

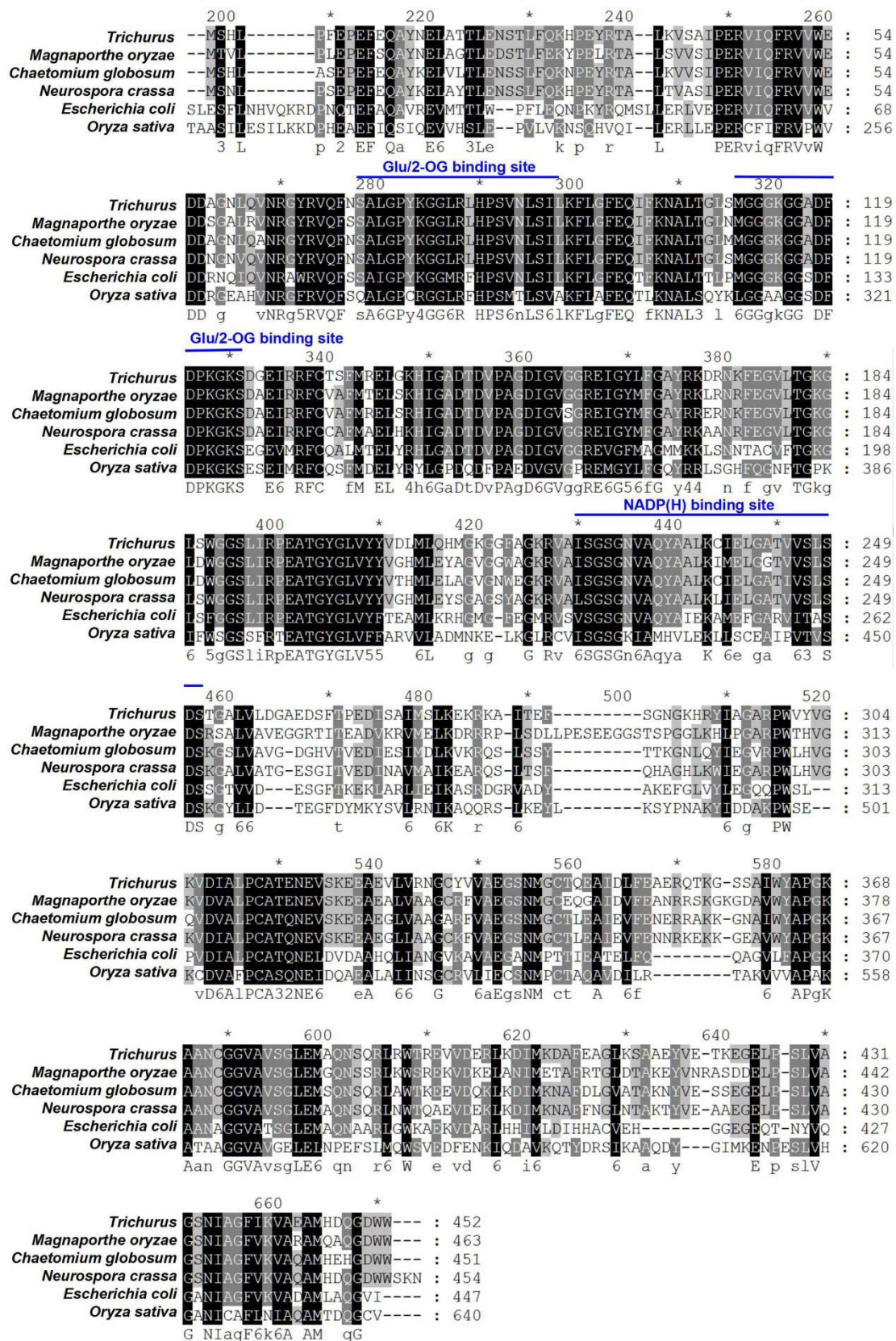
Start(0)

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   Met Ser His Leu Pro Phe Glu Pro Glu Phe Glu Gln Ala Tyr Asn Glu Leu Ala Thr Thr
   1         5         10         15         20
61  CTCGAGAACTCGACCCTCTTCCAGAAGCACCCCGAGTATCGCACCCGCGCTCAAGGTTTCC 120
   Leu Glu Asn Ser Thr Leu Phe Gln Lys His Pro Glu Tyr Arg Thr Ala Leu Lys Val Ser
   25         30         35         40
121 GCCATCCCCGAGCGTGTTCATCCAGTTCGCGGTTGTCTGGGAGACGATGCGGGCAACCTG 180
   Ala Ile Pro Glu Arg Val Ile Gln Phe Arg Val Val Trp Glu Asp Asp Ala Gly Asn Leu
   45         50         55         60
181 CAGGTCAACCGCGGTTACCGCGTTCAGTTCAACTCCGCGCTAGGCCCTTACAAGGGTGGC 240
   Gln Val Asn Arg Gly Tyr Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Arg
   65         70         75         80
241 CTGCGCCTCCACCCCTCGGTCAACCTGTCTATTCTTAAGTTCTTGGCTTCGAGCAGATC 300
   Leu Arg Leu His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu Gln Ile
   85         90         95         100
301 TTCAAGAATGCGCTCACTGGTCTTTCCATGGGCGGGCAAGGGAGGCGCCGATTTGAC 360
   Phe Lys Asn Ala Leu Thr Gly Leu Ser Met Gly Gly Gly Lys Gly Gly Ala Asp Phe Asp
   105        110        115        120
361 CCCAAGGGCAAGAGGACGGCGAGATCCGCCGTTTCTGCACCTCTTTCATGCGTGA GCTT 420
   Pro Lys Gly Lys Ser Asp Gly Glu Ile Arg Arg Phe Cys Thr Ser Phe Met Arg Glu Leu
   125        130        135        140
421 GGAAAGCACATCGGTGCCGACACTGACGTGCCCGCTGGTGACATCGGTGTGGGCGGTGCGC 480
   Gly Lys His Ile Gly Ala Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg
   145        150        155        160
481 GAGATCGGCTACCTGTTTCGGTGCCTACCGCAAGGACCGCAACAAGTTTCGAGGGTGTCTCTG 540
   Glu Ile Gly Tyr Leu Phe Gly Ala Tyr Arg Lys Asp Arg Asn Lys Phe Glu Gly Val Leu
   165        170        175        180
541 ACCGGCAAGGGCCTCAGCTGGGGGGGCGAGCCTGATCAGGCCCGAGGCCACCGGCTACGGT 600
   Thr Gly Lys Gly Leu Ser Trp Gly Gly Ser Leu Ile Arg Pro Glu Ala Thr Gly Tyr Gly
   185        190        195        200
601 CTCGTCTACTACGTTGACCTCATGCTCCAGCACATGGGCAAGGGCGGCTTCGCTGGCAAG 660
   Leu Val Tyr Tyr Val Asp Leu Met Leu Gln His Met Gly Lys Gly Phe Ala Gly Lys
   205        210        215        220
661 CGCGTCGCCATCTCCGGCTCCGGCAACGTCGCCCAAGTACGCGGGCGCTCAAGTGCAATTGAG 720
   Arg Val Ala Ile Ser Gly Ser Gly Asn Val Ala Gln Tyr Ala Ala Leu Lys Cys Ile Glu
   225        230        235        240
721 CTCGGTGCCACCGTCTCTCTCTCCGACTCCACCGGTGCCCTCGTCCCTCGACGGTGGC 780
   Leu Gly Ala Thr Val Val Ser Leu Ser Asp Ser Thr Gly Ala Leu Val Leu Asp Gly Ala
   245        250        255        260
781 GAGGACTCCTTCACTCCCGAGGATATCAGCGCCATCATGAGCCTCAAGGAGAAGCGCAAG 840
   Glu Asp Ser Phe Thr Pro Glu Asp Ile Ser Ala Ile Met Ser Leu Lys Glu Lys Arg Lys
   265        270        275        280
841 GCCATCACTGAGTTTACGCGGCAACGGCAAGCACAGGTACATCGCCGGCGCCAGGCCGCTGG 900
   Ala Ile Thr Glu Phe Ser Gly Asn Gly Lys His Arg Tyr Ile Ala Gly Ala Arg Pro Trp
   285        290        295        300
901 GTGTACGTCGGCAAGGTCGACATCGCGCTCCCTGCGCGACCGAGAAGGAGTCAAGCAAG 960
   Val Tyr Val Gly Lys Val Asp Ile Ala Leu Pro Cys Ala Thr Glu Asn Glu Val Ser Lys
   305        310        315        320
961 GAGGAGGCGGAGGTGCTCGTCCGCAACGGCTGCTACGTCGTCGCTGAGGGCTCCAACATG 1020
   Glu Glu Ala Glu Val Leu Val Arg Asn Gly Cys Tyr Val Val Ala Glu Gly Ser Asn Met
   325        330        335        340
1021 GGCTGCACCCAGGAGGGCCATCGACCTCTTCGAGGCCGAGAGGCAGACCAAGGGCAGCTCC 1080
   Gly Cys Thr Gln Glu Ala Ile Asp Leu Phe Glu Ala Glu Arg Gln Thr Lys Gly Ser Ser
   345        350        355        360
1081 GCCATCTGGTACGCCCCGGCAAGGCCGCCAACTGCGGTGGTGTGCGCCGTCTCGGGTCTC 1140
   Ala Ile Trp Tyr Ala Pro Gly Lys Ala Ala Asn Cys Gly Gly Val Ala Val Ser Gly Leu
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1141 GAGATGGCCCAGAACAGCCAGCGCCTCCGGTGGACCCGTGAGGTCGTCGACGAGAGGCTC 1200
   Glu Met Ala Gln Asn Ser Gln Arg Leu Arg Trp Thr Arg Glu Val Val Asp Glu Arg Leu
   385        390        395        400
1201 AAGGACATCATGAAGGACGCCTTCGAGGCGGGTCTCAAGAGCGCCGCCGAGTACGTCGAG 1260
   Lys Asp Ile Met Lys Asp Ala Phe Glu Ala Gly Leu Lys Ser Ala Ala Glu Tyr Val Glu
   405        410        415        420
1261 ACCAAGGAGGGCGAGCTTCTTCTGCTGCTTGGCGGTAGCAACATCGCCGGCTTCATCAAG 1320
   Thr Lys Glu Gly Glu Leu Pro Ser Leu Val Ala Gly Ser Asn Ile Ala Gly Phe Ile Lys
   425        430        435        440
1321 GTCGCGGAGGCTATGCACGACCAGGGTGA GACTGGTGGTGA 1359
   Val Ala Glu Ala Met His Asp Gln Gly Asp Trp Trp
   445        450

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Supplemental Fig. 1. The nucleotide sequence of *TrGDH* cDNA and its deduced amino acid sequence. The full-length *TrGDH* cDNA consists of 1,359 bp nucleotides, which was predicted to encode 452 amino acids with a molecular mass of 49.0 kDa and a calculated pI of 5.7.



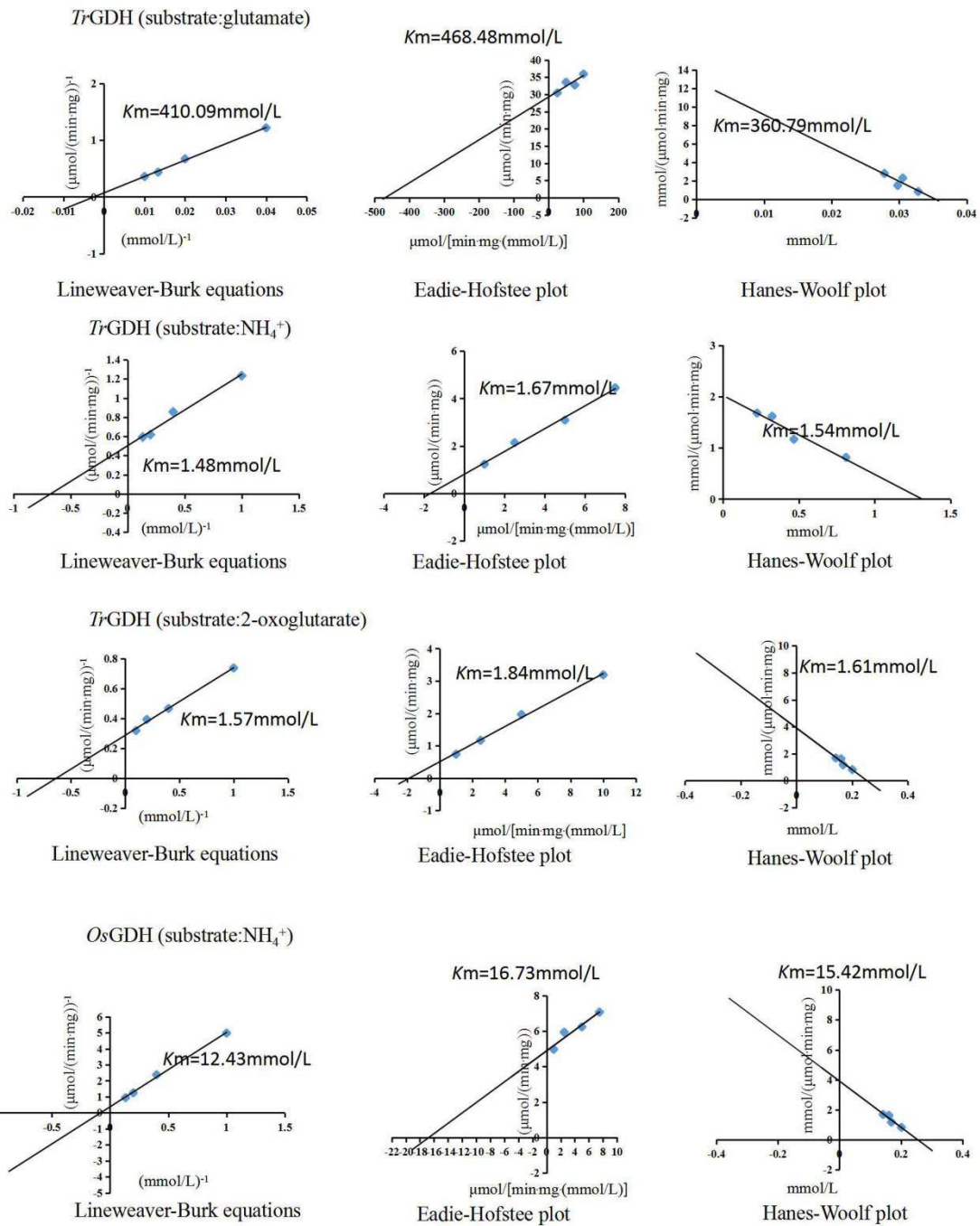
Supplemental Fig. 2. Protein sequence similarity between *TrGDH* and other representative reported GDHs from bacterial, fungal, and plants using MEGA 4.0 and GENEDOC.

The identical amino acids are indicated with black shading, and the similar with gray shading.

Dashes indicate a gap. The GDHs for the aligned sequences were as follows: *TrGDH*; *MoGDH*;

CgGDH; *NcGDH*; *EcoGDH*; *OsGDH4*. The blue line indicate Glu/2-OG binding site and

NADP(H) binding site. (Color figure online)



Supplemental Fig. 3. Lineweaver-Burk equations, Eadie-Hofstee plot and Hanes-Woolf plot used to calculate K_m values of *TrGDH* and *OsGDH4*.

The kinetic constant (K_m) of *TrGDH* and *OsGDH4* for different substrates was calculated with various NH_4Cl concentrations (1, 2.5, 5, 7.5 mM), various 2-oxoglutarate (2-OG) concentrations (1, 2.5, 5, 10 mM) or various L-glutamate concentrations (25, 50, 75, 100 mM).