Genome-wide identification, classification and transcriptional analysis of nitrate and ammonium transporters in Coffea

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Abstract

Nitrogen (N) is quantitatively the main nutrient required by coffee plants, with acquisition mainly by the roots and mostly exported to coffee beans. Nitrate (NO₃⁻) and ammonium (NH₄⁺) are the most important inorganic sources for N uptake. Several N transporters encoded by different gene families mediate the uptake of these compounds. They have an important role in source preference for N uptake in the root system. In this study, we performed a genome-wide analysis, including in silico expression and phylogenetic analyses of AMT1, AMT2, NRT1/PTR, and NRT2 transporters in the recently sequenced Coffea canephora genome. We analyzed the expression of six selected transporters in Coffea arabica roots submitted to N deficiency. N source preference was also analyzed in C. arabica using isotopes. C. canephora N transporters follow the patterns observed for most eudicots, where each member of the AMT and NRT families has a particular role in N mobilization, and where some of these are modulated by N deficiency. Despite the prevalence of putative nitrate transporters in the Coffea genome, ammonium was the preferential inorganic N source for N-starved C. arabica roots. This data provides an important basis for fundamental and applied studies to depict molecular mechanisms involved in N uptake in coffee trees.

Keywords: Coffee, nitrogen transport, nitrogen uptake, gene family evolution.

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Introduction

Nitrogen (N) is one of the primary macronutrients and is a critical nutrient for plant growth and development (Konishi and Yanagisawa, 2014). N is imported into the roots through specific ion transporters in root cells from several sources. The main N inorganic forms absorbed by plants are ammonium (NH₄⁺) and nitrate (NO₃⁻). NO₃⁻, due to nitrification reactions in the soil, is usually present in higher concentrations and is more mobile in soil when compared to NH₄⁺ (Marschner, 2012; Luo et al., 2013). Nonetheless, both ions can be utilized by plants, NH₄⁺ and NO₃⁻ have different energetic and biochemical characteristics for assimilation, resulting in different net fluxes of both ions and NH₄⁺ - NO₃⁻ preference in plants (Patterson et al., 2010; Alber et al., 2012). These preferences are still poorly understood in tropical woody dicots.

Plants have evolved different transport systems that effectively adapt to changes of N availability in the environment. Ammonium and nitrate in plants have two uptake systems: a low-affinity transport system (LATS) operating in the millimolar concentration range and a saturable high-affinity transport system (HATS) operating at submillimolar concentrations (reviewed in Forde, 2000; Wang et al., 2012). Mainly LATS accomplish the N uptake at high external concentrations, while at concentrations below 0.5 mM N, uptake is achieved through HATS.

Nitrate uptake by plant roots from soil solution is mediated by members of four gene families: NRT1/PTR (NPF, nitrate transporter 1/peptide transporter family), NRT2,
C. canephora species are hybrids involving two coffee species, and members seem to transfer net \( \text{NH}_3 \) yet no ionic currents (et al., 2000; Yuan et al., 2007), whereas at least some plant AMT2 members seem to transfer net \( \text{NH}_3 \), yet no ionic currents across the membrane (Guether et al., 2009). The physiological roles of the AMT2 proteins are less well understood than those of AMT1 proteins (Neuhäuser et al., 2009).

AMTs and NRTs have been characterized in several plant species and genera: Citrus (Carnañes et al., 2009), Arabidopsis thaliana (Wang et al., 2012; Xu et al., 2012), Solanum lycopersicon (Gräff et al., 2011), Medicago truncatula (Young et al., 2011; Pelizzaro et al., 2014), Cucumis sativus (Migocka et al., 2013), Zea mays (Sorgona et al., 2011), Sorghum bicolor (Koegel et al., 2013) and Puccinellia tenuiflora (Bu et al., 2013). However, there are no reports on the molecular mechanisms of \( \text{NH}_4^+ \) uptake in coffee, including preferential \( \text{N} \) source.

Coffee is one of the most traded commodities in the world, and Brazil has the largest production and is the second largest consumer of the beverage (Lashermes et al., 2008; Mondego et al., 2011). Fertilization practices are among the most important costs in coffee production (Fehr et al., 2012). The genus Coffea (Rubiacaeae) has 124 species (Davis et al., 2011), with Coffea arabica and C. canephora being the two species of greatest economic importance (Vidal et al., 2010). C. arabica is an allotetraploid \( (2n = 4x = 44 - \text{C}^4 \text{E}^4) \) and C. canephora is a diploid species \( (2n = 2x = 22 - \text{CC}) \), allogamous and self-incompatible (Denoued et al., 2014). C. arabica originated from a spontaneous hybridization between two diploid coffee species, C. canephora and C. eugenioides \( (2n = 2x = 22 - \text{EE}) \) (Vidal et al., 2010).

We present here a phylogenetic reconstruction of AMT1, AMT2, NRT1/PTR, and NRT2 gene families from the recently released Coffea canephora genome (Denoued et al., 2014). These phylogenies are supplemented with transmembrane domain and subcellular localization predictions, and in silico expression profiling in C. canephora organs. We have also investigated the transcriptional responses of selected transporters under N starvation in C. arabica, as well as identified preferential N sources for uptake in C. arabica roots under N starvation. This study provides the basis to develop future in-depth physiological and molecular studies to fully address N utilization in plants of the Coffea genus, and opens a perspective on the understanding of modules that control \( \text{NH}_4^+ \) and \( \text{NO}_3^- \) homeostasis in coffee roots, which are important targets for breeding and biotechnology.

Material and Methods

Identification and phylogenetic analysis of NRT and AMT gene families in coffee

Basic procedures of annotation followed a report on the evolution of nitrate and ammonium transporters (von Wittgenstein et al., 2014). Protein sequences of AMTs and NRTs annotated in Arabidopsis thaliana, Medicago truncatula, Populus trichocarpa and Vitis vinifera by von Wittgenstein et al. (2014) were used as queries for BLASTP searches against the C. canephora genome (http://coffee-genome.org/).

The parameters BLASTP used were also based on von Wittgenstein et al. (2014), with an expected threshold lower than 1e-50 and at least 30% of identity. Transmembrane (TM) domains were predicted using TMHMM v2 software (Krogh et al., 2001). Sequences with at least 8 TM domains were compared with the reference sequences, and only the ones that had a maximum difference of 50 amino acids in length were selected for further analyses. Subcellular localization was predicted using MultiLoc2 (Blum et al., 2009), with the MultiLoc2-HighRes (Plant), 10 Locations algorithm. For phylogenetic analyses, we included Oryza sativa, Zea mays, Sorghum bicolor and Brachypodium distachyon protein sequences for each transporter family. Sequences were aligned using MUSCLE (Edgar, 2004). This alignment was used to generate neighbor-joining trees (Saitou and Nei, 1987) based on distance matrices using the Jones-Taylor-Thornton model and pairwise deletion. The resampling method was bootstrapping and consisted of 1,000 replicates. All procedures were run using MEGA6 software (Tamura et al., 2013). Phylogenies were rooted using Arabidopsis sequences belonging to another family as outgroup.

Transcriptional profile of N transporters in C. canephora

For in silico expression profiling, RNAseq data from different organs and tissues of C. canephora were obtained from the “RNA-seq RPKM” track available on JBrowser at the Coffee Genome Hub database (http://coffee-genome.org/; Dereeper et al., 2015). This data was compiled to a spreadsheet to generate heatmaps that use a color coding to differentiate expression levels. The expression unit used was reads per kilobase per million reads (RPKM). The software Bio-Analytic Resource for Plant Biology (BAR) HeatMapper Plus (http://bar.utoronto.ca/) was used to generate the heatmaps of AMTs and NRTs genes.
Transcriptional profile of N transporters in C. arabica roots - N starvation experiment

We evaluated the transcriptional profile of 3 AMT and 3 NRT transporters in C. arabica roots submitted to N starvation (Table 1), which had homologs in ESTs of the Brazilian Coffee Genome Consortium database (Mondego et al., 2011). Basic procedures of N starvation experiment are summarized in Figure S1 (Supplementary material). Overall procedures and plant nutritive solution are detailed in de Carvalho et al. (2013). After 4 weeks on hydroponic devices for acclimation, C. arabica L. cv. IAPAR59 5-month old plants were harvested for time point 0 and then transferred to a modified N-free solution, where lateral roots were harvested at 1 day and 10 days after transfer into the N-free solution. Experiments were conducted twice, with a minimum of three biological replicates per experiment. All samples were harvested between 09:30 am and 10:30 am. Biological replicates were represented by pools of coffee lateral roots of at least nine plants each, at the same developmental stage. After harvesting, all samples were frozen immediately in liquid nitrogen and stored at -80 °C until RNA extraction.

RNA isolation, cDNA synthesis and semi-quantitative RT-PCR

Total RNA from C. arabica L. cv. IAPAR59 roots was isolated following the same procedures used by previous studies of our group (dos Santos et al., 2011). We treated RNA samples with DNase to remove traces of DNA contamination, and after dissolved in RNase-free water, the RNA concentration was determined using a NanoDrop® ND-100 spectrophotometer (Waltham, MA, USA). Complementary DNA (cDNA) was synthesized in a final volume of 20 μL using 5 μg of total RNA by using SuperScript® III Reverse Transcriptase (Invitrogen), following the manufacturer’s instructions.

Primers (Table 1) were designed using Primer Express (version 3.0) according to parameters established by the software to obtain amplicons of 100 base pairs with a Tm of 60 °C ± 1 °C (Table 1). Amplification was performed according to the following temperature profile: 2 min initial denaturation at 94 °C; 30 cycles of 94 °C for 1 min, 60 °C for 1 min, 72 °C for 1 min; end extension of 3 min at 72 °C; final hold at 4 °C. Cycles for RT-PCR analysis were based on Brandalise et al. (2009). Amplicons were verified in 2% agarose gel electrophoresis with sodium boric acid (SB) buffer (0.5 M NaOH, pH adjusted to 8.5 with boric acid), stained with ethidium bromide and photographed. The captured images were processed for densitometric analysis using the ImageJ 1.43 U software, as previously described by Freschi et al. (2009) and dos Santos et al. (2015). Transcriptional profiles were normalized using EF1α, a reference gene recommended by de Carvalho et al. (2013) for this condition. Semi-quantitative RT-PCR analysis was repeated at least three times for each sample.

Measurement of 15N influx in coffee roots

Coffea arabica L. cv. IAPAR59 seedlings were hydroponically grown under non-sterile conditions in a greenhouse according to the following regime: 14/10 h light/dark and temperature 28 °C/18 °C. Plants were grown in nutrient solution containing 1 mM KH2PO4, 1 mM MgSO4, 250 μM K2SO4, 250 μM CaCl2, 100 μM Na-Fe-EDTA, 50 μM KCl, 50 μM H3BO3, 5 μM MnSO4, 1 μM ZnSO4, 1 μM CuSO4, and 1 μM NaMoO4 (pH adjusted by 2 mM MES, pH 5.8, Sigma-Aldrich). The nutrient solution was replaced every two days during the first week. After the acclimation period, the plants were submitted to N sufficient (+N, 2 mM NH4NO3) or N starvation (-N, without N supply) nutrient solution for three days. Influx measurements of 15N-isotope in plant roots were conducted after rinsing the roots in 1 mM CaSO4 solution for 1 min, followed by an incubation for 10 min in nutrient solution containing 0.2 mM or 2 mM of 15N-isotope with the equimolar concentration containing either 15NH4NO3 (42.52 atom% 15N) or NH4Cl (41.62 atom% 15N) as a sole N source, and finally washed in 1 mM CaSO4 solution. Roots were harvested and stored at -70 °C before milled. Each sample was ground in liquid N2 and dried at 55 °C for five days. The 15N and %N determination was performed by isotope ratio mass spectrometry (ANCA SL da Sercon, England) with 5 mg of dried samples.

Table 1 - Coffea arabica transcriptional analysis: RT-PCR primers and orthologs in Arabidopsis and C. canephora genomes.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Forward Primer</th>
<th>Reverse Primer</th>
<th>NCBI Accession</th>
<th>Arabidopsis thaliana</th>
<th>Coffea canephora</th>
</tr>
</thead>
<tbody>
<tr>
<td>CaAMTa</td>
<td>AGCCGAATACATCTGCAACC</td>
<td>GAAGGTATGTGCTGATGG</td>
<td>GW473095</td>
<td>AT4G13510</td>
<td>Cc03-g06810</td>
</tr>
<tr>
<td>CaAM Tb</td>
<td>CATCCTCTGGCTCTTACA</td>
<td>GCAATGAGGCACTGTGTTAT</td>
<td>GW483659</td>
<td>AT4G13510</td>
<td>Cc01-g14140</td>
</tr>
<tr>
<td>CaAMTC</td>
<td>TCAGTGTCATGTACCTCTGGA</td>
<td>GCAAGCGATGGAGAAAGAGC</td>
<td>GT683246</td>
<td>AT2G38290</td>
<td>Cc07-g19360</td>
</tr>
<tr>
<td>CaNRTa</td>
<td>TGACGCTGTCGAGCACTTGGA</td>
<td>CCAAGCTTCTCAAAGGTCTCA</td>
<td>GW749551</td>
<td>AT1G66850</td>
<td>Cc02-g36020</td>
</tr>
<tr>
<td>CaNRTb</td>
<td>CTCGGAGAAAGAGATGAGCAG</td>
<td>GGAAGACCACCCACAGTTTTA</td>
<td>GW442751</td>
<td>AT2G26690</td>
<td>Cc06-g08580</td>
</tr>
<tr>
<td>CaNRTC</td>
<td>GCTGCTGTCGTGGAAGAAG</td>
<td>CCAAGCTTCTCAAAGGTCTCA</td>
<td>GT693501</td>
<td>AT5G62680</td>
<td>Cc04-g15770</td>
</tr>
</tbody>
</table>

Nitrate and ammonium transporters in Coffea
Statistical Analysis

Statistical analyses was done by one-way ANOVA using Sisvar software (Ferreira, 2011), followed by Tukey’s multiple comparison tests (p < 0.05 level).

Results and Discussion

Genome-wide analysis of ammonium transporters in C. canephora genome

All N transporter families in C. canephora had a copy number under the range found for most eudicots (von Wittgenstein et al., 2014; Pii et al., 2014; Table 2). We identified eight copies of ammonium transporter genes, four belonging to the AMT1 family and the others to AMT2. Three members of super-group A compose the C. canephora AMT1 family, and one member belongs to B super-group (Figure 1), which is highly contrasting to Populus, a tree that contains an expanded family of ammonium transporters (Couturier et al., 2007; von Wittgenstein et al., 2014). The presence of only one member in the coffee tree genome suggests that genome duplication mechanisms were not relevant to AMT1 evolution in coffee trees.

The AMT1 gene family comprises four members with 9-11 predicted TM domains. Almost all AMT1 transporters were predicted to be located in the endoplasmic reticulum, and only one AMT1 (Cc03_006810) has been indicated with subcellular localization in the Golgi apparatus. Members of AMT2 family have 11 TM domains and only one (Cc07_g11400, sub-group B-II-E) was localized on the Golgi apparatus. Other C. canephora AMT2 members (sub-group A-II-E and B-I-E) are located in the endoplasmic reticulum. Interestingly, we did not find any AMT2 transporter in C. canephora from super-group A-I, the sole group with biochemically characterized members (von Wittgenstein et al., 2014). Detailed information on TM prediction and subcellular localization are available in Tables S1 and S2.

Table 2 - Comparison of members from the AMT1, AMT2, NRT1/PTR and NRT2 gene families in Viridiplantae, based in von Wittgenstein et al. (2014) and Pii et al. (2014).

<table>
<thead>
<tr>
<th>Species</th>
<th>AMT1</th>
<th>AMT2</th>
<th>NRT1/PTR</th>
<th>NRT2</th>
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<tbody>
<tr>
<td>Arabidopsis thaliana</td>
<td>5</td>
<td>1</td>
<td>51</td>
<td>6</td>
</tr>
<tr>
<td>Coffea canephora</td>
<td>4</td>
<td>4</td>
<td>57</td>
<td>3</td>
</tr>
<tr>
<td>Glycine max</td>
<td>5</td>
<td>5</td>
<td>96</td>
<td>3</td>
</tr>
<tr>
<td>Oryza sativa</td>
<td>2</td>
<td>6</td>
<td>65</td>
<td>3</td>
</tr>
<tr>
<td>Physcomitrella patens</td>
<td>5</td>
<td>10</td>
<td>18</td>
<td>8</td>
</tr>
<tr>
<td>Populus trichocarpa</td>
<td>6</td>
<td>5</td>
<td>70</td>
<td>7</td>
</tr>
<tr>
<td>Selaginella moellendorfii</td>
<td>1</td>
<td>0</td>
<td>31</td>
<td>2</td>
</tr>
<tr>
<td>Setaria italica</td>
<td>2</td>
<td>6</td>
<td>74</td>
<td>7</td>
</tr>
<tr>
<td>Vitis vinifera</td>
<td>1</td>
<td>1</td>
<td>44</td>
<td>4</td>
</tr>
</tbody>
</table>

In silico expression analysis of putative C. canephora AMT1 genes (Figure 3A) showed Cc01_g14140 as the lowest expressed AMT1 gene. Two genes (Cc01_g17670 and Cc09_g03020) were preferentially transcribed in roots, whereas Cc03_g06810 had higher expression in aboveground organs. Cc01_g17670 is the ortholog of the AtAMT1;4 gene (At4g28700), with 75% of identity. Both genes belong to group A-1E (Figure 1). AtAMT1;4 is a pollen high-affinity ammonium transporter; the overexpression of this gene in roots of mutant plants demonstrated that this gene is able to mediate ammonium uptake into A. thaliana roots (Yuan et al., 2009). Thus, probably Cc01_g17670 is also a high-affinity ammonium transporter, but not specific to pollen as AtAMT1;4, due to the low expression in stamina (0.1 RPKM).

Cc03_g06810, the ortholog of the AtAMT1;1 gene of A. thaliana (At4g13510), was the only gene expressed in all tissues, with higher expression in perisperm, indicating that ammonium transport may have some impact in fruit development. Compared to other Arabidopsis AMT1 genes, AtAMT1;1 is expressed more broadly, including roots, sepals, and leaves (von Wittgenstein et al., 2014), which may also explain the expression of Cc03_g06810 in all C. canephora tissues.

Considering a RPKM > 1, two members of the AMT2 family had expression in roots and two in aerial parts (Table S2). Cc07_g19360 was the highest expressed AMT2 gene, with prevalence in roots (Figure 3B). The closest homolog in Populus, P0PTR_0001s31280, (Figure 2) has a prominent expression in reproductive tissues (von Wittgenstein et al., 2014), a pattern that is not observed in coffee.

Nitrile transporters in the C. canephora genome

The NRT1/PTR and NRT2 families were represented by 57 and three copies, respectively, in the C. canephora genome (Table 2). The C. canephora NRT1/PTR family is similar to the average for land plants, which has 54 family members (von Wittgenstein et al., 2014). Most of them were predicted as cytoplasmatic (25) or located in the plasma membrane (15) (Table S3). Other genes were located in Golgi apparatus (12), peroxisome (3), endoplasmic reticulum (Cc01_g06540) and extracellular regions (Cc01_g31780). The members of this family possess from 8-12 predicted TM domains. All 10 NRT1 superfamilies are represented in C. canephora (Figure S2). Considering an RPKM > 1, 12 NRT1/PTR members were expressed in all tissues and three genes (Cc01_g11750, Cc04_g15710, Cc01_g05330) were exclusively expressed in roots (Figure 4, Table S3).

Cc08_g12800, although expressed in aboveground organs, was the transcriptionally most active NRT transporter in roots (Figure 4, Table S3). The Arabidopsis ortholog of this gene is AtNRT1;1 (At1g12110); both genes are in
super-group B, group I E (Figure S2). AtNRT1;1 is highly expressed in roots, and is described as a dual transporter that acts in high and low-affinity nitrate uptake, mediated by phosphorylation (Liu and Tsay, 2003). Phylogenetic relations and expression profiles indicate that Cc08_g12800 probably has the same function as AtNRT1;1.

We observed that the gene Cc11_g13590 is the most expressed in aboveground organs (Table S3). This gene is in the super-group D, group IV E with the ortholog AtNRT1;7 (At1g69860) (Figure S2), that is expressed in phloem of older leaves, more specifically restricted to the sieve element and companion cell complex (Fan et al., 2009). Therefore, the probable function of this gene is to transport nitrate from older leaves to tissues demanding N (Fan et al., 2009). If the Cc11_g13590 gene shares the same function of its ortholog, this may be the reason for the higher expression of this gene in several tissues. In pistils, the most expressed gene of NRT1/PTR family was Cc04_g15770, whose ortholog in the Arabidopsis genome is AtNPF2.11 (At5g62680), also named as AtGTR2. This
Figure 2 - Neighbor joining phylogenetic analysis of the AMT2 family. The tree was rooted using an A. thaliana AMT1 gene as an outgroup. Percent bootstrap values from 1,000 replicates are given. All C. canephora genes are placed in clades with > 50% of bootstrap support. Taxonomic groups are colored based on groups: dark green and red refer to group A eudicot sequences; dark blue, dark grey, light grey and light green represent monocot sequences in group A-II; blue and purple illustrate dicot sequences in group B, grey represents group B monocot sequences. Accession numbers are shown. Codes were retrieved from the Coffee Genome Hub for C. canephora sequences and Phytozome for all other species. Phylogenetic groups were based in von Wittgenstein et al. (2014).
gene acts as a transporter for glucosinolates, suggesting that it possibly evolved through neo-functionalization of NRT1/PTR family members (Nour-Eldin et al., 2012). AtNPF2.11 has its higher transcription in petals, sepals, and stamina (von Wittgenstein et al., 2014). Since Cc04_g15770 had almost no expression in stamina, more studies are necessary to characterize the role of that C. canephora gene in reproductive tissues. In the seed and perisperm, the gene that had higher transcriptional values was Cc02_g05650, in agreement with the high expression profile of its ortholog oligopeptide transporter At2g40460 in Arabidopsis seeds (von Wittgenstein et al., 2014). These two genes are part of the super-group I, group I E (Figure S2).

The NRT2 family comprises three members (Figure 5) that were predicted with 11 TM domains, two of them predicted to be localized in peroxisome, whereas the other one (Cc01_g10620) was predicted to be in cytoplasm. The NRT2 gene family had two genes exclusively expressed in roots, considering RPKM > 1 (Table S4), where the most active was Cc01_g10640. The gene with higher expression in the aerial parts (Cc11_g15480) was also the less expressed in roots (Figure 6; Table S4).

AtNRT2;1 (At1g08090) shares higher identity with Cc01_g10640 than the other Arabidopsis NRT2 genes in group I E (Figure 5). AtNRT2;1 is the major inducible high-affinity transporter of nitrate (iHATS). When this gene was disrupted in Arabidopsis, 72% of the iHATS was reduced (Li et al., 2007). The transcriptional profile of Cc01_g10640 suggests that this gene probably acts in the same function as AtNRT2;1. AtNRT2;1 is targeted to the root plasma membrane (Chopin et al., 2007), but the predicted localization of Cc01_g10640 is in peroxisomes. According to von Wittgenstein et al. (2014), the high degree of peroxisome localization for NRT2 is unexpected, and it may be due to difficulties predicting hydrophobic, membrane bound proteins, added to inaccuracy in recently-released genome annotations.

The gene Cc11_g15480, that has been shown more expressed in aerial parts is related to AtNRT2;5 (At1g12940), and these genes are in group II E. AtNRT2;5 is highly expressed in senescing leaves, and is described as being a nitrate repressible gene, having maximum expression in the absence of nitrate (Okamoto et al., 2003).

Transcriptional responses of N transporters in C. arabica roots

We analyzed the transcriptional profile of three AMT and three NRT transporters in C. arabica in response to N depletion. Orthologs of these genes in C. canephora genome are indicated in Table 1 and Supplementary Tables S1 to S3. Since transcriptional changes related to the lack of N sources can also be species-specific, it is important to highlight that further work should address if the same transcriptional pattern is observed in C. canephora; but, to our knowledge, this is the first study that evaluates the transcriptional profile of N transporters in coffee tree roots.

CaAMTa and CaAMTb were induced by N starvation (Figure 7A and B). CaAMTb is an AMT1 transporter with low expression in roots of C. canephora (Figure 3, Table S1), which is in agreement with RT-PCR analysis, where this gene was the lesser expressed among the ammonium transporters under N-sufficient conditions. Under N suppression, CaAMTb was the most induced gene, suggesting its participation in ammonium uptake in N-deficiency conditions and warranting further studies in functional analyses to depict its transport capacity.

Nitrate transporters displayed distinct transcriptional patterns (Figure 8): CaNRTa and CaNRTc showed an increasing gradient of transcripts, suggesting a direct role in molecular responses to N starvation, while CaNRTb was down-regulated by short-term N-starvation and induced in long-term N-starvation.
The gene with most prominent changes in transcriptional values under N depletion was $\text{CaNRTa}$. Its ortholog in $\text{C. canephora}$, $Cc02\text{g36020}$, is expressed in several tissues, with prevalence in pistil. Kanno et al. (2012) demonstrated that the Arabidopsis ortholog of this N transporter (Table 1, Figure S2) is also involved in abscisic acid transport, suggesting that this transporter may have role in several abiotic stress responses.

Uptake of ammonium exceeds nitrate in $C. \text{arabica}$ roots

To determine the preferential inorganic N source of coffee roots, plants were acclimated in nutrient solution under N-sufficient or N-deficient conditions and short-term $^{15}$N-labeled influxes with equimolar concentrations of $^{15}\text{NH}_4\text{NO}_3$ or $^{15}\text{NH}_4\text{NO}_3$ were measured. For HATS activity, root $^{15}$N-label was measured at 0.2 mM, and the LATS activity was estimated for 2 mM of external $^{15}\text{NH}_4^+$ or $^{15}\text{NO}_3^-$ concentrations. At sufficient N supply, $^{15}\text{NH}_4^+$ uptake measured at high-affinity concentration rates exceeded that of $^{15}\text{NO}_3^-$ by 2.3-fold (Figure 9A), while in N-deficient plants, the ammonium influxes were 3.5-fold higher compared to nitrate uptake (Figure 9A). LATS activity became apparent at higher external N concentration, 2 mM $^{15}\text{NH}_4\text{NO}_3$ or $^{15}\text{NH}_4\text{NO}_3$, where $^{15}\text{NH}_4^+$ influxes were 2.3-fold increased under N sufficient and 1.6-fold higher for N deficient roots in comparison to low external N supply (Figure 9A and B). By contrast, the $\text{NO}_3^-$ LATS displayed less activity, since only 1.7-fold and 1.5-fold higher $^{15}\text{NO}_3^-$ influxes were observed under ample and limited N supply, respectively (Figure 9B), when compared to HATS. In addition, at low affinity external concentrations, $^{15}\text{NH}_4^+$ influxes were 3.5 times higher than those of $^{15}\text{NO}_3^-$, independent of the N nutritional status of the plants (Figure 9B). Taken together, these results demonstrate that high and low-affinity transport systems in coffee roots are active for both inorganic N forms, and that under low external N availability, the preference for ammonium uptake over nitrate indicates that the HATS is differentially regulated. Evidence for this come from the $^{15}$N-labeled influxes in contrasting N supply growth conditions, in which N deficiency for three days caused an induction of 1.3-fold of HATS activity for ammonium influxes but not for nitrate uptake rates (Figure 9A). Conversely, regulation of LATS activity was absent irrespective of N form or plant N status (Figure 9B).

Physiological studies have demonstrated the presence of two high affinity transport systems for nitrate and one for ammonium in higher plants (Crawford and Glass, 1998; Loqué and von Wirén, 2004). Influx measurements in roots of several species revealed that a low capacity, constitutive active transport system is responsible for acquisition of nitrate and ammonium from low external N concentrations, and the extent of this absorption is variable among different

**Figure 4** - *In silico* expression profile of $C. \text{canephora}$ NRT1/PTR gene family. RNAseq data from roots, stamen, pistil, leaves, perisperm, and endosperm were obtained from Coffee Genome Hub database.
species (Siddiqi et al., 1989; Serna et al., 1992; Wang et al., 1993; Kronzucker et al., 1997, 1998; Näsholm et al., 1998; Rawat et al., 1999; Zhuo et al., 1999; von Wirén et al., 2000; Tischner, 2000). Furthermore, for both N forms, an inducible high affinity transport system (iHATS) occurs in plants, in which HATS activity is transiently activated under N limited growth conditions and is repressed by high external N supply (Rawat et al., 1999; von Wirén et al., 2000; Nazoa et al., 2003; Orsel et al., 2006; Loqué et al., 2006). In addition, a key feature of the nitrate iHATS activity is that it can be rapidly induced in the presence of nitrate (Aslam et al., 1996; Kronzucker et al., 1999) although it seems to be less effective for ammonium (Loqué and von Wirén, 2004; Loqué et al., 2007; Lanquar et al., 2009).

The lack of activation of nitrate uptake by N deficient coffee roots might indicate that ammonium either causes a
repression on nitrate uptake mediated by HATS, or that NO$_3$-HATS is unable to be regulated under these conditions to sustain efficient nitrate acquisition in coffee roots. The inhibitory effect of ammonium on NO$_3$-HATS is a common feature previously shown in roots from several species, irrespective of plant N status (Minotti et al., 1969; Lee and Drew, 1986; Marschner et al., 1991; Orsel et al., 2006; Robinson et al., 2011). In contrast, the inability to regulate nitrate iHATS under N deficiency is unknown, despite the fact that iHATS were shown to be defective in Citrus roots under nitrate provision or decreased NH$_4$/NO$_3$ ratios (Camañes et al., 2009). In distinction to the regulation of the nitrate HATS, the LATS for ammonium and nitrate influx appeared to be insensitive to N status in coffee roots, as previously also shown for other higher plants (Siddiqi et al., 1990; Wang et al., 1993; Rawat et al., 1999; Cerezo et al., 2000), with exception for Arabidopsis (Okamoto et al., 2003). Considering that only a few physiological conditions have been investigated, the results presented here provide initial evidence for differential regulation of HATS activity for nitrate and ammonium in coffee roots and therefore, open questions and perspectives for further investigation.
Regardless of the mechanism responsible for this effect on nitrate uptake in coffee roots, our results show that when both inorganic N sources (\(\text{NH}_4^+\) and \(\text{NO}_3^-\)) are present in the nutrient solution, uptake of \(\text{NH}_4^+\), mediated by either transport system (HATS or LATS), is favored compared to that of \(\text{NO}_3^-\). This is commonly observed in several plant species and genera, including Citrus (Serna et al., 1992; Gessler et al., 1998; Gazzarrini et al., 1999; Min et al., 2000; Camañes et al., 2009), although, this situation results in greater availability of nitrate for leaching or denitrification, and further reduces the N use efficiency in coffee plants.

Conclusions

We presented in this study a genome-wide inventory of ammonium and nitrate transporter families in C. canephora, taking advantage of this recently released genome. We depicted transcriptional profile and phylogenetic patterns of N transporters in this tree species, and demonstrated that C. canephora genomic and transcriptional patterns follow the ones observed for most eudicots. Transcriptional analysis of selected transporters in C. arabica roots display distinct patterns, reinforcing that each member of the AMT and NRT families has a particular role in N uptake, which is influenced by N deprivation. N-starvation demonstrated that ammonium uptake is favored over nitrate, in C. arabica roots. In summary, our study shows that, although nitrate transporters are prevalent compared to ammonium transporters in the Coffea genome, ammonium uptake is a preferential inorganic N source compared to nitrate. Additional approaches to dissect N-regulatory networks and molecular mechanisms underlying the spatial and temporal nature of the N transport response according to N demand for coffee plants are still necessary for detailed comprehension of N metabolism in coffee trees.

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References

Alber A, Ehlting B, Ehlting J, Hawkins BJ and Rennenberg H (2012) Net \(\text{NH}_4^+\) and \(\text{NO}_3^-\) flux, and expression of \(\text{NH}_4^+\) and \(\text{NO}_3^-\) transporters in roots of Picea glauca. Trees 26:1403-1411.


Davis AP, Tosh J, Ruch N and Fay MF (2011) Growing coffee: Psilanthus (Rubiacceae) subsumed on the basis of molecular and morphological data; implications for the size, morphol-

Figure 9 - HATS (A) and LATS (B) under N starvation in C. arabica roots, using ammonium nitrate labeled with \(^{15}\text{N}\). Details of the uptake experiment are described in Material and Methods.


Grazziotto LF, Obladik P, Yuan L, Loqué D, Frommer WB and von Wirén N (2011) N-terminal cysteines affect oligomer stabil-


Supplementary material

The following online material is available for this article:

Figure S1 - N starvation experiment

Figure S2 - Neighbor joining phylogenetic analysis of the NRT1/PTR family.

Figure S3 - Semi-quantitative RT-PCR analysis of CaAMTs and CaNRTs.

Table S1 - Coffea canephora AMT1 gene family overall features.

Table S2 - Coffea canephora AMT2 gene family overall features.

Table S3 - Coffea canephora NRT1 gene family overall features.

Table S4 - Coffea canephora NRT2 gene family overall features.

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