

Table 1 Suppl. Primer sequences for reverse transcription (RT) semi-quantitative (sq) and quantitative (q) PCR of the Calvin cycle genes in sorghum (*Sorghum bicolor* L.) seedlings (*RbcL* - ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; *RbcS* - ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit; *RCA* - ribulose bisphosphate carboxylase/oxygenase activase; *SBPase* - sedoheptulose-1,7-bisphosphatase; *TPI* - triose-3-phosphate isomerase; *FBPase* - fructose-1,6-bisphosphate phosphatase; *PGK* - 3-phosphoglyceric acid kinase; *PRK* - ribulose-5-phosphate kinase; *GAPDH* - glyceraldehyde-3-phosphate dehydrogenase; *FBA* - fructose-1,6-bisphosphate aldolase.

Gene names	References	5' - 3' primer sequences
<i>Actin</i>	XM_002448995.1	CGGTGCCAATCTATGAAGGT GCGAGCTTTTCCTTGATGTC
<i>RbcL</i>	AM849341.1	CTTGAATGCGACTGCAGGTA GAAGAAAGTAGGCCGTTGTCTG
<i>RbcS</i>	AB564718.1	CCACTAGCTTCGCCAAAGTC TACACGAAGCCTTCCTTGCT
<i>RCA</i>	XM_002451283.1	GTACCTCAACGAGGCTGCTC ACAGGTGGGGGATCATCATA
<i>SBPase</i>	XM_002456602.1	CTTCACCGTTGGAACCATCT TGGTCGTGGTATCCTTGACA
<i>TPI</i>	XM_004146969.2	GGAGTCCCTGGTGTCAAGAA GCCTCGGGAATACAACAGAA
<i>FBPase</i>	XM_002438760.1	TCACTGCAAAGTGGAAGTCG AGGGGGTATTTGGATGGAAG
<i>PGK</i>	XM_002441268.1	GGCAAAGAAGTTGGCAGAAC GCAACAACCTCCTGGAAGCTC
<i>PRK</i>	XM_002448404.1	AAGCTCTCCTGCTCCTACCC ACCTCCCCGTAGAACTTGGT
<i>GAPDH</i>	XM_002444371.1	CGCAGATGCCGTAGTACAGA TGCTCCTTTCTCCTTTGCAT
<i>FBA</i>	XM_002453777.2	TGTTTGTGTCAGTCAGAGCCCA GCCCCCTCGATTACCATCGG

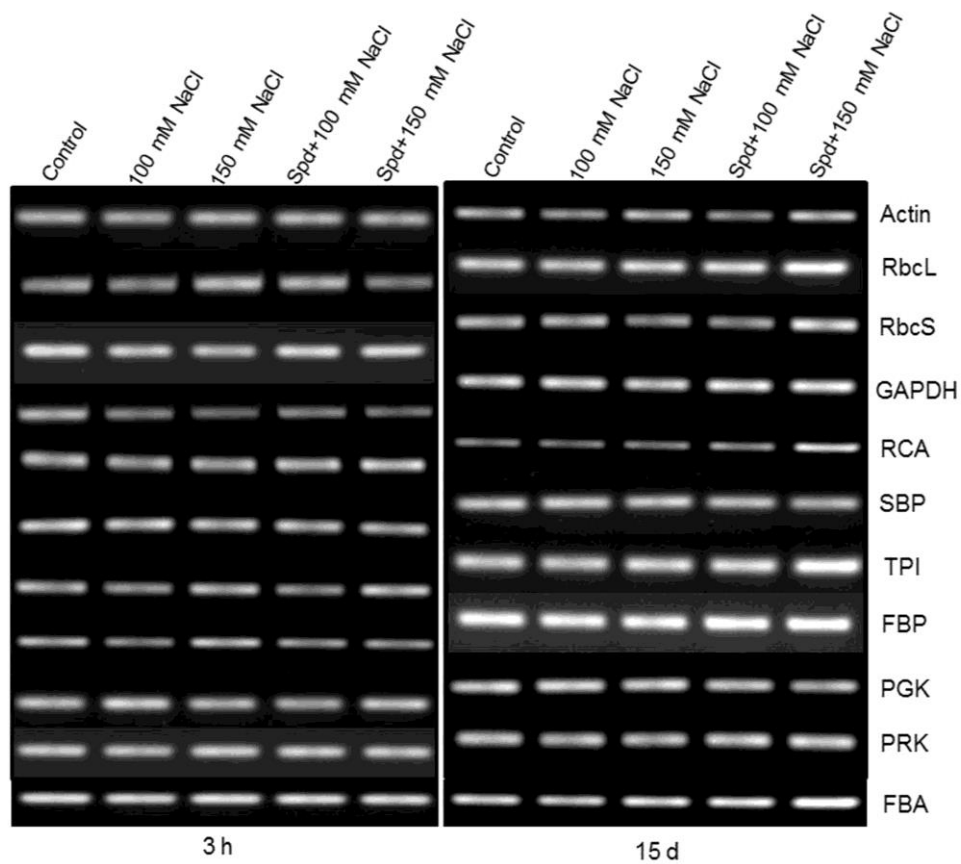


Fig. 1 Suppl. Reverse transcription (RT) semi-quantitative PCR of Calvin cycle genes in sorghum seedlings treated with exogenous spermidine (Spd) under salt stress and compared with control plants at different time points. Samples standardized to *actin*. RT-PCR products were separated on agarose gels (1.5 %, m/v) and visualized by ethidium bromide stain (RbcL - ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit; RbcS - ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit; RCA - ribulose bisphosphate carboxylase/oxygenase activase; SBP - sedoheptulose-1,7-bisphosphatase; TPI - triose-3-phosphate isomerase; FBP - fructose-1,6-bisphosphate phosphatase; PGK -3-phosphoglyceric acid kinase; PRK - ribulose-5-phosphate kinase; GAPDH - glyceraldehyde-3-phosphate dehydrogenase; FBA - fructose-1,6-bisphosphate aldolase.

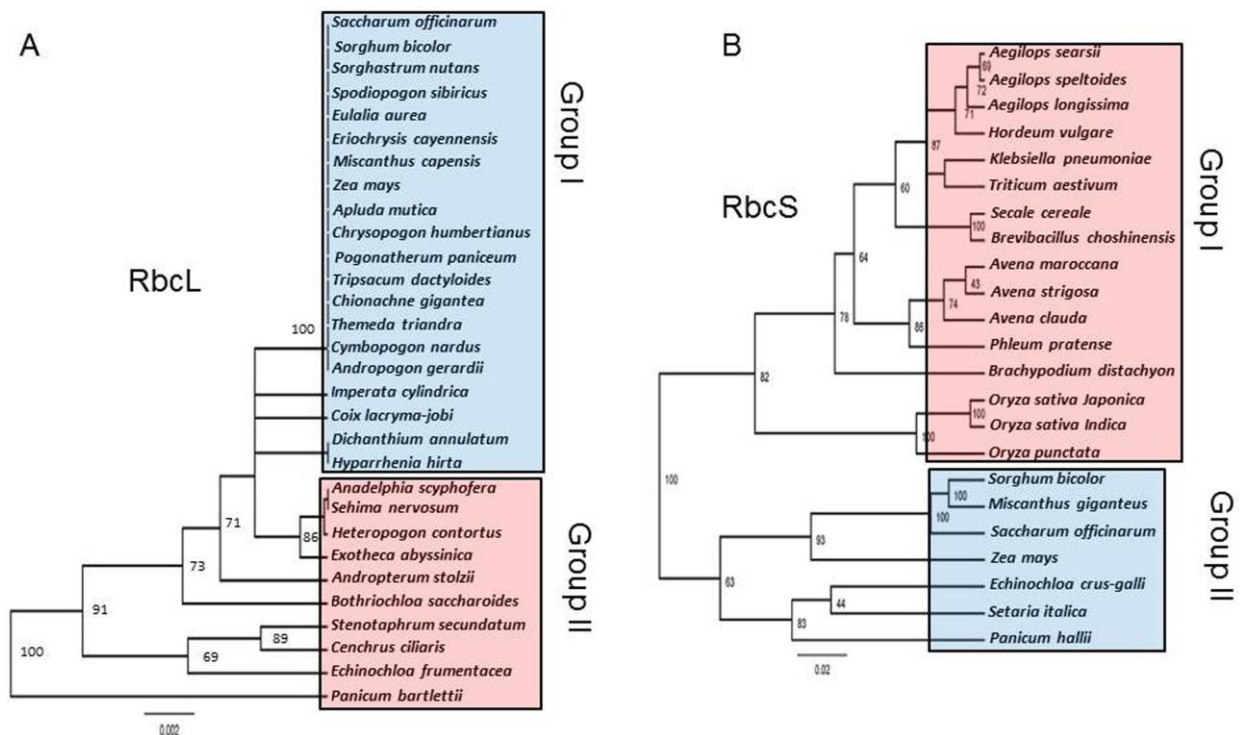


Fig. 2 Suppl. Phylogenetic analysis identified by BLASTP search was restricted to protein sequences of 10 genes related to enzymes involved in the Calvin cycle in sorghum and other plant species. Selected sequences from the plants were aligned using ClustalW, and the phylogenetic tree was inferred by using the maximum likelihood method using the Generious program. The scale bar shows the number of substitutions per amino acid. Bootstrap analysis of 500 replicates was performed. A - RbcL (ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit). YP_009389579.1[*Saccharum officinarum*], CAO94519.1[*Sorghum bicolor*], ABP01447.1[*Sorghastrum nutans*], CAH04931.1[*Imperata cylindrica*], CCC82899.1[*Spodiopogon sibiricus*], CAO94588.1[*Eulalia aurea*], YP_009245260.1[*Eriochrysis cayennensis*], CAJ86937.1[*Miscanthus capensis*], NP_043033.1[*Zea mays*], YP_009450767.1[*Apluda mutica*], CUU44311.1[*Chrysopogon humbertianus*], CAO94559.1[*Pogonatherum paniceum*], ATZ74756.1[*Tripsacum dactyloides*], CCD32651.1[*Chionachne gigantea*], YP_009384574.1[*Themeda triandra*], CUU44278.1[*Anadelphia scyphofera*], AIF72768.1[*Cymbopogon nardus*], ATZ74786.1[*Dichanthium annulatum*], CUU44348.1[*Exothea abyssinica*], CCC54994.1[*Sehima nervosum*], ATZ74783.1[*Andropterum stolzii*], YP_003208195.1[*Coix lacryma-jobi*], CCC82898.1[*Heteropogon contortus*], AAA80120.1[*Hyparrhenia hirta*], CAH04923.1[*Andropogon gerardii*], CAO94531.1[*Bothriochloa saccharoides*], ATZ74716.1[*Panicum bartlettii*], YP_009452455.1[*Stenotaphrum secundatum*], ATZ74751.1[*Echinochloa frumentacea*], ARJ58803.1[*Cenchrus ciliaris*], YP_003208195.1[*Coix lacryma-jobi*]. B - RbcS (ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit). Accession numbers of sequences are: BAJ40065.1[*Sorghum bicolor*], AFO59569.1[*Saccharum officinarum*], ABY66909.1[*Miscanthus giganteus*], CAA68419.1[*Zea mays*], AGJ76629.1[*Echinochloa crus-galli*], XP_004962302.1[*Setaria italica*], ASU47382.1[*Oryza punctata*], PAN20392[*Panicum hallii*], XP_015619408.1[*Oryza sativa Japonica*], EAY97115.1[*Oryza sativa Indica*], BAJ90202.1[*Hordeum vulgare*], XP_003576920.1[*Brachypodium distachyon*], WP_077271832.1[*Klebsiella pneumoniae*], AAC83374.1[*Avena clauda*], WP_083497141.1[*Brevibacillus choshinensis*], AAF07949.1[*Avena maroccana*], BAA35156.1[*Aegilops searsii*], AAC83373.1[*Avena strigosa*], BAA35161.1[*Secale cereale*], BAA35150.1[*Aegilops speltoides*], BAP82418.1[*Phleum pratense*], BAB19813.1[*Triticum aestivum*], BAA35151.1[*Aegilops longissima*].

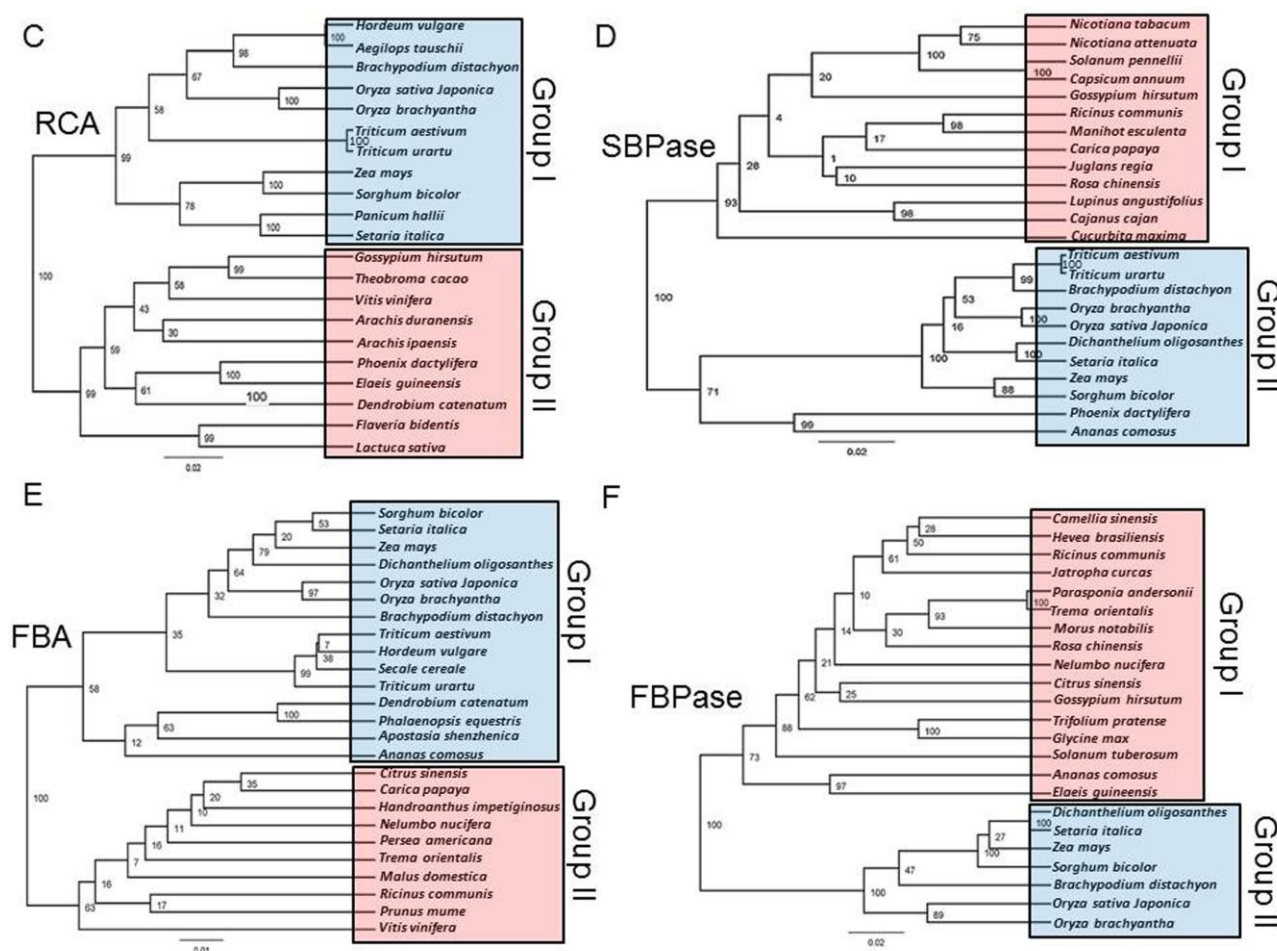


Fig. 2 Suppl. C - PGK 3-phosphoglyceric acid kinase. Accession numbers of sequences are: AQK86959.1 [*Zea mays*], NP_001347303.1 [*Glycine max*], OEL18219.1 [*Dichanthelium oligosanthos*], PNY13087.1 [*Trifolium pratense*], XP_002441313.1 [*Sorghum bicolor*], XP_002513353.1 [*Ricinus communis*], XP_003568189.1 [*Brachypodium distachyon*], XP_004139904.1 [*Cucumis sativus*], XP_004970259.1 [*Setaria italica*], XP_006422251.1 [*Citrus clementina*], XP_007213965.1 [*Prunus persica*], XP_008383150.1 [*Malus domestica*], XP_009763674.1 [*Nicotiana sylvestris*], XP_010269369.1 [*Nelumbo nucifera*], XP_010936574.1 [*Elaeis guineensis*], XP_015639410.1 [*Oryza sativa Japonica* Group], XP_015932386.1 [*Arachis duranensis*], XP_016170294.1 [*Arachis ipaensis*], XP_016707564.1 [*Gossypium hirsutum*], XP_019443705.1 [*Lupinus angustifolius*], XP_021298819.1 [*Herrania umbratica*], XP_021633936.1 [*Manihot esculenta*], XP_022149703.1 [*Momordica charantia*], XP_024157428.1 [*Rosa chinensis*]. D - GAPDH glyceraldehyde-3-phosphate dehydrogenase. Accession numbers of sequences are: AGT16863.1 [*Saccharum hybrid* cultivar R570], EMS58577.1 [*Triticum urartu*], NP_001105589.2 [*Zea mays*], OAY66532.1 [*Ananas comosus*], OEL15253.1 [*Dichanthelium oligosanthos*], PKA65492.1 [*Apostasia shenzhenica*], XP_002444416.1 [*Sorghum bicolor*], XP_003549550.1 [*Glycine max*], XP_003574540.1 [*Brachypodium distachyon*], XP_004973549.1 [*Setaria italica*], XP_006659448.1 [*Oryza brachyantha*], XP_010092210.1 [*Morus notabilis*], XP_010323179.1 [*Solanum lycopersicum*], XP_012442593.1 [*Gossypium raimondii*], XP_015650252.1 [*Oryza sativa Japonica* Group], XP_016200134.1 [*Arachis ipaensis*], XP_017408443.1 [*Vigna angularis*], XP_019231097.1 [*Nicotiana attenuata*], XP_019463393.1 [*Lupinus angustifolius*], XP_021276448.1 [*Herrania umbratica*], XP_021592506.1 [*Manihot esculenta*], XP_021650941.1 [*Hevea brasiliensis*], XP_022730068.1 [*Durio zibethinus*], XP_023733826.1 [*Lactuca sativa*]. E - TPI triose-3-phosphate isomerase. Accession numbers of sequences are: KHN39016.1 [*Glycine soja*], PON83414.1 [*Trema orientalis*], XP_002274871.1 [*Vitis vinifera*], XP_002529248.1 [*Ricinus communis*], XP_004147017.1 [*Cucumis sativus*], XP_004230885.1 [*Solanum lycopersicum*], XP_006423593.1 [*Citrus clementina*], XP_009140258.1 [*Brassica rapa*], XP_010090286.1 [*Morus notabilis*], XP_010268151.1 [*Nelumbo nucifera*], XP_010555242.1 [*Tarenaya hassleriana*], XP_010690445.1 [*Beta vulgaris* subsp. *vulgaris*], XP_011088504.1 [*Sesamum indicum*], XP_013450029.1 [*Medicago truncatula*], XP_013664312.1 [*Brassica napus*], XP_016208048.1 [*Arachis ipaensis*], XP_017612211.1 [*Gossypium arboreum*], XP_020425753.1 [*Prunus persica*], XP_021686085.1 [*Hevea brasiliensis*], XP_021819974.1 [*Prunus avium*], XP_022146193.1 [*Momordica charantia*], XP_022763099.1 [*Durio zibethinus*], XP_022987010.1 [*Cucurbita maxima*], XP_024167368.1 [*Rosa chinensis*]. F - FBA fructose-1,6-bisphosphate aldolase (also known as aldolase; ALD). Accession numbers of sequences are: ACO44683.1 [*Secale cereale*], ACO44684.1 [*Triticum aestivum*], ACO44685.1 [*Hordeum vulgare*], CAB77243.2 [*Persea americana*], EMS60368.1 [*Triticum urartu*], NP_001105336.2 [*Zea mays*], OEL13465.1

[*Dichanthelium oligosanthes*], PIN01633.1 [*Handroanthus impetiginosus*], PKA60228.1 [*Apostasia shenzhenica*], PKU74394.1 [*Dendrobium catenatum*], PON56017.1 [*Trema orientalis*], XP_002283381.1 [*Vitis vinifera*], XP_002453822.1 [*Sorghum bicolor*], XP_002528593.1 [*Ricinus communis*], XP_003564871.1 [*Brachypodium distachyon*], XP_004970966.1 [*Setaria italica*], XP_006481883.1 [*Citrus sinensis*], XP_006654377.1 [*Oryza brachyantha*], XP_008385438.1 [*Malus domestica*], XP_010243792.1 [*Nelumbo nucifera*], XP_015639252.1 [*Oryza sativa Japonica Group*], XP_020089073.1 [*Ananas comosus*], XP_021891171.1 [*Carica papaya*], XP_020577049.1 [*Phalaenopsis equestris*], XP_008241287.1 [*Prunus mume*].

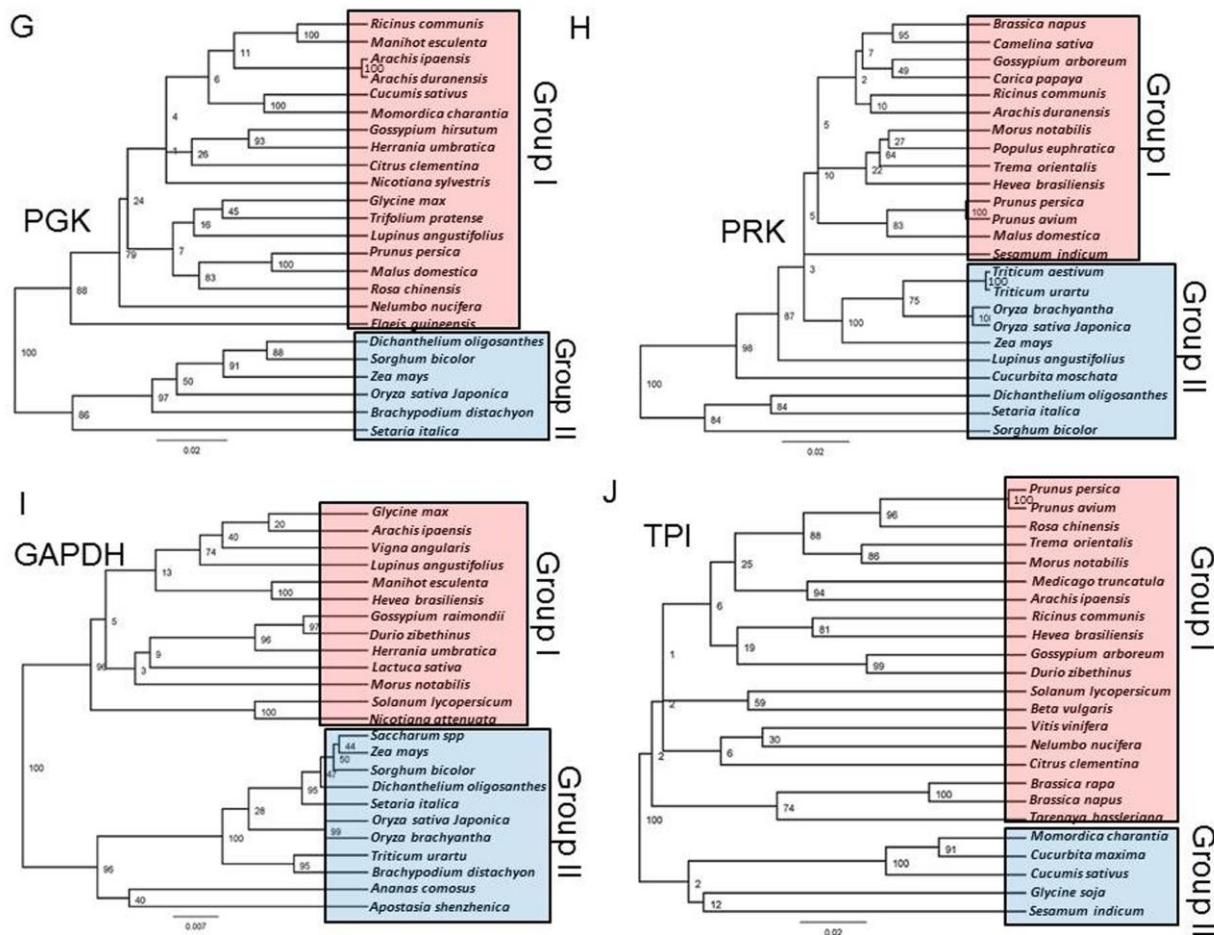


Fig. 2 Suppl. *G* - *FBPase* fructose-1,6-bisphosphate phosphatase. Accession numbers of sequences are: AHE93345.1 [*Camellia sinensis*], EXC43850.1 [*Morus notabilis*], NP_001147459.1 [*Zea mays*], OAY83076.1 [*Ananas comosus*], OEL23300.1 [*Dichanthelium oligosanthes*], PN94444.1 [*Trifolium pratense*], PON71828.1 [*Parasponia andersonii*], PON98347.1 [*Trema orientalis*], XP_002438805.1 [*Sorghum bicolor*], XP_002532766.1 [*Ricinus communis*], XP_003529262.1 [*Glycine max*], XP_003560409.1 [*Brachypodium distachyon*], XP_004965631.1 [*Setaria italica*], XP_006351721.1 [*Solanum tuberosum*], XP_006494687.1 [*Citrus sinensis*], XP_010254556.1 [*Nelumbo nucifera*], XP_010941718.1 [*Elaeis guineensis*], XP_012081371.1 [*Jatropha curcas*], XP_015642873.1 [*Oryza sativa Japonica Group*], XP_015693669.1 [*Oryza brachyantha*], XP_016715731.1 [*Gossypium hirsutum*], XP_021649834.1 [*Hevea brasiliensis*], XP_024168396.1 [*Rosa chinensis*]. *H* - *SBPase* sedoheptulose-1,7-bisphosphatase. Accession numbers of sequences are: AII99841.1 [*Nicotiana tabacum*], CBH32512.1 [*Triticum aestivum*], EMS67709.1 [*Triticum urartu*], NP_001148402.1 [*Zea mays*], OEL37223.1 [*Dichanthelium oligosanthes*], XP_002456647.1 [*Sorghum bicolor*], XP_002530415.1 [*Ricinus communis*], XP_003564625.1 [*Brachypodium distachyon*], XP_004970606.1 [*Setaria italica*], XP_006664812.1 [*Oryza brachyantha*], XP_008785431.1 [*Phoenix dactylifera*], XP_015076224.1 [*Solanum pennellii*], XP_015633459.1 [*Oryza sativa Japonica Group*], XP_016573389.1 [*Capsicum annuum*], XP_016742057.1 [*Gossypium hirsutum*], XP_018821822.1 [*Juglans regia*], XP_019259709.1 [*Nicotiana attenuata*], XP_019439410.1 [*Lupinus angustifolius*], XP_020102146.1 [*Ananas comosus*], XP_020211284.1 [*Cajanus cajan*], XP_021618564.1 [*Manihot esculenta*], XP_021904150.1 [*Carica papaya*], XP_022988647.1 [*Cucurbita maxima*], XP_022995950.1 [*Cucurbita maxima*], XP_024158398.1 [*Rosa chinensis*]. *I* - *PRK* ribulose-5-phosphate kinase. ACG42204.1 [*Zea mays*], CAA41020.1 [*Triticum aestivum*], EMS51337.1 [*Triticum urartu*], OEL23140.1 [*Dichanthelium oligosanthes*], PON94730.1 [*Trema orientalis*], XP_002448449.1 [*Sorghum bicolor*], XP_002519002.1

[*Ricinus communis*], XP_004976668.1 [*Setaria italica*], XP_006647733.1 [*Oryza brachyantha*], XP_007210511.1 [*Prunus persica*], XP_008373501.1 [*Malus domestica*], XP_010110407.1 [*Morus notabilis*], XP_011028086.1 [*Populus euphratica*], XP_011082329.1 [*Sesamum indicum*], XP_013660496.1 [*Brassica napus*], XP_015625719.1 [*Oryza sativa* Japonica Group], XP_015963222.1 [*Arachis duranensis*], XP_017607040.1 [*Gossypium arboreum*], XP_019091715.1 [*Camelina sativa*], XP_019423944.1 [*Lupinus angustifolius*], XP_021668642.1 [*Hevea brasiliensis*], XP_021830282.1 [*Prunus avium*], XP_021889428.1 [*Carica papaya*], XP_022923591.1 [*Cucurbita moschata*]. J - RCA Ribulose biphosphate carboxylase/oxygenase activase. Accession numbers of sequences are: AAA63163.1 [*Hordeum vulgare* subsp. *vulgare*], AAF71272.1 [*Triticum aestivum*], AAG61121.1 [*Gossypium hirsutum*], ABW80752.1 [*Flaveria bidentis*], EMS57011.1 [*Triticum urartu*], NP_001104921.1 [*Zea mays*], PAN43861.1 [*Panicum hallii*], XP_002270571.2 [*Vitis vinifera*], XP_002451328.1 [*Sorghum bicolor*], XP_007009268.1 [*Theobroma cacao*], XP_008801601.1 [*Phoenix dactylifera*], XP_010237360.1 [*Brachypodium distachyon*], XP_010923239.1 [*Elaeis guineensis*], XP_014661172.1 [*Setaria italica*], XP_015616897.1 [*Oryza sativa* Japonica Group], XP_015697867.1 [*Oryza brachyantha*], XP_015950170.1 [*Arachis duranensis*], XP_016190171.1 [*Arachis ipaensis*], XP_020172225.1 [*Aegilops tauschii* subsp. *tauschii*], XP_020694726.1 [*Dendrobium catenatum*], XP_023762211.1 [*Lactuca sativa*].