and inducible low-affinity (iLANT). The HANT systems operate at low external nitrate concentration (< 250 µM) and have different affinities and capacities to transport nitrate in plants. The LANT systems operate at high external nitrate concentration (> 1 mM), and thermodynamic evaluations and electrophysiology studies demonstrate that they also correspond to H<sup>+</sup>-dependent active transport [11, 12]. The regulation of the individual components of the NT systems is complex, and both upregulation by nitrate and feedback repression by N-metabolites resulting from nitrate reduction have been shown for several transporters [13–16].

The identification of genes encoding nitrate transporters in eukaryotes started with the cloning of the *Aspergillus nidulans* *CrnA* gene in 1991 [17]. The *crnA* mutants from

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*A. nidulans* are chlorate resistant and can use nitrate, though they are only deficient in N uptake in the conidiospore and young micelia stages [18]. Until now, at least 25 genes proposed to encode nitrate transporters have been identified, mainly in plants. According to their sequence analysis, nitrate transporter genes have been classified into two families: *Nrt1* and *Nrt2* [7, 8]. The nomenclature of these genes follows the rules proposed by the ISPMB [19]. Initially, *Nrt1* and *Nrt2* genes were related to LANT and HANT, respectively. However, the *Arabidopsis* NRT1;1, primarily proposed to be a LANT [12], is also involved in HANT [20, 21]. In addition, the NRT2;3 from *Chlamydomonas* is a LANT [22].

### Molecular characteristics of NRT1 and NRT2 transporters

The NRT2 transporters, also named NNP family (for nitrate-nitrite porter), belong to the Major Facilitator superfamily (MFS), which includes sugar transporters from mammals, plants, yeast, and bacteria; bacterial drug- $H^+$  antiporters; metabolite- $H^+$  symporters; and eukaryotic phosphate- $H^+$  symporters, among 17 transporter families [23] (see also article by Moir and Wood). The NRT2 proteins have a typical membrane topology of 12 transmembrane domains arranged as two sets of six, connected by a cytosolic loop. NRT2 proteins share a conserved sequence motif, D/N-R-X-G-R-R/K, between transmembranes 2 and 3, and another, I-X<sub>2</sub>-R-X<sub>3</sub>-G-X<sub>3</sub>-G, before and within transmembrane domain 4, which were present even among MFS members showing extensive divergence [23]. A consensus motif [FYK]-X<sub>3</sub>-[ILQRK]-X-[GA]-X-[VASK]-X-[GASN]-[LIVFQ]-X<sub>1,2</sub>-G-X-G-[NIM]-X-G-[GTA] within the fifth putative transmembrane domain has been proposed as the signature for the NNP family [23]. A portion of this sequence, A-G-W/L-G-N-M-G, present in the sequences from CRNA from *A. nidulans*, NRT2 from *Chlamydomonas* and *Hordeum vulgare*, and NARK from *Escherichia coli*, and absent in other MFS members, has been suggested as the substrate recognition motif [24]. The NRT1 transporters do not show significant conservation with members of the NRT2 family, and belong to the POT family, which includes numbers of  $H^+$ -dependent oligopeptide transporters from mammals, plants, fungi and bacteria [23, 25]. Although the POT family has sequence similarity to several members of the MFS, the small number of individuals and the short length of segments with significant similarity point to these two as distinct families [23]. NRT1 proteins are predicted to have 12 transmembrane domains, with a long loop containing many charged residues separating the first six transmembrane domains from the second

six, and short N- and C-terminal ends [12, 26]. Interestingly, this secondary structure resembles those predicted for *A. nidulans* CRNA [17] and *Hansenula polymorpha* YNT1 proteins [27], and differs from plant and algal NRT2 proteins, which contain a long hydrophylic C-terminal domain [28, 29].

### Functional and regulatory characteristics of NRT1 and NRT2 transporters

Even though many genes from both *Nrt1* and *Nrt2* families have been identified in eukaryotic organisms, the precise function for each transport system and their contribution to global N homeostasis remain to be elucidated. The functional and regulatory characteristics for some of these transporters are summarized in table 1.

The redundancy of nitrate transporters in many organisms results in a complicating factor when analysing the functionality of the transporters, which has been especially evident for AtNRT1;1. The *Arabidopsis* *Nrt1;1* (*chl1*) gene was isolated from a T-DNA insertion allele (*chl1*) resistant to chlorate [12]. *AtNrt1;1* was initially proposed to encode a LANT since its heterologous expression in *Xenopus* oocytes showed characteristics typical of a  $H^+$ -coupled NT in the millimolar range [12], and the phenotype of the *chl1* mutant was consistent with a significant reduction in LANT activity but not in the NT at the high-affinity range (below 1 mM) [30, 31]. Recently, AtNRT1;1 has also been implicated in HANT [20, 21]. The confirmation that NRT1;1 has a role in HANT derives from measurements of nitrate depletion from the external media by *Nrt1;1*-injected *Xenopus* oocytes, resulting in a  $K_m$  of 50  $\mu$ M [21]. The expression of *AtNrt1;1* transcript is upregulated by acid pH and by nitrate in the media at both low ( $\mu$ M) and high (mM) concentrations [12, 15]. This response to nitrate would agree with their proposed dual function in NT, which might also explain the reduced rate of uptake at both the low- and the high-affinity range in the *Arabidopsis* *chl1* mutant grown in ammonium nitrate [20, 21]. In contrast, *AtNrt1;1* expression is poorly sensitive to feedback regulation by N metabolites [15, 16].

The second *Nrt1* gene identified in *Arabidopsis* (*AtNrt1;2*, also named *NTL1*) corresponds to a cLANT system with no dual affinity for nitrite [26]. The *AtNrt1;2* is constitutively expressed in the absence of nitrate, and its functional analysis in *Xenopus* oocytes shows specificity for nitrate as a substrate ( $K_m$  5.9 mM), but it is not able to transport dipeptides or histidine [26]. Transgenic plants containing an antisense *AtNrt1.2* also confirm its role as a LANT, since a decrease in NT

rates was observed at 5 mM but not at 500  $\mu$ M [26]. Additional *Nrt1* homologous genes have been identified in *Arabidopsis* [32, 33] and tomato [34], but their function in NT is still unknown.

A gene phylogenetically close to *AtNrt1;1* has been identified in *Brassica napus* (*BnNrt1.2*) [35]. Both share the upregulation by low nitrate in the media, and activity for NT in the millimolar range when expressed in oocytes [35]. However, *BnNRT1.2* is able to transport L-histidine with similar efficiency to nitrate and, in contrast to *AtNRT1;1*, does not transport chlorate [31, 35].

*Nrt2* genes have been identified in fungi [17, 27], the alga *Chlamydomonas* [28, 36], and the plants barley [29], tobacco [37], *Arabidopsis* [15, 38] and soybean [39] (table 1). The *Arabidopsis* mutant *chl8* is defective in the cHANT, but the corresponding locus does not map to known *Nrt2* genes [40]. *Nrt2* genes have also been cloned in bacteria [41, 42]. NARK from *E. coli* appears to mediate the electrogenic nitrite export involved in anaerobic nitrate respiration [41], whereas NRTP from a marine cyanobacterium, *Synechococcus*, has an assimilatory function [42] (see also article by Moir and Wood).

In the eukaryotic green alga *Chlamydomonas*, nitrate assimilation genes are found in two gene clusters (fig. 1). A cluster of about 45 kb contains, among structural genes for nitrate (*Nia1*) and nitrite (*Nii1*) reduction, *Nrt2* genes for nitrate/nitrite transport [28, 43, 44]. A second cluster of about 15 kb contains a third *Nrt2* gene and a nitrate-regulated gene [36] which encodes a mito-

chondrial alternative oxidase [I. Gómez, A. Quesada and E. Fernández, unpublished]. Clustering of nitrate assimilation genes was previously reported in *A. nidulans* [45], and more recently in *H. polymorpha* [27] and *Arabidopsis* [38], which might represent a cell strategy to make the regulation of this important pathway efficient. Molecular and physiological studies on mutant strains defective in several of the nitrate-clustered genes allow identification of four high-affinity nitrate/nitrite transporters in *Chlamydomonas* (fig. 1). System I corresponds to a bispecific HANT/HANiT encoded by *Nrt2;1/Nar2*, system II to a monospecific HANT encoded by *Nrt2;2/Nar2* [28, 46], system III to a bispecific HANiT and LANT, encoded by *Nrt2;3* [22, 36, 47], and system IV to a bispecific HANT/HANiT probably encoded by *Nrt2;4* [22, 47]. The existence of an *Nrt2;4* gene is based on its functional characteristics and on Northern and Southern blot hybridization analysis with *Nrt2;3* probes, but it needs to be further substantiated (fig. 1).

These transport systems are differentially regulated by the carbon and nitrogen source. Systems I, II and III are optimally expressed at high CO<sub>2</sub>, and their activity is blocked by ammonium, whereas system IV is expressed optimally under limiting CO<sub>2</sub> and its activity is not inhibited by ammonium. In contrast to systems I, II and III, system IV activity is inhibited by CO<sub>2</sub>, chloride and a chloride channel inhibitor [46, 47]. Concerning the function for each of these systems, mutants deleted in systems I and II and carrying functional systems III and IV are unable to grow efficiently in nitrate media [28].

Table 1. Properties of some nitrate/nitrite transporters from eukaryotes.

Gene name (other name)	Species	Substrate	Upregulation	Feedback repression	Function	References
<i>Nrt1</i> Family						
<i>AtNRT1.1(CHL1)</i>	<i>A. thaliana</i>	NO <sub>3</sub> <sup>-</sup> , ClO <sub>3</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup> /low pH	No	HANT/LANT	16, 21
<i>AtNRT1.2 (NTL1)</i>	<i>A. thaliana</i>	NO <sub>3</sub> <sup>-</sup>	No	?	LANT	26
<i>BnNRT1;2</i>	<i>B. napus</i>	NO <sub>3</sub> <sup>-</sup> /his	NO <sub>3</sub> <sup>-</sup>	?	LANT	35
<i>LeNRT1;1</i>	<i>L. esculentum</i>	?	No	?	?	34
<i>LeNRT1;2</i>	<i>L. esculentum</i>	?	NO <sub>3</sub> <sup>-</sup>	?	?	34
<i>Nrt2</i> Family						
<i>AtNRT2;1</i>	<i>Arabidopsis</i>	NO <sub>3</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	HANT	15, 38
<i>AtNRT2;2</i>	<i>Arabidopsis</i>	?	NO <sub>3</sub> <sup>-</sup>	Yes	?	38
<i>CrnA</i>	<i>A. nidulans</i>	NO <sub>3</sub> <sup>-</sup> , NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	HANT/HANiT	17
<i>CrNrt2;1 (Nar3)</i>	<i>C. reinhardtii</i>	NO <sub>3</sub> <sup>-</sup> , NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	HANT/HANiT	28, 46, 51
<i>CrNrt2;2 (Nar4)</i>	<i>C. reinhardtii</i>	NO <sub>3</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	HANT	28, 46, 51
<i>CrNrt2;3</i>	<i>C. reinhardtii</i>	NO <sub>3</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	LANT/HANiT	36, 47, 22
<i>CrNrt2;4?</i>	<i>C. reinhardtii</i>	NO <sub>3</sub> <sup>-</sup> , NO <sub>2</sub> <sup>-</sup>	Low CO <sub>2</sub> /NO <sub>2</sub> <sup>-</sup>	No	HANT/HANiT	47, 22
<i>GmNrt2;1</i>	<i>G. max</i>	?	NO <sub>3</sub> <sup>-</sup>	?	?	39
<i>HvNrt2;1 (BCH1)</i>	<i>H. vulgare</i>	?	NO <sub>3</sub> <sup>-</sup>	?	?	29
<i>HvNrt2;2 (BCH2)</i>	<i>H. vulgare</i>	?	NO <sub>3</sub> <sup>-</sup>	?	?	29
<i>NpNrt2;1</i>	<i>N. plumbaginifolia</i>	?	NO <sub>3</sub> <sup>-</sup>	Yes	?	37
<i>HpYNT1</i>	<i>H. polymorpha</i>	NO <sub>3</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	Yes	HANT	27

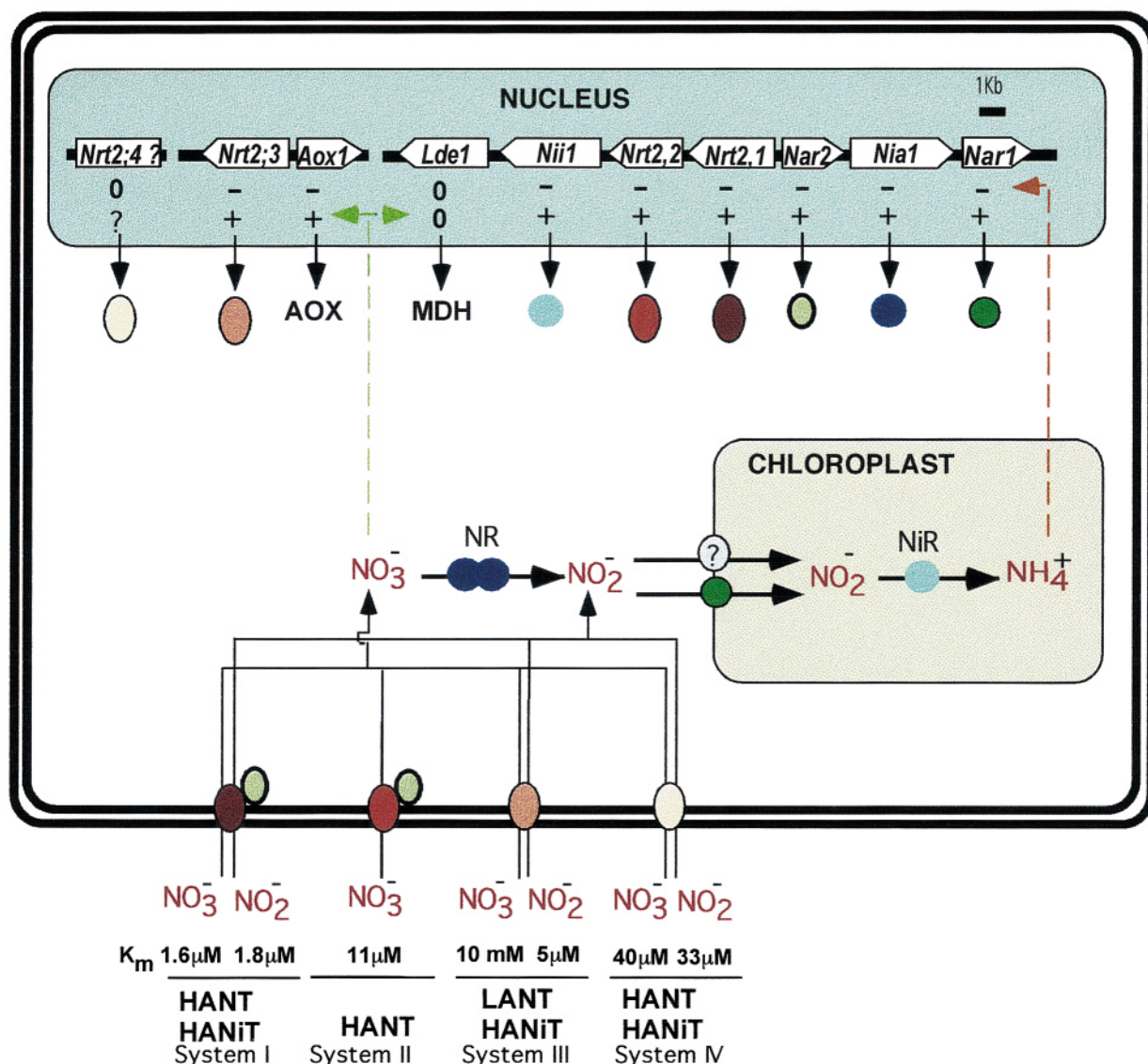


Figure 1. Scheme for the nitrate/nitrite transport systems in *Chlamydomonas*. Genes encoding transport systems I and II and the nitrite transporter to the chloroplast NAR1 are clustered in chromosome IX together with the NR and NiR genes. Location of the *Nrt2:3-Aox1* gene cluster and the putative *Nrt2:4* gene is unknown. Positive regulation by nitrate (+) and negative by ammonium (−) or no effect (0) is shown for each gene.

Thus, under sufficient  $\text{CO}_2$ , systems I and II have a primary function in the provision of nitrate for growth, and systems I and III in nitrite entry. Finally, system IV would allow nitrate and nitrite transport under limiting  $\text{CO}_2$ , even in the presence of ammonium. Under these conditions, ammonium cannot be incorporated efficiently into carbon skeletons, and nitrate and nitrite entry in the cells at amounts higher than those capable of being assimilated results in the excretion of ammonium [48, 49]. This activity of system IV might provide

the cells with an alternative way to dissipate excess reducing power generated photosynthetically. Deletion mutants lacking *Nar2*, *Nrt2:1* and *Nrt2:2* genes and having a functional *Nia1* gene recovered HANT activity and growth in nitrate when transformed with plasmids containing either *Nar2 + Nrt2:1* or *Nar2 + Nrt2:2*, but not with any of these genes alone [28]. Thus, systems I and II were proposed to require two protein components for activity [28, 46]. In addition, *Xenopus* oocytes injected with either *CrNrt2* messenger RNA

(mRNA) or *CrNar2* mRNA do not result in NT activity [50]. However, a HANT activity was measured in oocytes injected with the mixture of *CrNrt2;1* + *CrNar2* mRNAs, which is consistent with the participation of the two corresponding proteins in the appropriate makeup of the transporter, as previously proposed. CrNAR2 appears to have a single transmembrane domain and might correspond to a membrane protein type Ia [P. L. Lefebvre, personal communication], which could interact with CrNRT2;1 to modify its function. The pH dependence of the nitrate-elicited currents by CrNRT2;1 + CrNAR2 expressed in oocytes is consistent with a H<sup>+</sup>-cotransport mechanism [50]. Thus, the CrNRT2;1 and CrNRT2;2 proteins would be the first example of MFS proteins requiring two components for their functionality.

Nitrate at micromolar concentrations positively signals the expression of *CrNrt2;1*, *CrNrt2;2* and *CrNrt2;3*, *NpNrt2;1*, and *AtNrt2;1* [14, 15, 47, 51], and a negative feedback regulation by N-derivative metabolites from assimilated nitrate has also been reported for these genes [5, 14–16, 51]. In *Arabidopsis*, expression of *Nrt2;1* and *Nrt1;1* are also diurnally regulated in photosynthetically active plants, so that sucrose prevents the inhibition of the expression in the dark [16]. This regulation might be the result of the fluctuations of intracel-

lular nitrate and reduced C compounds, which signals the pathway [16]. An scheme of characterized NT systems in *Arabidopsis* is shown in figure 2.

A regulatory role has been assigned to nitrate reductase (NR) itself as proposed in fungi, where mutations in nitrite reductase (NiR) or NT genes do not lead to the overexpression of nitrate assimilation genes observed in NR mutants [52, 53]. In algae and plants, NR mutants also overexpress NR, NiR and HANT gene transcripts, without the requirement of a positive signal of nitrate [51, 54]. NiR mutants from tobacco, produced by an antisense strategy [55], show a similar overexpression pattern to NR mutants, which suggests that the absence of reduced N metabolites is responsible for the observed effects [55]. However, in *Chlamydomonas* as in fungi, no overexpression of nitrate assimilation genes was found in NiR mutants, thus pointing to NR activity as the cause of the deregulation in NR mutants [22]. *Chlamydomonas* strains carrying the NR *Nia1* gene promoter transcriptionally fused to the algal arylsulfatase gene has been used to study this regulation by NR itself [56, A. Llamas, M. I. Igeño, E. Fernández and A. Galván, unpublished]. It has been demonstrated that the reason for deregulation in NR mutants is the activity of system I, which is able to scavenge submicromolar concentrations of nitrate present in N-free media and thus to keep

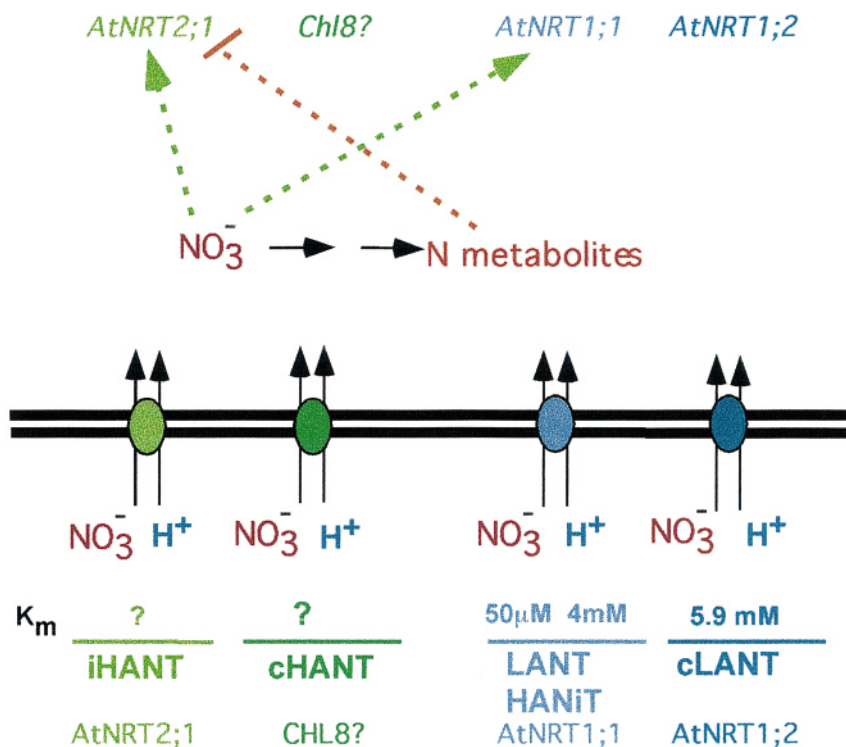


Figure 2. Scheme for functionality and regulation of some nitrate transport systems in *Arabidopsis*. Details are given in the text.

the NR promoter activity switched on [A. Llamas, M. I. Igeño, E. Fernández and A. Galván, unpublished]. The positive nitrate signaling on the NR promoter was also shown to depend directly on the activity of the NT systems.

Negative regulation of the *Nrt2* gene expression by NR activity is also evident in strains constitutively expressing the *Nia1* gene. Thus, expression of the *Nia1* gene under the *CabII-1* gene promoter in *Chlamydomonas* results in very low amounts of *Nrt2;1* and *Nar2* transcripts, which might be the result of a decrease in intracellular nitrate together with an increase in intracellular nitrite [57]. In agreement with this interpretation, transgenic *Nicotiana plumbaginifolia* plants carrying the *35S-Nia1* gene have a nitrate content in leaves significantly lower than normal plants [58]. A modulation by nitrite produced from nitrate and affecting expression of nitrate transporters has also been suggested [16, 22, 59, 60].

In addition to transcriptional regulation, ammonium has a immediate and strong negative effect on the activity of systems I, II and III from *Chlamydomonas* [46, 47]. The molecular mechanism of this regulation is unknown.

#### Chlorate resistance and nitrate/nitrite transporters

Chlorate as an analog of nitrate can be reduced by NR to produce chlorite, which is toxic for cells. Thus, mutants incapable of taking up chlorate or deficient in NR activity could be selected in chlorate media. This strategy has been widely used in fungi, algae and plants, and the mutants generated in this way were used to study the nitrate assimilation pathway [13, 52, 61]. Among mutants deficient in the structural genes of NR, genes for the biosynthesis of the molybdenum cofactor, essential for NR assembly and activity, and regulatory genes, mutants deficient in NT were also obtained in fungi [18], algae [43, 47] and plants [26, 30, 40].

Whether or not NR is responsible for chlorate toxicity has been evaluated by using *Chlamydomonas* mutants deficient in NR activity [62]. It has been shown that chlorate becomes toxic and causes mutagenesis in the cells by a process dependent on its transport and independent of NR activity [62]. Recently, *Chlamydomonas* strains deleted in genes for NR and HAN/NiT systems I and II, but possessing the HANiNT system III, were found to be resistant to chlorate. However, activation of system III by a nitrate signal causes chlorate sensitivity [47], which supports the view that chlorate toxicity is independent of its reduction by NR in cells. Notwithstanding, it cannot be ruled out that minor amounts of chlorite present in the chlorate solution account for the observed effects. In fact, chlorite concentrations 10

times lower than chlorate produce toxicity in *Chlamydomonas* [A. Galván and E. Fernández, unpublished]. Chlorate transport mediated by a nitrate transporter is well established for the AtNRT1;1 system [12, 31], but not well documented for the NRT2 systems. In tomato roots, chlorate has been shown not to be a useful analog for HANT, which is much more selective for nitrate, though nitrate interferes with root chlorate uptake [63]. Expression of *AnCrnA* mRNA in oocytes shows that this bispecific nitrate/nitrite transporter cannot transport chlorate, though chlorite is efficiently transported [8]. These data suggest that nitrate transporters each with different specificity towards chlorate and chlorite might determine cell toxicity, depending on their expression under the experimental conditions.

#### Regulatory genes

In plants, regulation of NR, NiR and HANT gene expression is coordinately regulated with respect to the nitrogen source, the intracellular amounts of reduced-nitrogen compounds, light, hormones and carbon status [1, 7, 14, 61]. Identification of genes directly involved in regulation of the nitrate pathway is well characterized in fungi [64] but scarce in plants. These aspects have been reviewed recently [6, 8].

In *Chlamydomonas*, expression of nitrate assimilation genes is coregulated (fig. 1). These genes are subject to repression by ammonium, induction by nitrate and control of the positive-acting regulatory gene *Nit2* [13, 51]. *Nit2* has been cloned and shown to be subject to ammonium repression, which implies an additional level of control [65]. A second regulatory locus, closely linked to *Nit2*, is also required for expression of the *Nrt2;3* and possibly other nitrate-inducible genes [47].

The regulatory mechanisms in algae appear to be different from those in fungi [64]. In fact, at least two pathway-specific genes, *Nrg1* and *Nrg2*, mediate ammonium repression of NT and reduction genes [66]. Mutant strains defective in *Nrg* genes are partially insensitive to ammonium and their phenotype is additive, so that the threshold concentration of insensitivity to ammonium is increased in the double mutant. The existence of several genes mediating positive effects of nitrate and negative effects of ammonium, whose deficiency leads to partial phenotypes, might explain the difficulties in the genetic dissection of the regulation both in algae and plants.

#### Nitrite transport to the chloroplast

The nitrite transport step to the chloroplast has not been sufficiently studied, probably because there exists a general belief that nitrite can diffuse freely as nitrous

acid to the chloroplast compartment, and thus there is no need for a plastidic transporter [67]. However, the nitrite uptake in intact pea chloroplasts shows a saturation kinetics, a preference for alkaline pH and a sensitivity to protein modifiers, which favors the existence of a nitrite-mediated channel or transporter versus the permeation of the nitrous acid [68, 69]. Nitrite transport into pea chloroplasts has been reevaluated by determining fluorometrically  $H^+$ -linked transport of nitrite [70]. A rate of  $H^+$ -linked nitrite transport much higher than the measured NiR activity in chloroplasts would imply that a nitrite transporter is not needed in illuminated chloroplasts [70]. The nitrite concentrations used in these experiments are at the millimolar range, more than five times higher than those estimated for cytosolic nitrite in shoots [71]. In addition, nitrite concentrations have been shown to change significantly in roots of barley seedlings, depending on the nitrate and nitrite availability in the environment [72], and in spinach leaves during light-dark transitions [73]. These fluctuations in cytosolic concentrations of nitrite, which should be maintained low because of its cellular toxicity, might make inefficient the nitrite reduction step if it depended on a nonregulated nitrite diffusion. Thus, molecular characterization of the plastidic nitrite transport is needed.

In *Chlamydomonas*, the *Nar1* gene, clustered with other nitrate assimilation genes (fig. 1), encodes an integral protein of the chloroplast membranes, as deduced from the sequence of its putative transit peptide and immunodetection of NAR1 in the chloroplast envelope membranes with specific antibodies [74]. NAR1 sequence analysis predicts a protein with six transmembrane-spanning segments and significant homology to putative nitrite transport proteins from bacteria [75]. In isolated chloroplasts from *Chlamydomonas* strains, the expression of *Nar1* corresponds with HANiR activity ( $K_m$  in the  $\mu M$  range) which operates at basic pH. NAR1 is also required for optimal cell growth under conditions of limiting nitrate. In addition to NAR1, other plastidic nitrite transporters seem to operate in *Chlamydomonas* [74]. Similarly to plasma membrane nitrate/nitrite transport, the picture of nitrite transport to the chloroplast also appears to be complex.

### Concluding remarks

Eukaryotic cells have provided themselves with many NT systems at the plasma membrane corresponding to two gene families, *Nrt1* and *Nrt2*. The redundancy of these systems in a single organism favors the multiplicity of functions needed to account for a regulated NT under changing environmental conditions, and for different requirements in plant tissues. Understanding the

complex network of these transporters would require future efforts in i) elucidating the particular functions and regulation for each of the putative nitrate transporters identified, ii) molecular identification of chloroplast nitrite transporters in plants: would they correspond to the *Chlamydomonas Nar1* gene? iii) post-translational regulation of nitrate transporters which modify their activity according to nutritional and environmental conditions, and iv) how nitrate and N metabolites are sensed. Is nitrate sensed extracellularly? Which are the protein factors that transduce the positive and negative signals?

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