

Table S1. Sequences of the primers used to amplify the cDNA of the RuBisCO, nitrogen transport and assimilation genes.

Gene	Acc. No.	Forward	Reverse
<i>TaRBCL</i>	EU492898	CATTCCGAGTAAGTCCTCAGC	CAGTAGAAGATTTCGGCAGCT
<i>TaRcaB</i>	AF251264	GGGATGTACAACAAGGAGGAG	CCCAGTAGAACTTCTCCATGC
<i>TaNRT1.3</i>	HF544990	CACCTGCATCCTCTTCTGG	AGGATGGAGAGGAAGAGGAAG
<i>TaNRT1.4</i>	HF544991	CTTACCTCCTATGCGCCATG	ACCAGCTAGCATTTCTCGTC
<i>TaNRT1.5</i>	HF544992	GCAACTACTTCAGCGACATC	GAGAGTATGGCTAGCAGGAAG
<i>TaNRT1.7</i>	HF544995	TCCTTTATCGCCCTAACTGC	CACCAATCCTATACCCTGTCTC
<i>TaNRT1.8</i>	HF544998	CTCGAGATAAAGAGGCTGGC	GGAAGTACTGAGGGATTTGCC
<i>TaNRT1.9</i>	HF544999	CCGTGAACCTCGTCTACTTTG	GTCATCGAGCCCAACATCTC
<i>TaGS2</i>	DQ124212	GTACATCTGGGTGGAGGATC	GGTGCTCGATCCGTCATAAT
<i>TaNIR</i>	FJ527909	AACCTCCTCTCCTCCTACATC	TACGCCAGGTCGTTGATATG
<i>TaActin</i>	AB181991	AGAGTCGGTGAAGGGGACTTA	TCCTGTACCCCTTATTCCTCTGA

Table S2. P and F values of the different parameters analysed Figures 2–4, based on one-way ANOVA. Bold values indicate statistical difference ($p < 0.05$).

Parameter	F-value	P-value
A _N	17.32	0.001
E	11.51	0.004
g _s	7.27	0.015
C _i	0.77	0.54
V _{Cmax}	1.42	0.33
J _{max}	4.26	0.06
V _{Cmax} /J _{max}	1.62	0.28
δ ¹⁸ O	15.62	0.001
δ ¹⁵ N non-labelled	2.09	0.179
δ ¹⁵ N labelled	12.77	0.002
δ ¹³ C-TOM	3.19	0.084
δ ¹³ C-WSC	29.09	0.000
RBCL	6.27	0.003
RcaB	5.58	0.005
NRT1.3	2.12	0.125
NRT1.5	0.38	0.766
NRT1.8	9.74	0.000
NRT1.4	8.83	0.000
NRT1.7	0.21	0.890
NRT1.9	1.61	0.214
GS2	7.68	0.001
NIR	2.40	0.094

Table S3. P and F values of the different parameters analysed in Table 1, based on one-way ANOVA. Values in bold indicate statistical significance ($p < 0.05$).

Parameter	F-value	P-value
ARG	21.52	0.000
LYS	16.48	0.001
LEU	14.90	0.001
ILE	15.63	0.001
MET	11.48	0.003
PHE	11.77	0.003
TRP	9.18	0.005
HIS	3.77	0.06
TYP	21.58	0.000
VAL	11.16	0.003
GLN	13.49	0.002
PRO	6.10	0.018
ASN	0.96	0.460
GABA	0.87	0.495
THR	3.68	0.062
SER	3.99	0.052
GLY	3.55	0.067
ALA	2.87	0.103
GLU	0.44	0.73
ASP	2.58	0.126