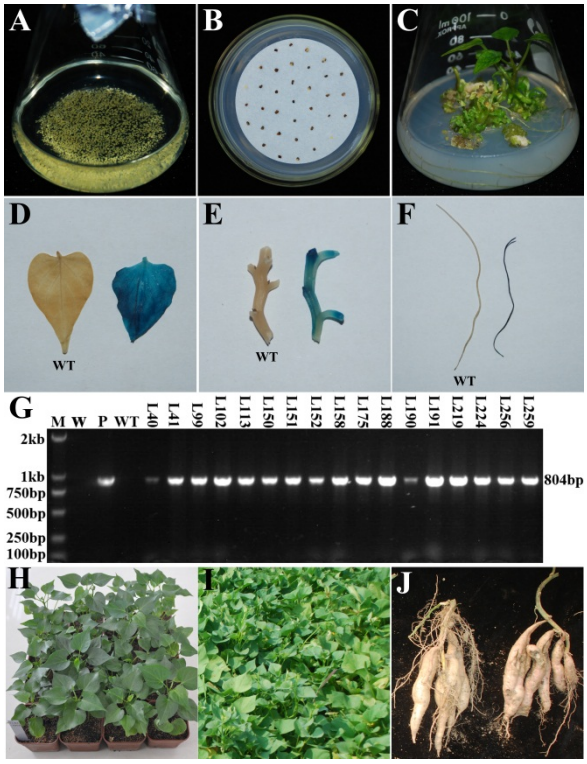

Appendix A Production of transgenic sweetpotato plants overexpressing the *IbAATP* gene. **A,** proliferation of embryogenic suspension cultures of Lizixiang in MS medium containing 2.0 mg L^{-1} 2,4-D. **B,** phosphinothricin (PPT)-resistant calluses (bright yellow) formed after 8 weeks of selection on MS medium with 2.0 mg L^{-1} 2,4-D, 300 mg L^{-1} cefotaxime sodium and 50 mg L^{-1} PPT. **C,** regeneration of plantlets from PPT-resistant calluses on MS medium with 1.0 mg L^{-1} ABA and 300 mg L^{-1} cefotaxime sodium. **D**, **E** and **F**, leaf, stem and root, respectively, of a transgenic plant that showed positive reactions in the GUS assay; GUS expression was not detected in the WT plant. **G**, PCR analysis of GUS-positive plants. Lane M: BL2000 DNA marker; Lane W: water as a negative control; Lane P: plasmid pCAMBIA3301-121-*IbAATP* as a positive control; Lane WT: WT as a negative control; Lanes 40-259: GUS-positive plant lines. **H**, transgenic plants grown in the greenhouse. **I**, transgenic plants grown in the field. **J**, storage roots of the transgenic sweetpotato.

Appendix B Sequences of the primers used in this study

Primer name	Primer sequence (5'-3')
DA-F	TGGGTBAAYYTGCCHATGGC
DA-R	GTHGCWGTYGARAARTCACCCAT
5GSP1	CGTTTAGAAGATTATCAGCAAG
5GSP2	TGAAGGGCAGAATAACGGTAT

5GSP3	GCCTGCTTGGACAACACATT
3GSP1	GCTTGAAGTTCTTGGCGTCT
3GSP2	TTGGTGGTAGCATATGGCAT
GA-F	TGGTGTTTGCGAGACAGGGA
GA-R	TCAGTGCAATCAATGCCTGATT
83A-F-*Spe*Ⅰ	GACTAGTATGGATGCCATATTACAATCTAGAG
83A-R-*Asc*Ⅰ	AGGCGCGCCCACATTCCGGCGGGGGT
OA-F-*BamH*Ⅰ	CGGGATCCATGGATGCCATATTACAATCTAGAG
OA-R-*Sac*Ⅰ	CGAGCTCTCACACATTCCGGCGGGGGTA
T35-F	TGCCATCATTGCGATAAAGG
TA-R	AGAAGATTATCAGCAAGAGCTGTG
QA-F (*IbAATP*)[a]	TCGAAGCCCAAAATCAGAGC
QA-R (*IbAATP*)	GAAATAGACAACCCATCAAACGG
Qactin-F (*IbActin*)	AGCAGCATGAAGATTAAGGTTGTAGCAC
Qactin-R (*IbActin*)	TGGAAAATTAGAAGCACTTCCTGTGAAC
QPGM-F (*IbPGM*)	TTCTGCTGGTGCAACAGTAAGAG
QPGM-R (*IbPGM*)	AGTTGGCTTCTCTCTTCCGGTA
QAGS1-F (*IbAGP-sTL1*)	AGAGAATTGACGGTGATGTTAGCA
QAGS1-R (*IbAGP-sTL1*)	ATGAACGGAGCAGTCCGAAC
QAGS2-F (*IbAGP-sTL2*)	CCAAAAGGAGAACAGTTGAAAGCTA
QAGS2-R (*IbAGP-sTL2*)	CTCCAGGGAACTTTTCTCGAAGTA
QAGL-F (*IbAGP-TLI*)	GAGATATCCCACATCCAACGACTT
QAGL-R (*IbAGP-TLI*)	TAGGGCCAAGTTAGCGTCGTAG
QGB-F (*IbGBSS Ⅰ*)	TGGCAACTATAACTGCCTCACAC
QGB-R (*IbGBSS Ⅰ*)	GGCACTGGTTCTCAATTGTAACAT
QS1-F (*IbSS Ⅰ*)	GCTGCAGACCGTCTTTGTGC
QS1-R (*IbSS Ⅰ*)	GAGCCATCCCTCTGTGCTCC
QS2-F (*IbSS Ⅱ*)	AGACTGTGGGATCTACTGAAAGGC
QS2-R (*IbSS Ⅱ*)	GTGAATCCACGTCCAGTGGC

QS3-F (*IbSSⅢ*)	TCTGTTATCCTGAGGAGGTAAAACC
QS3-R (*IbSSⅢ*)	CTCCCATGATCAATACATCAGGC
QS4-F (*IbSSⅣ*)	CTGCTTTCTCATTTCTGTCATCGT
QS4-R (*IbSSⅣ*)	GCTCAACTTCCACTTGACTCAGAG
QBE1-F (*IbSBE Ⅰ*)	ATTCTTGGCCTAGACCAAGGG
QBE1-R (*IbSBE Ⅰ*)	ACAATGCAGCCTTCTTCTTTGTTA
QBE2-F (*IbSBE Ⅱ*)	AGTCCGCTGTTTGGAGGCTT
QBE2-R (*IbSBE Ⅱ*)	CCTCAACTGGTTTTGCTTCGTC
QISA-F (*IbIsa1*)	GGAACGAGGTGGTTATCGGTG
QISA-R (*IbIsa1*)	TCTGGGCATAGCAACAGAATTATG
QPUL-F (*IbPUL*)	GCTGCTCGACGATGCCTCT
QPUL-R (*IbPUL*)	CATCCTCAACGTCCACATTCC

[a] The names of the primers used in the qRT-PCR reactions begin with the letter "Q", and the corresponding genes are shown in parentheses.

Appendix C GenBank accession numbers of the ATP/ADP transporter proteins used in the multiple sequence alignment and phylogenetic tree construction in this study.

Species	**Protein**	**GenBank accession number**
Arabidopsis thaliana	AtAATP1	NP_178146
Arabidopsis thaliana	AtAATP2	NP_173003
Cucumis sativus	CsAATP	XP_004147999
Mesembryanthemum crystallinum	McAATP1	AB190777
Manihot esculenta	MeAATP1	DQ071875
Manihot esculenta	MeAATP2	DQ071876
Medicago truncatula	MtAATP	KEH28732
Oryza sativa	OsAATP1	AAX58120
Oryza sativa	OsAATP2	BAD24996
Ricinus communis	RcAATP	XP_002517555
Solanum lycopersicum	SlAATP	XP_004235723

Solanum tuberosum	StAATP1	Y10821
Vitis vinifera	VvAATP	XP_002285232
Zea mays	ZmAATP	NM_001154379
Rickettsia prowazekii	TLCRp	M28816