Global transcriptome analysis of AtPAP2-overexpressing Arabidopsis thaliana with elevated ATP

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Abstract

Background: AtPAP2 is a purple acid phosphatase that is targeted to both chloroplasts and mitochondria. Over-expression (OE) lines of AtPAP2 grew faster, produced more seeds, and contained higher leaf sucrose and glucose contents. The present study aimed to determine how high energy status affects leaf and root transcriptomes.

Results: ATP and ADP levels in the OE lines are 30-50% and 20-50% higher than in the wild-type (WT) plants. Global transcriptome analyses indicated that transcriptional regulation does play a role in sucrose and starch metabolism, nitrogen, potassium and iron uptake, amino acids and secondary metabolites metabolism when there is an ample supply of energy. While the transcript abundance of genes encoding protein components of photosystem I (PS I), photosystem II (PS II) and light harvesting complex I (LHCI) were unaltered, changes in transcript abundance for genes encoding proteins of LHCII are significant. The gene expressions of most enzymes of the Calvin cycle, glycolysis and the tricarboxylic acid (TCA) cycle were unaltered, as these enzymes are known to be regulated by light/redox status or allosteric modulation by the products (e.g. citrate, ATP/ADP ratio), but not at the level of transcription.

Conclusions: AtPAP2 overexpression resulted in a widespread reprogramming of the transcriptome in the transgenic plants, which is characterized by changes in the carbon, nitrogen, potassium, and iron metabolism. The fast-growing AtPAP2 OE lines provide an interesting tool for studying the regulation of energy system in plant.

Keywords: Chloroplast, Mitochondria, LHC, Redox, Photosystem, Transcriptomes

Background

Purple acid phosphatases (PAPs) catalyze the hydrolysis of phosphoric acid esters and anhydrides [1]. In higher plants, PAPs are mostly related to the Pi response [2,3]. The only PAP that has been shown to affect carbon metabolism is AtPAP2, which is targeted to both chloroplasts and mitochondria by an additional transmembrane motif at the C-terminus compared to other related proteins [4]. PAPs with a transmembrane motif at their C-termini are conserved in green plants, including the smallest free-living photosynthetic eukaryote, Ostreococcus tauri [5]. Transgenic Arabidopsis thaliana overexpressing AtPAP2 grew faster, produced more seeds and contained higher leaf sucrose content (up to 30%) [6]. Transgenic Camelina sativa overexpressing AtPAP2 also grew faster and produced more seeds [7]. The pleiotropic growth-promoting effect of AtPAP2 is dependent on its C-terminal dual-targeting sequence [6].

Chloroplasts and mitochondria are two key organelles involved in energy metabolism in plant cells and how AtPAP2 affects the biology of these two organelles and supplies more energy for growth remains unknown. To study the impact of AtPAP2 overexpression on the energy status of plants, the levels of ATP and ADP in the leaves of 20-day-old AtPAP2 OE Arabidopsis were measured and compared with those of WT plants. The transcriptomes of leaves and roots were also compared. AtPAP2 overexpression resulted in a widespread changes of the transcriptome in the transgenic plants, which may reflect the impact of changes in energy supply that feed back to alter transcriptional programmes.

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Results
AtPAP2 OE lines contain elevated levels of ATP
To determine if the overexpression of AtPAP2 resulted in alteration in metabolites, LC-MS/MS analysis and bioluminescent based assays were carried out to measure the amount of ATP and ADP. As shown in Table 1, the leaves of AtPAP2 OE lines contained higher levels of ATP and ADP compared with the WT. In contrast, the AtPAP2 T-DNA line contained similar levels of ATP and ADP to the WT. The ATP/ADP ratios among these lines were also unchanged. The levels of ATP and ADP in the WT are similar to those measured in the other studies

| Methods                  | Lines    | ATP (nmol/gFW) | ADP (nmol/gFW) | ATP + ADP (nmol/gFW) | ATP/ADP |
|--------------------------|----------|----------------|----------------|----------------------|---------|
|                          | WT       | 34.17 ± 5.79<sup>a</sup> | 26.07 ± 0.79<sup>a</sup> | 60.24 ± 6.44<sup>a</sup> | 1.31 ± 0.19<sup>ab</sup> |
|                          | T-DNA    | 32.14 ± 1.47<sup>a</sup> | 28.72 ± 0.50<sup>a</sup> | 60.86 ± 1.94<sup>a</sup> | 1.12 ± 0.03<sup>a</sup> |
|                          | OE7      | 47.87 ± 4.36<sup>b</sup> | 32.03 ± 3.33<sup>b</sup> | 79.90 ± 6.55<sup>b</sup> | 1.50 ± 0.15<sup>b</sup> |
|                          | OE21     | 53.98 ± 3.09<sup>b</sup> | 40.73 ± 5.31<sup>b</sup> | 94.71 ± 7.48<sup>b</sup> | 1.34 ± 0.15<sup>ab</sup> |
| LC-MS/MS (n = 3 ~ 4)    | WT       | 25.26 ± 3.88<sup>a</sup> | 14.81 ± 2.12<sup>a</sup> | 40.07 ± 5.38<sup>a</sup> | 1.71 ± 0.22<sup>a</sup> |
|                          | T-DNA    | 21.47 ± 2.24<sup>a</sup> | 13.10 ± 1.51<sup>a</sup> | 34.57 ± 3.71<sup>a</sup> | 1.64 ± 0.05<sup>a</sup> |
|                          | OE7      | 32.72 ± 2.93<sup>b</sup> | 20.07 ± 1.57<sup>b</sup> | 52.79 ± 4.13<sup>b</sup> | 1.63 ± 0.11<sup>b</sup> |
|                          | OE21     | 32.73 ± 3.29<sup>b</sup> | 17.71 ± 1.23<sup>b</sup> | 50.45 ± 4.04<sup>b</sup> | 1.85 ± 0.16<sup>b</sup> |
| Bioluminescent assay (n = 5) | WT       | 34.17 ± 5.79<sup>a</sup> | 26.07 ± 0.79<sup>a</sup> | 60.24 ± 6.44<sup>a</sup> | 1.31 ± 0.19<sup>ab</sup> |
|                          | T-DNA    | 32.14 ± 1.47<sup>a</sup> | 28.72 ± 0.50<sup>a</sup> | 60.86 ± 1.94<sup>a</sup> | 1.12 ± 0.03<sup>a</sup> |
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Statistical differences (P < 0.05) in the same column for each line were based on one-way ANOVA analysis followed by Tukey’s Honestly Significant Differences (HSD) test using statistical program IBM SPSS 19. Within each column, the values marked by different letters (a, b, c) are significantly different (P < 0.05). The data were reproducible in at least 3 independent experiments.
In addition, GO annotation also showed very few gene changes in the AtPAP2 T-DNA line compared to the WT (data not shown), which is consistent with the WT-like phenotype of the AtPAP2 T-DNA line, implying a redundant function of AtPAP2 with other protein homologs in the genome.

Data for specific groups of genes were extracted and studied using the MapMan hierarchical ontology software (Figure 3 and Additional files 3, 4, 5, 6 and 7) [9] (http://www.gabipd.org/projects/MapMan/; Ath_AGI-TAIR9; Additional file 1 and 2). Again, more transcripts in leaves exhibited significant changes than in roots, including transcripts encoding proteins involved in carbohydrate metabolism (10.1% in leaves versus 3.4% in roots), cell wall metabolism (17.7% in leaves versus 3.5% in roots), glycolysis, mitochondria electron transport, ATP synthesis and the TCA cycle (9.3% in leaves versus 3.0% in roots), amino acid synthesis (11.6% in leaves versus 7.1% in roots) and lipid metabolism (8.0% in leaves versus 5.1% in roots). In addition, many genes encoding proteins associated with development (11.4% in leaves and 4.6% in roots), transcription (10.3% in leaves versus 4.4% in roots), protein modification and degradation (11.2% in leaves versus 5.6% in roots), stress (19.2% in leaves versus 12.4% in roots) and redox regulation (23.2% in leaves versus 7.6% in roots) exhibited remarkable changes (Additional files 3, 4, 5, 6 and 7).

Thus, widespread reprogramming of the transcriptome in the AtPAP2 OE plants corresponded with their fast-growing phenotypes. A complete list of altered genes, including their putative function, can be found in Additional file 1 (leaves) and Additional file 2 (roots).

Energy-harvesting system in leaves

When the expression profiles of the energy-harvesting system in the source leaves were compared, transcript levels of genes encoding PS I core proteins, PS II core proteins, LHC I proteins were not significantly altered (FC ≥ ±1.5) (Additional file 8a). In contrast, transcript levels of several genes encoding LHCII proteins, including Lhcb 1.4 (AT2G34430, FC ≤ 0.47), Lhcb 2.2 (AT2G05070, FC ≤ 0.06), Lhcb 2.3 (AT3G27690, FC ≤ 0.66), Lhcb 4.2 (CP29, AT3G08940, FC ≤ 0.38) and Lhcb 6 (CP24, AT1G15820, FC ≤ 0.44), were decreased (FC ≤ 0.66) in the AtPAP2 OE lines. The transcript levels encoding other components in the electron flow chain, including cytochrome b6f complex, ferridoxin (Fd), plastocyanin (PC), NADPH dehydrogenase (NDH) complex, were mostly unaltered, except one of the two ferredoxin-NAPD + reductases (FNR2, AT1G20020, FC ≤ 0.57), FdC2 (AT4G14890, FC ≤ 0.57) [10] and NdhO (AT1G74880, FC ≤ 0.66) [11], which was suppressed in the OE lines. Only two transcripts were up-regulated in the OE lines, including PGR5-like B (PGR5LB, AT4G11960, FC ≥ 2.30), and cyt c6a (AT5G45040, FC ≥ 2.50) [12]. All these changes reflected a reprogramming of energy harvest and electron transfer in the photosystems. Note that organelle-encoded genes are not poly-adenylated and therefore their cDNAs were not labeled in this study.
Redox regulated proteins in leaves and roots

In leaf, electrons excited by sunlight are the ultimate source of reducing equivalents in plants. Electron flow generated from the photosystems is used to reduce Fd, which in turn can be used for reduction of NADP to NADPH by FNR, for reduction of thioredoxins (Trx) by ferredoxin:thioredoxin reductase (FTR), for reduction of nitrite to ammonium by ferredoxin-nitrite reductase (NiR) [13] and for reduction of 2-oxoglutarate and glutamate to two glutamines by glutamate synthase (GOGAT). In the leaves and roots of the OE lines, there were no changes in the transcript abundance of four Fd genes, two FTR genes, nine Trx genes (Trx f1-2, m1-4, Trx x, Trx y1-2), or most enzymes regulated by Trx (GAPD1-3, SBPase, PRK, RCA, NADP-MDH) (Additional file 8b) [14]. In leaf, but not in root, the transcripts of two electron carriers FNR2 and

Figure 2 GO functional analysis of differentially expressed genes in leaves and roots. Functional category of differentially expressed genes in the leaves (A,B,C) and roots (D,E,F) in both AtPAP2 OE lines compared with the WT. Genes were annotated as “Cellular component” (A,D), “Molecular function” (B,E) and “Biological processes” (C,F) (1.5-fold change, P < 0.05).
Figure 3 Changes in transcripts associated with general metabolism. Compared with the WT, genes significantly up- and downregulated (1.5-fold change and $P < 0.05$) in the leaves (A) and roots (B) of AtPAP2 OE lines are visualized by MapMan and are indicated in red and blue, respectively. Scale bars display log2 fold changes.
FidC2 which play roles in photosynthesis, were downregulated. Interestingly, the transcripts of NiR (AT2G15620, FC ≤ 0.63) was downregulated in the roots, whereas G6PD4 (AT1G09920) were downregulated specifically in both leaves (FC ≥ 4.38) and roots (FC ≥ 1.95), whereas the transcript of AT01 (AT2G35010), a threodoxin in mitochondria, was upregulated in leaves (FC ≥ 1.55) but was downregulated in roots (FC ≤ 0.03), respectively.

Calvin cycle, starch and sucrose synthesis in leaves
Transcript abundance for the key enzyme of the Calvin cycle, a transketolase (AT2G45290, FC ≥ 1.97), was induced in the leaves of AtPAP2 OE lines. Uprogulation of the transcript implied an activated Calvin cycle activity and possible enhanced output of carbon skeletons for sucrose synthesis in the cytosol. AtPAP2 OE lines exhibited increased leaf sucrose content, a higher expression level of SPS protein and a higher SPS activity in leaves [6]. Among the four SPS genes in Arabidopsis, AtSPS2F (AT5G11110) exhibited a significant change in both leaves (FC ≥ 1.85) and roots (FC ≥ 1.73) of AtPAP2 OE lines (Additional files 8 and 9). Regarding sucrose cleavage enzymes that import sucrose in the sink tissues, two out of six sucrose synthases, SuSy1 (AT5G20830, FC ≥ 1.90) and SuSy3 (AT4G02280, FC ≥ 1.75) were upregulated in leaves, whereas transcripts of a gene for cell wall invertase (AT3G13790, FC ≤ 0.45) was significantly downregulated in the leaves of the OE lines (vs. WT). These results indicated an alternation of the gene expression pattern in sucrose metabolism. The transcript abundance of two key genes encoding enzymes in starch synthesis, plastid phosphoglucomutase (PGM, AT5G1820, FC ≤ 0.53) and ADP-glucose pyrophosphatase small subunit 2 (AT1G05610, FC ≥ 1.74) were altered in the leaves. In addition, the transcript abundance of three starch degradation enzymes: water dikinase (AT4G24450, FC ≥ 1.68), α-amylase 3 (AT1G69980, FC ≥ 3.0) and glucanphosphorylase (AT3G29320, FC ≤ 0.60), were significantly changed. Taken together, AtPAP2 OE lines exhibited altered gene expression patterns for sucrose and starch metabolism.

Glycolysis, the TCA cycle and the electron transport chain in mitochondria
Except for the upregulation of a cytosolic pyruvate kinase (AT5G56350, FC ≥ 1.64) in leaves and a downregulation of a pyruvate kinase (AT3G49160, FC ≤ 0.55) in roots, the expression levels of all of the genes of cytosolic enzymes involved in glycolysis were unaltered in leaves and roots (Additional files 8e and 9d). Likewise, the expression levels of all genes in the TCA cycle, except for the upregulation of a citrate synthase (CS)-like gene (AT2G11270, FC ≥ 5.30 in leaves and FC ≥ 2.53 in roots), were unchanged in the leaves and roots of both AtPAP2 OE lines (Additional files 8f and 9e). Regarding the respiratory chain in mitochondria, only components of Complex I, but not components of Complexes II, III, IV, V, UBQ and cytochrome c oxidase (COX) biogenesis, were altered in both leaves and roots (Additional file 10).

Cell wall synthesis
Thirty percent or more of cellular carbohydrate metabolism is consumed by the synthesis of wall components and cell shape morphogenesis [15]. Enhanced ATP production in source leaves of AtPAP2 OE lines could lead to a higher supply of sucrose for cell wall synthesis to support plant growth. AtPAP2 OE lines also exhibited significant changes in the expressions of genes encoding polygalacturonase, pectinesterase, cellulase and cellulose synthase (Additional files 8d and 9c). Transcripts from 87 genes (17.7%) in leaves (Additional file 1d) and 18 genes (3.5%) in roots (Additional file 2d) were altered, which correlated with a higher growth rate in leaves than in roots, arising from enhanced sucrose synthesis in leaves. Transcript of a gene encoding a protein similar to cellulose synthase (ATCSLA01, AT4G16590, FC ≥ 6.69) in the cellulose synthesis was induced up to 11-fold in the leaves of AtPAP2 OE lines. In addition, transcript levels of genes encoding expansin or expansin homologs (AT4G17030, FC < 0.35; AT1G69530, FC < 0.44; AT5G02260, FC < 0.59; AT2G20750, FC < 0.60; AT3G29365, FC < 0.62; AT1G20190, FC > 1.53; AT4G38400, FC > 1.91) and xyloglucan endotransglycosylase (AT4G25810, FC < 0.33; AT4G14130, FC ≥ 2.50) were also significantly upregulated in abundance. These alterations reflected an active state for cell wall growth and reorganization in leaves.

Nitrogen and amino acid metabolism
Faster plant growth and higher seed yield requires greater supply of nitrogen or re-allocation of available nitrogen sources. Plants obtain nitrogen via ammonium or nitrate transporters in roots. Nitrate is reduced to ammonium by two biochemical steps, nitrate reduction and nitrite reduction. The expression of the only nitrite reductase gene, NiR (AT2G15620), was significantly downregulated in the leaves (FC ≤ 0.63), Nitrate transporters, including AtNRT1.1 (AT1G12110, FC ≤ 0.55 in the leaves) [16], AtNRT1.2 (AT1G69850, FC ≤ 0.62 in the leaves and FC ≤ 0.58 in the roots) [17] were downregulated in the leaves and roots of both OE lines. Interestingly, a high affinity ammonium transporter (AMT1;2, AT1G64780, FC ≥ 3.12), was significantly induced in leaves. The reduced Fd generated from photosynthesis activates NiR activity posttranslationally; therefore, its lower mRNA expression in the OE lines could result from negative feedback by higher specific activities. If the NiR activity is indeed higher in the OE lines, more ammonium, but less nitrate, will be transported to the leaves. This could result in the upregulation of ammonium transporters, but downregulation of nitrate transporters in the leaves.
Amino acids serve as precursors of metabolites or intermediates for the stress response [18]. Noticeably, there was a clear tendency of repressed expression of genes associated with biosynthesis of the aspartate family amino acids (Asn, Asp, Lys, Met, Thr, Ile) in the roots of both OE lines. In the leaves, except for genes of enzymes involving in the biosynthesis of homoserine, genes for Pro, Cys, Ser and two genes for Met synthesis, were upregulated; all other genes involved in Trp and Lys synthesis, and Arg, Trp, and Ile degradation were downregulated.

The aromatic amino acids (AAA) metabolic pathway covers the synthesis of Trp, Phe and Tyr [19]. Nearly all the genes involved in this pathway were downregulated; all other genes involved in Trp and Lys synthesis, Cys, Ser and two genes for Met synthesis, were upregulated by a phosphatase (AIP1) [21]. Expression of CIPK23 (AT1G30270, FC ≥ 1.60) was significantly upregulated in the leaves of the OE lines (Additional file 8h). Regarding Fe uptake, one out of three Fe (II) transporters (IRT3, AT1G60960, FC ≥ 2.03) was significantly upregulated in leaves, and the expression of four out of eight ferric reductases including FRO1 (AT1G01590, FC ≥ 1.74; FRO4 (AT5G23980, FC ≥ 6.87), FRO3 (AT1G23020, FC ≤ 0.37) and FRO8 (AT5G50160, FC ≤ 0.60) changed significantly (Additional file 8i) whereas in the roots, transcripts of FRO3 (FC ≤ 0.62) and FRO8 (FC ≥ 1.57), were significantly altered in the roots (Additional file 9h).

Secondary metabolism
Sixty-three out of 395 genes involved in secondary metabolism in leaves were affected (Additional file 1). These include genes involved in phenylpropanoid and flavonoid biosynthesis (i.e. PAL2, PAL3, CHS, UGT71D1, CYP706A4, CYP706A5, UF3GT, DFR, ATN1C1, CAD5) and genes involved in phenols, glucosinolates, wax, and isoprenoids synthesis and degradation.

Transcription factors
Genes encoding transcription factors (TFs) constitute 5 to 7% of the Arabidopsis genes [22]. The Arabidopsis genome encodes at least 1550 TFs, classified into more than 50 families [23]. In this study, a larger amount of TFs were differentially expressed in the leaves (233 from 45 families) than in the roots (103 from 31 families) of AtPAP2 OE plants (Additional file 11). The number of upregulated TFs (6.3%) was higher than the number of downregulated TFs (3.7%) in the leaves; however, in roots, there were fewer upregulated genes (1.8%) than downregulated genes (2.5%) (Figure 2). In leaf, the transcriptional repressor NF-YA5, was up-regulated (AT1G54160, FC ≥ 1.74) at the transcriptional level. NF-YA5 could specifically bind to miR169, which targets mRNAs for cleavage or translational repression at multiple cellular processes [24]. The mRNA of the transcriptional activators such as MYB58 (AT1G16490, FC ≥ 2.00) in the lignin biosynthetic pathway [25], a FLOWERING BHLH transcriptional activator (AT4G09180, FC ≥ 1.74) control expression of the photo-periodic flowering [26], were also found with increased transcripts abundance in the leaves. These repressors or activators might affect targeted gene expression to some extent at the transcriptional level.

Nucleus-encoded chloroplastic and mitochondrial proteins
As AtPAP2 is targeted to the chloroplasts and mitochondria, the transcripts of genes encoding proteins of the “Chloroplast” and “Mitochondria” categories of TAIR were examined. About 6.8% genes in the “Chloroplast” and 6.6% genes in the “Mitochondria” of leaves and 3.9% genes in the roots “Mitochondria” transcripts were significantly changed. Among ~1500 nucleus-encoded proteins identified in chloroplasts by proteomics studies [27], more transcripts were significantly changed in the leaves (91 or 6.1%) than in the roots (43 or 2.7%) (Additional file 12). Among ~650 nucleus-encoded proteins identified in mitochondria by proteomics studies [28,29], again, more transcripts were significantly altered in leaves (37 or 5.7%) than in roots (10 or 1.5%) (Additional file 12).

Verification of candidate genes by real-time RT-PCR
To confirm the accuracy of the microarray data, real-time RT-PCR analysis was carried out on randomly selected genes from leaves. Candidate genes selected were: a C2 domain-containing protein (AT3G60950, FC ≥ 62.0), a member of the receptor kinase-like protein family (AT3G24660, FC ≥ 1.32), a phosphatidylinositol 3-kinase (AT1G23020, FC ≥ 1.32), a phosphatidylinositol 3- and 4-kinase family protein (AT5G24240, FC ≥ 10.2), a tyrosine specific protein phosphatase family protein (AT1G05000, FC ≥ 1.53) and a protein kinase family protein (AT1G28390, FC ≥ 2.38). Gene expression values from real-time RT-PCR of the five genes were also compared to their values from the microarray data. The expression of each gene was consistent between the microarray and real-time RT-PCR results (Additional files 13 and 14).

Microarray data is highly correlated with the physiology of AtPAP2 OE lines
High exogenous sucrose induces anthocyanin biosynthesis in Arabidopsis [30]. In the AtPAP2 OE plants,
most genes in the anthocyanin biosynthesis pathway were repressed (Figure 4). The key pathway gene \textit{dihydroflavonol 4-reductase} (\textit{DFR}) and downstream \textit{UF3GT} decreased 2-fold compared to WT. Other genes in the anthocyanin pathway also had attenuated gene expression in the OE lines. Thus, these microarray data predict opposite effects of endogenous and exogenous sucrose on anthocyanin biosynthesis.

To examine the correlation between the microarray data and phenotypes, the levels of anthocyanin production in various lines were examined on sugar-treated MS plates. \textit{AtPAP2} T-DNA insertion line had accumulated more anthocyanin than WT. In contrast, \textit{AtPAP2} OE7 line showed remarkably less purple color under the same treatment (Additional files 15 and 16). Mannitol and sorbitol are reduced forms of glucose and are not efficiently metabolized by plants [30]. Higher concentration of mannitol and sorbitol (8% and 9%; w/v) were added to the MS medium. These sugars also showed an anthocyanin background but there were few differences among the WT, \textit{AtPAP2} T-DNA line and \textit{AtPAP2} OE lines (Additional file 16). A semi-quantitative reverse transcription-PCR (RT-PCR) was employed to verify the transcriptional expression of genes involved in the pathway. In high sucrose (6%, w/v) MS medium, both WT and T-DNA lines exhibited strong induction of \textit{DFR} and \textit{Production of anthocyanin pigment 1,} (\textit{PAP1}) [30] whereas, the \textit{AtPAP2} OE7 line showed only weak induction of these 2 key genes (Additional file 17). Hence, the microarray data highly correlates with the physiology of the OE lines.

**Discussion**

Metabolomics analysis showed that \textit{AtPAP2} OE lines contained higher level of ATP (Table 1) and higher malate, citrate, fumarate and sucrose [6]. The fast growth, high seed yield and high sucrose phenotypes imply that the energy harvesting system of the OE lines may be more efficient, as the cell sizes and cell densities of the OE lines did not differ significantly compared to WT (data not shown).

The high ATP and sucrose contents of the OE lines must be generated by a higher output from the photosystems. Plant harvests light energy by PS I and PS II. In the leaves of both OE lines, while the mRNA transcripts of the genes of PS I and PS II core proteins and LHCII did not change significantly, many transcripts of the mobile LHCII components were altered (Additional file 8a). How could overexpression of \textit{AtPAP2} cause changes in the expressions of \textit{Lhcb} genes? A possible explanation is that \textit{AtPAP2} overexpression triggers the regulation of redox-dependent retrograde signaling [31]. The expression of \textit{Lhcb} genes are regulated by the redox state of the plastoquinone (PQ) pool [32]. PQ reduction suppresses \textit{Lhcb} family gene expression to avoid absorption of excess light energy [31]. In addition, \textit{Lhcb} genes could also be repressed by high sugar levels [33]. In addition to \textit{Lhcb} genes, the upregulation of \textit{PGRL1B}, a key component of the PGRL1-dependent CEF supercomplex [34] and the downregulation of \textit{FNRI} were also significant, whether these changes can lead to a higher output of ATP from the photosystems would be an interesting subject for future studies (Figure 5). Photosynthesis also supplies reducing powers and many biological pathways are redox-regulated. The transcription levels of all thioredoxins were not significantly changed in both leaves and roots, and among the many Fd- and Trx-regulated enzymes in chloroplasts, the transcription of \textit{NiR} and \textit{G6PD4} were specifically down- and up-regulated in both leaves and roots, respectively. This is reasonable because the activities of these proteins can be instantly regulated by the redox status (e.g. availability of light) instead of transcriptional regulation, which is more time-consuming. Our data indicates that the activities of \textit{NiR} and \textit{G6PD4} are subject to both redox and transcriptional regulations.

Generally, if there is a higher output of ATP from chloroplasts, the demand of ATP production in mitochondria would be less. The increase in organic acids in leaves is consistent with the changes observed in the transcriptome in this study. The transcript of the cytosolic \textit{ICDH} (AT1G65930) was strongly suppressed in the leaves of OE lines, which could account for the high citrate content in the OE lines [35]. Previous studies have shown that alterations of carboxylic acids can lead to alterations in photosynthesis and enhanced growth [36-38]. One mechanism shown to operate on altering organic acids is an effect on stomatal aperture, and increased growth by 25% [36]. Furthermore the role of citrate and malate in signaling changes in the transcriptome has been recently elucidated [39], showing interactions with hormone biosynthetic pathways such as gibberellin biosynthesis. Thus, overall the changes observed appear to mimic a reduction in carbon flow through the TCA cycle, which leads to an increase in sucrose and photosynthesis. Furthermore the changes due to increased levels of citrate, interact with hormone, ion (Fe$^{2+}$ and Ca$^{2+}$) and biotic defense pathways [39].

TCA metabolites are the substrates of various biomolecules. The OE lines contain a lower level of aspartate family amino acids (Asn, Asp, Lys, Met, Thr) than the WT, which could be caused by a higher capacity for malate production in the chloroplast. If excess malate is produced at the expense of OAA, the sole precursor of Asp family amino acids, and leads to a lower level of precursors of these amino acids. All of the above correlates with the results of metabolites analysis [6].

The fast-growing phenotypes of the \textit{AtPAP2} OE lines are dependent on the targeting of \textit{AtPAP2} to chloroplasts and mitochondria. While there are significant changes in energy harvesting and conversion processes
related to chloroplasts' functions (photosystem, starch and sucrose metabolism), the expression of most genes involved in catabolism, including glycolysis, TCA cycle and mitochondria respiratory chain, are unaltered in the OE lines. Similarly, the activities of many enzymes in these pathways are regulated by the energy status (e.g. ATP/ADP ratio, citrate, etc.) through allosteric regulation. Our data indicated that transcriptional regulation is not a major control mechanism of these pathways in the current study. Higher levels of energy production in chloroplasts would also alleviate the need for oxidative phosphorylation in mitochondria, which might cause the downregulation of the gene expression of Complex I components (Additional file 10). It would be interesting to measure the activity of Complex I in the OE lines. Reduced activity of Complex I may lower the rate of consumption of carbon, allocating more carbon to be used for anabolism and growth.
Leaves and roots are the source and sink of sucrose and energy and thus their carbon flows are different. Since the leaves of OE lines produced more sucrose, the supply of sucrose to roots would be increased. The changes in transcription profiles in the roots of OE lines thus likely reflect the impacts of higher sucrose supply. Cell wall invertase (cwINV) is a sucrose-cleavage enzyme and is responsible for hydrolyzing apoplastic sucrose. As shown in Figure 5, the transcription of a cwINV gene (AT3G13790) was downregulated in leaves but the transcription of another cwINV gene (AT3G13784, FC > 1.57 in OE21) was upregulated in roots. Furthermore, the transcriptions of two sucrose synthase (SuSy) genes were upregulated in leaves but not in roots. SuSy is a sucrose-cleavage enzyme which supplies hexose skeletons for cell wall synthesis. Their differential expression may affect the growth rates of leaves and roots. It is also true for the differential expression of certain genes of the starch synthesis pathway. Nonetheless, an SPS gene (AtSPS2F, AT5G11110) and a citrate synthase-like gene (AT2G11270) were upregulated in both leaves and roots, while a phosphoglucomutase (AT5G51820) was downregulated in both tissues.

Overall, the transcriptomic responses to AtPAP2 overexpression were consistent with the growth phenotypes and metabolite analysis [6]. A considerable amount of specific genes related to photosynthesis, sucrose metabolism, nitrogen metabolism and amino acid anabolism were significantly altered. A summary combining the transcriptome and metabolome for depicting the mechanisms responding to AtPAP2 overexpression is proposed (Figure 5). AtPAP2 overexpression may reprogram the photosystems and thus supply more ATP and carbon skeletons for sucrose and malate syntheses. The higher supply of malate causes the accumulation of organic acids, such as citrate and fumarate. The higher energy supply subsequently causes the alteration of many transcripts and metabolites.

Conclusions
This study reported the global changes in transcriptome of source (leaves) and sink (roots) tissues when there are
plenty of energy and sucrose. Overexpression of AtPAP2 enhances ATP production and sucrose synthesis in leaves, which provide more carbon skeleton for the roots. There are more than 30,000 genes in the genome of Arabidopsis and many gene families contain multiple members with highly homologous sequences or redundant functions. Our results reported the genes that are subject to transcriptional regulation when the energy status of the plant is elevated. Many scientists have attempted to enhance plant growth and yield by altering starch, sucrose, chloroplast or mitochondrial metabolism [40-43]. Other attempts included manipulation of transcription factors and hormones [44]. This study shows that alterations of other components feed into these pathways, and the identification of regulators or proteins that sense of mediate switches in metabolism offer an attractive avenue to increase biomass accumulation.

Methods
Plant materials and growth conditions
WT Arabidopsis thaliana ecotype Columbia (Col-0), an AtPAP2 T-DNA insertion mutant (Salk_013567) and two AtPAP2 OE lines (OE7 and OE21) were grown in soil under a 16-hr light (22°C)/8-hr dark (18°C) regime (long day, LD) at a light intensity of 120–150 μmol m−2 s−1 [6].

Determination of ATP and ADP by LC-MS/MS and bioluminescent assay
To extract ATP and ADP, 100 mg of leaves, freshly collected from 20-day-old plants at the middle of day, were ground in liquid nitrogen. 500 μL of 2.3% (w/v) trichloroacetic acid was then added to the sample and the mixture was incubated on ice for 10 min. After centrifugation for 30 min at 16,000 g at 4°C, the supernatant (500 μL) was transferred to an ice-cold Eppendoff tube and the pH was adjusted to 7.0 by addition of 2.5 M K2CO3 [8]. Measurement of ATP and ADP was carried out on a 3200 QTRAP LC-MS/MS System (AB Sciex, Foster City, USA) in negative mode [45]. To verify the LC-MS/MS results, ATP Bioluminescent Assay Kit (Sigma, FL-AA) was adopted [46]. The level of ATP was measured directly according to the kit's protocol. To measure ADP, ADP was first converted into ATP by pyruvate kinase and ADP content = Total ATP after pyruvate kinase conversion – ATP before conversion. All data were analyzed by the statistical program SPSS Statistics 19.

Microarray analysis
Leaves and roots were collected at the middle of the day and ground in liquid nitrogen. The roots were harvested from soil of 20-day-old Arabidopsis at the middle of day, and to avoid any interference caused by stresses or others, the harvest time did not exceed 1 hour. Total RNA extraction was performed using an RNeasy Mini Kit (Qiagen, USA) and quantified by the Bioanalyzer 2100 (Agilent Technologies, USA). First strand cDNA was synthesized using an oligo dT primer and 10 μg total RNA. NimbleGen Systems, Inc. (USA) performed the double stranded DNA synthesis and Cy 3 labeling from three biological replicates.

Normalized expression values were generated using a standard quantile normalization matrix [47] and the robust multiplex average (RMA) algorithm [48], resulting in a final data set of 30361 probe identifiers in the leaf and 37118 in the root. The signal-to-noise-ratio for each spot was greater than 2.6. ArrayStar 3.0 (DNASTAR, USA) was used to draw heatmaps. The log-transformed data were subsequently analyzed for differential expression of genes between AtPAP2 OE lines and WT using the paired Student’s t test [49]. GO annotation was carried out with the GO terms of the TAIR database (http://www.Arabidopsis.org/tools/bulk/go/index.jsp) and the corresponding Arabidopsis gene locus identifiers were mapped to the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (http://www.genome.jp/kegg/) using the KegArray tool (Version 1.2.1). The percent (%) of significantly changed genes in each TAIR annotated category was calculated as follows: percent = the number of significantly changed genes divided by N × 100, where N represents the total number of genes annotated in each ontology. Identified genes were subsequently mapped to the MapMan databases (http://www.gabipd.org/projects/MapMan/). The microarray data in this work are deposited at GEO (http://www.ncbi.nlm.nih.gov/geo/) with the accession number: GSE40307.

Quantitative real-time RT-PCR
Quantitative real-time RT-PCR analysis was carried out using cDNA samples transcribed from 20-day-old leaves of Arabidopsis. Primer3 Plus (http://www.bioinformatics.nl/cgi-bin/primer3plus/) was used to design the real-time RT-PCR primers. The PCR reactions were performed in a 20 μL volume containing a 2 × SYBR Green Master Mix (ABI systems), 50 ng cDNA, and 0.4 μM of forward and reverse primers in an ABI CFX96 thermocycler. The amplification parameters were 95°C for 1 min; followed by 40–50 cycles of 95°C, 15 s and 61°C, 30 s. β-actin was used as the internal control. For every transcript, each cDNA sample was analyzed in triplicate, and relative transcript abundance was calculated by normalizing to the maximum level. The comparative Ct method was used to calculate the relative gene expression levels across the samples. The relative expression level of each gene in one sample (ΔCt) was calculated as follows: 

\[ \Delta C_t = C_t - C_{b-actin} \]

where C_t is the cycle threshold of the target gene and C_{b-actin} is the cycle threshold of the reference gene. The relative expression of each gene in two different samples (ΔΔCt) was calculated as follows: 

\[ \Delta \Delta C_t = \Delta C_t - \Delta C_{t2} \]

where C_{t2} is the cycle threshold of the second sample. The primers used are shown in Additional file 13.
Sucrose treatment and anthocyanin measurement
Sucrose gradients from 0% to 15% (w/v) were employed to test the post-germination growth of Arabidopsis seedlings. Five–day-old seedlings grown on normal MS medium (2%, w/v, sucrose) were transferred to MS medium with different concentration of sucrose for 3 days. For mannnitol and sorbitol (8% and 9%; w/v) treatments, these sugars were added to the MS medium with 1% (w/v) sucrose. Anthocyanin content of seedlings was determined spectroscoically as described [50]. RT-PCR analysis was carried out according to Teng [51].

Additional files

Additional file 1: Leaf microarray data.
Additional file 2: Root microarray data.
Additional file 3: MapMan diagram of genes involved in sucrose synthesis and photosynthesis. Gene transcription significantly up- and downregulated (1.5-fold change and P < 0.05) in the leaves (A, B) and roots (C, D) of OE lines are indicated in red and blue, respectively. Scale bars display log2 fold changes.
Additional file 4: MapMan diagram of genes involved in regulation in Leaves (A) and Roots (B).
Additional file 5: MapMan diagram of genes associated with mitochondrial electron transport in Leaves (A) and Roots (B).
Additional file 6: MapMan diagram of genes of transcription factors in Leaves (A) and Roots (B).
Additional file 7: MapMan diagram of of genes associated with biotic stresses in Leaves (A) and Roots (B).
Additional file 8: Functional categories (Leaf).
Additional file 9: Functional categories (Root).
Additional file 10: Respiratory chain in mitochondria.
Additional file 11: Transcription factors.
Additional file 12: Nucleus-encoded chloroplastic and mitochondrial proteins in leaves and roots.
Additional file 13: RT-PCR Primers.
Additional file 14: Validation of leaf microarray data by real-time RT-PCR. Columns in white and black indicate microarray and real-time RT-PCR data, respectively.
Additional file 15: Induction of anthocyanin by sucrose. Five-day-old seedlings were transferred to MS medium containing different concentrations of sucrose for 3 days before RT-PCR analysis. Elongation factor (EF) was taken as a control.

Competing interests
The authors declare that they have no competing interests.

Authors’ contributions
FS carried out experimental design, sample collection, microarray data integration, anthocyanin measurement and drafted the manuscript, CL participated in the microarray data analysis and performed the ATP measurement experiments, JW, JF and PZ participated in the microarray data analysis and provided helpful suggestions, and BL was responsible for the overall concept, experimental design, data analysis, and revising manuscript. All authors read and approved the manuscript.

Acknowledgements
This project was supported by the Initiatives for Clean Energy and Environment (ICEE) of the University of Hong Kong, the General Research Fund (HKU772710M) and the Innovation and Technology Fund (ITS158/09 and Funding Support to Partner State Key Laboratories in Hong Kong) of the HKSAR, China.

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Received: 16 April 2013 Accepted: 19 October 2013
Published: 1 November 2013

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