Nitrogen metabolism of two contrasting poplar species during acclimation to limiting nitrogen availability

Jie Luo1, Hong Li2, Tongxian Liu2, Andrea Polle3, Changhui Peng4 and Zhi-Bin Luo1,4,*

1 College of Life Sciences and State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A&F University, Yangling, Shaanxi 712100, PR China
2 Key Laboratory of Applied Entomology, College of Plant Protection, Northwest A&F University, Yangling, Shaanxi 712100, PR China
3 Büsgen-Institute, Department of Forest Botany and Tree Physiology, Georg-August University, Büsgenweg 2, 37077 Göttingen, Germany
4 Key Laboratory of Environment and Ecology in Western China of Ministry of Education, College of Forestry, Northwest A&F University, Yangling, Shaanxi 712100, PR China

* To whom correspondence should be addressed. E-mail: luozbbill@163.com

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Abstract

To investigate N metabolism of two contrasting Populus species in acclimation to low N availability, saplings of slow-growing species (Populus popularis, Pp) and a fast-growing species (Populus alba × Populus glandulosa, Pg) were exposed to 10, 100, or 1000 μM NH4NO3. Despite greater root biomass and fine root surface area in Pp, lower net influxes of NH4+ and NO3– at the root surface were detected in Pp compared to those in Pg, corresponding well to lower NH4+ and NO3– content and total N concentration in Pp roots. Meanwhile, higher stable N isotope composition (δ15N) in roots and stronger responsiveness of transcriptional regulation of 18 genes involved in N metabolism were found in roots and leaves of Pp compared to those of Pg. These results indicate that the N metabolism of Pp is more sensitive to decreasing N availability than that of Pg. In both species, low N treatments decreased net influxes of NH4+ and NO3–, root NH4+ and foliar NO3– content, root NR activities, total N concentration in roots and leaves, and transcript levels of most ammonium (AMTs) and nitrate (NRTs) transporter genes in leaves and genes involved in N assimilation in roots and leaves. Low N availability increased fine root surface area, foliar starch concentration, δ15N in roots and leaves, and transcript abundance of several AMTs (e.g. AMT1;2) and NRTs (e.g. NRT1;2 and NRT2;4B) in roots of both species. These data indicate that poplar species slow down processes of N acquisition and assimilation in acclimation to limiting N supply.

Key words: Gene expression, glutamate synthase, glutamine synthetase, net flux, nitrate reductase, nitrite reductase, plasma membrane H+-ATPase, poplar, stable carbon isotope.

Introduction

As woody crops, forest plantations hold a great potential for the pulp and paper industry, carbon mitigation, and biomass production for biofuels (Luo et al., 2006; Luo and Polle, 2009; Novaes et al., 2009; Studer et al., 2011). Plantations of some fast-growing tree species such as Populus spp. have been widely established in recent years (Weih, 2004; Polle and Douglas, 2010; Rennenberg et al., 2010). As a riparian species, Populus in its natural habitat is supplied with sufficient nitrogen (N) derived from intensive N-fertilization application in agriculture (Rennenberg et al., 2010; Koyama and Kielland, 2011). Due to the high demand of fertile soil for agriculture, however, poplar plantations have often been established on marginal lands where soil N is limiting (Rennenberg et al., 2010; Bilodeau-Gauthier et al., 2011). In this context, it is of
particular importance to select poplar species with tolerance to low N availability.

The genus *Populus* contains about 30–40 species which may differ in N metabolism (Calfapietra et al., 2007; Finzi et al., 2007; Euring et al., 2012; Li et al., 2012). For instance, *Populus tremula* × *Populus tremuloides* is a species that often occurs on nutrient-poor soil. The growth and wood properties of this species are more responsive to different N levels than those of *Populus trichocarpa* which is adapted to fluctuating N supply (Euring et al., 2012). These results highlight that it is essential to better understand the distinctness of N metabolism in different poplar species in order to select poplars with tolerance to low N availability.

Although little information is available on responses of N metabolism in different woody plants to low N availability, distinct N metabolism has been reported in different herbaceous species or genotypes in response to N deficiency (Lawlor et al., 1987a, 1988, 1989; Lawlor, 2002; Hirel et al., 2007; Shen et al., 2013). For instance, some maize varieties displayed a higher capacity to absorb and utilize N than the others (Banziger et al., 1997; Toledo Marchado and Silvestre Fernandes, 2001). In cereal crops, earlier studies demonstrated that N deficiency in soil often led to altered root length and branching and decreased soluble protein concentration and photosynthetic activity (Maizlish et al., 1980; Lawlor et al., 1987b, 1989; Lawlor, 2002; Hirel et al., 2007). Plants with tolerance to low N are often associated with higher photosynthetic N use efficiency (PNUE), greater root length, and surface area per volume of soil (Lawlor, 2002; Hirel et al., 2007; Shen et al., 2013). However, the physiological and molecular mechanisms remain to be elucidated for plant species differing in tolerance to low N supply.

In plants, the N metabolism process involves uptake, transport, assimilation, and utilization for amino acid biosynthesis and ultimately for growth (Nunes-Nesi et al., 2010). Each of these steps may be regulated slightly different, leading to differences in N metabolism and performance of plants with distinct ecological requirements. In herbaceous plants, the N metabolism processes are well documented (Fig. 1), which may serve as a conceptual model to address N metabolism of different poplar species in response to low N availability.

In the N uptake process, NH$_4^+$ and nitrate NO$_3^-$ in soil solution are the two major inorganic N forms for plant absorption. Although both ions can be used by plants, the energetic, biochemical, and molecular features of NH$_4^+$ and NO$_3^-$ are different for metabolism, leading to distinct net fluxes of both ions at the root surfaces and NH$_4^+$ or NO$_3^-$ preference of plants (Jackson et al., 2008; Patterson et al., 2010). Using $^{15}$N labelling, it was demonstrated that some woody plants prefer NH$_4^+$ (Rennenberg et al., 2009, 2010). Additionally, net fluxes of NH$_4^+$ and/or NO$_3^-$ at the root surfaces have been investigated using ion-selective microelectrodes in herbaceous and woody plants (Plassard et al., 2002; Gobert and Plassard, 2007; Hawkins et al., 2008; Hawkins and Robbins, 2010; Alber et al., 2012; Luo et al., 2013), providing a better understanding of electrophysiological processes of NH$_4^+$ and NO$_3^-$ acquisition. The net fluxes of both NH$_4^+$ and NO$_3^-$ are coupled with the activities of plasma membrane (PM) H$^+$-ATPases in fine roots of *Populus popularis* (Luo et al., 2013). However, comparisons of fluxes of NH$_4^+$ and NO$_3^-$ at the root surface of poplar species with large differences in growth are missing.

The fluxes of NH$_4^+$ and NO$_3^-$ are mediated by various transporters for ammonium (AMTs) and nitrate (NRTs) (Rennenberg et al., 2010; Xu et al., 2012). Some AMTs and NRTs have been functionally elucidated in *Arabidopsis thaliana* (Wang et al., 2012; Xu et al., 2012). For instance, transcript abundance of AtAMT1;1 is strongly increased by N starvation and reduced upon NH$_4^+$ supply in *Arabidopsis* roots (Engelsberger and Schulze, 2012). Some NRT members such as AtNRT1;1, AtNRT1;2, AtNRT2;1, and AtNRT3;1 play pivotal roles in NO$_3^-$ uptake and signalling (Yong et al., 2010; Kotur et al., 2012; Wang et al., 2012). In the genome of *P. trichocarpa*, 14 putative AMTs have been documented (Tuskan et al., 2006; Couturier et al., 2007), whereas less is known about the NRT members (Plett et al., 2010; Rennenberg et al., 2010; Li et al., 2012). Several studies showed that transcripts of putative poplar transporters (e.g. AMT1;2, AMT1;6, AMT2;1, NRT1;1, NRT1;2, NRT2;4B, NRT2;4C, NRT3.1B, and NRT3.1C) were responsive to environmental fluctuations under non-limiting N conditions (Selle et al., 2005; Couturier et al., 2007; Dluzniewska et al., 2007; Ehlting et al., 2007; Plett et al., 2010; Li et al., 2012). However, it remains unknown how transcriptional regulation of these transporters responds to limiting N supply in different poplar species.

After uptake into the roots, a large amount of NH$_4^+$ can be assimilated locally and the remainder is translocated to leaves or other parts of the plant, whereas only a limited amount of NO$_3^-$ is assimilated in roots and most NO$_3^-$ is transported to leaves (Black et al., 2002; Xu et al., 2012). In the assimilation process, NO$_3^-$ is converted to NH$_4^+$ by nitrate reductase (NR) and nitrite reductase (NiR) (Xu et al., 2012). Subsequently, NH$_4^+$ can be assimilated to glutamine catalysed by glutamine synthetase (GS) (Castro-Rodriguez et al., 2011; Coleman et al., 2012). The formation of glutamate requires glutamine and 2-oxoglutarate in a reaction catalysed by glutamate synthase (GOGAT) (McAllister et al., 2012). Additionally, glutamate can be synthesized by glutamate dehydrogenase (GDH) under consumption of NH$_4^+$ and 2-oxoglutarate (McAllister et al., 2012). Very little is known about the response of these enzymes to low N supply in different poplar species.

Although forest plantations often grow on nutrient-poor soils (Johnson, 2006; Rennenberg et al., 2009), N-related studies in trees mainly addressed the effects of fertilization but less to uncover the responses to N-limitation (Cooke and Weih, 2005; Rennenberg et al., 2009, 2010; Lukac et al., 2010; Millard and Grelet, 2010). Recently, we found that growth, carbon, and N physiology, and wood properties of the fast-growing *Populus alba* × *Populus glandulosa* (Pg), which generally grows on relatively fertile soils, displays a stronger responsiveness to N-fertilization than the slow-growing *P. popularis* (Pp) which is often found on nutrient-deficient soils (Li et al., 2012). The differential responses are ascribed to prioritized resource allocation to the leaves and accelerated N physiological processes in the fast-growing Pg under
higher N supply levels. However, it remains unknown how N metabolism processes and key components involved in these processes of Pp and Pg respond to external low N availability. This study exposed Pp and Pg to low N levels. Measurements of morphological (root characteristics), physiological (e.g. photosynthesis, net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$, and other N-containing metabolites which can be utilized by plant growth. At the cellular level, N metabolism in plants can be affected by external low N availability. At the plant level, root characteristics, photosynthetic activity, and leaf properties can be altered in response to low N supply (this figure is available in colour at JXB online).
accumulation of NH$_4^+$, NO$_3^-$, and NO$_2^-$, total N concentration, and δ$^{15}$N), and molecular (transcript levels of representative genes involved in N metabolism) parameters known to be important for acclimation to low N availability were conducted. Furthermore, multivariate analysis was applied to dissect the importance of parameters as contributors to the acclimation of N metabolism in both poplar species to low N supply. The following questions were specifically addressed: (i) do root morphology, photosynthesis, and N metabolism of Pp and Pg display different response patterns to limiting N supply? and (ii) what are the physiological and transcriptional regulation mechanisms of Pp and Pg in acclimation to low N availability?

Materials and methods

Plant cultivation and N treatment

Cuttings of the slow-growing P. *populus* (Pp) and the fast-growing *P. alba* × *P. glandulosa* (Pg) were rooted as described previously (Li et al., 2012), and planted in pots (10 l) filled with fine sand. Plants were cultivated in a greenhouse (natural light, day/night 25/20 °C, 75% relative humidity) and provided with 50 ml Long Ashton (LA) nutrient solution, which contains 1000 μM NH$_4$NO$_3$ (Dluzniewska et al., 2007) every other day. After 6 weeks, plants with similar height (±0.6 cm) were selected for further study. The root systems of selected plants were carefully washed with tap water. Plants of each species were divided into three groups with 18 plants for each group. Subsequently, plants of three groups from each species were cultivated in hydroporons with modified LA solution (0.5 mM KCl, 0.9 mM CaCl$_2$, 0.3 mM MgSO$_4$, 0.6 mM KH$_2$PO$_4$, 42 μM K$_3$HPO$_4$, 10 μM Fe-EDTA, 2 μM MnSO$_4$, 10 μM H$_2$BO$_3$, 7 μM Na$_2$MoO$_4$, 0.05 μM CoSO$_4$, 0.2 μM ZnSO$_4$, and 0.2 μM CuSO$_4$) containing 10, 100, or 1000 μM NH$_4$NO$_3$, respectively, and the nutrient solution was adjusted to pH 5.5. The LA solution was refreshed every 2 days. In the greenhouse, the position of each plant was randomly assigned and altered once a week. At the beginning of the N treatment, the apex of each plant was marked by using a laboratory marker to distinguish the shoots formed during the N treatment. After hydroponic cultivation with N treatments for 3 weeks from 20 June to 10 July, 12 plants of each group were used for gas exchange determination prior to harvest and the remaining six plants of each group were used for measurements of net fluxes of NH$_4^+$ and NO$_3^-$.

Gas exchange and harvesting

The gas exchange of three mature leaves (leaf plastochron index = 8–10) formed during N treatment was determined for each plant. Net photosynthetic rates (A), stomatal conductance (gs), and transpiration rates were determined with a portable photosynthesis system (Li-Cor-6400, Li-Cor, Lincoln, NE, USA) and an attached LED light source (6400–02) as described by Cao et al. (2012). Harvested roots or leaves were wrapped with tinfoil and immediately frozen in liquid N. Root or leaf samples were ground into fine powder in liquid N with a mortar and pestle and stored at −80 °C. Frozen powder (c.100 mg) from roots or leaves of each plant was dried at 60 °C for 72 h to determine the fresh-to-dry-mass ratio. For further biochemical analysis, equal weight of fine powder from roots or leaves of two plants within each group was combined to form a well-mixed sample.

Analysis of net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$

To analyse net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$ at the root surface, three white fine roots (c.1.5 mm in diameter) were randomly selected from the root system of each plant. Net fluxes of these ions were measured non-invasively using scanning ion-selective electrode technique (SIET, SIET system BIO-003A, Younger USA Science and Technology, Falmouth, MA, USA) by Xuyue Science and Technology (Beijing, China). The SIET system and its application in net ion flux detection were described in detail (Li et al., 2010; He et al., 2011; Luo et al., 2013). The ion-selective microelectrode with 2–4 μm aperture was manufactured and siliconized with a backfilling solution and an ion-selective liquid cocktail.

To find out the positions along the root where the maximal net fluxes of NH$_4^+$ and NO$_3^-$ take place, a preliminary experiment was performed using plants treated with 100 μM NH$_4$NO$_3$ by taking an initial measurement at the root apex, followed by measurements at 300 μm intervals (in the region of 0–2100 μm) or 5 mm intervals (in the region of 5–30 mm) along the root tip (Supplementary Fig. S1A, available at JXB online). Ion gradients near the root surface were measured by moving the ion-selective microelectrode between two positions (±0.3 μm in distance) in a perpendicular direction to the root axis. The recording rate for these ion fluxes was one reading per 6 s and ion flux was recorded at each measurement point for 10 min. For the positions where the maximal net fluxes of NH$_4^+$ and NO$_3^-$ occur in roots, net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$ were further investigated in detail. A fine root was transferred to a Petri dish containing 10 ml measuring solution (0.1 mM KCl, 0.1 mM CaCl$_2$, pH 5.5) with 10, 100, or 1000 μM NH$_4$NO$_3$ according to the N treatment of the selected root, and equilibrated for 20 min. Prior to the measurement, the root was transferred to a new Petri dish containing fresh measuring solution and net NH$_4^+$ fluxes were monitored for 10 min. Afterwards, net NO$_3^-$ fluxes were measured for 10 min in the same root and finally, net H$^+$ fluxes were recorded for 10 min in the root.

Isolation of the PM and measurement of PM H$^+$-ATPase activity

PM vesicles of root cells were isolated according to the method of Sorgona et al. (2011) with minor modification. Briefly, fine powder of roots (c.2 g) was homogenized with 3 ml extraction solution containing 250 mM sucrose, 10% (v/v) glycerol, 10 mM glyceral-1-phosphate, 2 mM MgSO$_4$, 2 mM EDTA, 2 mM EGTA, 2 mM ATP, 2 mM DT T, 5.7% (w/v) choline chloride, 25 mM 1,3-bis(tris(hydroxymethyl)-methyl-aminoethylether)propane (BTP, pH 7.6 with 2(N-morpholino)ethanesulfonic acid, MES), 1 mM PMSF, and 20 μg ml$^{-1}$ chymostatin at 4 °C. After centrifugation (12,700 g, 4 °C, 30 min), the pellets were suspended over a 25/38% discontinuous sucrose gradient (5 mM MES containing all proteactins present in the extraction solution, pH 7.4). Afterwards, the gradient was centrifuged again (12,700 g, 4 °C, 60 min). The pellets were resuspended in a medium containing 20% glycerol (v/v), 2 mM EGTA, 2 mM EDTA, 0.5 mM ATP, 1 mM PMSF, 2 mM DT T, 20 μg ml$^{-1}$ chymostatin, 5.7% choline chloride, and 5 mM BTP buffered at pH 7.0 with MES and immediately frozen in liquid N and stored at −80 °C.


PM H⁺-ATPase activity was determined spectrophotometrically at 700 nm as described by Sorgona et al. (2011) with minor modifications. In brief, assays were carried out at 30 °C in 0.5 ml medium containing 30 mM BTP/MES (pH 6.5), 5 mM MgSO₄, 50 mM KCl, 4 mM ATP, 0.6 mM Na₂MoO₄, 100 mM KNO₃, 1.5 mM NaN₃, and 0.02% (w/v) polyethylene glycol 200001 either, with or without 100 μM vanadate (an inhibitor of P-type H⁺-ATPase). The difference between these two activities was attributed to the PM H⁺-ATPase. Sodium azide and KNO₃ were used as selective inhibitors of mitochondrial and tonoplast H⁺-ATPase, respectively (Zhu et al. 2009). The reaction was initiated by adding membrane vesicles (5–10 μg membrane protein) and stopped after 30 min with a solution containing 2% (v/v) concentrated H₂SO₄, 5% (v/v) SDS, 0.7% Na₂MoO₄, and 10% ascorbic acid. After solubilizing the membrane vesicles with 0.5 M NaOH (Gogstad and Krutnes, 1982), the total soluble protein was estimated according to Bradford (1976). PM H⁺-ATPase activity was expressed as that inhibited by 100 μM vanadate.

**Determination of NH₄⁺, NO₃⁻, and NO₂⁻ concentration**

NH₄⁺ concentration in roots and leaves was determined based on the Berthelot reaction (Brautigam et al. 2007; Luo et al., 2013). In brief, fine powder (c.100 mg) was homogenized in an extraction solution (1 ml 100 mM HCl and 500 μl chloroform). The extraction solution was centrifuged (10,000 g, 4 °C, 10 min) after shaking for 15 min at 4 °C. The aqueous phase was transferred to a 2 ml tube with 50 mg activated charcoal, mixed well, and centrifuged (12,000 g, 4 °C, 5 min) again. NH₄⁺ concentration in the supernatant was determined spectrophotometrically at 620 nm.

NO₃⁻ concentration in samples was analysed as suggested by Patterson et al. (2010). Fine powder (c.100 mg) was extracted in 1 ml deionized water at 45 °C for 1 h. After centrifugation (5000 g, 20 °C, 15 min), the supernatant was used for nitrate quantification. The supernatant (0.2ml) was mixed thoroughly with 0.8 ml of 5% (w/v) salicylic acid in concentrated H₂SO₄. After incubation at room temperature for 20 min, 19 ml of 2 M NaOH was added to raise the pH to above 12. The solution was cooled to room temperature before NO₃⁻ concentration was determined spectrophotometrically at 410 nm.

NO₂⁻ concentration in samples was quantified as described by Ogawa et al. (1999). Frozen fine powder (c.100 mg) was extracted by an extraction buffer containing 50 mM TRIS-HCl (pH 7.9), 5 mM cysteine, and 2 mM EDTA. After centrifugation (10,000 g, 20 °C, 20 min), 500 μl supernatant was mixed with 250 μl 1% sulfanilamide and 250 μl 0.02% N-(1-naphthyl)-ethylene-diamine dihydrochloride in 3.0 M HCl. NO₂⁻ concentration was quantified spectrophotometrically at 540 nm.

**Determination of enzyme activities**

Activities of NR (EC 1.7.99.4) and NiR (EC 1.7.2.1) were determined in roots and leaves according to the methods of Ehtling et al. (2007) and Ogawa et al. (1999), respectively. Briefly, frozen powder (c.200 mg) was extracted in an extraction buffer (100 mM HEPES-KOH (pH 7.5), 5 mM Mg-acetate, 5 mM DTT, 1 mM EDTA, 0.5 mM PMSF, 20 mM FAD, 5 mM Na₂MoO₄, 10% (v/v) glycerin, 1% (w/v) polyvinyl polypyrrolidone, 0.5% BSA, 0.1% (v/v) TritonX-100, and either 25 mM leupeptine for leaves or 25 mM chymostatin for roots). The crude extract was used for NR and NiR assays.

For NR, the extract was added to the reaction mixture (100 mM HEPES-KOH (pH 7.5), 6.0 mM KNO₃, 6.0 mM MEDTA, 0.6 mM NADH, 12 mM MFAD, 6 mM Na₂MoO₄, 3 mM DTT, and either 25 mM leupeptine for leaves or 25 mM chymostatin for roots) at 25 °C. The reaction was terminated after 20 min by adding 0.6 M Zn-acetate and 0.25 mM phenazinemethosulphate. NO₂⁻ formation in the solution was determined as in the assay of NO₃⁻ concentration.

For NiR, 500 μl supernatant from NO₃⁻ concentration assay was concentrated with a Amicon Ultra 10K filter (Millipore, Billerica, USA) to reduce nitrate ions. The concentrated supernatant was mixed with 500 μl solution containing 50 mM TRIS-HCl (pH 7.5), 1 mM cysteine, and 2 mM EDTA. The NiR activity was determined by following the reduction of NO₂⁻ in the assay. The assay solution contained 0.5 mM NaNO₃, 1 mM methyl viologen, and the extract. The reaction was started by adding the reagent (0.12 M Na₂SO₄, 0.2 M NaHCO₃) incubated at 30 °C for 60 min, and terminated by vigorous vortex until the colour of the methyl viologen disappeared completely. After adding 1 M Zn-acetate, the mixture was centrifuged (10,000 g, 25 °C, 10 min). The residual NO₂⁻ in the reaction solution was determined as in the assay of NO₃⁻ concentration.

GS (EC 6.3.1.2) activity was analysed spectrophotometrically as proposed by Wang et al. (2008). Frozen fine powder was homogenized at 4 °C in 50 mM TRIS-HCl extraction solution (pH 8.0) containing 2 mM MgCl₂, 2 mM DTT, and 0.4 M sucrose. After centrifugation (15,000 g, 4 °C, 20 min), the supernatant was used for GS activity assay. The assay solution contained 0.35 ml of 40 mM ATP and 0.8 ml of 0.1 M TRIS-HCl buffer (pH 7.4) with 20 mM Na-glutamate, 80 mM MgSO₄, 20 mM cysteine, 2 mM EGTA, and 80 mM NH₄OH. After adding the enzyme extract to the assay solution, the mixture was incubated at 37 °C, 30 min and the incubation was stopped by addition of the reagent (0.37 M FeCl₃, 0.2 M trichloroacetic acid, 0.6 M HCl). After centrifugation (5000 g, 4 °C, 15 min), the absorbance of the supernatant was recorded at 540 nm. GS activity was expressed as 1 μmol γ-glutamyl hydroxamate formed per min.

Activities of GOGAT (EC 1.4.7.1) and GDH (EC 1.4.1.2) were assayed in roots and leaves based on the method of Lin and Kao (1996). Fine powder (c.100 mg) was extracted with 10ml TRIS-HCl buffer (pH 7.6), 1 mM MgCl₂, 1 mM EDTA, and 1 mM β-mercaptoethanol at 4 °C. After centrifugation (15,000 g, 4 °C, 30 min), the supernatant was used for determination of enzyme activities. The GOGAT assay solution contained 0.2 ml of 20 mM L-glutamine, 25 μl of 0.1 M 2-oxoglutarate, 50 μl of 10 mM KCl, 0.1 ml of 3 mM NADH, and 0.25 ml enzyme extract in a final volume of 1.5 ml made up with 25 mM TRIS-HCl buffer (pH 7.6). After addition of L-glutamine, the decrease in absorbance was recorded spectrophotometrically at 340 nm. The GDH assay mixture contained 0.15 ml of 0.1 M 2-oxoglutarate, 0.15 ml of 1 M NH₄Cl, 0.1 ml of 3 mM NADH, and 0.5 ml of the enzyme extract in a final volume of 1.5 ml made up with 0.2 mM TRIS-HCl buffer (pH 8.0). After addition of enzyme extract, the decrease in absorbance was monitored spectrophotometrically at 340 nm.

**Determination of total carbon and nitrogen and stable isotopes**

Root samples and mature leaves used for gas exchange measurements were harvested for total C and N and stable isotope (13C and 15N) analysis. Total C and N concentration was determined according to the method of Luo and Polle (2009). The stable C isotope (13C) was analysed based on the protocol of Cao et al. (2012). Fine powder (c.50 mg) was dried in an oven at 80 °C. The dried powder (c.0.8 mg) was sealed under vacuum in a quartz tube with copper oxide and silver foil and combusted for at least 4 h at 800–850 °C. The CO₂ from the combustion tube was extracted and purified cryogenically. The isotopic ratio of the extracted CO₂ was determined by an elemental analyser (NA 1110, CE Instruments, Rodano, Italy) and a mass spectrometer (Delta Plus, Finnigan MAT, Bremen, Germany) with an interface (Confo III, Finnigan MAT, Bremen, Germany) according to the method of Werner et al. (1999). The 13C/12C ratio is expressed as parts per thousand deviation from the Pee Dee Belemnite standard. Carbon isotope composition (%) was calculated as δ13C = (Rsample – Rstandard) × 1000, where Rsample and Rstandard are the ratios of 13C to 12C of the sample and the standard, respectively. The standard was referred to CO₂ in air.

Stable N isotope composition (δ15N) was analysed similarly to 13C with minor modifications, according to the method of Yousfi et al. (2012). The standard was referred to N₂ in air.
**Results**

Root morphology and photosynthesis are sensitive to changes in resource (e.g., N availability). Thus, these characters were also examined in both poplar species (Table 1). Pp and Pg had distinct root distribution patterns. For Pp, the root biomass (g DW) was 123.3 ± 4.0, with a total fine root length (m) of 21.9 ± 2.0 and a total fine root surface area (cm²) of 123.3 ± 14.4. For Pg, the root biomass (g DW) was 22.0 ± 0.4, with a total fine root length (m) of 22.0 ± 8.5 and a total fine root surface area (cm²) of 71.2 ± 11.8.

**Table 1.** Root morphological, photosynthetic characteristics, and starch of P. popularis (Pp) and P. alba × P. glandulosa (Pg) exposed to 10, 100, or 1000 μM NH₄NO₃

<table>
<thead>
<tr>
<th>Species</th>
<th>N treatment (μM)</th>
<th>Root biomass (g DW)</th>
<th>Total fine root length (m)</th>
<th>Total fine root surface area (cm²)</th>
<th>Total root volume (cm³)</th>
<th>A (mmol CO₂ m⁻² s⁻¹)</th>
<th>WUE (mmol CO₂ mol⁻¹ H₂O)</th>
<th>PNUE (mol CO₂ (mg N)⁻¹ s⁻¹)</th>
<th>Foliar starch (mmol mol⁻¹)</th>
<th>Root starch (mg (g DW)⁻¹)</th>
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</thead>
<tbody>
<tr>
<td>Pp</td>
<td>10</td>
<td>4.4 ± 0.3</td>
<td>21.9 ± 2.0</td>
<td>123.3 ± 14.4</td>
<td>4.9 ± 0.0</td>
<td>6.8 ± 0.7</td>
<td>134.1 ± 26.8</td>
<td>1.8 ± 0.1</td>
<td>11.8 ± 0.1</td>
<td>12.3 ± 0.8</td>
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<td>11.2 ± 1.2</td>
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<td>10.8 ± 1.1</td>
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<tr>
<td>Pg</td>
<td>10</td>
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<td>11.4 ± 0.1</td>
<td>12.0 ± 0.9</td>
</tr>
</tbody>
</table>

Data indicate mean ± SE (n = 6). Different letters in the same column indicate significant difference (P < 0.05). P-values of the ANOVAs of species, N treatment, and their interaction are indicated: *P < 0.05; **P < 0.01; ***P < 0.001; ****P < 0.0001; ns, not significant. Pp, Populus popularis; Pg, Populus alba × Populus glandulosa; A, leaf net photosynthetic rate; PNUE, instantaneous photosynthetic N use efficiency; WUE, intrinsic water use efficiency.
root morphological characteristics under either the control N (1000 μM NH$_4$NO$_3$) or low N (100 and 10 μM NH$_4$NO$_3$) supply levels. Generally, Pg exhibited lower root biomass, total fine root length, and total fine root surface area, but higher root volume than Pp. Photosynthesis showed no differences between Pp and Pg under the control N level. Intrinsic water use efficiency was lower in Pg than that in Pp under the given N levels. As a stored photosynthetic, foliar starch concentration was higher in Pg than those in Pp under the three N supply levels. Root starch concentration was similar in Pp and Pg.

Low N availability affected root morphology and photosynthesis in both poplar species (Table 1). Total fine root surface area increased in Pp under both low N levels, but remained unaltered in Pg. Total root volume was unchanged in Pp but decreased in Pg under the lowest N supply level compared to that under the control N supply. Photosynthesis decreased stronger in Pp than those in Pg under N-limiting conditions. PNUE, was lower in both poplar species under limiting N supply levels in comparison with that under the control N condition. As a stored photosynthetic, foliar starch concentration was higher in both species under low N levels than those under the control N level. N supply levels had no effects on root starch concentration.

These data show that limiting N levels induces distinct responses of root morphology and photosynthesis in Pp and Pg, which is probably associated with interspecific differences in N metabolism.

Net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$, activities of PM H$^+$-ATPases, and accumulation of NH$_4^+$, NO$_3^-$, and NO$_2^-$

N uptake is the first crucial step, which may lead to distinct differences in N metabolism of Pp and Pg. Net fluxes of NH$_4^+$ and NO$_3^-$ measured along the root tips of Pg displayed large variation at different positions, and maximal net influxes of NH$_4^+$ and NO$_3^-$ occurred at the position of 15 mm from the root apex (Supplementary Fig. S1B). Based on these findings in Pg and previous observations in Pp (Luo et al., 2013), net fluxes of NH$_4^+$, NO$_3^-$, and H$^+$ were measured with greater detail at the position of 15 mm from the root apex of both species (Fig. 2).

Under control N, net NH$_4^+$ influx was similar in roots of Pp and Pg (Fig. 2A), but net NO$_3^-$ influx was higher in roots of Pg than those of Pp (Fig. 2B). Under 100 μM NH$_4$NO$_3$, Pg exhibited higher net influxes of NH$_4^+$ or NO$_3^-$ than Pp (Fig. 2A, B). Since net influxes of NH$_4^+$ and NO$_3^-$ are associated with H$^+$ fluxes (Luo et al., 2013), net H$^+$ fluxes were also determined in Pp and Pg under the three N supply levels (Fig. 2C). The net H$^+$ efflux was lower in Pg than in Pp under the control N level. Net H$^+$ flux at the root surface is coupled with activities of PM H$^+$-ATPases (Luo et al., 2013). Thus, PM H$^+$-ATPase activities were analysed in isolated plasma membranes of fine roots. The PM H$^+$-ATPase activity was similar in Pp and Pg under the control N condition (Fig. 3).

Low N supply levels always resulted in significant decreases in net NO$_3^-$ influxes in Pp and Pg compared to the control N condition (Fig. 2B). Both low N levels led to increased net H$^+$ efflux in Pg, but only the lowest N level elevated net H$^+$ efflux in Pg in comparison with the control N supply (Fig. 2C). In Pp, the PM H$^+$-ATPase activities decreased under low N supply compared to the control N condition, whereas no such effects were found in Pg (Fig. 3).

Different uptake rates of NH$_4^+$ or NO$_3^-$ at the root surface of Pg and Pp exposed to the three N levels may result in differences in NH$_4^+$, NO$_3^-$, and NO$_2^-$ content in plants. Therefore, these compounds were further analysed (Fig. 4).

![Fig. 2](https://academic.oup.com/jxb/article-abstract/64/14/4207/683851) Net fluxes of NH$_4^+$ (A), NO$_3^-$ (B), and H$^+$ (C) in 10 min at 15 mm from the root apex of fine roots of *P. popularis* (Pp) and *P. alba × P. glandulosa* (Pg). Data indicate mean ± SE (n = 6). The measuring solution (pH 5.5) contained 0.1 mM KCl and 0.1 mM CaCl$_2$ as well as 10, 100, or 1000 μM NH$_4$NO$_3$. Bars labelled with different letters indicate significant difference between the treatments. *P*-values of the ANOVAs of species, N treatment, and their interaction are indicated. *P* < 0.05; **P* < 0.01; ***P* < 0.001; ****P* < 0.0001; ns, not significant (this figure is available in colour at JXB online).
Activities of enzymes involved in N assimilation, total N, δ15\text{N}, and mineral nutrients

After the uptake of NH₄⁺ and NO₃⁻, enzymes play important roles in N assimilation. Therefore, this study determined the activities of enzymes (NR, NiR, GS, GOGAT, and GDH) involved in N assimilation in Pp and Pg (Figs. 5 and Supplementary Fig. S4). Root NR activity was higher in Pg than that in Pp under the control N level (Fig. 5A). Root NiR activities were similar in Pp and Pg under the control N supply, but lower in Pg than in Pp under low N supply conditions (Supplementary Fig. S4). Root GS activity was higher in Pg than that in Pp under 100 μM NH₄NO₃ (Fig. 5B). Activities of GOGAT or GDH in roots were unaffected by species (Supplementary Fig. S4). In leaves, analysed enzyme activities of Pg were higher than those of Pp (Figs. 5C, D and Supplementary Fig. S4).

Limiting N supply also influenced activities of enzymes implicated in N assimilation in both poplar species. Root NR activity reduced in both species in response to low N levels (Fig. 5A). Root NiR activity was stimulated in Pp by 10 μM NH₄NO₃ compared with that under the control N level, but remained unchanged in Pg under the three N levels (Supplementary Fig. S4). Activities of GOGAT or GDH in roots were unaffected by low N levels (Supplementary Fig. S4). In leaves, these enzyme activities in both species remained unaltered in response to low N availability except that foliar GDH activities decreased in Pg and stimulated in Pp exposed to 10 μM NH₄NO₃ (Figs. 5C, D and Supplementary Fig. S4).

Irrespective of N forms, total N concentration in plants may mirror N availability. Moreover, fractionation of 15\text{N} may occur in different steps of N metabolism in plants, reflecting active status of N metabolism. Therefore, total N and δ15\text{N} were analysed in Pp and Pg (Fig. 6). Total N concentration in roots of Pg was higher than those of Pp under the same N level (Fig. 6A). In contrast, δ15\text{N} in roots of Pg was lower than that of Pp under the same N treatment (Fig. 6B). Foliar N concentration of Pg was also higher than those of Pp under the same N level (Fig. 6C). Foliar δ15\text{N} was unaffected by species (Fig. 6D).

Total N concentration in roots reduced with decreasing N supply levels in both species (Fig. 6A). On the contrary, δ15\text{N} in roots of both species increased in response to both low N levels (Fig. 6B). Foliar N concentration in both species was also lower under low N levels compared to those under the control N condition (Fig. 6C). In contrast, foliar δ15\text{N} in both species increased in response to low N availability (Fig. 6D).

As N availability can also affect uptake of other nutrients and carbon metabolism, mineral nutrients, soluble sugars, total C, δ13\text{C}, soluble protein, and phenolics were analysed in Pp and Pg (Supplementary Figs. S5 and S6, Supplementary Table S2). There were complex patterns in the responses of nutrient elements and carbon-bearing compounds to N supply levels.

PCA of morphological and physiological responses

To unravel key parameters involved in the response patterns of both poplar species to N supply levels, a PCA was conducted using data of morphological and physiological parameters related to root morphology, photosynthesis, and N metabolism (Fig. 7, Supplementary Table S3). PC1 and PC2 accounted for 37 and 20% of the variation, respectively. PC1 clearly separated the variation of species effects, and PC2 uncovered the effects of N treatment levels. Foliar N concentration and root δ15\text{N} were key contributors to PC1, whereas A, net influxes of NH₄⁺ and NO₃⁻, and foliar starch...
concentration was important factors to PC2. In the PCA plot, a greater distance between symbols associated with N treatment levels suggests a stronger responsiveness of morphological and physiological parameters to changes in N supply levels. Thus, the greater distance between symbols related to the control N level and 100 μM NH₄NO₃ in Pp compared to that in Pg indicates that Pp is more sensitive to decreasing N supply than Pg in the range of given N availability. These PCA results indicate that Pp and Pg exhibit distinct morphological and physiological responsiveness in acclimation to limiting N availability, which mainly results from differences of Pp and Pg in uptake of NH₄⁺ or NO₃⁻, root ¹⁵N fractionation, foliar N and starch concentration, and A.

Transcriptional regulation of genes involved in N metabolism

Since Pp and Pg demonstrated distinct patterns of morphological and physiological responses in acclimation to limiting N availability, interspecific differences may also be expected in the transcriptional regulation pattern of key genes implicated in N metabolism. Therefore, transcript levels of representative genes involved in N acquisition and assimilation were assessed in roots and leaves of both species (Fig. 8). The cluster analysis of transcript changes of N uptake- and assimilation-related genes clearly separated Pg and Pp based on their responsiveness to N supply levels (Fig. 8).

In roots, NRT1;2, NRT2;4B, GDH, NRT1;1, and NRT3;1C formed a subcluster I (Fig. 8A). Under the control N level, the transcript abundance of genes in the subcluster I was higher in Pg than in Pp (Fig. 8A). The second subcluster consisted of NRT3;1B, GS1;3, GS2, AMT1;2, VHA1;1, and AMT1;6 and the transcript levels of these genes were similar or lower in Pg compared to those in Pp under the control N level (Fig. 8A). The subcluster III included NR, Fd-GOGAT, AMT2;1, NADH-GOGAT, and NiR, and the mRNA levels of these genes were lower in Pg than those in Pp under the control N level (Fig. 8A). The strongest differences existed for NRT2;4C and VHA2;2, which were strongly suppressed in Pg compared to those in Pp under the three N supply levels (Fig. 8A).
Limiting N supply affected transcript levels of genes involved in N metabolism in roots of both species (Fig. 8A). Generally, the transcript levels of genes from the subcluster I were increased in Pp in response to low N levels in comparison with those under the control N condition, but the transcript changes of these genes in Pg were diverse in response to low N availability (Fig. 8A). The transcriptional induction of genes from subcluster II except VHA 1;1 was detected in Pp in response to 10 μM NH₄NO₃ in comparison with those under the control N condition, but no such effects were found in Pg (Fig. 8A). The transcript levels of genes from subcluster III were suppressed in Pp in response to 100 μM NH₄NO₃ compared to those under the control N supply, but no such effects were observed in Pg (Fig. 8A). The strongest differences existed for NRT2;4C and VHA2;2 because NRT2;4C and VHA2;2 responded to N supply variation in Pp but not in Pg (Fig. 8A).

In leaves, NRT3;1B, NiR, NRT2;4B, GDH, and AMT2;1 formed a subcluster I (Fig. 8B). Under the control N level, the mRNA levels of genes in the subcluster I except AMT2;1 were higher in Pg than those in Pp (Fig. 8B). GS2, NRT1;1, GSI;3, and NADH-GOGAT constitute the second subcluster (Fig. 8B). The transcript levels of genes from this subcluster were similar or slightly lower in Pg than those in Pp (Fig. 8B). The third subcluster consisted of NRT3;1C, NRT2;4C, Fd-GOGAT, and NR (Fig. 8B). Under the control N level, genes from subcluster III showed lower transcript levels in Pg than those in Pp (Fig. 8B). The mRNA level of AMT1;2 was higher in Pg than that in Pp under the control N condition (Fig. 8B).

In leaves, transcript levels of genes related to N metabolism were also affected by N supply. NRT2;4B, GDH, and AMT2;1 from subcluster I had lower transcript levels in Pp in response to low N availability compared to those exposed to the control N supply, but the transcript levels of these genes were relatively stable in Pg under the three N levels (Fig. 8B). In the second subcluster, the mRNA levels of GS2 were stable in Pp in response to low N availability, but repressed in Pg under low N levels compared to that under the control N condition (Fig. 8B). In comparison with the control N supply, the transcript levels of genes from subcluster III were increased in Pp exposed to 10 μM NH₄NO₃, but suppressed or unaltered in Pg (Fig. 8B). The other three genes (i.e. NRT1;2, AMT1;6, and AMT1;2) displayed the strongest differences between Pp and Pg in response to N availability (Fig. 8B). NRT1;2 and AMT1;6 showed lower mRNA levels in Pg in response to low N availability, but no such effects were observed in Pg
The mRNA level of AMT1;2 was increased in Pp but not in Pg in response to low N availability (Fig. 8B).

To find out which genes are the most important ones in response to differences in species and/or N supply levels, a PCA was performed using data of fold-changes of transcripts in Pp and Pg under the three N levels (Supplementary Table S4). PC1 clearly separated species effects and PC2 the N treatment impacts. PC1 and PC2 accounted for 48 and 26% of the variation, respectively. Leaf NRT2;4C and AMT1;6, and root NRT2;4C were the most important contributors to PC1, whereas NADH-GOGAT, AMT1;2, and NRT1;2 in roots were essential factors in PC2.

Discussion

Differences between Pp and Pg in N metabolism under limiting N supply

The greater root biomass and larger fine root surface area of Pp compared with Pg suggest that root morphological features of Pp are more responsive to limiting N availability than those of Pg. More stimulation of root growth in Pp than in Pg can be critical for different acclimation patterns of both species to limiting N availability because N acquisition in these poplars depends on root characteristics. The greater root biomass and fine root surface area in Pp indicate that Pp may better exploit nutrient resources in rhizosphere in comparison with Pg. The higher growth rates of plants may need more N metabolites to support (Lawlor, 2002). Thus, growth can be a driving force for N metabolism of plants. Consequently, the higher root growth of Pp can lead to greater N demand, further triggering a stronger responsiveness to decreasing N availability. Despite lower total N concentration in Pp roots than in Pg roots, the greater root biomass of Pp resulted in higher N amount (14–38%) in Pp roots, suggesting that Pp can acquire more N to support higher root growth.

The greater root growth in Pp, however, does not necessitate higher net influxes of N compared to those in Pg. Actually, Pp displayed lower net influxes of NH$_4^+$ and NO$_3^-$ compared to those of Pg under 100 μM NH$_4$NO$_3$, which is likely associated...
with PM H⁺-ATPase activities, activities of enzymes implicated in N assimilation, and functioning of AMTs and NRTs (Hawkins et al., 2008; Hawkins and Robbins, 2010; Alber et al., 2012; Luo et al., 2013). PM H⁺-ATPases play a central role in the uptake of NH₄⁺ and NO₃⁻ because H⁺ ions pumping to the apoplast through PM H⁺-ATPases create the proton motive force, driving the absorption of NH₄⁺ and NO₃⁻ in roots (Hawkins and Robbins, 2010; Luo et al., 2013). The lower activity of PM H⁺-ATPases is in line with the lower net influxes of NH₄⁺ and NO₃⁻ in Pp compared with Pg under 100 μM NH₄NO₃. Additionally, in most cases, the lower activities of enzymes involved in N assimilation and the lower total N concentration in roots and leaves of Pp versus Pg correspond well to the lower N uptake rates in Pp under 100 μM NH₄NO₃. In contrast to the lower total N concentration in Pp than in Pg, the higher δ¹⁵N in roots of Pp indicates that ¹⁵N is more rapidly enriched in the process of N metabolism in roots of Pp than in Pg. Since the processes of N metabolism in plants discriminate against the heavier N isotope leading to the depletion of ¹⁵N in plant dry mass compared with that in the soil (Tcherkez and Hodges, 2008; Falxa-Raymond et al., 2012; Gauthier et al., 2013), higher δ¹⁵N in roots of Pp indicates less fractionation of ¹⁵N occurs in Pp than in Pg. This is consistent with the lower net influxes and content of NH₄⁺ and NO₃⁻, activities of NR and GS, and total N concentration in Pp compared with Pg. Based on morphological and physiological parameters related to N metabolism, the PCA results suggest that Pp is more sensitive to decreasing N supply than Pg under 100–1000 μM NH₄NO₃, which is mainly due to differences between Pp and Pg in the uptake of NH₄⁺ or NO₃⁻, root ¹⁵N fractionation, foliar N and starch concentration, and A.

The distinct patterns of transcriptional regulation of genes implicated in N metabolism of Pp and Pg may be associated with the different morphological and physiological responses of both species to limiting N availability. This study group’s previous study suggests that, under N fertilization, differential expression of genes involved in N uptake (AMTs and NRTs) of Pp and Pg leads to accelerated N physiological processes in Pg than in Pp (Li et al., 2012). Under limiting N conditions, however, the current data show that transcriptional regulation of key genes involved in N metabolism of Pp is more responsive than that of Pg. These results indicate that Pp and Pg can differentially manage transcriptional regulation of key genes involved in N metabolism under low and high N availability. These results are consistent with previous studies. *Arabidopsis* plants manage N metabolism differently under deficient and sufficient N conditions (Lemaître et al., 2008; Chardon et al., 2010; Ikram et al., 2012). These studies highlight that it is necessary to investigate the responses of plants not only to high N fertilization but also to low N availability.

Overall, Pp and Pg displayed different patterns of morphological, physiological, and transcriptional regulation in response to limiting N availability, which is mainly associated with the difference of both species in net influxes of NH₄⁺ and NO₃⁻, root δ¹⁵N, foliar N and starch concentration, A, and the transcriptional regulation of genes (e.g. AMT1:2, NRT1:2, and NRT2:4C in roots and AMT1:6 and NRT2:4C in leaves) that are involved in N acquisition and assimilation.

![PCA plot](https://academic.oup.com/jxb/article-abstract/64/14/4207/683851)

**Fig. 7.** Principal component analysis (PCA) plot of the first two principal components in *P. popularis* (Pp) and *P. alba × P. glandulosa* (Pg). The analysis was conducted using data of physiological parameters of Pp and Pg exposed to 10 (yellow), 100 (orange), or 1000 (brown) μM NH₄NO₃, respectively (this figure is available in colour at JXB online).

The physiological and transcriptional regulation mechanisms of N metabolism of poplars in acclimation to low N availability

Root morphology responds highly plastic to N availability (Forde and Walch-Liu, 2009; Chapman et al., 2012). Increases in fine root surface area of poplars exposed to low N levels indicate that poplars stimulate growth of fine roots to forage for nutrients under limiting N availability. Consistently, *Arabidopsis* roots adopt an ‘active-foraging strategy’ by outgrowth of lateral roots under limiting N conditions, but a ‘dormant strategy’ by inhibited growth of lateral roots under sufficient N supply (Ruffel et al., 2011). Most plants can increase root growth, resulting in greater fine root surface area under short-term N deficiency, but exhibit stunted root growth under long-term limiting N availability due to lack of internal N (Kraiser et al., 2011; Shen et al., 2013). The current data indicate that poplar roots adopt an active-forage strategy to acquire N resources and other essential minerals under low N supply. Although poplar roots actively forage for nutrients under low N conditions, the acquired N appears insufficient for the biosynthesis of photosynthetic enzymes and metabolic precursors, leading to decreased A and PNUE. In other higher plants, N deficiency also inhibits photosynthetic capacity and growth (Sardans and Penuelas, 2012).

Gradual decreases in net influxes of NH₄⁺ and NO₃⁻ at the root surface under decreased concentration of external NH₄NO₃ supply indicate that NH₄⁺ and NO₃⁻ concentration in the external solution play important roles in net influxes of these ions. This was also found for seedlings of Douglas fir (*Pseudotsuga menziesii*) and soybean (*Glycine max*) (Hawkins...
and Robbins, 2010). However, net influxes of $\text{NH}_4^+/\text{NO}_3^-$ are greater at the root surface of white spruce ($Picea glauca$) exposed to 50 μM $\text{NH}_4\text{NO}_3$ than those of 1500 μM $\text{NH}_4\text{NO}_3$ (Alber et al., 2012). These results suggest that impacts of external $\text{NH}_4\text{NO}_3$ concentration on net fluxes of $\text{NH}_4^+/\text{NO}_3^-$ are also related to plant species. Decreases in PM H$^+$-ATPase activities and transcript levels of genes ($VHA1:1$ and $VHA2:2$) encoding PM H$^+$-ATPases, root $\text{NH}_4^+$ and foliar $\text{NO}_3^-$ content, foliar GDH activity, total N concentration in roots and leaves, and soluble protein in roots and leaves of both poplar species are in agreement with lower net influxes of $\text{NH}_4^+/\text{NO}_3^-$ under limiting N supply. Moreover, correlations between different enzymes involved in N metabolism, enzymes, gene expression levels, and transcript levels of different genes in both poplar species (Supplementary Fig. S7) indicate that poplar plants coordinate each step of N metabolism processes to acclimate to low N availability. These results indicate that the processes of N uptake and assimilation have slowed down in both poplar species in acclimation to low N availability. In plants, N and C metabolism is interconnected because the production of N metabolites such as amino acids needs C skeletons (Nunes-Nesi et al., 2010). The lower total C concentration in roots and foliar $\delta^{13}\text{C}$, the elevated starch concentration in leaves, and the correlations between $\delta^{13}\text{C}$ and parameters of N metabolism in both poplar species under low N levels (Supplementary Figs. S5 and S7) suggest

**Fig. 8.** Cluster analysis of transcriptional fold-changes of key genes involved in N uptake and assimilation in roots (A) and leaves (B) of *P. populiris* (Pp) and *P. alba × P. glandulosa* (Pg) exposed to 10, 100, or 1000 μM $\text{NH}_4\text{NO}_3$. The colour scale indicates fold-changes of mRNAs. For each gene, the expression levels in roots or leaves of Pp exposed to 1000 μM $\text{NH}_4\text{NO}_3$ were defined as 1, and the corresponding fold-changes under 100 and 10 μM $\text{NH}_4\text{NO}_3$ were calculated (this figure is available in colour at JXB online).
that C export and/or phloem transport is inhibited under N deficiency. Foliar starch accumulation is also observed in herbaceous plants in response to low N availability, which is ascribed to the reduced demand of C skeletons for N compounds such as amino acids and proteins under low N levels (Lemaître et al., 2008; Ikram et al., 2012; Schluter et al., 2012). In the same line, earlier studies indicate that foliar starch accumulation is a consequence of photosynthesis exceeding the demands of respiration and growth under N deficiency conditions (Lawlor et al., 1987b; Lawlor, 2002).

Increases in $\delta^{15}$N in roots and leaves of poplars under low N levels are contrary to decreases in total N concentration, indicating that $^{15}$N is enriched in both poplar species under limiting N availability. N starvation also stimulates whole-plant $\delta^{15}$N in some genotypes of wild barley (Hordeum spontaneum) (Robinson et al., 2000). The higher $\delta^{15}$N values in both poplar species under low N conditions compared with that under the control N supply are probably associated with slowing down of N metabolism which leads to less depletion of $^{15}$N in poplars under low N availability. In other words, poplar plants are forced to utilize $^{15}$N to meet their N demands under limiting N conditions, leading to $^{15}$N enrichment in dry mass. Although the mechanisms underlying the variation in natural $^{15}$N are not completely known in plants under various environmental conditions (Cernusak et al., 2009; Tcherkez, 2011), $^{14}$N/$^{15}$N fractionation can occur in the processes of N absorption, assimilation, recycling, and reallocation in plants and N release from plants (e.g. foliar NH$_3$ volatiles and N-containing exudates of roots; Robinson et al., 2000; Ariz et al., 2011; Gauthier et al., 2013; Youssi et al., 2013). Additionally, changes in environmental factors such as nutrients, can cause substantial alterations in $\delta^{15}$N in plants (Ariz et al., 2011; Gauthier et al., 2013; Youssi et al., 2013). Furthermore, negative correlations between $\delta^{15}$N and transpiration rate were observed in wheat under salinity (Youssi et al., 2013). Consistently, negative correlations occur between $\delta^{15}$N and transpiration rate, $g_s$, $A$, or PNUE, in poplars (Supplementary Fig. S7). These results indicate that $^{15}$N enrichment in poplars exposed to low N levels is probably associated with (i) less active N metabolism in poplars under low N availability and/or (ii) elevated N release from roots and leaves. The latter possibility needs further studies.

Although transcriptional regulation of genes involved in N metabolism plays a fundamental role in response to N deficiency or starvation in herbaceous plants (Hirai et al., 2004; Bi et al., 2007; Krouk et al., 2010; Patterson et al., 2010; Krapp et al., 2011; Ruffel et al., 2011; Engelsberger and Schulze, 2012; Kiba et al., 2012; Schluter et al., 2012), little is known on transcriptional regulation underlying N metabolism in trees under limiting N availability (Rennenberg et al., 2009, 2010). Transcriptional induction of several AMTs (e.g. AMT1;2) and NRTs (e.g. NRT1;2, NRT2;4A, and NRT3;1B) in poplar roots exposed to low N levels indicates that poplar roots increase mRNAs of key transporters for NH$_4^+$ and NO$_3^-$ as the result of acclimation to low N availability. Induced transcript abundance of AMT1;2 is also found in roots of Populus tremula × tremuloides exposed to low N supply (Selle et al., 2005) and in P. tremula × alba under N starvation (Couturier et al., 2007).

Similarly, transcription of OsAMT1;2 in roots of rice (Oryza sativa) is induced by NH$_4^+$ deficiency (Perandio et al., 2011). NRT2;1 (i.e., NRT2;4C re-defined in this study) displays higher transcript levels in NO$_3^-$-fed P × canescens roots than in NH$_4^+$-fed roots (Ehlting et al., 2007) and is induced upon application of NO$_3^-$ to N-deprived roots of peach (Prunus persica) seedlings (Nakamura et al., 2007). NRT3;1 (also called NAR2;1) is a key player in a two-component system including NRT2s for nitrate transport in Arabidopsis (Yong et al., 2010; Korur et al., 2012) and rice (Yan et al., 2011). Correlation analysis between transcript levels of NRT3;1B or NRT3;1C and other NRTs (i.e., NRT1;1, NRT2;4B, and NRT2;4C) in Pp and Pg under normal and low N levels detected positive relationships (Supplementary Fig. S7). These correlations, combined with this study group’s previous findings where positive correlations also occurred under N-fertilization conditions (Li et al., 2012), indicate that NRT3;1B and/or NRT3;1C may also act as partners of other NRTs for nitrate transport in poplars under various N levels. In contrast to induction of several AMTs and NRTs in poplar roots, reduced transcript levels of most AMTs and NRTs in leaves and genes (e.g. NR, NiR, GOGAT) involved in N assimilation in roots and leaves of poplars indicate that N assimilation (downstream processes after N uptake) is inhibited due to shortage of N-containing precursors under low N availability. These results suggest that overexpression of AMTs and NRTs in poplar roots and downregulation of most AMTs and NRTs in leaves and genes involved in N assimilation in roots and leaves of poplars play fundamental roles in acclimation to limiting N availability.

Taken together, increased fine root growth, slowed down N acquisition and assimilation, overexpressed transcripts of AMTs and NRTs in roots, and repressed transcript levels of AMTs and NRTs in leaves and key genes involved in N assimilation are primary mechanisms of both poplar species in acclimation to limiting N availability.

In summary, Pg exhibited greater root biomass and total fine root surface area, lower net influxes of NO$_3^-$ at the root surface, higher $\delta^{15}$N in roots, and more responsiveness of transcriptional regulation of 18 genes involved in N uptake and assimilation in roots and leaves than Pg under limiting N supply. These results indicate that N metabolism of Pg displays a stronger responsiveness to decreasing N availability than that of Pg. Under low N conditions, decreased net influxes of NH$_4^+$ and NO$_3^-$ at the root surface are consistent with lower root NH$_4^+$ and foliar NO$_3^-$ content, root NR activity, total N concentration in roots and leaves, and mRNA of most AMTs and NRTs in leaves and genes involved in N assimilation in roots and leaves. Moreover, low N supply levels increased fine root surface area, foliar starch accumulation, $\delta^{15}$N in roots and leaves, and transcript levels of several AMTs (e.g. AMT1;2) and NRTs (e.g. NRT1;2, NRT2;4B, and NRT3;1B) in roots of both poplar species. These data suggest that poplar species slow down processes of N acquisition and assimilation in acclimation to limiting N supply. These morphological, physiological, and molecular data suggest that poplar plants can differentially manage N metabolism under deficient and sufficient N conditions and that it is important to consider low N tolerance when selecting woody plants such
as *Populus* spp. for energy plantations on nutrient-poor sites. Using technologies including genomics, transcriptomics (e.g. microarray, RNA sequencing), and metabolomics in future experiments, a deeper understanding of poplars in acclimation to low N availability may be obtained.

**Supplementary data**

Supplementary data are available at *JXB* online.

- **Supplementary Table S1.** Primers used for qRT-PCR.
- **Supplementary Table S2.** Concentrations of mineral nutrients.
- **Supplementary Table S3.** PCA of physiological parameters of both poplar species.
- **Supplementary Table S4.** PCA of transcriptional changes of representative genes.
- **Supplementary Fig. S1.** Net fluxes of NH$_4^+$ and NO$_3^-$ along the root tip.
- **Supplementary Fig. S2.** Alignments of representative genes.
- **Supplementary Fig. S3.** NO$_3^-$ content in roots and leaves.
- **Supplementary Fig. S4.** Activities of NiR, GOGAT, and GDH in roots and leaves.
- **Supplementary Fig. S5.** Soluble sugars, C concentration, and δ$^{13}$C.
- **Supplementary Fig. S6.** Soluble protein and phenolics.
- **Supplementary Fig. S7.** Correlations of related parameters.

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**References**


Falxa-Raymond N, Patterson AE, Schuster WSF, Griffin KL. 2012. Oak loss increases foliar nitrogen, $\delta^{15}$N and growth rates of Betula lenta in a northern temperate deciduous forest. Tree Physiology 32, 1092–1101.


Li Q, Li BH, Kronzucker HJ, Shi WM. 2010. Root growth inhibition by NH4+ in Arabidopsis is mediated by the root tip and is linked to NH4+ efflux and GMPase activity. Plant, Cell and Environment 33, 1529–1542.


Sperandio MVL, Santos LA, Bucher CA, Fernandes MS, de Souza SR. 2011. Isoforms of plasma membrane H\(^+\)-ATPase in rice root and shoot are differentially induced by starvation and resupply of NO\(_3^-\) or NH\(_4^+\). *Plant Science* **180**, 251–258.


Tcherkez G. 2011. Natural \(^{15}\)N/\(^{14}\)N isotope composition in C\(_3\) leaves: are enzymatic isotope effects informative for predicting the \(^{15}\)N-abundance in key metabolites? *Functional Plant Biology* **38**, 1–12.


