

Supplementary Material

Possible involvement of phosphoenolpyruvate carboxylase and NAD-malic enzyme in response to drought stress. A case study: a succulent nature of the C₄-NAD-ME type desert plant, *Salsola lanata* (Chenopodiaceae)

Zhibin Wen^A and Mingli Zhang^{A,B,C}

^AKey Laboratory of Biogeography and Bioresource in Arid Land, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, CN-830011 Urumqi, China.

^BInstitute of Botany, Chinese Academy of Sciences, CN-100093 Beijing, China.

^CCorresponding author. Email: zhangml@ibcas.ac.cn

Table S1. Primers used for PCR

Abbreviations: *18S rRNA*, ribosomal RNA 18S; *cyt*, cytosolic; *EF1- α* , elongation factor- α ; *GAPDH*, glyceraldehyde 3-phosphate dehydrogenase; NAD-ME, NAD-malic enzyme; PEPC, phosphoenolpyruvate carboxylase

Gene	Sequences (5' to 3')
Target genes	
PEPC	Forward: GGKGACATACATYATCTCCATG Reverse: GGTGTCCTCAAGGCCAGGAG
α -NAD-ME	Forward: TCCTACWGTWGGTCTTGTGTTGCC Reverse: AATYTTTGTTAGGGAAGTCAATCA
Candidate reference genes	
β -actin	Forward: ACATCWGCCAACGGGAAA Reverse: CAACCTTGATCTCATGCTGCTAG
<i>EF1-α</i>	Forward: TCAYRTCAGTTGGTGGTTATTGGA Reverse: CCAAGRGTGAAGGWAAGAAGRGC
<i>18S rRNA</i>	Forward: GCTCGTAGTTGGACCTTGGG Reverse: AAGGGCAGGGASGTAGTCAAC
α -tubulin	Forward: TSGACATTGAGCGWCCCACWT Reverse: CACAGCAGCRTTSACATCCTT
<i>GAPDH</i>	Forward: CAGAGRGAYGATRTYGAGCTTGT Reverse: GARCTGTAWCCCCATTCGTTGTCAT

Table S2. Primers used for gene expression of *Salsola lanata* under drought for RT-qPCR

Abbreviations: *18S rRNA*, ribosomal RNA 18S; *cyt*, cytosolic; *EF1- α* , elongation factor- α ; *GAPDH*, glyceraldehyde 3-phosphate dehydrogenase; NAD-ME, NAD-malic enzyme; NADP-ME, NADP-malic enzyme; PEPC, phosphoenolpyruvate carboxylase

Gene	Sequences (5' to 3')	Annealing temperature (°C)
Target genes		
PEPC	Forward: GTTATGGCGAACCAAAGACC Reverse: TGCCTGGCAAACATTAGGAT	Forward: 59.0 Reverse: 59.9
α -NAD-ME	Forward: AGAAGGCCACGAGGAATGTA Reverse: CTAGGTCTCCAAGTCCAAAAT	Forward: 57.2 Reverse: 57.1
Candidate reference genes		
β -actin	Forward: TCCACGAAACAACCTACAACTC Reverse: CAGCAATACCGGGGAACAT	Forward: 57.0 Reverse: 58.0
<i>EF1-α</i>	Forward: TCAGTTGGTGGTTATTGGACA Reverse: ACCTCTTGTTCATCTCAGCAGC	Forward: 58.0 Reverse: 58.6
<i>18S rRNA</i>	Forward: GGGCATT CGTATTTCATAGTCA Reverse: CGGCATCGTTATGGTTGA	Forward: 57.3 Reverse: 57.5
α -tubulin	Forward: CCATACCCCAGGATTCACTTC Reverse: CACACTTGCCATCATAGACGA	Forward: 58.4 Reverse: 58.7
<i>GAPDH</i>	Forward: AACGAGCACGAATACAAGTCAG Reverse: AGCCCCTCAAGAATACCGA	Forward: 57.4 Reverse: 57.0

Table S3. The expression stability value (SV) of candidate reference genes in all samples

Abbreviations: *18S rRNA*, *ribosomal RNA 18S*; *EF1- α* , *elongation factor- α* ; *GAPDH*, *glyceraldehyde 3-phosphate dehydrogenase*

Software programs	Five candidate references				
	<i>β-actin</i>	<i>α-tubulin</i>	<i>GAPDH</i>	<i>EF1-α</i>	<i>18S rRNA</i>
NormFinder	0.004	0.009	0.013	0.047	0.049
geNorm	0.041	0.044	0.045	0.073	0.076

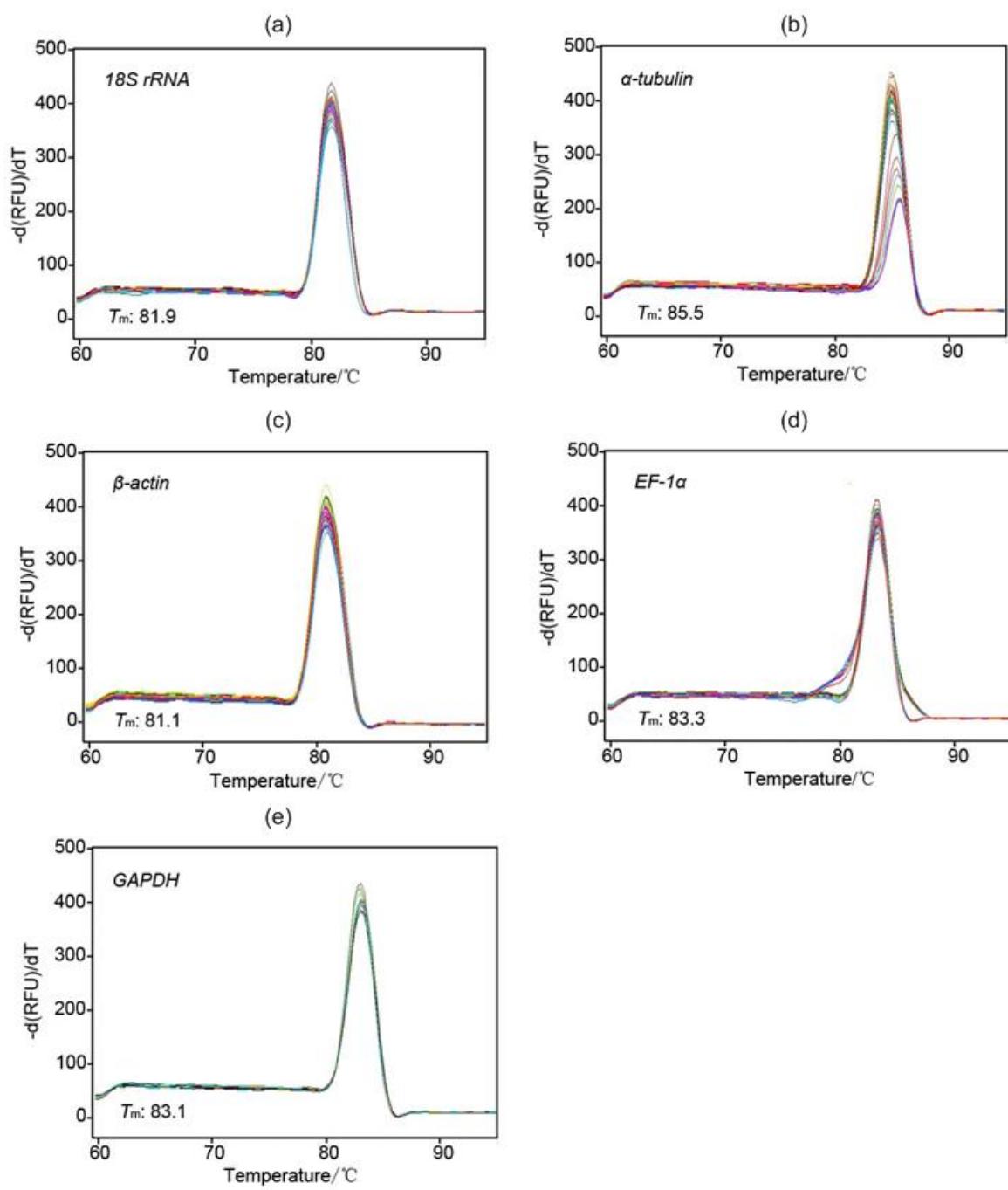


Fig. S1. RT-qPCR melting curves of five candidate reference genes of *Salsola lanata*.

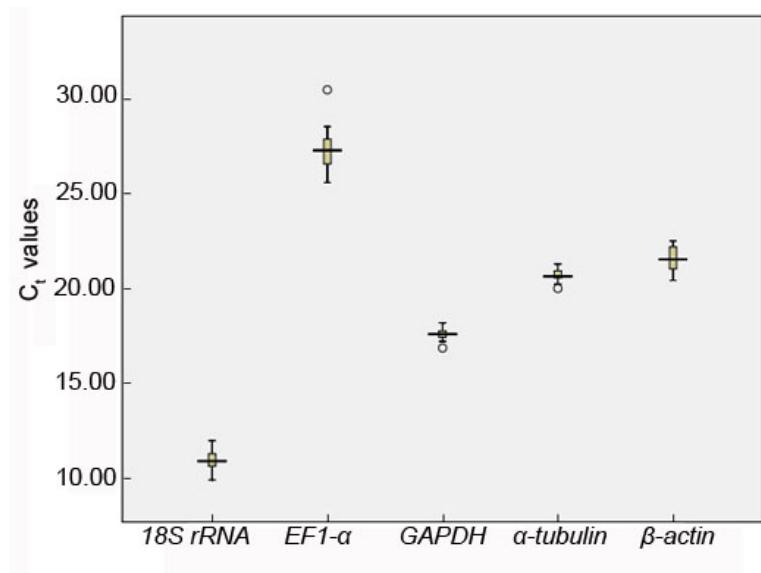


Fig. S2. Distribution of C_t values of five candidate reference genes across all samples. The Box-plot contains the mean, interquartile range, non-outlier range, and outlier.