

Table 1 Suppl. Primer sequences.

Primer name	Primer sequence
F1	5'- GGIGCIGGITAYGTIGGIGG -3'
F2	5'- GGIGCIGGIAARGCIGCIG -3'
R1	5'- GGRTGRTCCCARTCRAAYTT -3'
R2	5'- GCIGGIGTYTCICKIGTRTC -3'
5'R1	5'- GGGTTTCCCTGCCTCCAATAAGA -3'
5'R2	5'- CCAGTAGCCTCACAGAGAGCAGACA -3'
3'F1	5'- ATGTCTGCTCTCTGTGAGGCTA -3'
3'F2	5'- CGACTATCAGAAGAACCGTTTT -3'
Universal Primer Mix Long primer	5'- CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT -3'
Universal Primer Mix Short primer	5'- CTAATACGACTCACTATAGGGC -3'
BpUGDH-full-F	5'- AGAGTGATAAAGGAGCAAAGATGG -3'
BpUGDH-full-R	5'- TCTTCTAACAAAGGAACGGACAG -3'
BpUGDH-SP-F	5'- GCTACTGGGGCTAACATCTC -3'
BpUGDH-SP-R	5'- AACGGTTCTTCTGATAGTCG -3'
BpActin-F	5'- CTACCTTGATCTTCATGCTG -3'
BpActin-R	5'- AGCAACTGGGATGACATGGAG -3'
BpUGDH-P-SP1	5'- TGAAGAAGAGGTTTTTGCCACGG -3'
BpUGDH-P-SP2	5'- CGACCACAATTTTGTGCACTTTGA -3'
BpUGDH-P-SP3	5'- CCAGTGTGCATAAACAGCCTTCAA -3'
AD1	5'- AAATGCTGCAGCCTCCCTCTCACCC -3'
AD2	5'- AATACCAGAAATGTGCCCTCCCGTG -3'
AD3	5'- TGAGCTGGCAGGTTGTAGTCTCTGT -3'
BpUGDH- <i>Bam</i> H1-F	5'- CACGGGGGACTCTAGAACATGAGAGTGATAAAGGAGCAAAGATGG -3'
BpUGDH- <i>Bam</i> H1-R	5'- ACGTTGCAAACGTAAGTGTTGTCTTCTAACAAAGGAACGGACAG -3'
BpUGDH- <i>Xba</i> I-F	5'- GCCCAACGTTCTCGAGTTTTTGTCCAAACACGATTTTACGAT -3'
BpUGDH- <i>Xba</i> I-R	5'- CCCGGGTGGATCCAAGGCCTTCTTTGCTCCTTTATCACTCTAT -3'
Atactin2-F	5'- CTGGATTCTGGTGATGGTGTGTCT -3'
Atactin2-R	5'- GAACCACCGATCCAGACACTGTAC -3'
GUS-F	5'- TCAACGGGGAAACTCAGCAAGCGC -3'
GUS-R	5'- CCTCATTGTTGCCTCCCTGCT -3'

Table 2. Suppl. Putative *cis*-acting elements and their positions in the *Broussonetia papyifera* uridine diphosphate glucose dehydrogenase promoter.

Name of <i>cis</i> -element	Sequence	Function	Position strand
<u>ATCT-motif</u>	AATCTAATCC	part of a conserved DNA module involved in light responsiveness	-458
<u>Box 4</u>	ATTAAT	part of a conserved DNA module involved in light responsiveness	-967
<u>CAAT-box</u>	CCAAT/CAAAT/CAAT/TGC CAAC	common <i>cis</i> -acting element in promoter and enhancer regions	-57; +44; -513; -559; +644...
<u>CAT-box</u>	GCCACT	<i>cis</i> -acting regulatory element related to meristem expression	-381
<u>CGTCA-motif</u>	CGTCA	<i>cis</i> -acting regulatory element involved in the MeJA-responsiveness	-828
<u>ERE</u>	ATTTCAAA	ethylene-responsive element	+273
<u>G-box</u>	CACGAC	<i>cis</i> -acting regulatory element involved in light responsiveness	-396
<u>GARE-motif</u>	TCTGTTG	gibberellin-responsive element	+374; +1045
<u>LAMP-element</u>	CTTTATCA	part of a light responsive element	-1308
<u>LTR</u>	CCGAAA	<i>cis</i> -acting element involved in low-temperature responsiveness	-915
Myb-binding site	CAACAG		-375; -1046
<u>TATA-box</u>	ATATAT/TATA/TATAA/TAT ATA/TACAAAA/ATATAA	core promoter element around -30 of transcription start	+170; -1275; -1300; +171; -507; +172...
<u>TCA-element</u>	TCAGAAGAGG	<i>cis</i> -acting element involved in salicylic acid responsiveness	-986
<u>TCT-motif</u>	TCTTAC	part of a light responsive element	-61; +856
<u>TGA-element</u>	AACGAC	auxin-responsive element	-625; -1016
<u>TGACG-motif</u>	TGACG	<i>cis</i> -acting regulatory element involved in the MeJA-responsiveness	+828

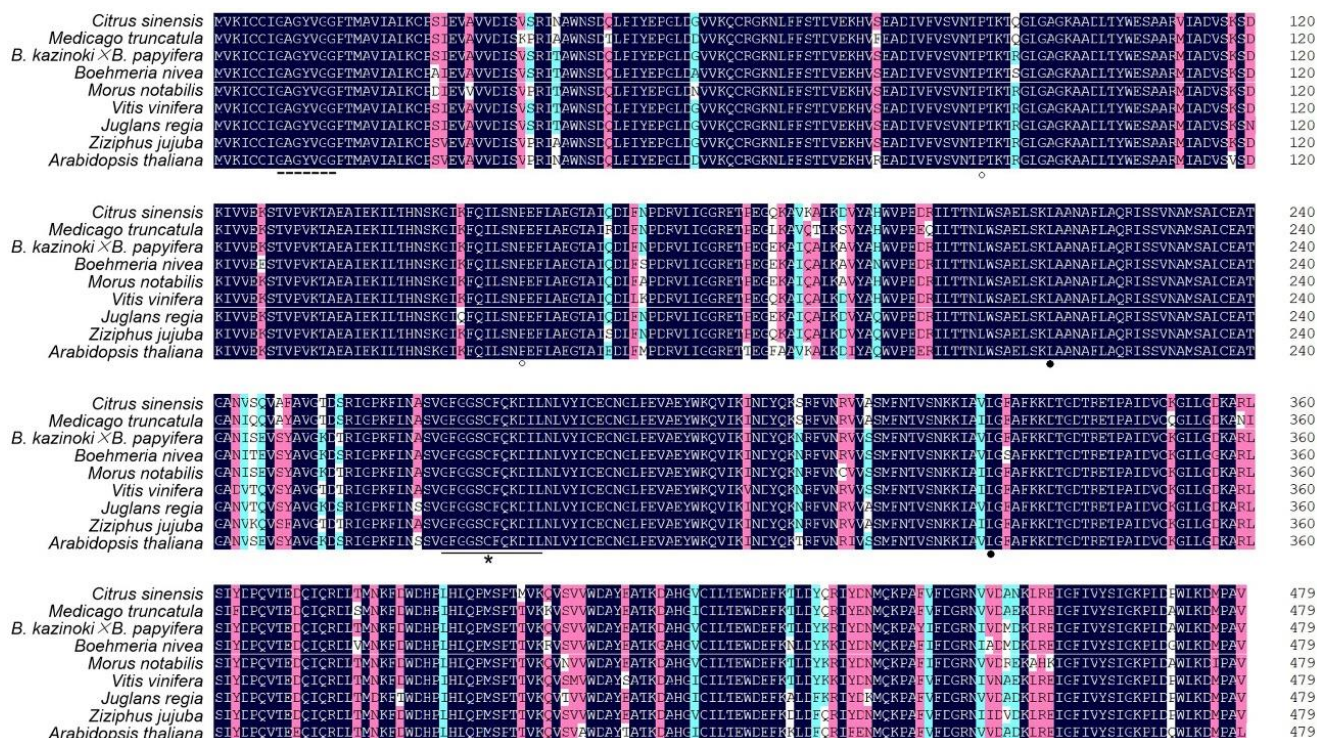


Fig. 1 Suppl. The alignment of amino acid sequences of uridine diphosphate glucose dehydrogenase (UGDH) proteins from *Vitis vinifera* (VvUGDH XP_010661131.1), *Morus notabilis* (MnUGDH XP_010089612.1), *Ziziphus jujuba* (ZjUGDH XP_015879845.1), *Behmeria nivea* (BnUGDH ABM55267.3), *Citrus sinensis* (CsUGDH XP_006482729.1), *Juglans regia* (JrUGDH XP_018816674.1), *Arabidopsis thaliana* (AtUGDH BAB02581.1), and *Medicago truncatula* (MtUGDH XP_003621403.1). The putative NAD⁺ cofactor-binding motif (G-A-G-Y-V-G-G) is indicated by a dashed line undern the sequences. The key catalytic site (G-F-G-G-S-C-F-Q-K-D-I-L) is underlined and Cys-272, which is supposedly involved in enzyme catalysis during the second-half reaction catalyzed by UGDH, is indicated by an asterisk under the sequences. Two Lys residues at positions 217 and 330 are indicated by solid circles under the sequences (one of these Lys residues is probably involved in the conversion of UDP-glucose to UDP- aldehydoglucose). Pro residues at positions 89 and 156 are indicated by open circles under the sequences, which are conserved in all of the eukaryotic UGDHs and are believed to correspond to the main bends in the protein structure.

+ TCCAAACACG ATTTTACGAT CTTGACCTTT CCGACGCACC TGCCAAATGG AAAATAATTG GTAAGACAAA
 -1304 AGGTTTGTGC TAAAAATGCTA GAACTGGAAA GGCTGCGTGG ACGGTTTACC TTTTATTAAC CATTCT GTTI
 -----TCT-motif-----
 + AATAAATAAA TAAAAATGTTT GTTCGACAGC TTCCACCAG ACAAGCACCG GCTTGTAATT TCCTAGAAAT
 -1234 TTATTTATTT ATTTTACAAG CAAGCTGTCG AAGGGTGGTC TGTTCTGTGGC CGAACATTAA AGGATCTTTA

 + GTTAGGGGTA GATCTGGAAC ATACATTGGA TATATAAAG AGCTCCGCAT TCGTCTTCTT CGTGCTTCTC
 -1164 CAATCCCATC CTAGACCTTG TATGTAACCT ATATATTGTC TCGAGGCGTA AGCAGAAGAA GCACGAAGAG

 + TCCTTCTCTC TCGCGTAGAA ACACCAGAGC AGGATTTCAG GAGGTAAAAAT TCCGACCTTG CGATTTCAAA
 -1094 AGGAAGAGAG AGCGCATCTT TGTGGTCTCG TCCTAAAGTC CTCCATTITA AGGCTGGAAC GCTAAAGTTT
 -----ERE-----
 + TCTCCATGCA TTTTCTTCT CTTTTGCTT GATTTGTCC GTTTTTCATT CGATTTTCTT CGGTTTCCGA
 -1024 AGAGGTACGT AAAAGAAAG AAAAAACGAA CTAACACAGG CAAAAAGTAA GCTAAAGAA GCCAAAGGCT
 -----AAGAA-motif-----
 + GATCAAATTA CAGTGATTTC TTATCTGTTC AGTGGCGAAT TCTCAGTCGT GTTCGTTTTT TGATCTGAAT
 -954 CTAGTTTAAT GTCATAAAG AATAGACAAC TCACCGCTTA AGAGTCAGCA CAAGCAAAAG ACTAGACTTA
 -----GARE-motif-----
 -----Myb-binding site-CAT-box-----G-box-----
 + TTGATGCCAG ATTTGATTG CGCTGTTTCT TGATACTGGA TTCGATTCTG ATGTTTGAT TAAGCAGATC
 -884 AACTACGGTC TAACTAAAC GCGACAAAG ACTATGACCT AAGCTAAGAC TACAAACGTA ATTCTGTCTAG
 -----ATCT-motif-----
 + TAGCGTCTTT TCCGGTTTT GTATTGTTTT GATGGTCAAT TATGGTGTCTG GGAATGTGAA TTGAGCTTGT
 -814 ATCGCAGAAA AAGGCCAAAA CATAACAAA CTACCAGTTA ATACCACAGC CCTTACACTT AACTCGAACA

 + TGGCATTGGA TCTGATTGAA TTTTGGTTA TCAATTAGGA TTTTATGCTA ATCAAGGTTT TTTGGTCGTT
 -744 ACCGTAACCT AGACTAECTT AAAAACCAAT AGTTAATCCT AAAATACGAT TAGTTCCTAAA AAACCAGCAA
 -----TGA-element-----
 + TAATTACAGG ATTTGCCAAC ATTTTGTG TTGAAAATAT TCTTTTACCT GTTTTGTGAT TGTTAAGCAT
 -674 ATTAATCTCC TAAACGGTTG TAAAAACAC AACTTTTATA AGAAAATGGA CAAAACTAC ACAATTCTGA
 -----Box 4-----
 + TATTTTGGTA AGCTAGTTGT CGGCTTCCAC CCATATGGGT TGGATCCGGT TTTGTCTTAG CTCTAATTAT
 -604 ATAAAAACCT TCGATCAACA GCCGAAGGTG GGTATACCCA ACCTAGGCCA AAACAGAATC GAGATTAATA

 + TGCTATTGG CTAAAGGAAA TATCTTCTTC TTCTTCTTCT TTTCATGCTT GTTCGATTGA CGTCTCTTGC
 -534 ACAGATAACC GATTTCCTTT ATAGAAGAAG AAGAAGAAGA AAAGTACGAA CAAGCTAACT GCAGGAAACG
 -----TGACG-motif-----
 -----CGTCA-motif-----
 + TGATGTGTTA GTCTCTCTTA CGTTCCTAGA TCCGCCTACT CTGTAAATTT ATTCTTCATC CCGAATACCG
 -464 ACTACACAAT CAGAGAGAAT GCAAGAATCT AGGCGGATGA GACAATTTAA TAAGAAGTAG GGCCTATGGC
 -----TCT-motif-----
 + GACTTTTCGG ATTTGATGAA ACGGGATTCTG TATTACTAGA ATTCTGTGAA ACTCGGATTA ATATTGTTTT
 -394 CTGAAAAGCC TAAACTACTT TGCCCTAAGC ATAATGATCT TAAGACACTT TGAGCCTAAT TATAACAAAA
 -----LTR-----
 + GTGTTCTCTT TTTGAACAAG TTAGCACATT TCTAGTCGT TTGAGGTTAC TCTTAGTTCT CTAATCTGTT
 -324 CACAAGGAGA AACTTGTTT AATCGTGTA AGAATCAGCA AACTCCAATG AGAATCAAGA GATTAGACAA
 -----TCA-element-----TGA-element-----GARE-moti
 -----Myb-binding si
 + GTGAAAATTG ATGGCAAGAA AAGGATTGGA GGTTTTACT CTTAAGGGCC CAGATCTAGG AAAAAGTCTC
 -254 CACTTTTAAC TACCGTTCTT TTCTTAACCT CCAAAACTGA GAATTCCTGG GTCTAGATCC TTTTCAGAG

 + ATGAGTGACC AGATCTTCTT TAAGTATAAT AATTGATTAT GGAGGCATGA GATAGTTTAT TTGCTTTATG
 -184 TACTCACTGG TCTAGAAGGA ATTCATATTA TTAATAATA CCTCCGTA CTATCAAATA AACGAAATAC

 + AAAAAAATAA TGATTGAAA AGTGCTAAAA TAAGTTTAC CGTTTGCATG TTTTGCATG GTTGTCTTT
 -114 TTTTATTAT ACTAACCTTT TCACGATTTT ATTCAAAGTG GCAAACGTAC AAAAACGTTA CAACAAGAAA

 + TTATCTCTCT GATCTATATG AAACCTCATC GTGGACAGGT TATAGAGTGA TAAAGGAGCA AAGATG
 -44 AATAGGAGGA CTAGATATAC TTTGGAGTAG CACCTGTCCA ATATCTCACT ATTTCCTCG TTCTAC
 -----LAMP-element-----

Fig. 2 Suppl. Putative cis-acting regulatory elements detected in the promoter region of the *Broussonetia papyifera* uridine diphosphate glucose dehydrogenase gene using the *PlantCARE* database are indicated by *underlining*. ‘A’ represents the transcriptional start site, and ATG represents the starting codon.

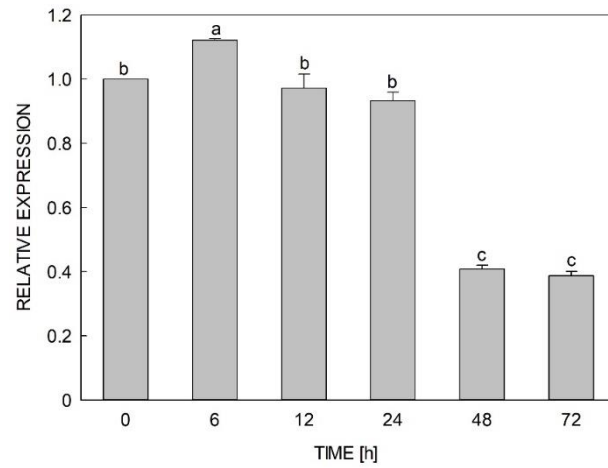


Fig. 3 Suppl. Real-time PCR was used to measure a relative expression of the *Broussonetia papyifera* uridine diphosphate glucose dehydrogenase gene in paper mulberry seedlings cultivated at 4 °C for 0 - 72 h. Error bars represent SDs of three independent biological replicates. Different lowercase letters represent significant differences among the groups of samples ($P < 0.05$).