Mitochondrial uncoupling protein contributes to the regulation of carbon and nitrogen metabolism and seed yield under low nitrogen stress in Arabidopsis

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Research Article

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Abstract

Nitrogen (N) availability is a critical factor for plant development and yield, and it closely correlates to carbon (C) metabolism. Uncoupling protein (UCP) and alternative oxidase (AOX) in mitochondria exhibit a strong correlation with N and C metabolism. Here, we investigated the respective functions of UCP and AOX by using ucp1, aox1a and aox1a/ucp1 mutants under low-N condition. Low-N markedly increased AOX1a and UCP1 expression, alternative pathway capacity and UCP activity. Eight-day-old aox1a/ucp1 seedlings were more sensitive to low-N condition than Col-0 and single mutants, i.e., the lower primary root length and higher anthocyanin accumulation. The net photosynthetic rate (A) and electron transport rate (ETR) under low-N stress were markedly decreased in ucp1 and aox1a/ucp1 compared to those in Col-0, but not in aox1a. The leaf area, total C and N content in shoots showed a similar profile as A and ETR. Nitrate acquisition rate was accelerated in aox1a/ucp1, but its transport activity from root to shoot was decreased, which resulted in the low nitrate content and nitrate reductase activity in shoots upon low-N condition. Additionally, the low C and N content in ucp1 and aox1a/ucp1 seeds led to the decreased seed yield compared to Col-0 upon low-N stress. RNA-seq analysis revealed that a large number of genes involved in photosynthesis, C/N metabolism were markedly down-regulated in aox1a/ucp1 compared to Col-0 under low-N stress. These results highlight the more key role of UCP1 than AOX1a in modulating C and N metabolism and seed yield in Arabidopsis adaptation to low-N stress.

Introduction

The availability of nitrogen (N) in soil is essential for plant growth and defense [1–3]. However, plants often encounter limited N sources under nature environmental conditions, which leads to chlorophyll degradation, decreased photosynthesis and protein synthesis [4, 5]. Moreover, application of N fertilizers results in contamination of groundwater and production of nitrogenous greenhouse gases [6, 7]. Ammonium (NH\textsubscript{4}\textsuperscript{+}) and Nitrate (NO\textsubscript{3}\textsuperscript{−}) are two major forms of useable N for plants. NH\textsubscript{4}\textsuperscript{+} can be directly assimilated into amino acids by glutamine synthetase and glutamate synthase [8]. However, NO\textsubscript{3}\textsuperscript{−} is first reduced to nitrite (NO\textsubscript{2}\textsuperscript{−}) by nitrate reductase (NR) in cytoplasm using NAD(P)H as the electron donor; then NO\textsubscript{2}\textsuperscript{−} is reduced to NH\textsubscript{4}\textsuperscript{+} by nitrite reductase (NiR). The reduction of NO\textsubscript{2}\textsuperscript{−} and assimilation of NH\textsubscript{4}\textsuperscript{+} occur in plastids/chloroplasts and the reduced ferredoxin is used as the reductant [8]. Inhibition of the reductant output via the malate-oxaloacetic acid (Mal-OAA) shuttle from chloroplasts decreases the NO\textsubscript{3}\textsuperscript{−} assimilation rate [9, 10]. Therefore, plants need to balance the photosynthetic energy partition between carbon (C) and N assimilation at different development stages.

N assimilation is in closely related to C metabolism. The balance of N and C in plants is essential for the optimal growth and development [5]. NO\textsubscript{3}\textsuperscript{−} availability affects transcriptions of a variety of genes involved in C metabolism, while C depletion decreases protein biosynthesis and alters N metabolism [11, 12]. It is well accepted that low N inevitably results in low photosynthetic capacity and yield in plants [5]. Photosynthesis and respiration provide not only the reducing power but also C skeletons (2-oxoglutarate, citrate, and isocitrate) for N assimilation [9, 13]. Many reports have confirmed that photosynthesis and
respiration rates highly correlate to the intracellular N level [5, 9, 10]. Glycolytic pathway and the tricarboxylic acid cycle could be up-regulated in plant adaptation to low N condition [11, 14, 15]. Additionally, the capacity of alternative electron transport pathways (aETPs) in the respiratory chain also exhibits a strong correlation with the intracellular NO$_3^-$ level [9, 10, 16]. aETPs are essential for plant adaptation to various stresses [17–19]. Particularly, they play key roles in maintaining a high photosynthetic capacity by dissipating the excess reductant from chloroplasts [10, 20]. However, it is not well understood how aETPs coordinate and contribute to optimizing the C metabolism and N assimilation under low-N stress in plants.

Alternative pathway (AP) and uncoupling pathway are two major pathways of aETPs, which are mediated by alternative oxidase (AOX) and the uncoupling protein (UCP), respectively. AOX can directly transport electron from ubiquinone to O$_2$, but it did not transfer H$^+$ across the mitochondrial inner membrane, thus dissipating energy as heat [21]. Comparatively, UCP increases the permeability of H$^+$ across the mitochondrial inner membrane, which destroys the H$^+$ gradient and decreases the ATP formation [22]. In Arabidopsis, five AOX genes (AOX1a, AOX1b, AOX1c, AOX1d, AOX2) and six UCP genes (UCP1-6) have been reported [23]. Recently, it was found that the AOX1a or UCP1 mutation can alter foliar N and C assimilation rates in Arabidopsis fed with NO$_3^-$ or NH$_4^+$ [9]. Moreover, the transcripts of AOX1a and UCP1 are significantly up-regulated by low-N stress [10, 16]. Excessive carbohydrates are preferentially respired by AOX, which suppresses the increase of the C/N ratio upon low-N condition [15, 24]. However, it is indicated that AOX induced by low-N condition does not play important roles on C/N ratio regulation [16]. Sweetlove et al. [20] reported that the UCP1 mutation markedly decreases the AOX protein content, but does not affect other aETPs in ucp1 plants. Moreover, UCP1 is essential for the efficient photosynthesis mainly through maintaining photorespiratory rate in Arabidopsis [20]. However, it is still unknown whether UCP1 participates in regulating C/N ratio upon low-N condition at the whole plant level; and the respective contribution and coordination of UCP1 and AOX in Arabidopsis adaptation to low-N stress remain unclear.

Although above promising results have been reported, the authors rarely analyzed the effects of AOX1a and UCP1 mutation on the C/N ratio and yield of seeds as well as their respective roles in plant adaptation to low-N condition. The aim of this study is to clarify the functions of AOX1a and UCP1 in Arabidopsis tolerance to low-N stress by using the aox1a, ucp1 and aox1a/ucp1 mutants. In particular, we focused on the effects of AOX1a and UCP1 mutation on C and N assimilation processes, photosynthetic capacity, C/N ratio, and seed yield.

**Materials And Methods**

**Plant materials and growth conditions**

Arabidopsis wild type (Col-0) and the T-DNA insertion lines of AOX family genes [aox1a (Salk_084897), aox1c (CS804611, CS877307), aox1d (CS390166), aox2 (CS766955)] and UCP family genes [ucp1 (CS821384), ucp2 (Salk_037074), ucp3 (Salk_006106), ucp4 (CS373159), ucp6 (Salk_111403C)] were
purchased from the Arabidopsis Biological Resource Center (ABRC). *aox1b* point mutants [*aox1b* (1-2-5), *aox1b* (14-9-7)] were provided by Dr. Aigen Fu at Northwest University, China. The *aox1a/ucp1* double mutant was generated by crossing *aox1a* and *ucp1*. The *aox1a* mutant was identified by using two primer pairs (Salk_084897-RP and LBB1; Salk_084897-RP and Salk_084897-LP). The *ucp1* mutant was identified by using two primer pairs (CS821384-RP and LB1; CS821384-RP and CS821384-LP).

For the experiments at seedling stage (0-10 d), the seeds were vernalized at 4°C for 48 h, then germinated and cultured in half-strength solid MS (1/2 MS) medium (pH 5.8). For the experiments at the vegetative stage and the reproductive stage, the seedlings were cultured with the hydroponic method [25]. After vernalized at 4°C for 48 h, the seeds were germinated and grew in the germination solution for 10 d. Then the seedlings were transferred to the growth solution. All the solutions were replaced every 2 d. The seedlings were cultured in a growth chamber with 120 μmol m⁻² s⁻¹ light intensity, 60-70% humidity and a 16 h/8 h light/dark cycle at 22 ± 2°C.

**Generation of proAOX1a: GUS and proUCP1: GUS transgenic lines**

The promoter sequences of *AtAOX1a* and *AtUCP1* were amplified by using the primer pairs (*proAOX1a*-FP and *proAOX1a*-RP; *proUCP1*-FP and *proUCP1*-RP), respectively. Then, they were cloned into the expression vector pBIB-GUS by using the Gateway technology. *Agrobacterium*-mediated transformation was used to deliver the recombinant plasmids into Col-0 by floral-dipping method. The T₀ seeds were screened for positive lines by using the herbicide Basta.

**Low nitrogen treatment**

For the low nitrogen experiment at the seedling stage (0-10 d), NH₄NO₃ and KNO₃ were removed from the 1/2 MS medium, then KNO₃ as the only nitrogen source was added at the concentrations of 0, 0.1 mM, and 1 mM, which were denoted as 0 N, 0.1 N, and 1 N medium, respectively, in this study. The depleted K⁺ was supplied with KCl. The seeds were germinated and grew in 0 N, 0.1 N, or 1 N medium for treatments.

For the low nitrogen experiment of the hydroponically grown plants, NH₄NO₃ and Ca(NO₃)₂ were removed from the growth solution, and KNO₃ was added at concentrations of 1mM (low) or 5 mM (moderate), which were denoted as 1 N or 5 N medium, respectively. The depleted Ca²⁺ was supplied with CaCl₂. The 14-day-old seedlings were used for experiments.

**The extraction of DNA and RNA and qRT-PCR analysis**

Genomic DNA was extracted from Arabidopsis leaves on the basis of Tan et al. [26]. The extraction of total RNA and subsequent cDNA synthesis were performed by using the Plant RNA Extraction Kit (Thermo Fisher) and the Prime Script RT Reagent Kit with gDNA Eraser Kit (TRANS), respectively. qRT-PCR were carried out by using Transtart Green qPCR Super Mix Kit (TRANS). The primers are described in Table. S1. The qRT-PCR was programmed as 94°C for 2 min; 94°C for 30 s; 58°C for 15 s; 72°C for 20 s with 40
cycles according to the ABI PRISM7500 real-time PCR system (China). The gene expressions were normalized to *ACTIN2* (AT3G18780) and analyzed by using the $2^{-\Delta \Delta Ct}$ method.

**Analysis of anthocyanin content**

Anthocyanin content was determined as described previously by Vandenbussche et al.[27]. 0.1 g of fresh tissues were put into a tube containing 600 µl of extract buffer [methanol/HCl (v/v)=99/1] for 24 h at 4°C in dark. 400 µl of chloroform and 400 µl of H$_2$O were added in sequence and then centrifuged at 10,000 g for 10 min. The absorbance at 530 nm was recorded.

**Measurement of nitrate content**

The nitrate content was determined according to Cataldo et al. [28]. 0.3 g of fresh tissues were ground with ddH$_2$O. After treated for 30 min at 100°C, the homogenate was centrifuged at 13,000 g for 15 min. The supernatant was mixed with 5% salicylic acid. After 20 min, 2 M NaOH were added. The absorbance at 410 nm was recorded.

**Measurement of respiratory rates**

The 14-day-old hydroponically grown seedlings were grown under control (11 N) or low nitrogen (1 N) conditions for 16 d. The shoots were collected and used for isolation of mitochondria [29] and the analysis of alternative pathway capacity ($V_{alt}$) and UCP activity [30]. The O$_2$ consumption was detected in a Chlorolab II liquid-phase oxygen electrode (Hansatech, UK) in 1.5 ml of reaction buffer [10 mM TES (pH 7.5), 0.3 M mannitol, 5 mM KH$_2$PO$_4$, 2 mM MgSO$_4$, 10 mM NaCl and 0.1% BSA]. For the measurement of $V_{alt}$, 5 mM pyruvate, 10 mM succinate, 10 mM malate, 0.15 mM ADP, 1 mM NADH, 10 mM glutamic acid, 2 mM KCN were added. KCN was used to inhibit the cytochrome c oxidase activity. For UCP activity analysis, 10 mM malate, 0.15 mM ADP, 10 mM glutamic acid, 10 µM linoleic acid (LA), oligomycin (2.5 µg/mg protein), 2 mM GDP (added or not) were added. LA and GDP are the activator and inhibitor of UCP, respectively.

**Determination of chlorophyll (Chl) contents**

The Chl was extracted with the solution [80% acetone/80% ethanol (v/v) = 1/1, 31]. Chlorophyll content was calculated based with the following formulas.

\[
\text{Chl a (mg/L)} = 12.63 \times \text{OD}_{664.5} - 2.52 \times \text{OD}_{647}; \\
\text{Chl b (mg/L)} = 20.47 \times \text{OD}_{664.5} - 4.73 \times \text{OD}_{647}.
\]

**Measurement of photosynthetic fluorescence parameters**

Photosynthetic fluorescence parameters were analyzed using the LI-6400XT photosynthesis system (LI-COR). The leaf temperature was maintained at 22°C during measurements. Photosynthesis was
determined under ambient growth condition by using 300 PAR light intensity and 400 ppm CO$_2$. The photosynthetic light-response curve was determined at 0-1200 PAR light intensity and 400 ppm CO$_2$.

**Measurement of C and N contents**

The contents of C and N were analyzed by using a C/N element analyzer (Elementar vario EL cub). The dry samples were powdered and used for analysis.

**GUS staining assay**

GUS staining assay was performed as described by Pelagio-Flores et al. [32]. Briefly, the proAOX1a::GUS and proUCP1::GUS transgenic lines were incubated in the staining buffer containing 0.1 M sodium phosphate (pH 7.0), 1 mM X-Gluc, 0.5 mM K$_3$[Fe(CN)$_6$], 0.5 mM K$_4$[Fe(CN)$_6$], 10 mM EDTA, and 0.1 % Triton X-100 for 3 h at 37°C. After destained with 75% ethanol, samples were photographed with Nikon camera or Olympus stereoscopic microscope.

**Determination of nitrate reductase (NR) and nitrite reductase (NiR) activity**

The NR activity was analyzed as described by Du et al. [33]. The fresh tissues were homogenized with the buffer [0.1 M HEPES-KOH (pH 7.5), 3 % polyvinylpolypyrrolidone, 1 mM EDTA and 7 mM cysteine], and centrifuged at 10,000 g for 10 min. The supernatant was used for NR activity analysis.

The activity of NiR was determined according to Datta and Sharma [34]. Leaves were homogenized with the buffer [50 mM phosphate buffer (pH 8.8), 3% BSA, 1 mM EDTA and 25 mM cysteine]. Homogenate was centrifuged at 13,000 g for 15 min at 4°C. The supernatant was used directly for NiR activity measurement.

**Determination of nitrate uptake and transport**

The uptake and transport of nitrate were analyzed by using $^{15}$N-KNO$_3$ (Sigma-Aldrich 57654-83-8) according to Gandi et al. [9]. 14-day-old seedlings were treated for 10 d on low-N (1 N) condition and then 24 h on 0 N condition, then transferred to the growth medium containing 10 mM $^{15}$N-KNO$_3$ (CK) or 1 mM $^{15}$N-KNO$_3$ (1 N) for 6 h. After 6 h of labelling, samples were washed and oven-dried, and then ground to fine powder. Total $^{15}$N enrichment was measured using a gas stable isotopic ratio mass spectrometer (IRMS).

**RNA-Seq analysis**

The 14-day-old hydroponically grown seedlings were treated under control (11 N) or low nitrogen (1 N) conditions for 16 d. The shoots were collected and used for the high-throughput sequencing in Bai Mike Company (http://www.biocloud.net/). Gene expression levels were estimated by fragments per kilobase of transcript per million fragments (FPKM) mapped. Differential expression analysis of two groups was performed using the DESeq2 [35]. The $p$ values were adjusted using the Benjamini and Hochberg’s
approach for controlling the false discovery rate (FDR). Genes with an adjusted $p < 0.01$ found by DESeq2 were assigned as differentially expressed. The FDR < 0.01 and $|\log_2(FC)| \geq 2$ were set as the threshold for significantly differentially expressed genes (DEGs). The KOBAS software was used to test the statistical enrichment of DGEs in KEGG pathways [36].

**Statistical analysis**

The data were expressed as means ± SD ($n \geq 3$). All statistical analysis were conducted via one-way ANOVA and SPSS17.0. In the figures, the lowercase letters indicate the significant difference at $P<0.05$.

**Results**

**Double mutant aox1a/ucp1 has compromised tolerance to low nitrogen stress**

It has been reported that *ALTERNATIVE OXIDASE 1a (AOX1a)* and *UNCOUPLING PROTEIN 1 (UCP1)* respond to low nitrogen (N) stress at the transcriptional level in plants [16]. To further investigate the function of *AOX* and *UCP* genes upon low-N condition, the physiological responses of *AOX* mutants [aox1a (Salk_084897), aox1c-1 (CS804611), aox1c-2 (CS877307), aox1d (CS390166) and aox2 (CS766955)] and *UCP* mutants [ucp1 (CS821384), ucp2 (Salk_080118C), ucp3 (Salk_006106), ucp4 (CS373159), ucp6 (Salk_111403C)] were analyzed under low-N condition. Fig. S1 and S2 showed that low N (0.1 N) resulted in the increased primary root length, accumulation of anthocyanin, but decreased fresh weight in Col-0 and the mutants. However, there were no significant differences among them. qRT-PCR results showed that low N significantly induced the expressions of *AOX1a*, *AOX1c* and *AOX2*, which were increased by 9.3-fold, 5.6-fold and 17.0-fold, respectively; while *AOX1b* and *AOX1d* expressions were decreased (Fig. S1d). Similarly, the transcripts of *UCP1*, *UCP2* and *UCP3* were increased by 1.8-fold, 2.0-fold and 1.3-fold, respectively; but *UCP4*, *UCP5* and *UCP6* transcripts were decreased (Fig. S2d). The highest expression of *AOX1a* in the *AOX* family and *UCP1* in the *UCP* family suggests their essential function in Arabidopsis tolerance to low N.

To explore the function and relationship of *AOX1a* and *UCP1* in Arabidopsis tolerance to N deficiency, the *aox1a* and *ucp1* were crossed to generate the double mutant *aox1a/ucp1*. PCR analysis confirmed the screened homozygous lines (Fig. S3). Phenotypic analysis of 8-day-old single and cluster seedlings showed that there was no difference among Col-0, *aox1a*, *ucp1* and *aox1a/ucp1* on 1/2 MS and 1 N conditions (Fig. 1a). However, under 0.1 N and 0 N conditions, the primary root length of *aox1a/ucp1* seedlings was shorter than that of Col-0 seedlings (Fig. 1a, d), and the difference reached the maximum at day 8 (Fig. S4). Under 0.1 N condition for 8 d, the primary root length of *aox1a/ucp1* was reduced by 25.4% compared to Col-0 (Fig. 1d). Moreover, the anthocyanin content and the purple rate of *aox1a/ucp1* cotyledons were higher than that of Col-0 and single mutants under 0.1 N condition (Fig. 1b, c, e). The cotyledon purple rate of Col-0, *aox1a*, *ucp1* and *aox1a/ucp1* seedlings was 60.2%, 58.4%, 61.1%, and 82.8%, respectively (Fig. 1e). Thus, AOX1a and UCP1 might be collaboratively involved in the adaptation of Arabidopsis seedlings to low-N stress.
UCP1 plays more important roles in regulating photosynthesis than AOX1a upon low-N condition

To further investigate the mechanism of AOX1a and UCP1 involvement in Arabidopsis adaption to low-N stress, we analyzed the rosette leaf area, shoot biomass and photosynthetic capacity of Col-0, aox1a, ucp1 and aox1a/ucp1 seedlings. In order to accurately control the N concentration in the medium, seedlings were grown hydroponically. Results showed that the rosette leaf area, fresh weight (FW) and dry weight (DW) of ucp1 and aox1a/ucp1 seedlings were markedly lower than that of Col-0 under moderate-N (5 N) and low-N (1 N) conditions, while aox1a had no significant difference compared to Col-0 (Fig. 2). Under low-N condition, the rosette leaf area, FW and DW in ucp1 were reduced by 24.4%, 29.0% and 27.7%, respectively, and by 44.6%, 26.3%, and 27.3% in aox1a/ucp1, respectively, compared to Col-0 (Fig. 2b-d). These results indicate that loss of UCP1 function results in more significant inhibition of growth than loss of AOX1a function under low-N condition.

The total chlorophyll content (chlt) in ucp1 and aox1a/ucp1 plants were decreased by 7.4% and 9.2%, respectively, in comparison with that in Col-0 upon low-N condition. However, in aox1a, it did not change (Fig. 3a). Under the control condition, the net photosynthetic rate (A) and electron transfer rate (ETR) in ucp1 were significantly lower than that in Col-0. However in aox1a and aox1a/ucp1 plants, A and ETR were not different from that in Col-0 (Fig. 3b, c). Under low-N condition, A and ETR in aox1a was similar to that in Col-0. In contrast, they were significantly lower in ucp1 and aox1a/ucp1 than that in Col-0. A and ETR were reduced by 27.4% and 31.0%, respectively, in ucp1, and by 29.8% and 26.5%, respectively, in aox1a/ucp1 (Fig. 3b, c). The analysis result of light response curve showed that the light saturation point in ucp1 was markedly lower than that in Col-0 when the light intensity exceeded 200 µmol photons m$^{-2}$ s$^{-1}$ (PAR) under the control condition (Fig. 3d). Under low-N condition, the light saturation point in both ucp1 and aox1a/ucp1 plants were significantly lower than that in Col-0 and aox1a, but there was no difference between ucp1 and aox1a/ucp1 (Fig. 3e). These results indicate that aox1a/ucp1 and ucp1 plants have low photosynthetic capacity under low-N stress. UCP1 plays more important roles in regulating photosynthesis than AOX1a does in Arabidopsis tolerance to low-N stress.

**Mutation of AOX1a and UCP1 decreases C and N contents in the shoots of aox1a/ucp1**

Above results confirmed that mutation of AOX1a and UCP1 affects the photosynthetic capacity of aox1a/ucp1. We subsequently analyzed the changes of C and N contents under low-N stress. Upon low-N and moderate-N conditions, the percentage of C in Col-0, aox1a, ucp1, and aox1a/ucp1 shoots was decreased. Interestingly, there was a marked difference only between ucp1 and Col-0 under 1 N condition (Fig. 4a). Low N similarly decreased the percentage of N in all plants (Fig. 4b). The total C and N contents in ucp1 and aox1a/ucp1 shoots were significantly lower than that in Col-0 upon low-N condition (Fig. 4c, d), which were reduced by 21.6% and 26.1%, respectively, in ucp1 and by 24.2% and 23.11%, respectively, in aox1a/ucp1 under 5 N condition. Under 1 N condition, the total C and N contents were reduced by 29.6% and 28.6%, respectively, in ucp1 and by 27.0% and 27.9%, respectively, in aox1a/ucp1. However, in aox1a, the total C and N contents were similar to that in Col-0 under all N conditions. Thus, the photosynthetic C fixation and N assimilation capacity in ucp1 and aox1a/ucp1 were lower than that in...
Col-0 and axo1a plants under low-N condition, and this explained the decreased biomass in ucp1 and aox1a/ucp1 plants.

**Expression patterns of AOX1a and UCP1 and changes of respiratory rates upon low-N condition**

To investigate the expression patterns of AOX1a and UCP1 upon low-N condition, the proAOX1a:GUS and proUCP1:GUS transgenic lines were generated. GUS staining results showed that 0.1 N treatment induced marked increase of AOX1a and UCP1 expression in 6-day-old seedlings. AOX1a was expressed in the whole seedling, whereas UCP1 was mainly expressed in cotyledons and the maturation zone of primary roots (Fig. 5a-d). Under low-N condition, the AOX1a expression was higher than UCP1 in rosette leaves (Fig. 5e-h). At the reproductive stage, low N also increased the expression of AOX1a and UCP1 in flowers and stamens (Fig. 5i-p). Specifically, the expression of AOX1a was mainly increased in the anthers of stamens (Fig. 5n), while UCP1 was mainly expressed in the filaments of stamens (Fig. 5p).

qRT-PCR results reported that low N induced the expression of AOX1a and UCP1 at almost every developmental stage. When Arabidopsis seeds were germinated and grown for 6 d in 0.1 N medium, the expression of AOX1a and UCP1 were enhanced by 9.3-fold and 1.8-fold, respectively (Fig. 5q). In rosette leaves, the response of AOX1a expression to low-N condition was higher than that of UCP1 (Fig. 5r). However, in flowers and siliques, the AOX1a expression increased about 1.5-fold and 2.1-fold upon low-N condition, respectively, while the UCP1 expression was increased by 1.7-fold and 2.3-fold (Fig. 5s, t).

To clarify the relationship between AOX1a and UCP1 as well as the effect of low N on the alternative pathway capacity (V_{alt}) and UCP pathway activity (V_{ucp}), the respiratory rates were analyzed. Fig. S5 showed that low N significantly increased V_{alt} and V_{ucp} in Col-0. Under high-N (control) condition, V_{alt} in ucp1 was decreased by 84.3% and V_{ucp} in aox1a was decreased by 42.1% compared to Col-0. Interestingly, the mutation of UCP1 in ucp1 stimulated the V_{alt} by 63.5% upon low-N condition (Fig. S5a). Similarly, V_{ucp} was also increased in aox1a and Col-0 upon low-N condition. Thus, there should be the close relationship between AOX1a and UCP1 under normal growth condition.

**Mutation of AOX1a and UCP1 affects N metabolism upon low-N condition**

To investigate the effects of AOX1a and UCP1 mutations on N metabolism in Arabidopsis in response to low N, the differences of the uptake, assimilation and transport of N were analyzed in Col-0, aox1a, ucp1, aox1a/ucp1 plants. The results showed that low N decreased the NO$_3^-$ content and NR activity, but increased NiR activity in Col-0, aox1a, ucp1 and aox1a/ucp1 shoots (Fig. 6a-c). Compared to Col-0 under 1 N condition, the NO$_3^-$ content, NR and NiR activities were reduced by 11.5%, 9.5%, 15.0%, respectively, in ucp1 and by 34.0%, 21.8%, 13.3%, respectively, in aox1a/ucp1; however, there was no significant difference between aox1a and Col-0.

To analyze the uptake rate of NO$_3^-$ and the transport from root to shoot, Arabidopsis seedlings were starved under 0 N condition for 24 h, and then transferred to the growth solution containing 10 mM $^{15}$N-
KNO₃ (control) or 1 mM ¹⁵N-KNO₃ (1 N) for 6 h. Results showed that low N decreased the uptake rate of NO₃⁻ in Col-0, aox1a, ucp1 and aox1a/ucp1 roots (Fig. 6d). However, compared to Col-0, the uptake rate of NO₃⁻ in aox1a, ucp1 and aox1a/ucp1 were elevated by 15.4%, 16.7% and 21.6%, respectively, under the control condition, and by 6.9%, 12.0% and 21.2%, respectively, under 1 N treatment (Fig. 6d). In contrast, the transport activity of NO₃⁻ from root to shoot in aox1a, ucp1 and aox1a/ucp1 was significantly decreased compared to Col-0 under both control and low-N conditions (Fig. 6e). Based on these results, although mutations of AOX1a and UCP1 resulted in acceleration of NO₃⁻ uptake under low-N stress, the low assimilation rate and transport activity of N in aox1a/ucp1 seedlings impaired the N metabolism.

**Mutation of AOX1a and UCP1 decreases the seed yield and the C/N content in aox1a/ucp1 under low-N stress**

N deficiency inevitably limits the reproductive growth of plants. Our results showed that low N significantly reduced the silique number and seed yield of Col-0, aox1a, ucp1 and aox1a/ucp1 plants (Fig. 7a, b). Loss of function of AOX1a and UCP1 resulted in more decrease of silique number and seed yield in aox1a/ucp1 (by 22.3% and 23.6%, respectively) than that in Col-0. A similar trend was also found in ucp1 mutant. However, there was no difference between aox1a and Col-0 (Fig. 7a, b). Figure 7c, d showed that the percentage of N was decreased in seeds of four genotypes upon low-N condition. However, the percentage of C in seeds had no significant changes compared to the control. Further result confirmed that the AOX1a mutation alone in aox1a did not affect the total C and N contents in seeds, but in ucp1 and aox1a/ucp1 seeds, the total C content was reduced by 21.1% and 21.8%, respectively, and the total N content was reduced by 27.4% and 34.1%, respectively (Fig. 7e, f). Thus, the decrease of C and N distribution in seeds accounted for the low seed yield in both ucp1 and aox1a/ucp1 plants.

**Distinct transcript profiles in Col-0, aox1a, ucp1 and aox1a/ucp1 plants under low-N stress**

The different physiological response of Col-0, aox1a, ucp1, and aox1a/ucp1 seedlings to low-N stress might be caused by differential expressions of downstream genes involved in different metabolic pathways. To test the hypothesis and elucidate the molecular metabolism of UCP1 and AOX1a in Arabidopsis tolerance to low N, we compared gene expression profiles in Col-0, aox1a, ucp1, and aox1a/ucp1 shoots by using RNA sequencing. Compared to Col-0, transcriptomes of aox1a, ucp1, and aox1a/ucp1 had marked changes (Fig. S6). With thresholds of log₂(FC) ≥ 2 and FDR < 0.01, there were 1605 up-regulated genes and 1559 down-regulated genes in Col-0 upon low-N condition. The up- and down-regulated genes were 1656 and 1153, respectively, in aox1a, 687 and 1378, respectively, in ucp1, and 2321 and 1796, respectively, in aox1a/ucp1 (Fig. S6a-d). KEGG functional enrichment analysis indicated that the DEGs in Col-0 were mainly enriched in ribosome, plant hormone signal transduction, biosynthesis of amino acids, and plant-pathogen interaction. DEGs were mainly enriched in ribosome, biosynthesis of amino acids and carbon metabolism in aox1a; in plant hormone signal transduction, plant-pathogen interaction and photosynthesis in ucp1; and in carbon metabolism, biosynthesis of amino
acids, and photosynthesis in $a_{ox}1a/u_{cp}1$ (Fig. S6e-f). Thus, mutation of $UCP1$ and $A0X1a$ in $a_{ox}1a/u_{cp}1$ markedly disturbed the photosynthesis and carbon metabolism pathways upon low-N condition.

To further investigate the mechanism of decreased resistance to low N in $a_{ox}1a/u_{cp}1$, DEGs in Col-0 and $a_{ox}1a/u_{cp}1$ were analyzed. Venn diagram showed that 1233 and 923 genes were co up- and down-regulated, respectively, in Col-0 and $a_{ox}1a/u_{cp}1$ (Fig. 8a). KEGG results showed that DEGs in both Col-0 and $a_{ox}1a/u_{cp}1$ were mainly enriched in ribosome, biosynthesis of amino acids, photosynthesis and N metabolism. DEGs in Col-0 only (1961 genes) were mainly enriched in ribosome, plant hormone signal transduction, plant-pathogen interaction. DEGs only in $a_{ox}1a/u_{cp}1$ (1008 genes) were mainly enriched in C metabolism, amino acid synthesis, C fixation in photosynthesis organisms, and glycolysis (Fig. 8b-d). The numbers of DEGs involved in the N metabolism, C metabolism, photosynthesis, por and chl metabolism and ribosome were 4, 44, 11, 6, 12, respectively, in $a_{ox}1a/u_{cp}1$, but were 2, 3, 1, 2, 57, respectively, in Col-0 (Fig. 8e, f). Figure 8g further showed that most DEGs in both Col-0 and $a_{ox}1a/u_{cp}1$ in the aforementioned metabolism pathways were generally down-regulated. However, the decrease was more significant in $a_{ox}1a/u_{cp}1$ than in Col-0 under low-N stress (Fig. 8g). qRT-PCR was performed to validate some of the DEGs in Col-0 and $a_{ox}1a/u_{cp}1$. Among the six genes examined, they all showed similar expression patterns as the RNA-seq results (Fig. 8h). Thus, the decreased expressions of genes related to C metabolism, photosynthesis, N metabolism in $a_{ox}1a/u_{cp}1$ could be one of the reasons for the low photosynthetic capacity and C/N level in seeds.

**Discussion**

Nitrogen (N) assimilation is essential for leaf metabolism and seed yield. In plants, carbon (C) metabolism are closely related to the N levels and its assimilation capacity [5, 37–38]. The energy generated by light reaction not only supply C fixation, but also N assimilation [8, 9]. Therefore, plants must balance the energy distribution between C and N metabolism. Many reports have indicated that the alternative pathway and the uncoupling protein (UCP) pathway play key roles in decreasing photooxidation damage and maintaining photosynthesis rate by dissipating excessive reductants in chloroplasts under stresses [10, 20]. Moreover in plants, the dysfunction of AOX1a or UCP1 disturbs the N assimilation and C metabolism [9, 10]. In the study, we investigated the functions of AOX1a and UCP1 involved in regulating the balance of C and N metabolism in Arabidopsis adaptation to low-N stress.

**Dysfunction of AOX1a and UCP1 decreases the tolerance of Arabidopsis to low-N stress at the seedling stage**

Alternative pathway is extensively involved in plant tolerance to environmental stresses, *i.e.*, cold, salt, drought, low-N and so on [10, 16, 30, 39]. qRT-PCR results showed that low-N significantly induces the expressions of $A0X1a$, $A0X1c$ and $A0X2$, but decreases the expressions of $A0X1b$ and $A0X1d$. It has been reported that the expression of $A0X1a$ is tightly related to the N level in plants [10, 16] and is involved in regulating N metabolism and the intensity of mitochondrial stress signal pathway [40]. However, the primary root length and fresh weight of seedlings of $A0X$ mutants exhibit no significant
difference to Col-0 upon low-N condition. Watanabe et al. [16] reported that low N can stimulate \( AOX1a \) expression, however, dysfunction of \( AOX1a \) did not affect the biomass of Arabidopsis. Thus, there should be additional compensation mechanisms when the alternative pathway is affected in plant adaptation to low N.

The functions of AOX and UCP are closely coordinated, as demonstrated in plant heat generation, cell energy balance and adversity defenses [22, 30, 41]. The effect of UCP1 dysfunction on N metabolism is more significant than \( AOX1a \) deficiency [16, 18]. qRT-PCR showed that low N significantly increases \( UCP1, UCP2 \) and \( UCP3 \) expression. However, the phenotypes of 8-day-old \( UCP \) mutants are also similar to that of Col-0 under low-N condition. Double mutation of \( AOX1a \) and \( UCP1 \) in \( aox1a/ucp1 \) results in reduced primary root length and accumulation of anthocyanin compared to Col-0 and the single mutants. It is well known that increase of the root/shoot ratio, the accumulation of anthocyanin and the recycling of N from old leaves to young leaves are common features during plant tolerance to low-N condition [4, 42]. \( pap1 \), a mutant defective in anthocyanin biosynthesis, shows decreased tolerance to low-N stress [43]. Our results suggest that \( aox1a/ucp1 \) has lower tolerance to low N than Col-0 and the single mutants. The high anthocyanin level and purple ratio of cotyledons could facilitate \( aox1a/ucp1 \) seedlings adaptation to low-N stress. In the process, AOX1a and UCP1 collaboratively function in the adaptation of Arabidopsis seedlings to low-N stress.

**Mutation of UCP1 leads to low photosynthetic capacity as well as C and N content in \( aox1a/ucp1 \) under low-N stress**

It has been reported that loss of \( UCP1 \) function leads to photorespiration limitation and reduction of C assimilation rate under high light condition, but not loss of \( AOX1A \) function [9, 20]. Under the control condition (high N), \( A \) and ETR in \( ucp1 \) are markedly decreased compared to that in Col-0. Furthermore, the light saturation point in \( ucp1 \) is significantly lower than that in Col-0, but not in \( aox1a \) and \( aox1a/ucp1 \). Interestingly, \( UCP1 \) mutation results in low AOX protein content under normal growth condition, but does not affect other mETPs [20]. The present result further showed that \( UCP1 \) mutation significantly decreases \( V_{alt} \) under high-N condition. Similarly, \( AOX1a \) mutation also significantly decreases the activity of the UCP pathway. Under low-N stress, higher \( V_{alt} \) is induced in \( ucp1 \) seedlings. These results indicate that there is a close correlation between the alternative pathway and the UCP pathway in Arabidopsis.

The photosynthetic capacity in plants is positively related to N levels in leaves [5, 44]. The N availability in plant affects leaf growth and photosynthetic area through influencing protein synthesis [37]. Under moderate and low-N conditions, the total rosette leaf area of \( ucp1 \) and \( aox1a/ucp1 \) is lower than that of Col-0. N mainly exists in photosynthetic enzymes and chlorophyll in plant shoots, so its level will affect the function and the number of chloroplasts [45, 46]. The chlorophyll content, \( A \) and ETR in \( ucp1 \) and \( aox1a/ucp1 \) are significantly reduced under low-N condition. However, \( AOX1a \) mutation does not affect the photosynthesis capacity and leaf area. Moreover, there is a similar trend in above parameters between \( ucp1 \) and \( aox1a/ucp1 \) under low-N stress, indicating that the dysfunction of UCP1 is responsible for the low photosynthetic capacity and biomass in \( aox1a/ucp1 \) under low-N condition.
It has been reported that mutation of AOX1a and UCP1 affects the assimilation rate of C and N in Arabidopsis leaves [9]. Under low-N condition, the relative C and N contents in aox1a, ucp1, aox1a/ucp1 and Col-0 shoots are decreased. However, the total C and N contents in ucp1 and aox1a/ucp1 shoots are lower than that in aox1a and Col-0 shoots. Moreover, accumulation of shoot biomass shows a similar trend to the total C and N contents as well as the photosynthetic capacity under low-N condition. Watanabe et al., [16] reported that the balance of C and N in plants might be strictly modulated by pathways other than AP upon low-N condition. Thus, the low photosynthetic capacity in ucp1 and aox1a/ucp1 under low-N condition results in decreased total C levels and biomass in shoots; in the process, UCP1 plays a more essential role than AOX1a.

**Mutation of UCP1 disturbs the C/N ratio and leads to low seed yield in aox1a/ucp1 upon low-N condition**

The seed yield and pod setting rate in plants are closely related to N level and its assimilation capacity [5, 47, 48]. ^15^N tracing results indicate that mutation of AOX1a and UCP1 accelerates the NO\textsubscript{3}^- acquisition in aox1a/ucp1 roots under the control and low-N conditions. However, the transport activity of NO\textsubscript{3}^- from roots to shoots is lower in aox1a/ucp1 than that in Col-0, which eventually results in a significant decrease of NO\textsubscript{3}^- level in aox1a/ucp1 leaves upon low-N condition; moreover, the NR activity in leaves of Col-0, aox1a, ucp1, and aox1a/ucp1 is significantly decreased, but the activity decreases the most in aox1a/ucp1. NR activity has a significant positive correlation with protein content in leaves, and it can be used as a biochemical indicator to weigh grain yield and protein content [46, 49]. Under low-N stress, the seed yield and siliQue number were decreased more in ucp1 and aox1a/ucp1 than that in Col-0 and aox1a. Gandi et al. [9] confirmed that UCP1 plays a more key role than AOX1a in the N and C metabolism under normal and high light conditions in Arabidopsis. Based on our results, we propose that loss of UCP1 function, not AOX1a, leads to the low seed yield in aox1a/ucp1 upon low-N condition.

The total C and N levels in seeds are positively correlated with the protein and fat contents in seeds, which also determines the quality and yield of seeds [50, 51]. Loss of function of UCP1 and AOX1a in aox1a/ucp1 did not affect the C content in seeds, but significantly decreased the N content under low-N stress, which resulted in a high C/N ratio in aox1a/ucp1 seeds. Comparatively, the total C and N content in ucp1 and aox1a/ucp1 seeds were significantly lower than those in Col-0 and aox1a. Watanabe et al. [16] indicated that AOX induced by low-N condition does not play an important role on the C/N ratio, instead it could be controlled by pathways other than alternative pathway. In short, the low N utilization efficiency in aox1a/ucp1 disturbs the metabolism of C and N, and eventually results in low seed yield and high C/N ratio under low-N stress; and UCP1 plays a key role for the maintenance of C/N ratio.

RNA-Seq analysis of Col-0 and aox1a/ucp1 shoots reveals the molecular mechanism for their differences in C and N metabolism as well as seed yield upon low-N condition. KEGG results indicate that low N disturbs ribosomes, photosynthesis, N metabolism, C metabolism, amino acid synthesis, porphyrin (por) and chlorophyll (chl) metabolism in Col-0 and aox1a/ucp1. Noticeably, by comparing different DEGs between Col-0 and aox1a/ucp1, we found that aox1a/ucp1 has more DEGs enriched in photosynthesis, N metabolism, C metabolism, and por and chl metabolism than Col-0; and most of their expressions are
down-regulated. Moreover, the expression of common DEGs in photosynthesis and C/N metabolism is more down regulated in \textit{aox1a/ucp1} than that in Col-0 upon low-N condition. Thus, the decreased expressions of genes related to C metabolism, photosynthesis, and N metabolism in \textit{aox1a/ucp1} might be responsible for the low photosynthetic capacity as well as C and N levels in seeds.

Taken together, 8-day-old \textit{aox1a/ucp1} seedlings showed higher sensitivity to low-N stress in comparison with Col-0 and single mutant seedlings, suggesting that \textit{AOX1a} and \textit{UCP1} are both involved in the Arabidopsis tolerance to low N at the seedling stage. The photosynthetic rate and the N assimilation capacity in \textit{ucp1} and \textit{aox1a/ucp1} plants are markedly weakened, leading to decreased leaf area, total C and N content, shoot biomass as well as seed yield compared to Col-0 and \textit{aox1a}. These results indicate UCP1 plays more essential roles than AOX1a in Arabidopsis adaptation to low N at the vegetative and reproductive stages. RNA-seq analysis confirmed that \textit{AOX1a} and \textit{UCP1} mutation leads to more significant down-regulation of genes in photosynthesis and C/N metabolism in \textit{aox1a/ucp1} shoots in comparison with Col-0, which provides powerful evidence for the low seed yield, C and N levels in \textit{aox1a/ucp1}. Noticeably, compared to \textit{AOX1a}, \textit{UCP1} plays a more important role in regulating C/N ratio and yield of seeds in Arabidopsis adaptation to low-N stress.

**Declarations**

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**Author contributions** XW and YB designed the project; XQ, TY, MR, CC\textsuperscript{a}, YZ, FL, SW performed the experiments; XQ, MJ, CC\textsuperscript{b}, XN analyzed the data; XW and TY wrote the paper. All authors have read and approved the manuscript.

**Availability of data and materials**

Sequencing data is available at NCBI SRA under BioProject ID:PRJNA722574.

**Conflict of interest**

The authors declare no competing interest.

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Figures
Figure 1

Effects of low N on Col-0, aox1a, ucp1, aox1a/ucp1 seedlings. (a) Phenotypes of individual and clustered seedlings grown in different media for 8 d. Bar = 1 cm. (b) Magnified images of cotyledons under 0.1 N condition for 8 d. Bar = 50 μm. (c) Anthocyanin content in cotyledons under 0.1 N condition for 8 d. (d) Primary root length under 0.1 N condition for 8 d. (e) Purple ratio of cotyledons under 0.1 N condition for 8 d. Data were expressed as mean ± SD (n≥3, P<0.05).
Figure 2

Effects of AOX1a and UCP1 mutation on leaf area and biomass of Arabidopsis under low N stress. (a) Phenotypes of plants and images of rosette leaves under the different N conditions. Bar = 1 cm. (b) Rosette leaf area. (c) Fresh weight of shoots. (d) Dry weight of shoots. 14-day-old Col-0, aox1a, ucp1, and aox1a/ucp1 seedlings were grown under low-(1 N), moderate-(5 N), or high-N (10 N, CK) conditions for 16 d. Data were expressed as mean ± SD (n≥3, P<0.05).
Figure 3

Effects of low N on chlorophyll content and photosynthetic parameters in Col-0, aox1a, ucp1, aox1a/ucp1. (a) Total chlorophyll (Chlt) content. (b) Net photosynthetic rate (A). (c) Electron transport rate (ETR). (d, e) Light responsive curves under CK (d) and low N (e) conditions. The concentration of CO2 is 400 ppm. 14-day-old seedlings were grown under low-(1 N), moderate-(5 N), or high-N (10 N, CK) conditions for 16 d. Data were expressed as mean ± SD (n≥3, P<0.05).
Figure 4

Effects of AOX1a and UCP1 mutation on C and N content upon low N condition. (a) Percentage of C content in shoots. (b) Percentage of N content in shoots. (c) Total C content in shoots. (d) Total N content in shoots. The 14-day-old seedlings were treated as in Fig. 2. Data were expressed as mean ± SD (n≥3, P<0.05).
GUS-staining and qRT-PCR analysis of AOX1a and UCP1 expression under low N condition. (a-d) 6-day-old seedlings under 1/2 MS (a, c) or 0.1 N (b, d) conditions, bar = 50 μm. (e-h) Shoots under CK (e, g) and 1 N (f, h) conditions, bar = 1 cm. (i-l) Flowers under CK (i, k) and 1 N (j, l) conditions, bar = 20 μm. (m-p) Stamens under CK (m, o) and 1 N (n, p) conditions, bar = 40 μm. (q-t) qRT-PCR analysis of AOX1a and UCP1 expressions in 6-day-old seedlings (q), leaves (r), flowers (s), and siliques (t). In a-d and q, seeds were germinated and grown for 6 d under 1/2 MS or 0.1 N condition. In e-p and r-t, 14-day-old seedlings were transferred to CK (10 N) or low N (1 N) medium for 16 d (e-h, r) or 30 d (i-p, s, t). ACTIN 2 was used as the internal reference gene. Data were expressed as mean ± SD (n = 3). *, P<0.05; ** P<0.01.
Effect of AOX1a and UCP1 mutation on N metabolism under low N condition. (a) NO3- content. (b) NR activity. (c) NiR activity. (d) NO3- uptake. (e) The root to shoot transport activity of NO3-. In a, b and c, 14-day-old seedlings were cultured in low N (1 N) medium for 16 d. In d and e, CK: after the 24-day-old seedlings were starved under 0 N condition for 24 h, they were cultured in the medium containing 10 mM 15N-KNO3 as the sole N source for 6 h. 1 N treatment: after the 14-day-old seedlings were treated under 1
N condition for 10 d and 0 N for 24 h, they were cultured in the medium containing 15N-KNO₃ (1 mM) as the sole N source for 6 h. Data were expressed as mean ± SD (n=3, P<0.05).

Figure 7

Effects of low N on seed yield and C/N content of Col-0, aox1a, ucp1, aox1a/ucp1 plants. (a) Total siliquae number per plant. (b) Seed yield per plant. (c) The percentage of C content in seeds. (d) The percentage of N content in seeds. (e) Total seed C content per plant. (f) Total seed N content per plant. 14-day-old seedlings were transferred to low N (1 N) medium for treatment. Data were expressed as mean ± SD (n ≥ 8, P<0.05).
Figure 8

RNA-Seq analysis of the transcripts in Col-0 and aox1a/ucp1 shoots under low N condition. (a) Venn diagram of DEGs between Col-0 and aox1a/ucp1. (b-d) KEGG enrichment of DEGs in Col-0 (b), aox1a/ucp1 (c), and both Col-0 and aox1a/ucp1 (d). (e) DEGs in Col-0 (green) or in aox1a/ucp1 (grey) that are involved in C metabolism (I), N metabolism (II), photosynthesis (III), porphyrin (por) and chlorophyll (chl) metabolism (IV), and ribosome (V). (f) DEGs in e and their expressions. (g) Low-N
responsive patterns of DEGs in Col-0 and aox1a/ucp1 involved in N metabolism (I), C metabolism (II), photosynthesis (III), and por and chl metabolism (IV). (h) Validation of DEGs in Col-0 and aox1a/ucp1 by qRT-PCR. ACTIN 2 was used as the internal reference gene. Corresponding gene IDs are: NiR (AT2G15620), G6PD3 (AT1G24280), RBCS1A (At1G67090), RBCS1B (At5G38430), PSBP-1 (AT1G06680), PSAD-2 (AT1G03130). Data were expressed as mean ± SE (n = 3, * P<0.05).

**Supplementary Files**

This is a list of supplementary files associated with this preprint. Click to download.

- QiaoXYSupplementaldata20210417.doc