Physiological and transcriptomic characterization of a yellow-green leaf mutant of maize

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Abstract

Background Chlorophylls, green pigments in chloroplasts, are essential for photosynthesis. Reduction in chlorophyll contents may result in retarded growth, dwarfism, and sterility. In this study, a yellow-green leaf mutant of maize, indicative of abnormality in chlorophyll contents, was identified. The physiological parameters of this mutant were measured. Next, global gene expression of this mutant was determined using transcriptome analysis and compared to that of wild-type maize plants. **Results** The yellow-green leaf mutant of maize was found to contain lower contents of chlorophyll a, chlorophyll b and carotenoid compounds. It contained fewer active PSII centers and displayed lower values of original chlorophyll fluorescence parameters than the wild-type plants. The real-time fluorescence yield, the electron transport rate, and the net photosynthetic rate of the mutant plants showed reduction as well. In contrast, the maximum photochemical quantum yield of PSII of the mutant plants was similar to that of the wild-type plants. Comparative transcriptomic analysis of the mutant plants and wild-type plants led to the identification of differentially expressed 1122 genes, of which 536 genes were up-regulated and 586 genes down-regulated in the mutant. Five genes in chlorophyll metabolism pathway, nine genes in the tricarboxylic acid cycle and seven genes related to the conversion of sucrose to starch displayed down-regulated expression. In contrast, genes encoding a photosystem II reaction center PsbP family protein and the PGR5-like protein 1A (PGR1A) exhibited increased transcript abundance. **Conclusions** The yellow-green leaf mutant of maize contained fewer active PSII centers with lowered net photosynthesis rate, but have the similar value of the maximum photochemical quantum yield of PSII with that of the wild-type plants. Analysis of differentially expressed genes through transcriptome analysis revealed the down-regulated genes which may be responsible for chlorophyll deduction and changes of photosynthetic characteristics. The up-regulated genes would be helpful to maintain the active PSII centers of the yellow-green leaf mutant.

Background

Chlorophylls are essential pigments for photosynthesis, playing the main role in the conversion of light energy to stored chemical energy [1]. Chlorophyll contents directly determine photosynthetic potential and primary productivity of green plants [1-3]. The formation of chlorophyll consists of four steps including synthesis of 5-aminolevulinic acid, formation of a pyrrole ring porphobilinogen, synthesis of protoporphyrin IX and insertion of Mg^{2+} to the protoporphyrin IX [4]. The functional genes of the chlorophyll metabolism pathway have been identified.

Generally, the leaf color is green for its common content of chlorophyll. Nevertheless, a large number of leaf color mutants have been identified in many seed plant species, such as *Arabidopsis*, maize, soybean, barley, rice, and wheat [5]. Among the leaf color mutants, a number of abnormal phenotypes have been identified, such as yellow, pale green, spots, and stripes. Due to reduced levels of chlorophyll, retarded growth, dwarfism, and sterility were characterized in most color mutants. Recently, with the progressive characterization of various leaf color mutants, a significant number of genes have been isolated and verified to be responsible for the abnormal phenotype. For example, in carrot, a *YEL* locus was mapped in a linkage group with a total length of 33.2 cM, and the mutant had a yellow-leaf phenotype [6]. In maize, a semi-dominant oil yellow 1 (*Oyl*) mutant was identified to be deficient in the conversion of protoporphyrin IX to magnesium protoporphyrin IX [7]. The *Oyl* gene was demonstrated to encode the I subunit of magnesium chelatase (*ZmCHL*). In cabbage, the *ygl-1* locus was located on chromosome C01; mutation in the *ygl-1* gene exhibited a yellow-green leaf phenotype [8]. In rice, mutation in the *VIRESCENT YELLOW LEAF* (*VYL*) gene, which encodes a subunit of chloroplast Clp (*OsClpP6*), resulted in temperature-insensitive and developmental stage-dependent *virescent yellow leaf* (*vyt*) phenotype [9]. *Fgl* is located in the coding region of *OsPORB*, and its mutation resulted in the presence of the yellow/white leaf [10]. Mutation in the *FdC2* gene, which encodes a ferredoxin-like protein with a C-terminal extension, caused the yellow-green leaf phenotype in rice [11]. Mutation in the rice YS83 (LOC_Os02g05890) gene resulted in the yellow-green-leaf phenotype as well [12]. In addition, a number of chloroplast signal recognition particle (cpSRP) mutants were identified with chlorophyll deficiency in *Arabidopsis*, rice and maize [13-15]. Although these studies have provided many insights into the key genes controlling chlorophyll deficiency, the analyses of physiological parameters of such mutants and their underlying molecular mechanisms have been generally lacking.

Chlorophyll-deficient mutants are important tools for studying the formation and development of photosynthetic pigments in plants. Their phenotypes could be used as crop trait markers in hybrid breeding [16]. In this work, a new yellow-green leaf

mutant inbred line of maize was isolated. The chlorophyll contents, chlorophyll fluorescence parameters, and photosynthesis characteristics were determined. Using comparative transcriptomic analysis, differentially expressed genes were compared between the yellow-green leaf mutant and the normal green leaf inbred line. These results not only provide valuable genetic resources for further studies of chlorophyll-deficient mutants in maize, but also contribute to our understanding of the relationship between physiological changes and gene expression changes. The latter may pave the way to further dissecting the molecular basis of morphological and physiological characteristics of the yellow-green leaf mutant.

Results

Identification of a maize yellow-green leaf mutant and measurement of its pigment contents

A yellow-green leaf mutant inbred line was firstly isolated from an F2 [segregating population](#) of the cross recombination inbred line C033 and inbred line LH102, both of which have a green leaf phenotype. After successive self-pollination of F2, F3 and F4 generations, a stable F5 generation was obtained. In this study, a stable yellow-green leaf mutant inbred line and a normal green leaf inbred line from the F5 generation were selected for downstream characterizations. The yellow-green leaf mutant had a yellow color in the entire above-ground portion of the plant (Fig. 1A).

Leaf color could indicate the amount and proportion of chlorophyll in leaves. Deficiency of chlorophyll leads to the leaf color change from green to yellow. In this study, in contrast with the normal green leaf inbred line, the content of chlorophyll *a* and chlorophyll *b* in the yellow-green leaf mutant was reduced by 35.22% and 34.48%, respectively, which may directly result in the presence of yellow-green color in the mutant plants (Fig. 1B). Otherwise, the contents of seven kinds of carotenoid compounds including neoxanthin, violaxanthin, capsanthin, zeaxanthin, β -carotene, β -carotene and lutein were significantly decreased in the yellow-green leaf mutant (Fig. 1C).

Measurement of chlorophyll fluorescence parameters of the yellow-green leaf mutant

For further analysis, chlorophyll fluorescence parameters were determined to evaluate the changes of light absorption and energy transfer in the light-harvesting complexes. F_0 indicates the minimum fluorescence yield after dark-adaptation with all PSII centers open. F_m represents the maximum fluorescence yield after dark-adaptation with all PSII centers closed. Both F_0 and F_m were decreased in the yellow-green leaf mutant, suggesting that the yellow-green leaf mutant has fewer active PSII centers than the normal green leaf inbred line (Fig. 2A). However, the yellow-green leaf mutant and the normal green leaf inbred line had the similar value of the maximum photochemical quantum yield of PSII (F_v/F_m), suggesting that light absorption and energy transfer of the light-harvesting complexes is still efficient in the yellow-green leaf mutant plants.

F_t is the real-time fluorescence yield recorded during the slow kinetics induction with the continuous monitoring mode. The changes of F_t reflect the light-adaption status of the PSII centers. Although the F_t kinetics curve in the yellow-green leaf mutant had the same light-adaption pattern as that in the normal green leaf inbred line, the F_t values were much lower in the yellow-green leaf mutant (Fig. 2B). Accordingly, the values of the minimal and maximal fluorescence yield in the light-adapted state (F_0' and F_m') were significantly lower in the yellow-green leaf mutant than in the normal green leaf inbred line (Fig. 2C). Photochemical quenching parameters (Φ_{PSII} , qP , and qL), non-photochemical quenching parameters (Φ_{NO} , Φ_{NPQ} , NPQ , and qN), and the PSII electron transport rate (ETR) were also evaluated. The values of Φ_{PSII} , qP , qL , Φ_{NO} , Φ_{NPQ} , NPQ , and qN were similar between the yellow-green leaf mutant and the normal green leaf inbred line (Fig. 2C). But the value of ETR was significantly lowered in the yellow-green leaf mutant.

Net photosynthesis in response to light intensities of the yellow-green leaf mutant

Net photosynthesis (P_n) in response to different light intensities was also determined (Fig. 3). P_n was lower in the yellow-green leaf mutant than in the normal green leaf inbred line when the light intensity was $1200 \mu\text{mol photons m}^{-2}\text{s}^{-1}$ or higher. But the rate of dark respiration was higher in the yellow-green leaf mutant.

Comparative transcriptomic analysis of the yellow-green leaf mutant and the normal green leaf inbred line: overall changes

To explain the physiological changes in the yellow-green leaf mutant, comparative transcriptome analysis was performed to identify differentially expressed genes in chlorophyll biosynthesis, light-harvesting antenna complex formation, photosynthesis, and other metabolism pathways. Three independently repeated sequencing of cDNA was carried out by using the HiSeq 2500 platform. After data processing, the clean reads were obtained. Pearson correlation was calculated for the three independent experiments. The data from NGL_1, NGL_3, YGL_2, and YGL_3 were collected for the following analysis for the higher correlation rate between the same color leaves (Additional file: Fig. S1). Further studies were performed to identify differentially expressed genes, using DGE methods. A total of 1122 genes were found to be differentially expressed in the normal green leaf inbred line and the yellow-green leaf mutant: 536 genes were up-regulated, and 586 genes were down-regulated in the yellow-green leaf mutant (Fig.4A). Among these differentially expressed genes, 1092 genes were categorized into 33 metabolic pathways (Fig.4B): 14 in photosynthesis, 19 in lipid metabolism, 40 in hormone metabolic, 53 in transport, 52 in secondary metabolism, and 55 in stress response, 106 in RNA synthesis, and another 106 in protein metabolism. The remaining 328 genes could not be mapped to specific metabolism pathways.

Differentially expressed genes in chlorophyll biosynthetic pathways

Chlorophylls are synthesized from the precursor protophorphyrin IX. As shown in Fig. 5, three chlorophyll metabolic genes (*magnesium-chelatase subunit ch1D* [Zm00001d013013], *protochlorophyllide reductase A* [Zm00001d001820], and *chlorophyllide a oxygenase* [Zm00001d004531] showed decreased expression levels in the yellow-green leaf mutant. Similarly, two protophorphyrin biosynthetic genes (*coproporphyrinogen III oxidase* [Zm00001d026277] and *uroporphyrinogen decarboxylase 1* [Zm00001d044321]) displayed decreased expression in the yellow-green leaf mutant. However, genes encoding chlorophyllide a oxygenase (Zm00001d002358) and protoporphyrinogen oxidase (Zm00001d008203) showed increased transcript abundance in the yellow-green leaf mutant.

Differentially expressed genes in photosynthetic reactions

As shown in Fig.6, 22 genes in photosynthesis were differentially expressed in the yellow-green leaf mutant and the normal green leaf inbred line. Of these genes, two are related to photosynthetic light reactions, 11 genes participate in photorespiration, and nine are involved in the Calvin cycle. Among the two genes in photosynthetic light reactions, one encodes a Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein (Zm00001d041824) and the other encodes PGRL1A (PGR5-like protein 1A, Zm00001d034904). These two genes exhibited increased transcript abundance in the yellow-green leaf mutant. However, genes encoding two ribulose biphosphate carboxylase/oxygenase (RuBisCO) large chain precursors (Zm00001d00279 and GRMZM5G815453), which are involved in the Calvin cycle and photorespiration, showed decreased transcript abundance in the yellow-green leaf mutant. Genes encoding two *RuBisCO large subunit-binding protein subunit alpha* genes (Zm00001d031503 and Zm00001d051252) displayed decreased transcript abundance in the yellow-green leaf mutant as well. Genes encoding chloroplast chaperonin 60 subunit beta (Zm00001d035937), RuBisCO methyltransferase family protein (Zm00001d020437), TCP/cpn60 chaperonin family protein (Zm00001d045544), and RuBisCO large subunit-binding protein subunit alpha (Zm00001d00399) showed increased transcript abundance in the yellow-green leaf mutant. The expression of phosphoglycolate phosphatase (Zm00001d034887) and glycerate dehydrogenase (Zm00001d014919) was enhanced in the yellow-green leaf mutant. Whereas the expression of glycine dehydrogenase (Zm00001d023437) and aldolase superfamily protein (Zm00001d040084) was decreased.

Differentially expressed genes in the tricarboxylic acid cycle

The tricarboxylic acid cycle (TCA cycle) is responsible for the production of most of the ATP yield. As shown in Fig.7, a total of nine genes in the TCA cycle were down-regulated in the yellow-green leaf mutant. Among these genes, *pyruvate phosphate dikinase* (Zm00001d010321) catalyzes the conversion of pyruvate to phosphoenolpyruvate (PEP), *aconitate hydratase* (Zm00001d015497) catalyzes the stereo-specific isomerization of citrate to isocitrate, and *isocitrate dehydrogenase* (Zm00001d025690) catalyzes the conversion of isocitrate to alpha-ketoglutarate and CO₂. The other six genes are involved in oxidative phosphorylation: *NADH-ubiquinone oxidoreductase 20 kDa subunit* (Zm00001d043619), *NADH dehydrogenase* (Zm00001d016864), *ubiquinol-cytochrome c reductase iron-sulfur subunit* (Zm00001d016619), *cytochrome c*

(Zm00001d042600), member of uncoupling protein PUMP2 family (Zm00001d048583), and cytochrome c oxidase (Zm00001d051055).

Differentially expressed genes in the sucrose-to-starch pathway

In Fig.8, nine genes in the sucrose-to-starch pathway were found to be differentially expressed between the yellow-green leaf mutant and the normal green leaf inbred line. Among these genes, two were up-regulated and seven were down-regulated in the yellow-green leaf mutant. Among the two up-regulated genes, one encodes aglycosyl hydrolase family 32 protein (Zm00001d025943), which may function as the invertase that split sucrose into glucose and fructose. The other gene is annotated as fructokinase-like protein (Zm00001d033181), which may catalyze the conversion of fructose to fructose-6-phosphate. Among the seven down-regulated genes, three are annotated as granule-bound starch synthase 1b (Zm00001d027242, Zm00001d029360, and Zm00001d019479), two encode soluble starch synthase (Zm00001d0002256 and Zm00001d0045261) and one encodes 1, 4- α -glucan branching enzyme IIB (Zm00001d003817). These six genes participate in starch synthesis. The other down-regulated gene is annotated as α -1, 4 glucanphosphorylase L isozyme (Zm00001d034074), which catalyzes the conversion of starch to glucose-1-phosphate.

Validation of unigenes and gene expression profiling

To evaluate the validity of sequence data, nine known transcripts were selected for examination by real-time RT-PCR. Information for these genes and their gene-specific primers are showed in Supplementary Table 1. The results showed that the expression patterns determined using both RT-qPCR and DGE were consistent for nine genes, which suggesting that the transcriptome analyses were very reliable (Fig. 9).

Discussion

In maize, a yellow-green leaf mutant SN62 has been identified [16]. Photosynthetic characteristics of SN62 revealed that its chlorophyll content, the quantum efficiency of PSII and maximal quantum yield of PSII photochemistry were significantly lower than those of a medium-green leaf inbred line SN12[16]. In this study, another yellow-green leaf mutant was identified. The values of photosynthetic parameters in this newly identified yellow-green leaf mutant were comparable to those in the previously identified yellow-green leaf mutant (SN62). The chlorophyll content and the values of chlorophyll fluorescence parameters (F_t , F_o , F_m , F_o' , F_m' and ETR) in the yellow-green leaf mutant were significantly lower than those in the normal green leaf inbred line. These data indicate that the yellow-green leaf mutant has fewer opened PSII reaction centers than the normal green leaf inbred line. However, the yellow-green leaf mutant and the normal green leaf inbred line had the similar value of the maximum photochemical quantum yield of PSII (F_v/F_m). This suggests that light absorption and energy transfer of the light-harvesting complexes is still efficient in the yellow-green leaf mutant plants. In addition, there were no obvious differences in F_{PSII} , F_{NO} , F_{NPQ} , NPQ, qN, qP, and qL between the yellow-green leaf mutant and the normal green leaf inbred line. Furthermore, Pn was only lower in the yellow-green leaf mutant than in the normal green leaf inbred line when the light intensity was at 1200 $\mu\text{mol photons m}^{-2}\text{s}^{-1}$ or higher.

In seed plants, most of the genes responsible for the chlorophyll biosynthesis pathway have been identified [17]. Magnesium-protoporphyrin chelatase catalyzes the first step in chlorophyll synthesis. This enzyme contains three subunits (ChlH, ChlD and ChlI) and catalyzes the insertion of Mg^{2+} into protoporphyrin IX. Mutation in ChlD resulted in a chlorina (yellowish-green) phenotype in rice [18]. Protochlorophyllide reductase catalyzes the conversion of pchlde to chloro-phyllide. Chlorophyllide *a* oxygenase (CAO) is responsible for chlorophyll *b* biosynthesis [19]. Overexpression of *CAO* was found to enlarge the antenna size of photosystem II in *Arabidopsis* [20]. Mutation in the barley CAO (*fch2*) gene leads to chlorophyll *b* deficiency, which may affect electron transfer in photosystem II [21]. Coproporphyrinogen III oxidase is a key enzyme in the biosynthetic pathway of chlorophyll and heme. The deficiency in coproporphyrinogen III oxidase caused lesion formation in *Arabidopsis* [22]. Uroporphyrinogen decarboxylase is responsible for the decarboxylation of four acetate groups of uroporphyrinogen III to yield coproporphyrinogen III, resulting in heme and chlorophyll biosynthesis [23]. In this study, these genes were found to have

decreased transcript abundance in the yellow-green leaf mutant, which may directly cause chlorophyll deficiency and reduced formation of light-harvesting antenna complexes.

Photosynthesis begins with the light reactions. In this work, the gene encoding Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein and the gene annotated as PGRL1A were found to have increased transcript abundance. PsbP is necessary for the retention of Ca^{2+} and Cl^{-1} , the assembly of PSII complex, and the maintenance of normal thylakoid architecture in PSII [24]. PGRL1A is associated with PSI and it interacts with PGRL1 [25]. The PGRL1-PGR5 complex was found to facilitate cyclic electron flow [25]. In this work, the expression of both genes was up-regulated in the yellow-green leaf mutant, which may make the fewer opened PSII reaction centers work efficiently in the yellow-green leaf mutant.

TCA cycle plays a central role in generating ATP and providing reducing agent NADH and precursors for a number of amino acids in both heterotrophic and photosynthetic tissues [26]. In this work, totally nine genes were identified with down-regulated expression in the yellow-green leaf mutant, including *pyruvatephosphate dikinase*, *aconitatehydratase*, *isocitrate dehydrogenase*, *NADH dehydrogenase*, and *NADH-ubiquinone oxidoreductase 20 kDa subunit*. Pyruvate phosphate dikinase is the key enzyme in cellular energy metabolism; it catalyzes the ATP- and phosphate (P_i)-dependent conversion of pyruvate to phosphoenol pyruvate in C4 plants [27]. Aconitate hydratase catalyzes the conversion of citrate to cis-aconitate [28]. Isocitrate dehydrogenase catalyzes oxidative decarboxylation of isocitrate [29]. The other six genes are involved in the mitochondrial electron transport chain and ATP synthesis, which requires the participation of large protein complex I (NADH-ubiquinone oxidoreductase), II (NADH dehydrogenase), III (ubiquinol-cytochrome *c* reductase) and IV (cytochrome *c* oxidase) [30, 31]. The decreased expression of these genes may have negative effects on ATP generation in the mitochondria of the yellow-green leaf mutant. Furthermore, seven genes involved in the conversion of sucrose to starch were found to have decreased transcript abundance in the yellow-green leaf mutant. Of these genes, granule-bound starch synthase 1b is responsible for amylose synthesis [32]. Soluble starch synthase is a key enzyme in the biosynthesis of amylopectin [33]. Moreover, the analysis of enzymes activities in starch biosynthesis pathway further demonstrated the results. The enzymes activities of SS, SSS, SPS and GBSS were significantly lower in yellow-green leaf if compared with that in normal green leaf (Additional file: Fig. S2). But there were no obvious difference in the contents of starch and total reducing sugar, though the content of the water-soluble total sugar was high in normal green leaf (Additional file: Fig. S3).

Conclusions

In summary, a number of genes in chlorophyll biosynthesis, photosynthesis, tricarboxylic acid cycle, and sucrose-to-starch conversion were found to be differentially expressed in the yellow-green leaf mutant and the normal green leaf inbred line. These findings provide potential explanations for observed morphological and physiological changes in the yellow-green leaf mutant. Further investigations are needed to unravel the molecular basis of the morphological, physiological and transcriptional changes in the yellow-green leaf mutant plants.

Methods

Plant material

The maize inbred line C033 and LH102 were obtained from preserved breeds in rural areas of Anhui province which were stored in Tobacco Research Institute, Anhui province, People's Republic of China. The yellow-green leaf mutant inbred line was isolated from an F2 [segregating population](#) of the recombination between inbred line C033 and LH102 in the farm of Tobacco Research Institute. After successive self-pollination of F2, F3 and F4 generations, a stable F5 generation was obtained. The yellow-green leaf mutant inbred line and a normal green leaf inbred line from the F5 generation were selected for downstream analyses. The inbred lines were cultivated with regular water and fertilizer management in the farm of Tobacco Research Institute in the year of 2017. After the third leaf was fully expanded, seedlings were selected for physiological parameter determination, RNA extraction, and gene expression analysis.

Measurement of chlorophyll contents

Leaf samples (100 mg) were cut into small pieces, and soaked in 10 mL of 80% acetone (acetone: water = 4:1) at 4°C in the dark for 24 h. The supernatant was collected after centrifugation at 6000 rpm for 10 min. The absorbance was recorded at 663 and 645 nm on a UV-1800 spectrophotometer (Shimadzu Corporation, Japan). The concentrations of Chl *a* and Chl *b* were calculated using the method described by Arnon [34].

Measurement of carotenoid compounds

To analyze the carotenoid compounds, 200 mg leaf samples were grinded into powder with 2 ml absolute alcohol containing 1% butylated hydroxytoluene. After water bath for 5 min at 85°C, 40 µl 80% KOH and 1 ml N-hexane were added into the extraction buffer followed by water bath and vortex. The supernatant were eventually collected and dried with nitrogen, then dissolved in 500 µl acetonitrile solution containing 1% butylated hydroxytoluene, 25% methanol, and 5% dichloromethane for following analysis.

The Ultimate 3000 UHPLC system (Thermo Fisher Scientific, USA) was employed to quantitatively and qualitatively determine the components. Carotenoids were resolved and analyzed on a reverse phase YMC Carotenoid column (250*4.6mm, 5µm; YMC, Kyoto, Japan) set at a temperature of 40°C with the flow rate of 1ml/min. The solvent system consisted of solvent A with methanol: methyl tert-butyl ether: water (81:15:4, by vol) and solvent B with methanol: methyl tert-butyl ether (6.5:93.5, by vol). The gradient program was set as follows: 2 min hold on 100% solvent A, followed a 1 minute linear gradient to 32.5% solvent A and 67.5% solvent B, then 2 min hold on 100% solvent B, and 2 min hold on 100% solvent A lastly. Carotenoid compounds were detected at 450 nm.

Measurement of the total starch, total sugar and enzymes activities

The contents of the total starch, the total soluble sugar and the total reducing sugar were measured using the methods described by McCleary et al., Irigoyen et al. and Miller et al. [35-37]. The enzymes activities of SS (Sucrose synthase) and SPS (Sucrose phosphate synthase) were assayed according to Echeverria and Humphreys' method [38]. The enzymes activities of SSS, GBSS and AGP were determined using the methods described by wang et al. and Nakamura et al [39-40].

Measurements of chlorophyll fluorescence parameters

By using the PAM-2500 chlorophyll fluorometer (Walz, German), chlorophyll fluorescence parameters were determined for the leaves from the yellow-green leaf mutant inbred line and the normal green leaf inbred line. The procedure was described as follows. After the leaf was adapted in the dark with the dark adapting clip for 20 min, the slow kinetics of chlorophyll *a* fluorescence induction was triggered with a continuous mode to measure dark- and light-adapted parameters. The leaf was initially subjected to a measuring light of 95 µmol photons m⁻² s⁻¹. After *F_o* was recorded, a saturating pulse of 2000 µmol photons m⁻² s⁻¹ was automatically turned on, and *F_m* was measured accordingly. At that time, an actinic light of 145 µmol photons m⁻² s⁻¹ was activated to simulate normal irradiance conditions. *F*, *F_m'* and *F_o'* were subsequently measured with saturating pulses every 20 s. The parameters Φ_{PSII}, Φ_{NPQ}, Φ_{NO}, NPQ, qN, qP, qL and ETR were derived from the final measurements obtained after a 10-min light adaptation.

The maximum photochemical quantum yield of PSII (*F_v/F_m*) was calculated according to Stefanov and Terashima [41]: *F_v/F_m* = (*F_m*-*F_o*)/*F_m*.

The effective photochemical quantum yield of PSII (Φ_{PSII}), the quantum yield of non-regulated heat dissipation and fluorescence emission (Φ_{NO}), and quantum yield of light-induced non-photochemical quenching (Φ_{NPQ}) were calculated as described by Kramer et al. [42]: Φ_{PSII} = (*F_m'*-*F*) / *F_m'*, Φ_{NO} = 1/(NPQ + 1 + qL (*F_m/F_o* -1)), Φ_{NPQ} = 1-Φ_{PSII}-(1/(NPQ + 1 + qL (*F_m/F_o* -1))).

The coefficient of photochemical quenching (qL) was calculated as described by Kramer (2004): qL = qP×*F_o'*/F.

The coefficients of photochemical quenching (qP), non-photochemical quenching (qN and NPQ) were calculated as described by Stefanov and Terashima (2008): qP = (*F_m'*-*F*)/(*F_m'*-*F_o*), qN = 1-(*F_m*- *F_m'*)/(*F_m*- *F_o*), NPQ = (*F_m*-*F_m'*)/*F_m'*.

The relative apparent photosynthetic electron transport rate (ETR) was calculated using the equation: $ETR = \Phi_{PSII} \times PAR \times 0.5 \times 0.84$.

Measurement of photosynthesis parameters

The net photosynthetic rate (Pn) was measured using a Li-6400XT portable photosynthesis system (Li-Cor Inc., USA) equipped with a 6400-02B chamber and a red-blue LED light source with intensities up to 2000 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$ over an area of 6 cm^2 . The flow rate was adjusted to 500 $\mu\text{mol s}^{-1}$ with the absolute CO_2 concentration of 380 $\mu\text{mol mol}^{-1}$ at 26°C inside the chamber. The light response curve of Pn was determined at nine photosynthetically active radiation (PAR) levels (0, 50, 100, 200, 400, 800, 1200, 1600 and 2000 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$).

Total RNA extraction for RNA-Seq and qRT-PCR

Total RNA from the yellow-green leaf mutant and the normal green leaf inbred line was extracted with the RNeasy Pure Plant Kit (Qiagen, China) using 200 mg tissue homogenized in liquid nitrogen. The quality and concentration of extracted RNA were determined using NanoDrop 2000 (Thermo, USA).

cDNA library construction and sequencing

By using Illumina TruSeq™ RNA Sample Preparation Kit (Illumina, San Diego, USA), the cDNA library was constructed. After the quality detection, the Illumina sequencing was carried out at Beijing Novogene Biological Information Technology Co. Ltd. (Beijing, China) ([HTTP://www.novogene.cn/](http://www.novogene.cn/)). The index-coded samples were clustered following the manufacturer's instructions using TruSeq PE Cluster Kit v3-cBot-HS (Illumina). After cluster generation, the library was sequenced on an Illumina HiSeq 2500 platform with 200 bp paired-end reads.

Data filtering and assembly

By removing reads from adaptor sequences, duplicated sequences, poly-N (reads with unknown nucleotides) and low-quality reads, high-quality clean reads were obtained for downstream analyses. The cleaned sequences were mapped to the maize B73 reference genome (AGPv4) (ftp://ftp.ncbi.nlm.nih.gov/genomes/genbank/plant/Zea_mays/latest_assembly_versions/GCA_000005005.6_B73_RefGen_v4). The final transcriptome assembly was generated using TopHat 2 as previously described [43, 44]. Transcript counts were normalized by calculating reads per kilobase million mapped reads (RPKM) as described by Mortazavi et al. [45].

Identification of differential expressed genes

According to standard digital gene expression (DGE) methods as described by Zhang et al. [46], the read counts were adjusted by using edge R program package through one scaling normalized factor. Differentially expressed genes were screened by using the DESeq R package (1.12.0; TNLIST, Beijing, China). A P-value of 0.005 was used as the threshold for significant differential expression according to the Benjamini and Hochberg's method [47].

Gene functional annotation and metabolic pathway analysis

The functions of differentially expressed genes were annotated using Blast X (E-value < 10^{-5}) queries searched against three databases: NCBI non-redundant (Nr) protein database (<ftp://ftp.ncbi.nlm.nih.gov/blast/db/>), Pfam (annotated Protein family) (<http://pfam.xfam.org/>), and SwissProt protein database (https://web.expasy.org/docs/swiss-prot_guideline.html). By using the Blast2GO program, the genes were annotated according to molecular function, biological process, and cellular component ontology. Functionally annotated genes were assigned to different metabolic pathways based on the Kyoto Encyclopedia of Genes and Genomes Pathway database (KEGG <http://www.genome.jp/kegg>). The MapMan software (V3.6.0 RC1) was used to map the target genes to metabolic pathways and draw the profile frames as described by Kakumanu et al. [48].

Additional File

Table S1 Primers for qRT-PCR analysis

Table S2 The list of differentially expressed genes between yellow-green leaf and normal green leaf

Table S3 The GO enrichment result of differentially expressed genes between yellow-green leaf and normal green leaf

Table S4 The KEGG pathway enrichment result of differentially expressed genes between yellow-green leaf and normal green leaf

Fig. S1 The Pearson correlation between individual RNA samples from the yellow-green leaf mutant and the normal green leaf inbred line.

Fig. S2 The activities of enzymes SS, SSS, SPS, GBSS and AGP involved in starch biosynthesis pathway

Fig. S3 The contents of starch, total reducing sugar and the water-soluble total sugar

Fig. S4 The Blast2GO analysis of differentially expressed genes between the yellow-green leaf mutant and the normal green leaf inbred line.

Abbreviations

F_o: the minimum fluorescence yield; F_m: the maximum fluorescence yield; F_t: the real-time fluorescence yield; F_v/F_m: The maximum photochemical quantum yield of PSII; Φ_{PSII} : the effective photochemical quantum yield of PSII; Φ_{NO} : the quantum yield of non-regulated heat dissipation and fluorescence emission; Φ_{NPQ} : quantum yield of light-induced non-photochemical quenching; q_L: the coefficient of photochemical quenching; q_P: the coefficient of photochemical quenching; NPQ: the coefficient of non-photochemical quenching; q_N: the coefficient of non-photochemical quenching; ETR: the relative apparent photosynthetic electron transport rate; P_n: The net photosynthetic rate; RuBisCO: ribulose biphosphate carboxylase/oxygenase; TCA: the tricarboxylic acid cycle; PEP: phosphoenol pyruvate; Chl: chlorophyll; CAO: Chlorophyllide *a* oxygenase;

Declarations

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Availability of data and materials

The datasets generated and analyzed in this study are available from the corresponding author on reasonable request.

Author Contributions

TL and HY performed experiments, generated figures, and wrote the draft manuscript. YL helped with data interpretation and revision of the manuscript. Q Dand GL helped in performing experiments and preparation of the materials. FC helped with data interpretation and revision of the manuscript. YZ designed the plan and significantly revised the manuscript. All authors have read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable

Competing Interests

The authors declare that they have no competing interests.

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Figures

A

B

C

Figure 1

Phenotypic characteristics change of yellow-green leaf mutant plants. The letter A indicated two yellow-green leaf mutant plants (left) and a normal green leaf plant at the same age (right). Maize plants in this image were at the five-leaf stage. The letter B showed the contents of chlorophyll a and chlorophyll b in the normal green leaf inbred line and the yellow-green leaf mutant. The letter C showed the contents of eight carotenoid compounds including neoxanthin, violaxanthin, capsanthin, zeaxanthin, β-cryptoxanthin, α-carotene, β-carotene and lutein. Small letters a and b above the columns indicate differences between the yellow-green leaf mutant and the normal green leaf inbred line at $P < 0.05$, according to least significant difference (LSD) tests. FW is the abbreviation of the fresh weight.

Figure 2

Chlorophyll fluorescence parameters in the yellow-green leaf mutant inbred line and the normal green leaf inbred line. The letter A indicated the original chlorophyll fluorescence parameters. The letter B showed real-time fluorescence yield Ft in the normal green leaf inbred line and the yellow-green leaf mutant. The point pointed by the arrows indicated the turned on of the actinic light. The letter C indicated additional chlorophyll fluorescence parameters of the normal green leaf inbred line and the yellow-green leaf mutant. Small letters a and b indicate differences between the yellow-green leaf mutant and the normal green leaf inbred line at $P < 0.05$, according to least significant difference (LSD) tests.

Figure 3

Light response curves of net photosynthesis in the yellow-green leaf mutant and the normal green leaf inbred line. Pn is the net photosynthesis rate. The light response curves were measured at nine PAR levels (0, 50, 100, 200, 400, 800, 1200, 1600 and 2000 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$). The dark respiration rate is defined as the Pn value when the light response curve intersects the Y-axis. The measurement was performed for three times. The error bars represented the standard errors.

Figure 4

Differentially expressed genes and its enriched metabolic pathways between the yellow-green leaf mutant and the normal green leaf inbred line. The letter A indicated differentially expressed genes between the yellow-green leaf mutant and the normal green leaf inbred line. Differentially expressed genes were selected by $q\text{-value} < 0.005$ and $|\log_2(\text{fold change})| > 1$. The X axis indicates gene expression changes in different samples, and the Y axis indicates the significant degree of gene expression changes. Scattered points represent each gene, the red dots represent differentially up-regulated genes, the green dots represent differentially down-regulated genes, and the blue dots represent no significant difference gene. YGL, yellow-green leaf mutant; NGL, normal green leaf inbred line; $-\log_{10}(\text{padj})$, the corrected p-value ($\text{padj} < 0.05$). The letter B showed the pie chart of enriched metabolic pathways of genes differentially expressed in the yellow-green leaf mutant and the normal green leaf inbred line. The pie chart was generated by submission of the differentially expressed genes to the online Mercator sequence annotation tool (<http://www.plabipd.de/portal/mercator-sequence-annotation>).

Figure 5

Comparative expression analysis of differentially expressed genes involved in chlorophyll metabolism between the yellow-green leaf mutant and the normal green leaf inbred line.

Figure 7

Comparative expression analysis of differentially expressed genes in the tricarboxylic acid cycle between the yellow-green leaf mutant and the normal green leaf inbred line.

Figure 8

Comparative expression analysis of differentially expressed genes involved in sucrose to starch conversion between the yellow-green leaf mutant and the normal green leaf inbred line.

Figure 9

Validation of unigenes and DGE genes expression profiling

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