Na₂CO₃-responsive mechanisms in halophyte *Puccinellia tenuiflora* roots

revealed by physiological and proteomic analyses

Qi Zhao^{1,2}, Jinwei Suo², Sixue Chen³, Yudan Jin², Xiaolin Ma², Zepeng Yin², Yuhong Zhang¹, Tai

Wang⁴, Ji Luo⁵, Wenhai Jin⁵, Xia Zhang⁴, Zhiqiang Zhou^{1,#} & Shaojun Dai^{1,2,*}

¹Key Laboratory of Forest Plant Ecology, Ministry of Education, Northeast Forestry University,

Harbin 150040, China;

²Alkali Soil Natural Environmental Science Center, Northeast Forestry University, Key Laboratory

of Saline-alkali Vegetation Ecology Restoration in Oil Field, Ministry of Education, Harbin 150040,

China;

³Department of Biology, Genetics Institute, Plant Molecular and Cellular Biology Program,

Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, FL 32610,

USA;

⁴Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China;

⁵AB Sciex Asia Pacific Application Support Center, Shanghai 200233, China

*Correspondence: Professor Shaojun Dai, Northeast Forestry University, Harbin 150040, China

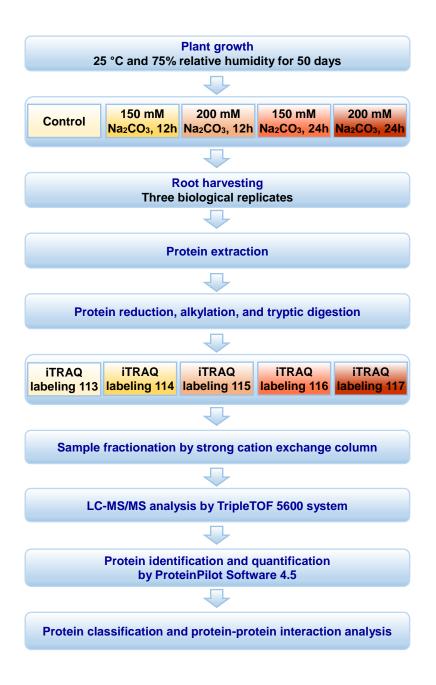
Tel: 86-451-82192237; Fax: 86-451-82192237

E-mail: daishaojun@hotmail.com

***Co-corresponding author Tel:** 86-451-82190338; **Fax:** 86-451-82190338

E-mail: zhiqianqzhou@hotmail.com

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Supplementary Figure S1. iTRAQ-based proteomics strategy for analysis of Na₂CO₃-responsive proteins in *Puccinellia tenuiflora* roots

gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	MGNACGGSLRSKYLSFKQ	GNHSRPEENSKSTTTTVSSVHSPTTDQDFSKQNTNPALVIPV TASQRHDTDDNNNAAAADSPKKPSRPPAAAKTDDHPVSASAP
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	AAAMRRGQAPADLGSVLG	HKTPNIRDLYTLSRKLGQGQFGTTYLCTDIATGVDYACKSIS HPTPNLRDLYAMGRKLGQGQFGTTYLCTELSTGVDYACKSIS
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	KRKLITKEDIEDVRREIQ	IMHHLAGHKNIVTIKGAYEDPLYVHIVMELCAGGELFDRIIH IMHHLSGHKNVVAIKGAYEDQLYVHIVMELCAGGELFDRIIQGHLTGHRNIVELHGAYEDRHSVNLIMELCEGGELFDRIIA**.**.*.*************************
gi 30679935 AtCPK6 gi 10944296 0sCDPK7 Contig720 PtCDPK consensus	RGHYSERKAAELTRIIVG RGHYSERAAAALCREIVS	VVEACHSLGVMHRDLKPENFLLVNKDDDFSLKAIDFGLSVFF VVEACHSLGVMHRDLKPENFLLANKDDDLSLKAIDFGLSVFF VVHSCHSMGVFHRDLKPENFLFLNDKEDSPLKATDFGLSVFF *****.**.*************************
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	KPGQTFTDVVGSPYYVAP KHGEQFKDLVGSAYYVAP	EVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAV EVLLKHYGPEADVWTAGVILYILLSGVPPFWAETQQGIFDAV EVLKRHYGAEADIWSAGIILYILLSGVPP
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	LKGFIDFDSDPWPVISES	AKDLIRKMLCSSPSERLTAHEVLRHPWICENGVAPDRALDPA AKDLITKMLNPRPKERLTAHEVLCHPWIRDHGVAPDRPLDPA
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	VLSRIKQFSAMNKLKKMA	LKVIAESLSEEEIAGLRAMFEAMDTDNSGAITFDELKAGLRR LRVIAESLSEEEIAGLKEMFQTMDADNSGAITYDELKEGLRK
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	YGSTLKDTEIRDLMDAAD FGQTLR	VDNSGTIDYSEFIAATIHLNKLEREEHLVSAFQYFDKDGSGY IDNSGTIDYIEFIAATLHLNKLEREEHLVAAFSYFDKDGSGYMAYLRLSCLARISHLTLGLQYL*******
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	ITVDELQQACKEHNMPDA	FLEDIIKEVDQDNDGRIDYEEFVAMMQKGNAGVGRRTMKNSL FLDDVINEADQDNDGRIDYGEFVAMMTKGNMGVGRRTMRNSL MAQKIWR
gi 30679935 AtCPK6 gi 10944296 OsCDPK7 Contig720 PtCDPK consensus	NISMRDV NISMRDAPGAL	

Supplementary Figure S2. Multiple amino acid sequence alignment of calcium-dependent protein kinases from Arabidopsis (AtCPK6), rice (OsCDPK7), and

Puccinellia tenuiflora (PtCDPK). The Gi numbers of AtCPK6 and OsCDPK7, and encoding unigene name of PtCDPK were listed on the left side. Completely conserved residues among all three proteins were presented in red fonts and marked with asterisks in the consensus line. The dot indicates conserved region between two proteins. Conserved residues between PtCDPK and AtCPK6/OsCDPK7 were presented in blue fonts.