

Table S1 Primer sequences used for q-PCR in this study.

Genes	Forward (5'→3')	Reverse (5'→3')
<i>Actin</i>	TAGAGAGTCCCCCGTATGCT	CACAAGAATCCGACACGCAT
<i>AACT</i>	GATGTTGTTGTGGCAGGTGG	TCAGCACAATTCCCCATGCT
<i>HMGS</i>	GATCTTGAGAAGGCGAGCCA	CCGGCCAGAGAGCTACTTTT
<i>HMGR1</i>	GGAAAATCTCTCGCCGGACT	GAAGGAGTGGCCCTGCTATG
<i>MK</i>	ATGTTGTGGGAGCAGAGAGTG	AAGCATCATGGCCACCAACT
<i>PMK</i>	TCTGCTCCTGGGAAGGTTTTG	GGGTTCCTCGAGTCACTTCC
<i>MDD2</i>	GCCTGGTCTTCTCATTGGCT	CCCCTTGACGAATCCACCA
<i>DXS</i>	CAGGAAAACAGGCAAAGAGTA	TGGAGGAACGACGAGTAGAT
<i>DXR</i>	CGCCCAAAAAGGGGTTTTGTT	TCTCTTGCCCGCACTGTATC
<i>MCT</i>	AAGACCTCTCGTGTTGGCTG	GCGAGTAGTAAGTCGTCGGG
<i>CMK</i>	ACTCCGGCTTTTGACGTTCT	AACTGAGGTGGATCGGGAGA
<i>MDS</i>	GGGCTTCCAGACATTGGTCA	CCCGAGCAACAGGCATAGAT
<i>HDS</i>	CCAAGGCTGCAGAATGAGGA	GAAACTCCGGGCAAGTGAGA
<i>HDR</i>	GCTTGTGGTAGGTGGGTTCA	TGCACCTGAAGTTATGCCGA
<i>GGPS</i>	AGGTGGTGGACGACATCCTA	CTCCCTCTTCAGCTGCTCTG
<i>CPS</i>	CCATGGGCGACGGAGAAATA	ACGCAGCTACGCATCCTAAT
<i>UGT73AU1</i>	GGGGGAGGTGAACTTGGATG	ACTCTTCCACCACGAGGGTA
<i>NIA2</i>	TTACCGGATCGGAGAGCTGA	CATCGTGTGAGAGCGAGGTT
<i>GS1</i>	AGTTTCAAGTCGGCCCTAGC	TTTGTGGCGAAGCGATAGGT
<i>GS2</i>	TCCACTCTCCACTCCTCACC	AGCCTCCGACCCAGATGTAT
<i>NDAH-GOGAT</i>	AGGAAGTCGAAGGTTCTGCG	AATCCCAGTTTCTCCGCCAG
<i>Fd-GOGAT</i>	CCCGGCGATCTCGTCAATTA	CCAAGGTCGATGTGCTGAGT
<i>GDH</i>	TGCTGATTTTAATGGCGCGG	TCCGGGTCAGTAGGATGGTT
<i>GAD</i>	TCGTGTCCAAGGATAACGGC	GTGTATGCGGGGACAATCCA
<i>GABA-TP3</i>	GGCGAGATTAGGGGAACAGG	ACTCGCACCAACATCCCATT
<i>NAGK</i>	GGACAAGGACAGGGCGATAA	CCGCGCCTCATAAACCAATC
<i>ADC</i>	GCCTCTCCCTACGCTTTTCTC	AGTGAAGTAAGAAGCGCCCC

<i>glnD</i>	GCCGACGTAATGCGAACAAT	CCGATGGAACGACTGGAGTT
<i>ACO</i>	GCTGTCCAGTCGGAGATCAG	GTTGGAGACGGGGAGATGAC
<i>EIN3</i>	AGGGTCTTCAATCAGTGGCG	GCCCTTCTGGCTCACATTCT
<i>AOAT</i>	GACCGAGATGAACGGGCAAT	AGCGAAGTGTTGAGCGAGAA
<i>AODA</i>	CCTGGAGGTGGCATCAATCA	CTGGCGTTCTCCTCTGGAAG
<i>OAT</i>	ACTGCACTTACAGGCAACAC	AAAGTGGACTGGGACGTTCTG
<i>AGDI</i>	ACCGGAACCCCGATTTAACC	ACAACGCTCGTATTGTGGGT
<i>CuAO</i>	GTGGAGATGGTTGTGCCGTA	AGAAAGCACGATCGAGGCAA

Table S2 Parameters of *A-Ci* curve. V_{cmax} , J_{max} and TPU were calculated by the FvCB model [74]. Data were represented by means \pm SD ($n=4$). Different letters in the same column indicates significant difference at $P < 0.05$ level according to one-way ANOVA combined with Duncan's multiple range method. NN, nitrate nitrogen; AN, ammonium nitrogen; UN, urea nitrogen; GN, glycine nitrogen.

Treatment	V_{cmax} $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$	J_{max} $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$	TPU $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$
NN	47.82 \pm 0.35 ab	45.85 \pm 1.08 a	9.00 \pm 0.07 ab
AN	52.66 \pm 1.61 a	51.00 \pm 2.37 a	9.78 \pm 0.41 a
UN	50.09 \pm 2.04 ab	49.00 \pm 2.00 a	9.29 \pm 0.35 ab
GN	46.66 \pm 0.94 b	43.76 \pm 1.14 a	8.53 \pm 0.14 b

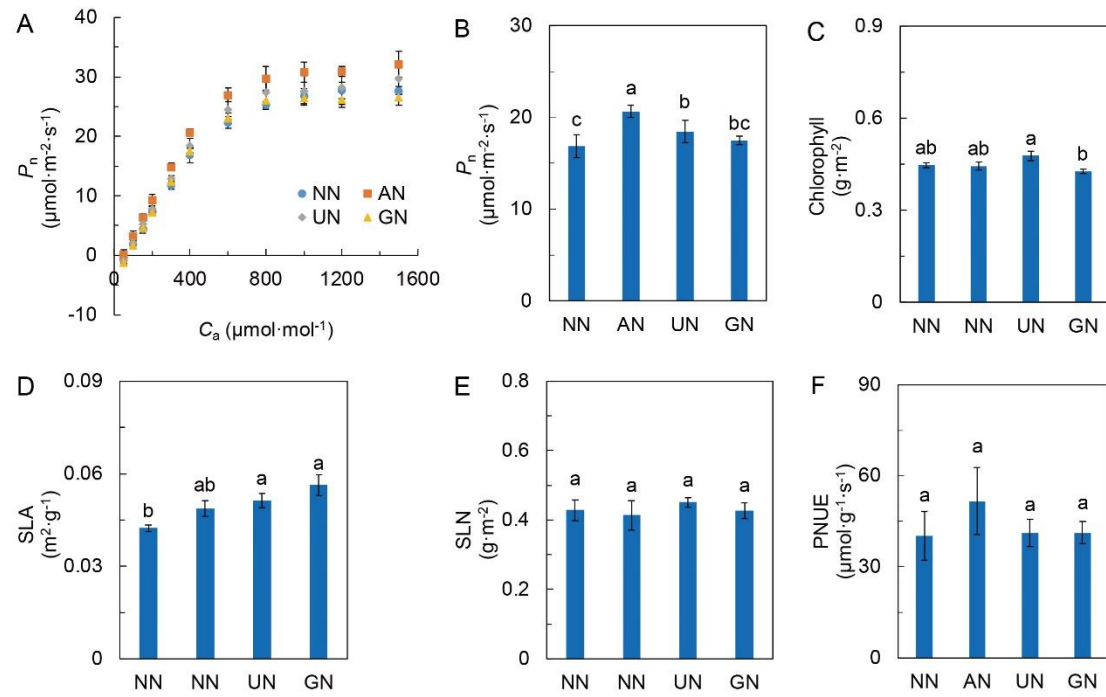


Fig.S1 Photosynthetic CO_2 response curve, chlorophyll, SLA and SLN in response to N forms in *A. paniculata*. **(A)** Photosynthetic A - C_a curve; **(B)** Photosynthetic rate at 400 $\mu\text{mol}\cdot\text{mol}^{-1}$ C_a (ambient CO_2 concentration); **(C)** Chlorophyll content based on leaf are; **(D)** Specific leaf area; **(E)** Specific leaf N content; **(F)** Photosynthetic N use efficiency. Data were represented by means \pm SD ($n=4$). Different letters in the same column indicates significant difference at $P < 0.05$ level according to one-way ANOVA combined with Duncan's multiple range method. NN, nitrate nitrogen; AN, ammonium nitrogen; UN, urea nitrogen; GN, glycine nitrogen.

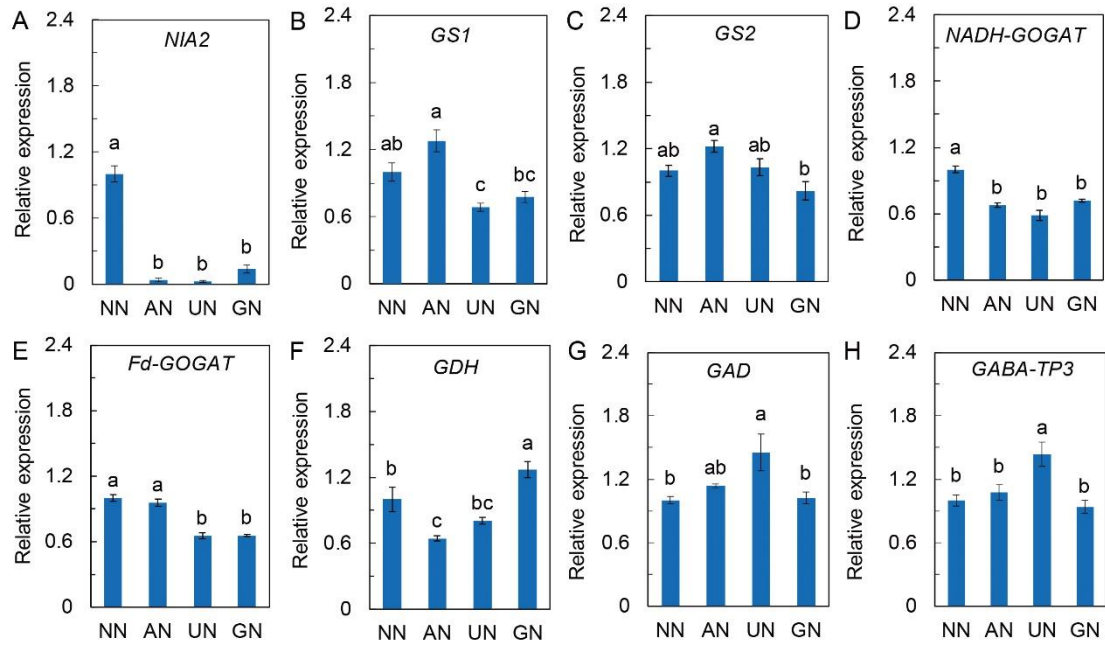


Fig.S2 Expression of N metabolic genes in response to N forms. Data were represented by means \pm SD ($n=4$). Different letters in the same column indicates significant difference at $P < 0.05$ level according to one-way ANOVA combined with Duncan's multiple range method. NN, nitrate nitrogen; AN, ammonium nitrogen; UN, urea nitrogen; GN, glycine nitrogen.

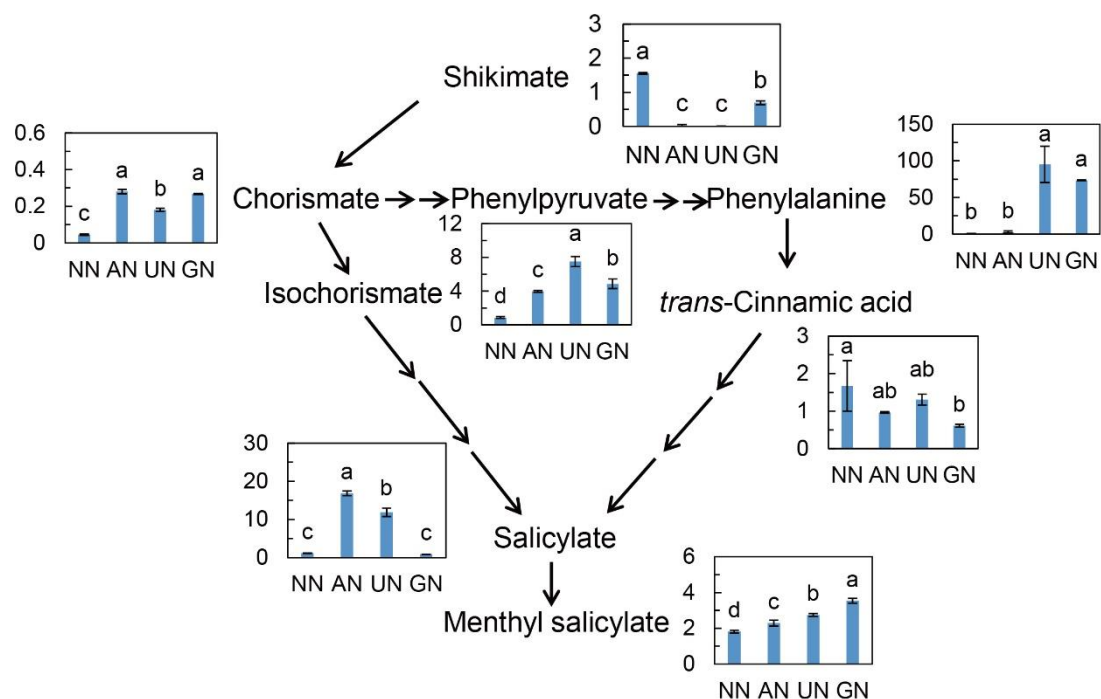


Fig.S3 Salicylic acid synthetic pathway in response to N forms. Data were represented by means \pm SD ($n=4$). Different letters in the same column indicates significant difference at $P < 0.05$ level according to one-way ANOVA combined with Duncan's multiple range method. NN, nitrate nitrogen; AN, ammonium nitrogen; UN, urea nitrogen; GN, glycine nitrogen.

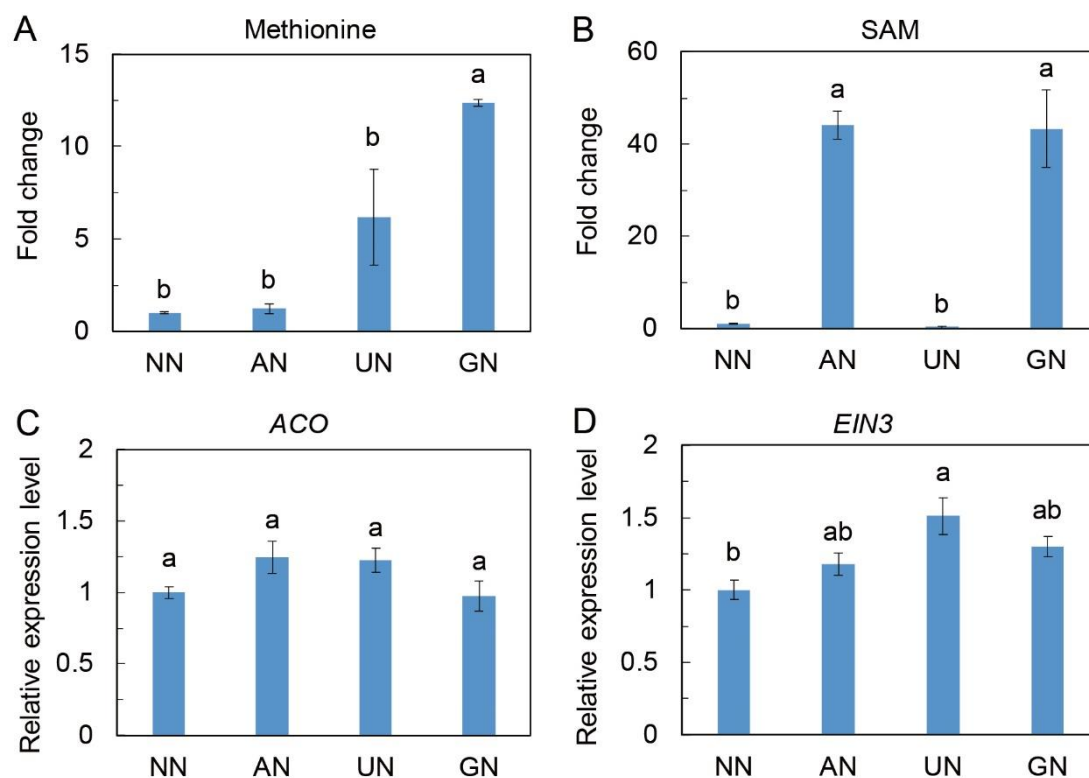


Fig.S4 Methionine and S- S-adenosylmethionine (SAM) levels and expression of *ACO* and *EIN3* in response to N forms. Data were represented by means \pm SE ($n=4$). Different letters in the same column indicates significant difference at $P < 0.05$ level according to one-way ANOVA combined with Duncan's new complex range method. NN, nitrate nitrogen; AN, ammonium nitrogen; UN, urea nitrogen; GN, glycine nitrogen.