

Supplementary Materials: In Situ Dark Adaptation Enhances the Efficiency of DNA Extraction from Mature Pin Oak (*Quercus palustris*) Leaves, Facilitating the Identification of Partial Sequences of the 18S rRNA and Isoprene Synthase (*IspS*) Genes

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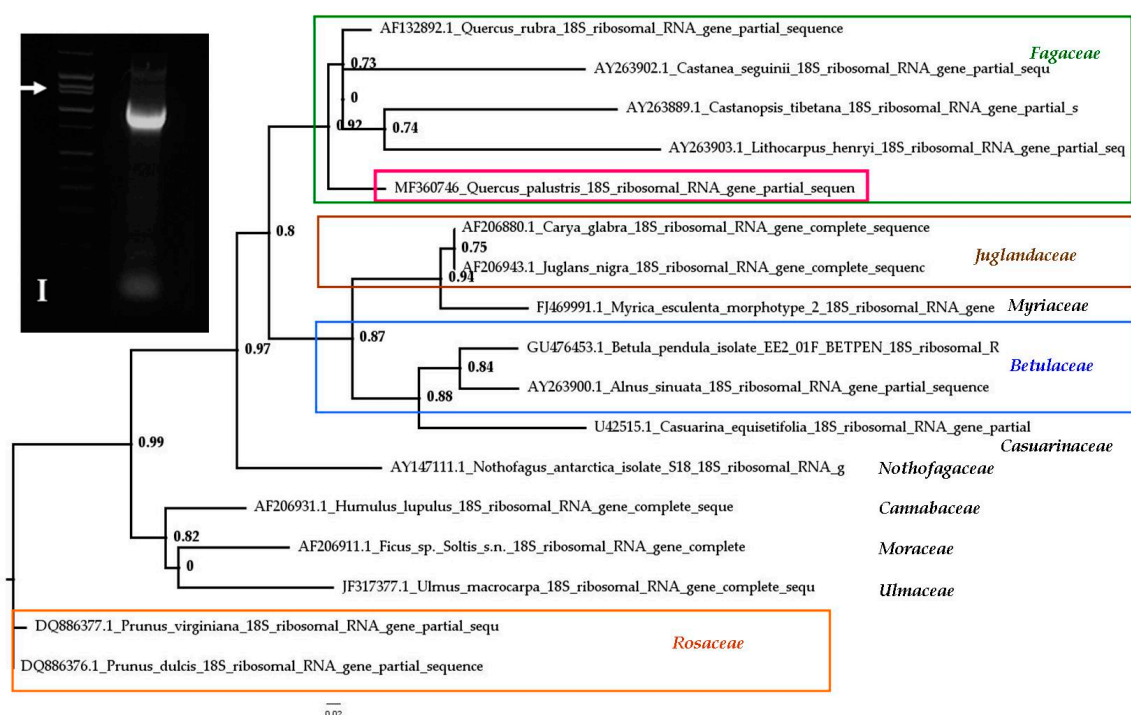


Figure S1. Phylogenetic relationship between the gene encoding for the 18S rRNA fragment (18S rDNA) identified in this study from pin oak (*Q. palustris*) leaves (Accession # MF360746) and other 18S rDNA sequences from families of the Fagales order. The phylogenetic tree was constructed based on maximum likelihood analysis. Bootstrap analysis was done with 1,000 replicates. Colored boxes enclose sequences of representative species belonging to distinct families (labeled with color identical to that of the boxes). Numbers at nodes represent confidence values for splits. Branch length is proportional to the number of substitutions per site. The figure inset (I) shows a representative example of the amplified 930 bp fragment of the gene encoding for the 18S rRNA, in a 2% agarose gel stained with 0.5µg/mL ethidium bromide. The fragment was excised from the gel, the DNA purified and sequenced for genomic sequence identification. The white arrow annotates the position of the 1400 bp marker band.

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AY263889.1	-----
AY263902.1	-----
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AF206911.1	-----TGCTTGTCTCAAAGATTAAGCCATGCATGTGTAAGTATGAACTAATTCAGAC
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DQ886377.1	-----
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U42515.1_C	-----AGANTAAGCCATGCATGTGTAAGTATGAACTAATTCAGAC
AY263900.1	-----
GU476453.1	-----
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AY263902.1	-----
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AY263900.1	-----
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AF206911.1	CTCGACGGATCGCACGGCCACCGTGCCGGCGACGCATCATTCAAATTTCTGCCCTATCAA
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JF317377.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTATGTTGGCCTTCGGGATCGGAGTA
DQ886376.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTCTGTTGGCCTTCGGGATCGGAGTA
DQ886377.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTCTGTTGGCCTTCGGGATCGGAGTA
AY147111.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTCTGTTGGCCTTCGGGATCGGAGTA
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GU476453.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTGTTGGCCTTCGGGATCGGAGTA
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FJ469991.1	TAGCATGGGATAACATCATAGGATTTCCGGTCCTATTGTTGGCCTTCGGGATCGGAGTA
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AY263902.1 ATGATTAAACAGGGACAGTCGGGGGCATTTCGTATTTCATAGTCAGAGGTGAAATTCCTTGGA
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JF317377.1 ATGATTAAACAGGGACAGTCGGGGGCATTTCGTATTTCATAGTCAGAGGTGAAATTCCTTGGA
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DQ886376.1	GAAAGTTGGGGGCTCGAAGACGATCAGATACCGTCCTAGTCTCAACCATAAACGATGCCG
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AY263902.1	ACCAGGGATCGGTGGATGTTACTTATAGGACTCCGCCGGCACATTATGAGAAATCAAAGT
AF132892.1	ACCAGGGATCGGCGGATGTTACTTATAGGACTCCGCCGGCACCTTATGAGAAATCAAAGT
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JF317377.1	ACCAGGGATCGGCGGATGTTGCTTATAGGACTCCGCCGGCACCTTATGAGAAATCAAAGT
DQ886376.1	ACCAGGGATCGGCGGATGTTACTTTTAGGACTCCGCCGGCACCTTATGAGAAATCAAAGT
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FJ469991.1	ACCAGGGATCGGCGGATGTTGCTTTAAGGACTCCGCCGGCACCTTATGAGAAATCAAAGT
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JF317377.1	TTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
DQ886376.1	TTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
DQ886377.1	TTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
AY147111.1	CTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
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AY263900.1	CTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
GU476453.1	CTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
AF206943.1	CTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
FJ469991.1	CTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGG
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AY263902.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
AF132892.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
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AF206911.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
JF317377.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
DQ886376.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
DQ886377.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
AY147111.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
U42515.1_C	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
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GU476453.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
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FJ469991.1	CACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTTACCAGGTC
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AY263902.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTNTATGGGTGGTGGTGCA
AF132892.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
MF360746_Q	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
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AF206911.1	CAGACATAGCAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
JF317377.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
DQ886376.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
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GU476453.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
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FJ469991.1	CAGACATAGTAAGGATTGACAGACTGAGAGCTCTTCTTGATTCTATGGGTGGTGGTGCA
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AY263902.1	TGGCCGTTCTTAGTTGGTGGAGTGATTTGTATGGTTAATTCGGTTAAGGAACGAGACCTC
AF132892.1	TGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
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AF206931.1	TGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
AF206911.1	TGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
JF317377.1	TGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
DQ886376.1	TGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
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FJ469991.1	TGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTC
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AY263902.1	AGCCTGCTAACTAGCTATGCGGAGGTGACCCTCCGCGGCCAGCTTCTTAGAGGGAATATG
AF132892.1	AGCCTGCTAACTAGCTATGCGGAGGTGACCCTCCGCGGCCAGCTTCTTAGAGGGAATATG
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AF206911.1	AGCCTGCTAACTAGCTATGCGGAGGATACCCTTCGCGGCCAGCTTCTTAGAGGGAATATG
JF317377.1	AGCCTGCTAACTAGCTATGCGGAGGTATCCCTCCGCGGCCAGCTTCTTAGAGGGAATATG
DQ886376.1	AGCCTGCTAACTAGCTATGCGGAGGAT - CCCTCCGCGGCCAGCTTCTTAGAGGGAATATG
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GU476453.1	AGCCTGTTAACTAGCTATGCGGAGGATCCCTCCGCGGCCAGCTTCTTAGAGGGAATATG
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AY263902.1	GCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGATGTTTCTG
AF132892.1	GCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGATGTTTCTG
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AF206911.1	GCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTG
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FJ469991.1	GGCCGCACGCGGCTACACTGATGTATTCAACGAGTTTATAGCCTTGCCCGCAGGCCCG
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AY263902.1	GGTAATCTTTGAAATTTTCATCGTAATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
AF132892.1	GGTAATCTTTGAAATTTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
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AF206911.1	GGTAATCTTTGAAATTTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
JF317377.1	GGTAATCTTTGAAATTTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
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AY147111.1	GGTAATCTTTGAAATTTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
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AF206943.1	GGTAATCTTTGAAATTTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACG
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AY263902.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AF132892.1	ARGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
MF360746_Q	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AF206931.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AF206911.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
JF317377.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
DQ886376.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
DQ886377.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AY147111.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
U42515.1_C	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AY263900.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
GU476453.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
AF206943.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT
FJ469991.1	GAGAATTTCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCCCTGCCCTTTG-
AF206880.1	AGGAATT-CCTAGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCC-TGCCCTTTGT

AY263903.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTC-----
AY263889.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
AY263902.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTC-----
AF132892.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
MF360746_Q	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
AF206931.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGAGGCGA
AF206911.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGAGGCGA
JF317377.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
DQ886376.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
DQ886377.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
AY147111.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTG-----
U42515.1_C	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
AY263900.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA
GU476453.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTG-----
AF206943.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGAGGCGA
FJ469991.1	-----
AF206880.1	ACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCCGATCGCGGCGA

AY263903.1	-----
AY263889.1	CG-GGGCGGTTTCGCTGCCGGCG------
AY263902.1	-----
AF132892.1	CGTGGGCGGTTTCGCTGCCGGCGACNTCGCGAGAAGTCCACTGAACCTTATCATTAGAG
MF360746_Q	CGTGGGCGGTTTCGCTGCCGGCGACGTCGCGAGAAGTCCACTGAACCTTATCATTAGAGG
AF206931.1	CGTGGGCGGTTTCGCTGCCGGCGACGTAGCGAGAAGTCCACTGAACCTTATCATTAGAGG
AF206911.1	CATGGGCGGTTCCGCTGCCCGTGACGTCGCGAGAAGTCCACTGAACCTTATCATTGAGAGG
JF317377.1	CGTGGGCGGTTTCGCTGCCGGCGACGTCGCGAGAAGTCCATTGAACCTTATCATTAG---
DQ886376.1	CGTGGGTGGTTTCGCTGCCGGCGACGTCGCGAGAAGTCCACTGAACCTTATCATT-----
DQ886377.1	CGTGGGTGGTTTCGCTGCCGGCGACGTCGCGAGAAGTCCACTGAACCTTATCATT-----
AY147111.1	-----
U42515.1_C	CGTGGGCGGTTTCGCTGCCGGCGACGTCGCGAGAAGTCCACTGAACCTTATCATTAG---
AY263900.1	CGTGGGCGGTTTCG-----
GU476453.1	-----
AF206943.1	TGTGGGCGGTTTCGCTGCCGGCAACGTCGCGAGAAGTCCACTGNACCTTATCATNTAGNGG
FJ469991.1	-----
AF206880.1	TGTGGGCGGTCCGCTGCCGGCAACGTCGCGAGAAGTCCACTGAACCTTATCATTAGAGG
AY263903.1	-----
AY263889.1	-----
AY263902.1	-----
AF132892.1	AAGGA-----
MF360746_Q	AAGGAGAAGTCGTAACAAG
AF206931.1	AAGGAGAA-----
AF206911.1	AAGGAGC-----
JF317377.1	-----
DQ886376.1	-----
DQ886377.1	-----
AY147111.1	-----
U42515.1_C	-----
AY263900.1	-----
GU476453.1	-----
AF206943.1	A-----
FJ469991.1	-----
AF206880.1	AAGGA-----

Figure S2. DNA sequence alignment of the 18S rDNA segments used for phylogenetic analyses (tree presented in Figure S1). The 18S rDNA segment identified for the first time in this study is highlighted in yellow. Nucleotide identity in given positions is denoted by the asterisk * at the bottom of the alignment.

(a)

5'AGTGTTCCTTATGGACAATGGGATTATTGTTTCAGCCACAATTTGGATATTTTAGGAGAAC
AATAGCAAAGTTCTTTGCACTAATAACAGTAATAGATGATATTTATGATGCATATGGCACTT
TGGAAGAACTGGAGTGCTTCACAAATGCTATCGAGAGATGGGA3'

(b)

BAD98243.1	MATELLCLHRPISLTHKLFRNPLP-----KVIQATPLTLKLRCVSTENVSFTETET
AAQ16588.1	MATELLCLHRPISLTHKLFRNPLP-----KVIQATPLTLKLRCVSTENVSFSETET
CAL69918.1	MATELLCLHRPISLTHKLFRNPLP-----KVIQATPLTLKLRCVSTENVSFTETET
AEK70970.1	MATELLCLHRPISLTPKLFNRNPLP-----KVILATPLTLKLRCVSTENVSFTETET
AAQ84170.1	MATNLLCLSNKLSSPTPTPSTRFPQSKNFITQKTS LANPKPWRVICATSSQFT--QITEH
CUR52979.1	MATNPSCSLSTPFLSSTPALSTRFPLSENFT-QKTSLVNPKPWPLISAVSSQFS--QIAED
AEK70968.1	-----
AEK70969.1	-----
BAS30551.1	--MIMATDQLLCMNPGCFFFAHKL-----TSQSARRPLQGIASSTSRPSQLVRCSA
BAS30550.1	MIHIMAT-ELLYMSPGCFFFAHKL-----TSQSARRPLQGIASSTSRPSQMVRCSA
AAP40638.1	-----MALRLLSTPHLP-----QLCSRRVSGRVHCSASTQVSDAQ----
BAF02831.1	-----MALRLLFTPHLP-----VLSSRRANGRVRCASASTQISDPQ----
UQP00000.1	-----
BAS30549.1	-MELSLAASLANCNFTRLLPSKTS-----ISLVSRRASIRPAVLCMAISETSTES
BAD98243.1	EARRSANYEPNSWDYDYLSSDTD-----ESIEVYKDKAKKLEAEVRREINNEKAEFLT
AAQ16588.1	ETRRSANYEPNSWDYDYLSSDTD-----ESIEVHKDKAKKLEAEVRREINNEKAEFLT
CAL69918.1	ETRRSANYEPNSWDYDYLSSDTD-----ESIEVYKDKAKKLEAEVRREINNEKAEFLT
AEK70970.1	ETRRSANYEPNSWDYDYLSSDTD-----ESIEVYKDKAKKLEAEVRREINNEKAEFLT
AAQ84170.1	NSRRSANYQPNLWNFEFLQSLEND-----LKVEKLEEKATKLEEEVRCMINRVDTQPLS
CUR52979.1	NSRRSANYHPNLWDFEFLQSLEND-----SKMEKLEEKATKLEEEVRNMMNEAKTEALS
AEK70968.1	---RSANYQPNLWNFEFLQSQEYD-----LMVETLQERATKLEEEVRRLINRVDTIEPLK
AEK70969.1	--RRSGNYQPNLWNFDLQSQKND-----LKEEMLQERAGKLEEEVRGLINEVDTEPLS
BAS30551.1	SQRLSANFQPSWSYDFLQSLEA-----YHVETYKEKVEKLEKEVKRMINKEDASLMT
BAS30550.1	DQRLSANYQPSWSYDFLQSLEA-----YHVETYKEKVEKLEKEVRHIINKEDASLMT
AAP40638.1	GGRRSANYQPSVWTYNYLQSLVADDIRRSRREVEQEREKAQILEEDVRGALNDGNAEPMA
BAF02831.1	EGRRSANYQPSVWTYNYLQSI VAGEGRQSRREVEQQKEKVQILEEEVRGALNDEKAETFT
UQP00000.1	-----
BAS30549.1	VVRRSANFQPAIWHYDFIQSLRSD-----YTEESCSQRIDKLKGEVRMMLQKA-VDPLE
BAD98243.1	LLELIDNVQRLGLGYRFESDIRRALDRFVS--SGGFDAVTKTSLHGTALSFRLLRQHGF-
AAQ16588.1	LLELIDNVQRLGLGYRFESDIRRALDRFVS--SGGFDGVTKTSLHGTALSFRLLRQHGF-
CAL69918.1	LPELIDNVQRLGLGYRFESDIRRALDRFVS--SGGFDAVTKTSLHATALSFRLLRQHGF-
AEK70970.1	LLELIDNVQRLGLGYRFESDIRRALDRFVS--SGGFDAVTKTSLHATALSFRFLRQHGF-
AAQ84170.1	LLELIDDVQRLGLTYKFEKDI I KALENIVL--LDENK-KNKS DLHATALSFRLLRQHGF-
CUR52979.1	LLELIDDVQRLGLTYKFEKDI I KALEKIVP--LDE-----SGLHVTSLSFRILRQHGF-

AEK70968.1	LLELVDNVQRLGLTYKFEDDINKALERIVS--LDE---REKSLGHATALIFRLLRQHGF-
AEK70969.1	LLELIDNVERLGLTYKFQEDINKALGRIVS--SDIN---KSLGHAAALTFRLLRQHGF-
BAS30551.1	TLELIDDIQRLGLGYRFEEEEIREALERISS--LEGFNSGIEKSLHATALGFRLLRQHGFN
BAS30550.1	TLELIDDIQRLGLGYRFEEDIRKALERISS--LEGFDSGIEKSLHAAALGFRLLRQHGFN
AAP40638.1	IFALVDDIQRLGLGRYFEEDISKALRRCLS--QYAVTGSLOKSLHGTALSFRVLRQHGF-
BAF02831.1	IFATVDDIQRLGLGDHFEEDISNALRRCVS--KGAVFMSLOKSLHGTALGFRLLRQHGY-
UQP00000.1	-----
BAS30549.1	RLELIDVLQRLGLSYHFDEEIQKILESIDANYGGKIPSNKENIYATALEFRLLRQLGY-
BAD98243.1	EVSQEAFSGFKDQNGNFLENLKEDIKAILSLYEASFLALEGENILDEAKVFAISHLKELS
AAQ16588.1	EVSQEAFSGFKDQNGNFLENLKEDIKAILSLYEASFLALEGENILDEAKVFAISHLKELS
CAL69918.1	EVSQEAFSGFKDQNGNFLKNLKEDIKAILSLYEASFLALEGENILDEAKVFAISHLKELS
AEK70970.1	EVSQEAFGGFKDQNGNFLENLKEDIKAILSLYEASFLALEGENILDEAKVFAISHLKELS
AAQ84170.1	EVSQDVFERFKDKEGGFSGELKGDVQGLLSLYEASYLGFEGENLLEEARTFSITHLKNNL
CUR52979.1	EVSQDVFKRFKDKEGGFCAELKDDVQGLLSLYEASYLGFEGESLLDEARAFSITHLKNNL
AEK70968.1	EVSQDVFESTRDKEGRFKAIEIKGDVQGLLSLYEASYLGFEGENLLDEAREFSMTHLKN-L
AEK70969.1	QISQDVFEKFKDKEGRFSAEIKGDVQGLLSLYEASYLGFEGENVLEEARAFSTTHLRN-I
BAS30551.1	YVSQDISKIIKDQNGSFKESLSKDVKGMLSLYEASHLAFQGESPWGEAREFTRTHLNDLI
BAS30550.1	YVSQDIFKIIKDQNGSIKESLSKDVKGMLSLYEASHLAFQGESLWDEAREFTRTHLNDLI
AAP40638.1	EVSQDVFKIFMDESGSFMKTLGGDVQGMMLSLYEASHLAFEEDILHKAKTFAIKHLENLN
BAF02831.1	EVSQDVFKIFLDESGSFVKTLGGDVQGVLSLYEASHLAFEEEEILHKARSFAIKHLENLN
UQP00000.1	-----
BAS30549.1	GVPQEIFNSFRNEQGNFKASLCDDIKGILCLYEASFLLEVEGETILEETRDFTTKQLKEYI
BAD98243.1	EKIGK-ELAEQVNHALELPLHRRRTQRLEAVWSIEAYRKKEDANQVLELAILDYNMIQS
AAQ16588.1	EKIGK-ELAEQVSHALELPLHRRRTQRLEAVWSIEAYRKKEDANQVLELAILDYNMIQS
CAL69918.1	EKIGK-DLAEQVNHALELPLHRRRTQRLEAVWSIEAYRKKEDADQVLELAILDYNMIQS
AEK70970.1	EKIGK-DLAEQVNHALELPLHRRRTQRLEAVWSIEAYRKKEDANQVLELAILDYNMIQS
AAQ84170.1	KEGINT-KVAEQVSHALELPYHRLRLEARNWFLDKYEPKEPHHQLLELAKLDFNMVQT
CUR52979.1	NKGINT-KVAQQVSHALELPYHRRLEARNWLLDKYEPKEPHHLLHELAKLDFNLVQS
AEK70968.1	NEGVVTPKLAEQINHALELPYHRRFQRLEARNWFIENYEVKEPHDRLLVELAKLDFNMVQS
AEK70969.1	KQGVST-KMAEQISHALELPYHRRLQRLEARRFIDKFEIKEPQDRLLLELAKLDFNMVQT
BAS30551.1	RSGDLSKDVAAEIRHALELPLHQRMNRLEARRYIEGYAKRSDANRVLLEFAKWDFNMVQS
BAS30550.1	RSDDLKDVAAEIRHALELPLHQRMNRLEARRYIEGYAKRSDANRVLLEFAKWDFNMVQS
AAP40638.1	--HDIDQLQDHVNHELELPLHRRMPLLEARRFIEAYSRRSNVNPRIELAVMKFNSSQL
BAF02831.1	--SDVDKDLQDQVKHELELPLHRRMPLLEARRSIEAYSRRGYTNPQILELALTDFNVSQS
UQP00000.1	-----
BAS30549.1	KQSTDE-NLTDLVSHALEVPLHWRMLRLETRRFIDVYRSREDANPILLELATLDFNLVQT
BAD98243.1	VYQRDLRETSRWRRVGLATKLHFARDRLIESFYWAVGVAFEPQYSDCRNSVAKMFSFVT
AAQ16588.1	VYQRDLRETSRWRRVGLATKLHFARDRLIESFYWAVGVAFEPQYSDCRNSVAKMFSFVT
CAL69918.1	VYQRDLRETSRWRRVGLATKLHFARDRLIESFYWAVGVAFEPQYSDCRNSVAKMFSFVT

AEK70970.1	VYQRDLRETSRWRRVGLATKLHFARDRLIESFYWAVGVAFEPQYSDCRNSVAKMFSFVT
AAQ84170.1	LHQKELQDLSRWWTETMGLASKLDFVRDRLMEVYFWALGMAPDPQFGECKRAVTKMFGGLVT
CUR52979.1	LYQKELRELSLWWREIGLTSKLDLDFVRDRLMEVYFWALGMAPDPQFSECKRVVTKMFGGLVT
AEK70968.1	LQKKEVGELSRWWKEIGLTSKLDLDFVRDRLVEVYFWASGMAPDPQLSECKRAVTKMFGGLVT
AEK70969.1	LQKELRDLRSRWWEIGLARKMEFVRDRLMEVYFWAVGMAPDPLSDCRKAIKMGGLVT
BAS30551.1	TLQNDLKDLRSWWKEVGLTNKLSFARDRLVESFFWSVGMAFEPQYSRLREELTKVFAFVT
BAS30550.1	TLQNDLKDLRSWWKDVGLTNKLSFARDRLVESFFWSVGMAFEPQYSRLREELTKVFAFVT
AAP40638.1	TLQRDLQDMLGWNNVGLAKRLSFARDRLMECFFWAVGIAREPALSNCRKGVTKAFSLIL
BAF02831.1	YLQRDLQEMLGWNNNTGLAKRLSFARDRLIECFFWAVGIAHEPSLSICRKAVTKAFALIL
UQP00000.1	-----CFLWTMGLLFQPPQFGYFRRTIAKFFALIT
BAS30549.1	SHQEDVKEISRWWKNTGLGEKLSFARDRLMESFLWSAGVMFPQPYGYSRRIFTKIFALIT
	: *: *: *: * . * . : * * . :
BAD98243.1	IIDDIYDVYGTLDLELELFTDAVERWDVNAINDLPDYMKLCFLALYNTINEIAYDNLKDKG
AAQ16588.1	IIDDIYDVYGTLDLELELFTDAVERWDVNAINDLPDYMKLCFLALYNTINEIAYDNLKDKG
CAL69918.1	IIDDIYDVYGTLDLELELFTDAVERWDVNAIDDLPDYMKLCFLALYNTINEIAYDNLKDKG
AEK70970.1	IIDDIYDVYGTLDLELELFTDAVERWDVNAINDLPDYMKLCFLALYNTINEIAYDNLKEKG
AAQ84170.1	IIDDVYDVYGTLDLQLFTDAVERWDVNAINTLPDYMKLCFLALYNTVNDTSYSILKEKG
CUR52979.1	IIDDVYDVYGTLDLQLFTDAVERWDVNAINTLPDYMKLCYLALYNTVNDTAYSILKEKG
AEK70968.1	IIDDVYDVYGTLDLELELFTNAVERWDVNAVDTLPDYMKLCFFALYNTVNDTAYNLLKEKG
AEK70969.1	IIDDVYDVYGTLDLQLFTDAVERWDVNALDTLPDYMKLCFLALYNTVNDTAYSLLRERG
BAS30551.1	VIDDVYDVYGTVDELELFTDAIERWDVQAVQNLPAYMRICFLALYSTVNDLVYETLKERD
BAS30550.1	VIDDVYDVYGTVDELELFTDAIERWDVQAVQNLPDYMRIKFLALYNTVNDLVYETLKERD
AAP40638.1	VLDDVYDVFGTLDELELFTDAVRRWHEDAVENLPGYMKLCFLALYNSVNDMAYETLKETG
BAF02831.1	VLDDVYDVFGTLEELFTDAVRRWDLNAVEDLPVYMKLCYLALYNSVNEMAYETLKEKG
UQP00000.1	VIDDIYDAYGTLEELCFTNAIERW-----
BAS30549.1	ILDDVYDVYGTLDLELELFTNAIERWDTNTIDQLPYMKICFLTLHNSINEIAYDILRERG
	:: **: ** . : *: *: *: *: *: *: *: *: *: *
BAD98243.1	ENILPYLTKAWADLCNAFLQEAKWLYNKSTPTFDDYFGNAWKSSSGPLQLVFAYFAVVQN
AAQ16588.1	ENILPYLTKAWADLCNAFLQEAKWLYNKSTPTFDDYFGNAWKSSSGPLQLIFAYFAVVQN
CAL69918.1	ENILPYLTKAWADLCNAFLQEAKWLYNKSTPTFDEYFGNAWKSSSGPLQLVFAYFAVVQN
AEK70970.1	ENILPYLTKAWADLCNAFLQEAKWLYNKSTPTFDDYFGNAWKSSSGPLQLVFAYFAVVQN
AAQ84170.1	HNNLSYLTWSRELCKAFLQEAKWSNNKIIPAFSKYLENASVSSSGVALLAPSYFVCQQ
CUR52979.1	HNNISYLTWSCELCKAFLQEAKWSNNKIIPAFNKYLDNASVSSSGVALLAPSYFLVCQE
AEK70968.1	DNNLPYLAKSWSDLCKAFLQEAKWSNNKIIPSFNKYIENASVSSSGGALLTPCYFSIRQ-
AEK70969.1	DNSLPYLAKSWSELCKAFLQEAKWSNKKTIPEFREYLDNASVSSSGGALLTPCYFSLITQ
BAS30551.1	EYILPYLTKAWADMCKAFLQEKKWTQNEETPSFEDYLENGWRSSSGGVFLVNAYLLMSQD
BAS30550.1	EYILPYITKAWADMCKAFLQEKKWTQNKETPSFEDYLENGWMSSSGGVFLVNSYLLVSQD
AAP40638.1	ENVTPYLTKVWYDLCKAFLQEAKWSYNKITPGVEEYLNNGWVSSSGQVMLTHAYFLSSPS
BAF02831.1	ENVIPYLAKAWYDLCKAFLQEAKWSNSRIIPGVEEYLNNGWVSSSGSVMLIHAYFLASPS
UQP00000.1	-----
BAS30549.1	VNVIPSLRKVWTDLCRSFLLEATWYHKKHTPTFEEYLQNAWVSVLGPSVLHVHYSITNP

BAD98243.1	--- IKKE --- E I E N L Q K Y H D T I S R P S H I F R L C N D L A S A S A E I A R G E T A N S V S C Y M R T K -
AAQ16588.1	--- IKKE --- E I E N L Q K Y H D I I S R P S H I F R L C N D L A S A S A E I A R G E T A N S V S C Y M R T K -
CAL69918.1	--- IKKE --- E I D N L Q K Y H D I I S R P S H I F R L C N D L A S A S A E I A R G E T A N S V S C Y M R T K -
AEK70970.1	--- IKKE --- E I E N L Q K Y H D I I S R P S H I F R L C N D L A S A S A E I A R G E T A N S V S C Y M R T K -
AAQ84170.1	Q E D I S D H --- A L R S L T D F H G L V R S S C V I F R L C N D L A T S A A E L E R G E T T N S I I S Y M H E N D
CUR52979.1	Q - D I S D Q --- A L H S L T N F H G L V R S S C T I F R L C N D L A T S S A E L E R G E T T N S I T S Y M H E N -
AEK70968.1	--- D I T N Q --- A L D S L T N Y H G P V R S S C A I F R L C N D L A T S A A E L E R G E T T N S I T S Y M Q D N -
AEK70969.1	D V A V T S Q F H S S T I D S L T N F H G V V R S S C T I F R L C N D L A T S A A E L E R G E T T N S I T S Y M R E K -
BAS30551.1	--- F T K Q --- G L E S L E N Y H N L L R W P S I I F R L N D L A T S S A E L E R G E T T N S I S C I M S D T -
BAS30550.1	--- I T K Q --- G L E S L E N Y H N L L R W P S I I F R L T N D L A T S S A E L E R G E T T N S I S C I M S D T -
AAP40638.1	--- L R K E --- E L E S L E H Y H D L L R L P S L I F R L T N D L A T S S A E L G R G E T T N S I L C Y M R E K -
BAF02831.1	--- I R K E --- E L E S L E H Y H D L L R L P S L I F R L T N D I A S S S A E L E R G E T T N S I R C F M Q E K -
UQP00000.1	-----
BAS30549.1	--- I T E E --- T T R F L E E Y P N I I R W S S T I F R L N D L E T S E D E I E R G D V S K S L Q C Y M H E T -

BAD98243.1	G I S E E L A T E S V M N L I D E T W K K M N K E K L G G S L - F A K P F V E T A I N L A R Q S H C T Y H N G D A H T S
AAQ16588.1	G I S E E L A T E S V M N L I D E T W K K M N K E K L G G S L - F A K P F V E T A I N L A R Q S H C T Y H N G D A H T S
CAL69918.1	G I S E E L A T E S V M N L I D E T W K K M N K E K L G G S L - F A K P F V E T A I N L A R Q S H C T Y H N G D A H T S
AEK70970.1	G I S E E L A T E S V M N L I D E T W K K M N K E K L G G S L - F P K P F V E T A I N L A R Q S H C T Y H N G D A H T S
AAQ84170.1	G T S E E Q A R E E L R K L I D A E W K K M N R E R V S D S T L L P K A F M E I A V N M A R V S H C T Y Q Y G D G L G R
CUR52979.1	E T S E E Q A C K E L R N L I D A E W K K M N E E R V S N S T - L P K A F R E I A I N M A R I S H C T Y Q Y G D G L G R
AEK70968.1	G I S E E Q A R D E L R N L I D A E W K Q I N R E R V F D Q T - F P K A F I E T A I N M A R V S H C T Y Q Y G D G L G R
AEK70969.1	G V G E E E A R E E L S K L I D V E W M K L N R E R V L D I G P F P K A F M E T A V N M A R V S H C T Y Q H G D G L G R
BAS30551.1	G L S E E S A R Q H L T N L I E E T W K Q M N K D T M S G E S P F T K P F M E T A I N L A R I A Q C Q Y Q H G D G H G N
BAS30550.1	G L S E E S A R Q H L R N L I E E T W K Q M N K G T M S G E S P F T K P F M E T A I N L A R I A Q C Q Y Q H G D G H G N
AAP40638.1	G F S E S E A R K Q V I E Q I D T A W R Q M N K - Y M V D H S T F N R S F M Q M T Y N L A R M A H C V Y Q D G D A I G A
BAF02831.1	G I S E L E A R E C V K E E I D T A W K K M N K - Y M V D R S T F N Q S F V R M T Y N L A R M A H C V Y Q D G D A I G S
UQP00000.1	-----
BAS30549.1	G K S Q E E S R K Y I S S L I E T T W K K M N K E R A V G S S - L F Q T Y V E I G I N L A R T A Q C M Y Q H G D G L S V

BAD98243.1	PDELTRKRVLSVITEPILPFER---
AAQ16588.1	PDELTRKRVLSVITEPILPFER---
CAL69918.1	PDELTRKRVLSVITEPILPFER---
AEK70970.1	PDELTRKRVLSVITEPILPFER---
AAQ84170.1	PDYATENRIKLLLLIDPFPINQLMYV
CUR52979.1	PDYTTENRIKLLLLIDPFPIN-----
AEK70968.1	PDNTAENRIKLLLLIDPFPPI-----
AEK70969.1	PDNTAQNRIKLLLLNPIPS-----
BAS30551.1	PDTKSKNRVLSLIIDPIK-----
BAS30550.1	PDTKSKNRVLSLIIDPIK-----
AAP40638.1	PDDQSWNRVHSLIIKPVSLAPC---
BAF02831.1	PDDLSDNRVHSLIIKPISPAA----
UQP00000.1	-----
BAS30549.1	SDRETKDRIQSVLINPIPLR-----

Figure S3. *IspS* DNA sequence and protein sequence alignment. (a) DNA sequence of the 165 bp segment of the gene (*IspS*) encoding for the isoprene synthase protein in pin oak (*Quercus palustris*), identified for the first time in this study. (b) protein sequence alignment of the pin oak *IspS* protein segment and known *IspS* proteins of other species, used for phylogenetic analyses (tree presented in Figure 6). The *Quercus palustris* *IspS* segment is highlighted in yellow. Amino acid identity in given positions is denoted by the asterisk * at the bottom of the alignment. The amino acid F338 unique to isoprene synthases is highlighted in bold in the novel pin oak segment. Also highlighted is the highly conserved DDXXD sequence.