Supplement

The following supplementary materials are available for this article: Li, W., Zhang, Z., Zhou, Z. 2025 Identification and functional analysis of ammonium transporter family in potato. Taiwania 70(4): 721-732. doi: *10.6165/tai.2025.70.721*

Table S1. qRT-PCR, PCR and NPTII detection primers

Primer	Sequence (5′-3′)	Role
Ef1a-F	ATTGGAAACGGATATGCTCCA	
Ef1a-R	TCCTTACCTGAACGCCTGTCA	
Atactin-F	TGCAGACCCTATGAGCAAAG	
Atactin-R	CTGGAAAGTGCTGACGGAAG	
StAMT1.1-F	CCTTGTTTGGACGAAGGTTATTG	
StAMT1.1-R	CACTGAACAACCTGAAGTGATTG	
StAMT1.2-F	TGTACCCAATTGTCTCACACTG	
StAMT1.2-R	CGATAACACCCGAACCGAATAA	
StAMT1.3-F	CGGATCCGGTGTTATCGATTT	
StAMT1.3-R	CCGATTCTCGGACCTTCAATTA	Quantitative PCR
StAMT2.1-F	TTACTGCGGCTTATTGGGTAG	primers
StAMT2.1-R	CCAGTCCAACCCATCCATAAA	
StAMT2.2-F	TCATCTGGAGTTGCTGGATTT	
StAMT2.2-R	CACCTCCAAGCATGTGAATTATG	
StAMT2.3-F	GGCTTTACTGCTGCTTATTGGG	
StAMT2.3-R	CTCCATTGAACCCTGACCACC	
StAMT2.4-F	AGTGTTCCAGGTCTTGTCATCC	
StAMT2.4-R	CCAACCCAACAAACAAGGACTG	
StAMT2.5-F	TGGATTCACCGCTGCTTATT	
StAMT2.5-R	TGAAACCTGACCAACCCATC	
StAMT1.1-F	TTGGAGAGAACACGGGGGACTCTAGAATGGATTCTTCATGGGAAGCTAGTGT	
StAMT1.1-R	AACATCGTATGGGTACTCGAGTTGTTGTTGCATCCTTAAATACTCGC	
StAMT1.2-F	TTGGAGAGAACACGGGGGACTCTAGAATGGCTTCCGCCGTGACTT	
StAMT1.2-R	AACATCGTATGGGTACTCGAGCACAACCACATTGTGATGATGATGA	
StAMT1.3-F	TTGGAGAGAACACGGGGGACTCTAGAAGCCCAATGGCTTGTTCCGT	
StAMT1.3-R	AACATCGTATGGGTACTCGAGAGTTGAGCTTGTTGGTTCAATTCTC	
StAMT2.1-F	TTGGAGAGAACACGGGGGACTCTAGAATGGAACTTCCCTCAAATTTATCAC	
StAMT2.1-R	AACATCGTATGGGTACTCGAGTACCATTTGGAGTTCACTCAAAGTCT	PCR
StAMT2.2-F	TTGGAGAGAACACGGGGGACTCTAGAATGGACCCAAAATATTCAGTCCTCC	primers
StAMT2.2-R	AACATCGTATGGGTACTCGAGATGACTGGTTCCATGACGTCGA	
StAMT2.3-F	TTGGAGAGAACACGGGGGACTCTAGAATGAGTTTATCATCTCCACCAGCCT	
StAMT2.3-R	AACATCGTATGGGTACTCGAGGACCATTTCGACCTGACTTCTAGACG	
StAMT2.4-F	TTGGAGAGAACACGGGGGACTCTAGAATGGCATACTTGTACTTGCCTAGAA	
StAMT2.4-R	AACATCGTATGGGTACTCGAGAAGTCCATAGCCACTTTTAGACAACT	
StAMT2.5-F	TTGGAGAGAACACGGGGGACTCTAGAAAATAATTAGCCATGTCCATACCA	
StAMT2.5-R	AACATCGTATGGGTACTCGAGTAAATCAAATGTCAATACTGTAGTTGTTTG	
NPTII-F	GCTATGACTGGGCACAACAG	PCR detection primers for
NPTII-R	ATACCGTAAAGCACGAGGAA	positive transgenic plants

Table S2. Analysis of CAEs of the promoter regions of 8 *StAMTs*

	StAMT1.1	StAMT1.2	StAMT1.3	StAMT2.1	StAMT2.2	StAMT2.3	StAMT2.4	StAMT2.5
3-AF1 binding site								1
AAGAA-motif	1	1		1		1		3
A-box								1
ABRE	2	1	1			3	2	
ABRE3a	2					1	1	
ABRE4	2					1	1	
ACA-motif				1				
ACE	1						1	
AC-I								1
AE-box	1	1						2
ARE	3	4	1		2	1		
as-1	5		2	1	3	1	1	
AT~TATA-box	5	4	5	1	3	1	5	4
ATC-motif			1					
ATCT-motif					1		1	
AT-rich element	1				1			
AT-rich sequence			1					
AuxRE							1	
AuxRR-core								1
Box 4	4	8	9		3	3	4	1
Box III			1					
CAAT-box	33	52	32	35	53	47	38	39
CAT-box							1	
CCAAT-box	1							
CGTCA-motif	5		2	1	3	1	1	
chs-CMA1a				1	1	1		
chs-CMA2a					1			
chs-Unit 1 m1							1	
CTAG-motif					1			
ERE	2	3	5	2	8		1	1
F-box			2					
GA-motif		2			1			1
GARE-motif						1	1	
GATA-motif				2				1
G-Box		1				1		
G-box	4	1	2			2	2	1
GCN4_motif						1		
GT1-motif	1	3	2	1	3	1	1	
HD-Zip 1				1	1		1	
HD-Zip 3			1					
I-box						1	2	
LAMP-element		1						
LTR	1		1			1	1	1
MBS				1	1	1		2
MBSI							1	
MRE	1	2						2
MYB	2	3	2	3	4	4	2	1
Myb		2	1	2	1	3	2	2
MYB recognition site	1							
Myb-binding site						2	1	
MYB-like sequence	1	2	1	2	2	1	1	
MYC	8	4	3	3	5	3	3	5
Myc			1				1	
O2-site	1	1				3	1	1
P-box				1		1		
RY-element		1						
STRE	1	2	1	1		2	2	
TATA	1	2	3		1			2
TATA-box	52	109	72	60	72	30	47	65
TATC-box				1			3	
TCA		1	2			1		
TCA-element					2			
TCCC-motif			1				1	
TC-rich repeats					2			
TCT-motif	1			1	1	1	3	2
TGACG-motif	5		2	1	3	1	1	
TGA-element	1					1		
Unnamed__1	4	1					1	
Unnamed__4	5	4	5	8	4	13	9	7
Unnamed__6		1			1			
W box		1		1				2
WRE3		1						
WUN-motif	2	1		2		1	2	1

Different numbers indicated the number of cis-acting elements

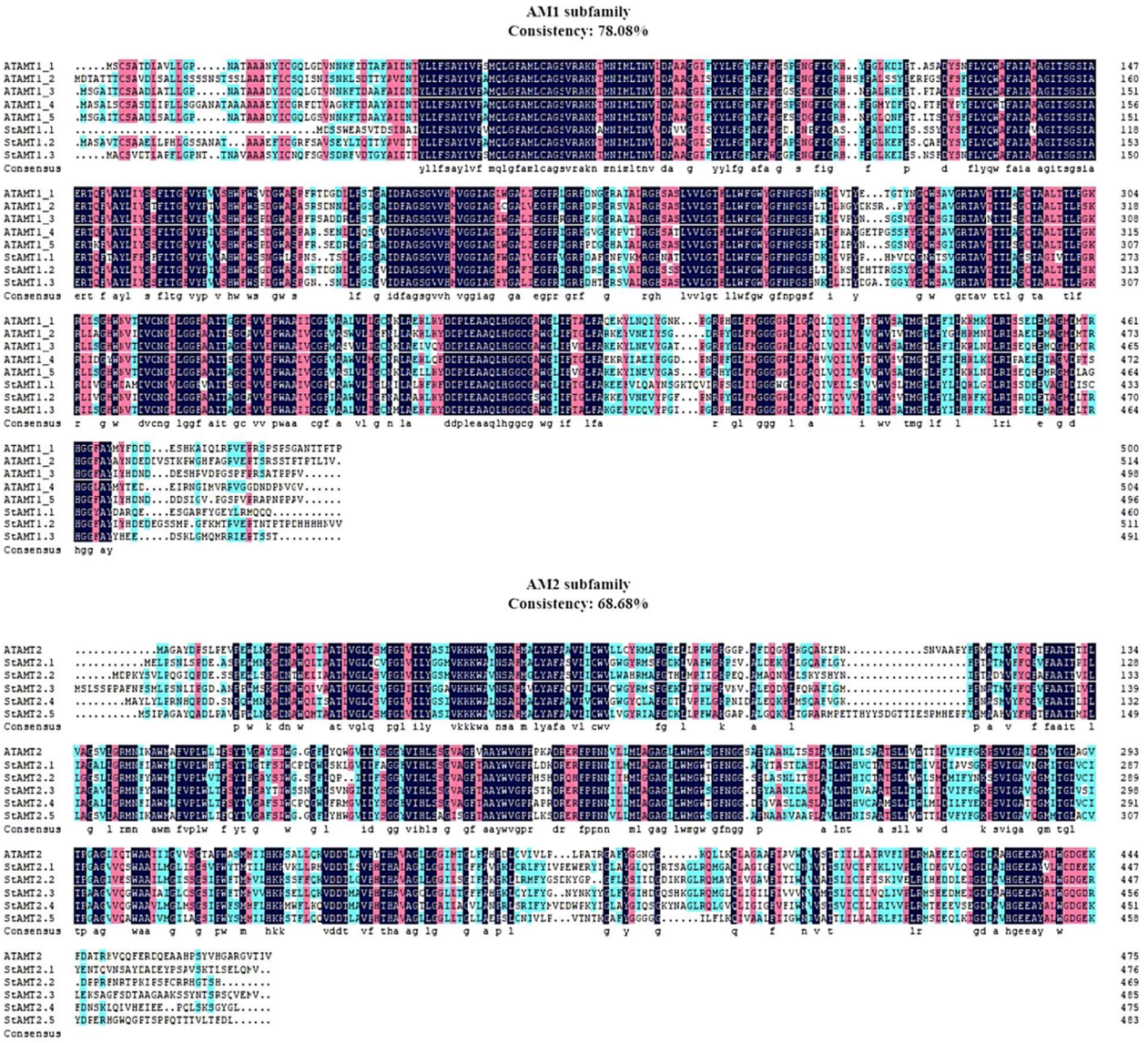

Fig. S1. Sequence alignment of AMT1 subfamily and AMT2 subfamily between potato and ***A. thaliana***

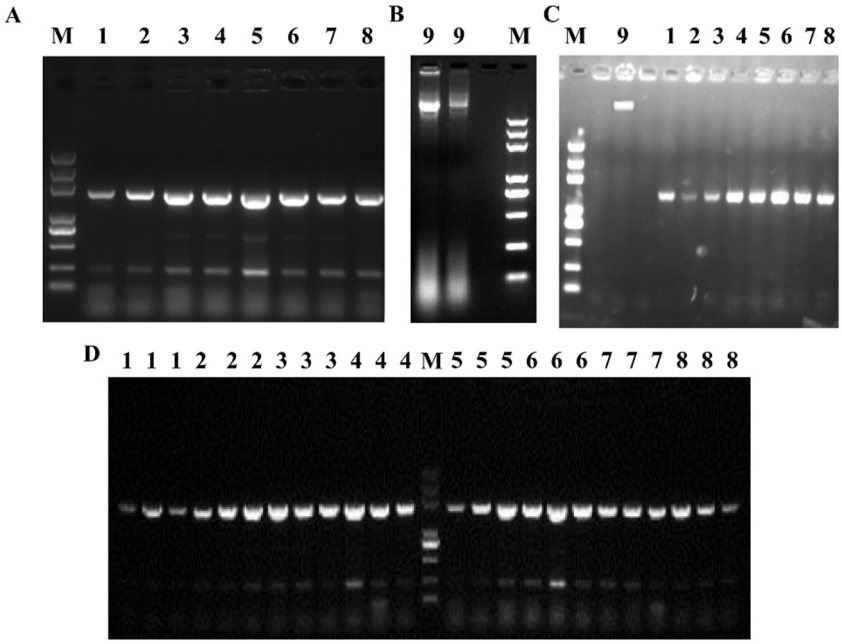

Fig. S2. Construction of recombinant vectors for StAMTs and pBI121-HA. M: DNA molecular weight marker (bp). The bans showed 5000, 3000, 2000, 1000, 750, 500, 250, 100 from top to bottom. "1-8" were PCR amplification bands of 8 *StAMTs*, respectively. "9" represented the linearized band of the vector pBI121-HA. **A.** PCR amplification form potato cDNA. **B.** Double enzyme digestion of pBI121-HA by *Xba* I and *Xho* I. **C.** Gel purification products detection of linearized vector and PCR amplification. **D.** PCR detection of positive transformants of ***Agrobacterium tumefaciens*** contained the recombinant plasmids of *StAMTs* and pBI121-HA.

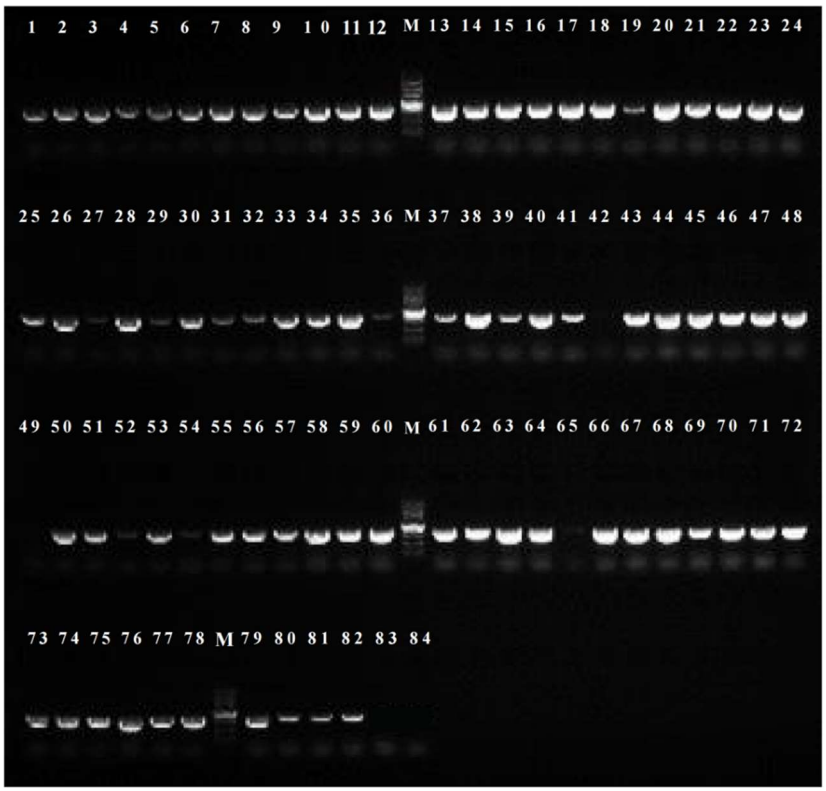

Fig. S3. PCR detection of positive transgenic ***A. thaliana*** plants. M: DNA molecular weight marker (bp). "1-10", "11-18", "19-33", "34-38", "39-49", "50-58", "59-66" and "67-80" were PCR amplification bands of genome DNA of the plants that have been transformed with StAMT1.1-StAMT2.5, respectively. 81~82 were positive controls. 83-84 were negative controls, the templates were sterile ddH_2O and genome DNA of Columbia-0, respectively. The marker gene was neomycin phosphotransferase II gene (*NPTII*). The corresponding plants of the templates that can be amplified by PCR to obtain bands were selected for qRT-PCR detection.

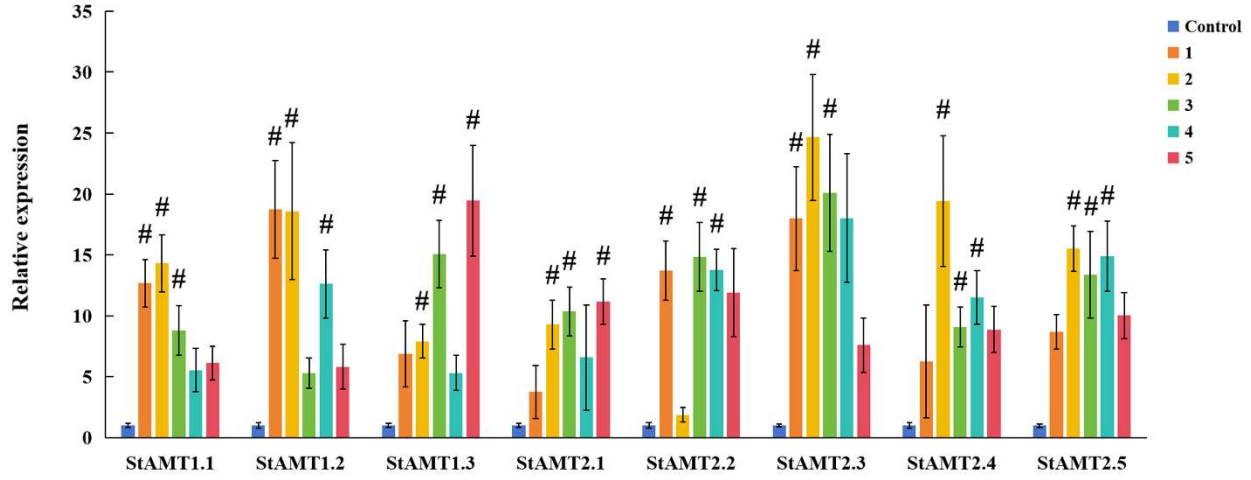

Fig. S4. qRT-PCR detection of positive transgenic ***A. thaliana*** plants. 1-5 indicated different lines. # indicated the transgenic lines selected for the next study.

Fig. S5. Growth phenotype of transgenic ***A. thaliana*** and Columbia-0 under Control, NH_4^+ sufficiency and NH_4^+ deficiency conditions. 1-8 indicated transgenic ***A. thaliana*** lines overexpressing *StAMT1.1~StAMT2.5*, respectively.