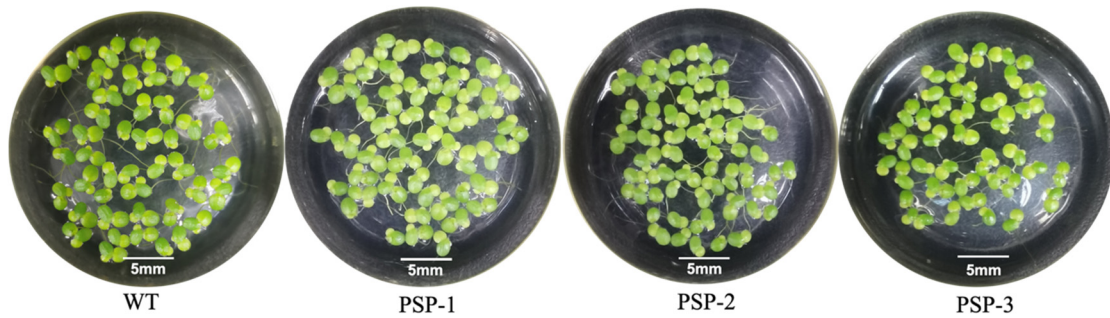# Supplementary Materials

Figure S1. Phenotype of WT and three *AtPSP1* transgenic lines. The photoes were taken after WT and *AtPSP1* transgenic lines were cultivated after full nutrition condition (Datko) for 9 days.
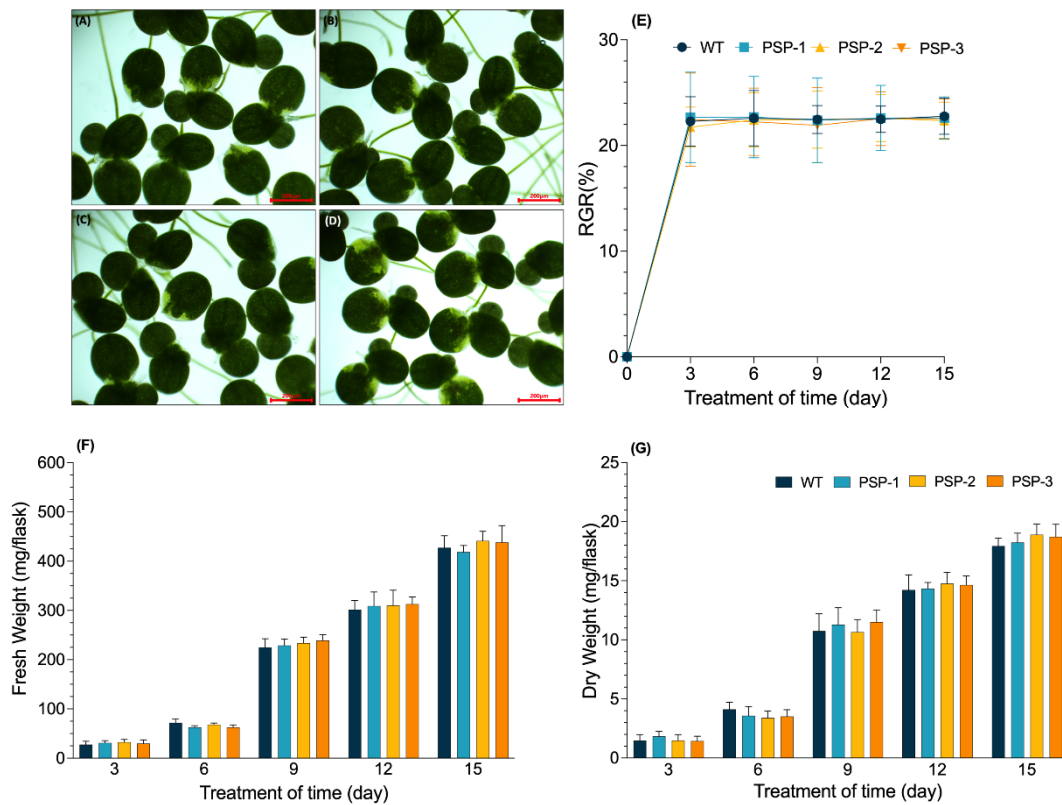

Figure S2. Analysis of phenotype, relative growth rate (RGR), fresh weight and dry weight in WT and three *AtPSP1* transgenic lines under Datko condition. **(A)** WT, **(B)** PSP-1, **(C)** PSP-2, **(D)** PSP-3 indicate the phenotype of WT and *AtPSP1* transgenic lines were cultivated under Datko condition for 9 days with dissecting microscope; **(E)** The RGR; **(F)** The fresh weight; **(G)** The dry weight. Each statistic is the mean ± standard error (n=9, from three independent experiments with three repeats of each).
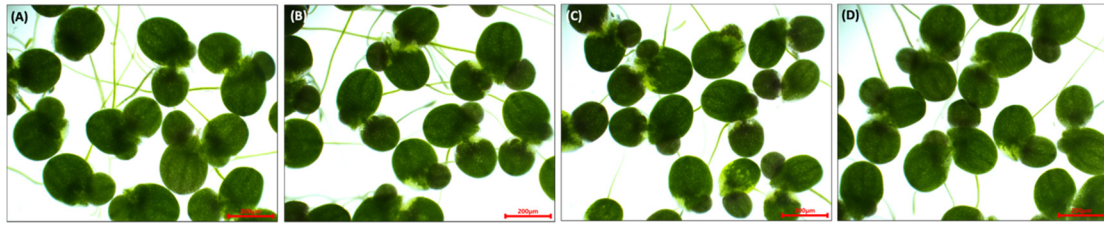
Figure S3. Phenotype of WT and three *AtPSP1* transgenic lines under sulfur-deficiency condition. **(A)** WT, **(B)** PSP-1, **(C)** PSP-2, **(D)** PSP-3 indicate the phenotype of WT and *AtPSP1* transgenic lines were cultivated under sulfur-deficiency condition for 9 days with dissecting microscope.
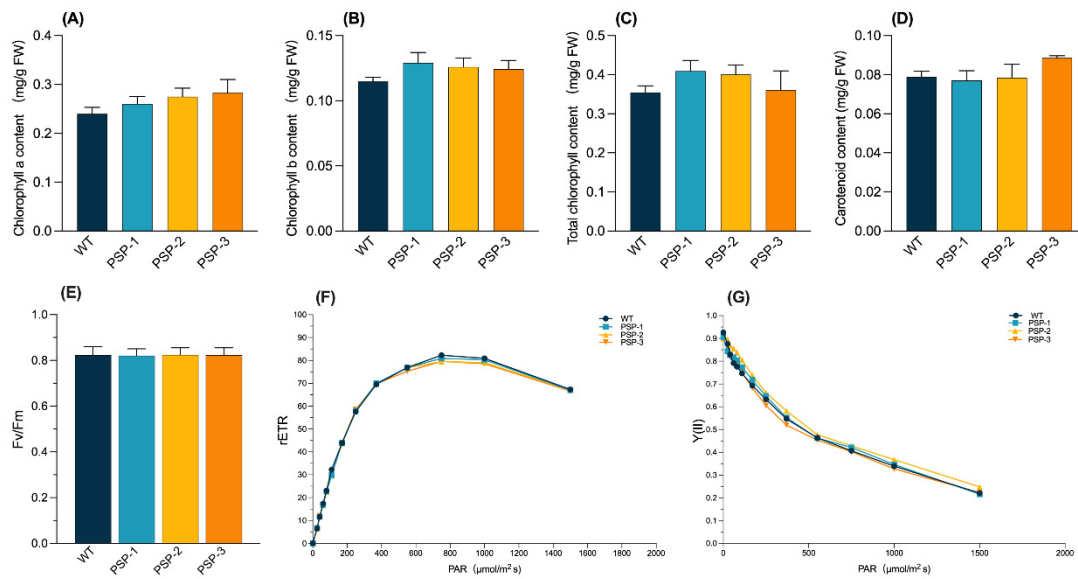

Figure S4. The analysis of photosynthetic pigment and chlorophyll fluorescence-related parameters in duckweed under full nutrition condition (Datko). **(A)** Content of Chlorophyll a; **(B)** Content of Chlorophyll b; **(C)** Total chlorophyll content; **(D)** Carotenoid content. The content of photosynthetic pigment was measured after the samples were cultivated under full nutrition condition for 9 days; **(E)** The value of Fv/Fm; **(F)** The value of rETR; **(G)** The value of Y(II), the chlorophyll fluorescence-related parameters were measured after the samples were cultivated under full nutrition condition for 6 days. Each statistic is the mean ± standard error (n=9, from three independent experiments with three repeats of each, the data no average value in Figure **F** and **G**).
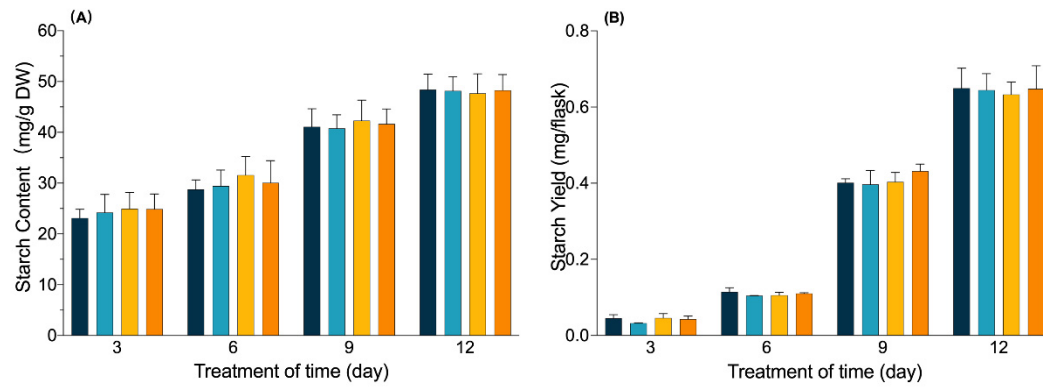
Figure S5. The content of starch , yield and the soluble protein in WT and three *AtPSP1* transgenic lines under full nutrition condition in different treatment of time. **(A)** The starch content; **(B)** The starch yield. Each statistic is the mean ± standard error (n=9, from three independent experiments with three repeats of each).

Table S1 The primer sequences in the study.

Primer name	Primer sequence （5′-3′）	Note	
AtPSP1-F	CCATGGGGATGGAAGCATTAACTACTTCA	The primers for genes amplification	
AtPSP1-R	GGGTTACCCTTAGTCCAATGAGTTTATGAG		
AtPSP1-RT-F	GAAAGGCTGTTGCTGAAT	The primers of genes for RT-PCR	
AtPSP1-RT-R	TCGTTCTCATCAAATCCC		
Lt18S-RT-F	ATACCGTCCTAGTCTCAACCA		
Lt18S-RT-R	ACAAATCGCTCCACCAAC		
AtPSP1-qRT-F	GGTTGTGCCAGTTCAGGT	The primer of AtPSP1	The primers of genes for qRT-PCR
AtPSP1-qRT-R	ACGAAGCAATTTGGGATG		
Lt18S-qRT-F	ATAAACGATGCCGACCAG	The primer of Lt18S	
Lt18S-qRT-R	TCAGCCTTGCGACCATAC		
LtAPK1-qRT-F	GAAGGAGCCAGTGGTGAA	The primer of sulfur assimilation related genes	
LtAPK1-qRT-R	AGTCGATACAGGGCGAAG		
LtAPR1-qRT-F	TCGCCATAGCTTTCAGTG		
LtAPR1-qRT-R	TTTCAGGGTTCAATCTTCC		
LtPAPSS1-qRT-F	ATGTCTGTTCCCATCGTTC		
LtPAPSS1-qRT-R	TCTTCTTTGTGGTGCTTGT		
LtSERAT1-qRT-F	GCGGCTAATCAAGTGCTG		
LtSERAT1-qRT-R	TTTCGGCGTAACTCCTCA		
LtSIR1-qRT-F	GTGAGCGTCCAGGATTTA		
LtSIR1-qRT-R	CCGATGCGATTAGTGAAG		
LtSULTR1-qRT-F	TTTCTTCGGAGTCATCTT		
LtSULTR1-qRT-R	CATTACACCAGGAATCTTT		
LtSULTR2-qRT-F	AGCTCTGGCTGCAAGACT		
LtSULTR2-qRT-R	ATGGCTGTAGGAGTGAAGTA		
LtSULTR3-qRT-F	TCGCCAACGCCTGCTACT		
LtSULTR3-qRT-R	CGCCCAAGTCCAAGACCACA		
LtSULTR4-qRT-F	TGGGTCTGGTGGACTATGA		
LtSULTR4-qRT-R	ACAAATGCAAGGGAGGAG		
LtSUOX1-qRT-F	GGCGTATGAAATGAATGG		
LtSUOX1-qRT-R	GTCAACTATGGGTGGGAAC		
LtAPS1-qRT-F	ATAGAGCATAGCGTCGTTG	The primer of starch metabolism related genes	
LtAPS1-qRT-R	TTCATCCTCCGTCTCATAG		
LtSSS1-qRT-F	TGTGGCTCTTTGCCTGTA		
LtSSS1-qRT-R	TTCAACTTCGTGCTCTGC		
LtGBSS1-qRT-F	CGGGTAACAGGAAGGGTG		
LtGBSS1-qRT-R	TCCGGTTCTTTGGTGATTGA		
LtAPL1-qRT-F	CACCGTATCCCAAGTCCC		
LtAPL1-qRT-R	TCACCGTCTCGAAATCGT		

LtISA1-qRT-F	GCACGCCTCTGAGCAACCCT	The primer of starch metabolism related genes	The primers of genes for qRT-PCR
LtISA1-qRT-R	TGCCCATTCCATTCTGACCACA		
Ltα-Amy1-qRT-F	ATAATCCGCTCAGAGTTCG		
Ltα-Amy1-qRT-R	ACCGATACCTTACCCTCC		
Ltβ-Amy1-qRT-F	GGCATTCATTGGTGGTAC		
Ltβ-Amy1-qRT-R	GTCGTGCTTCTTGAGGGT		
LtPFK1-qRT-F	TCGGAATAATCGCTGTCTC	The primer of carbon metabolism related genes	
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LtFBA1-qRT-R	TCCACCTTACCTGCCCAC		
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LtPK1-qRT-R	CTGGGTTCCCGAGAAAGT		
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LtACO1-qRT-F	GGAGTGACCGCAACAGAT		
LtACO1-qRT-R	GCACCGTATTCAGGAGACA		
LtIDH1-qRT-F	AACGACATACGGCTTCTA		
LtIDH1-qRT-R	TTACCCATTACCTGACAAC		
Lt2OG-DH1-qRT-F	ATTCACGGAGATGGGAGTT		
Lt2OG-DH1-qRT-R	CAGCGGTCGGATCAGTAG		
LtSDH1-qRT-F	AATGTAACCAAGGAGCCG		
LtSDH1-qRT-R	TTTGCGCCATGAACTGAT		
LtFUM1-qRT-F	AACGACATACGGCTTCTA		
LtFUM1-qRT-R	ATTACCCATTACCTGACAAC		
LtMDH1-qRT-F	GCTTCATCGGGTCTGGT		
LtMDH1-qRT-R	CGTTCGTCATCGTCGTTA		
LtCS1-qRT-F	TTGGACTATGGCGGAAAT		
LtCS1-qRT-R	GCAGTATGGGCGCTAACA		

The sequence of genes

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Lt18S

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LtSULTR4

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LtSUOX1

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LtAPS1

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Ltα-Amy1
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Ltβ-Amy1
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LtPDC1
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LtSDH1

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LtFUM1

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LtMDH1
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LtCS1
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