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Protocol Note

Annotation and re-sequencing of genes from de novo transcriptome assembly of *Abies alba* (Pinaceae)[1]

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- *Premise of the study:* We present a protocol for the annotation of transcriptome sequence data and the identification of candidate genes therein using the example of the nonmodel conifer *Abies alba*.
- *Methods and Results:* A normalized cDNA library was built from an *A. alba* seedling. The sequencing on a 454 platform yielded more than 1.5 million reads that were de novo assembled into 25 149 contigs. Two complementary approaches were applied to annotate gene fragments that code for (1) well-known proteins and (2) proteins that are potentially adaptively relevant. Primer development and testing yielded 88 amplicons that could successfully be resequenced from genomic DNA.
- *Conclusions:* The annotation workflow offers an efficient way to identify potential adaptively relevant genes from the large quantity of transcriptome sequence data. The primer set presented should be prioritized for single-nucleotide polymorphism detection in adaptively relevant genes in *A. alba*.

Key words: *Abies alba*; adaptation; annotation; candidate genes; de novo sequencing; Pinaceae.

To gain insights into the molecular level of adaptation, attention has turned to the investigation of adaptively relevant genes (candidate genes). For nonmodel organisms, access to candidate genes is limited and the transfer of primers, e.g., from expressed sequence tag (EST) libraries, if available, requires high labor costs. For instance, the resequencing of 800 genes selected from more than 7000 ESTs from *Pinus taeda* L. yielded only 70 candidate genes for *Abies alba* Mill. (Mosca et al., 2012). Because sequencing costs are decreasing rapidly, de novo sequencing in nonmodel organisms is now achievable. For the identification of candidate genes in de novo–sequenced organisms, the use of differential expression profiling (e.g., Street et al., 2006; Huang et al., 2012) can be performed, but it requires the sequencing of several samples. The sequencing of a single transcriptome, in contrast, is very cost-effective. However, the reduction of the data remains challenging. Blasting against available databases is the standard method, which results in outputs of large quantities and is therefore mainly used for annotation only (e.g., Parchman et al., 2010). Here, we present a protocol for the efficient reduction of transcriptomic data down to 283 candidate gene sequences that were used for immediate primer development. The protocol is applicable for species that lack genomic resources. It combines a standard and a specific annotation approach and led to the resequencing of 88 gene fragments in *A. alba*.

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METHODS AND RESULTS

A normalized transcriptome of a 1-yr-old *A. alba* seedling from the Black Forest (Forest District Calw, Germany; voucher MB-P-001007, Herbarium Marburgense, University of Marburg) was sequenced on a 454 GS FLX Titanium platform (cDNA library preparation: Vertis Biotechnology AG, Freising, Germany; sequencing: Genoscreen, Lille, France). The 454 run yielded 1 521 698 reads with an average length of 359 nucleotides (nt). Trimming and de novo assembly of the raw reads into contigs using Newbler software version 2.3 (454 Life Sciences, Branford, Connecticut, USA) resulted in 25 149 contigs consisting of 381 808 complete and 619 615 partially assembled reads. The contig length was between 100 nt and 2394 nt, with an average length of 498 nt. A total of 484 576 reads remained as singletons (Table 1). Contigs were submitted to the Transcriptome Shotgun Assembly database (TSA) at the National Center for Biotechnology Information (NCBI) (accession no.: JV134525–JV157085).

In the specific approach (Fig. 1), we tested a novel annotation protocol: After a literature survey with key words "adaptation," "candidates," "drought," "evolution," "RT-PCR," and "selection" in various combinations using the Web of Science database, we selected 5349 unique proteins and downloaded them from UniProt or NCBI (downloaded in November 2011). The proteins were subsequently searched against the contigs coming from the de novo transcriptome sequencing that were formatted as the reference database using the BLAST+ 2.2.24 toolkit (tBLASTn parameters: softmasking = threshold 15 max_target_seqs 10 000). To increase reliability of alignments and to avoid too-short amplicons, only alignments with a length of at least 100 amino acids and an identity of at least 90% were considered further. From the contigs that passed the filter, 157 were selected for primer design. In the standard approach (Fig. 1), contigs were searched against the refseq_protein database (downloaded from NCBI 14 June 2011) with strict BLAST-settings (BLASTx parameters: threshold 999, window-size 4, gapopen 32767, gapextend 32767, *E*-value $1e^{-20}$) (Altschul et al., 1990). Gene ontologies (Ashburner et al., 2000) were assigned to contig-protein hits using Blast2GO 2.5.0 (Conesa et al., 2005) and subsequently filtered as described above. To select for well-described proteins, contig sequences were used for primer design if they could be assigned to enzyme IDs with the Kyoto Encyclopedia of Genes and Genomes (KEGG) (Ogata et al., 1999) in the final annotation step. Primers were developed specifying the amplified range according to the contig-protein alignment boundaries using default standard PCR settings of PerlPrimer (version 1.1.12; Marshall, 2004). Primers were tested in a 30 µL PCR reaction with 17.28 µL double-distilled water, 3 µL 10× PCR buffer with $MgCl_2$ (20 mM), 1.2 µL $MgCl_2$ (25 mM), 3 µL Primermix (forward and reverse each 2 µM), 1.44 µL dNTPs (each 5 mM),

TABLE 1. Statistics of the 454 transcriptome sequencing run and metrics of the Newbler assembly software.

Sequence type	Number	%	Nucleotides	Average (nt)	Size (nt) in quantiles				
					0%	25%	50%	75%	100%
Reads trimmed	1 521 698	100	546 346 058	359.0	<21	<303	<395	<444	<1088
Reads assembled	381 808	25.1							
Reads partial	619 615	40.7							
Reads singleton	484 576	31.8	175 198 711	361.6	<50	<307	< 397	< 443	<876
Reads repeat	1617	0.1							
Reads outlier	20 389	1.3							
Reads too short	13 693	0.9							
Contigs	25 149		12 511 848	498	<100	<365	<468	<601	<2394
N50 Contig[a]			704						

[a] Half of all bases are assembled in contigs of this size or longer.

0.24 µL bovine serum albumin (BSA) (20 mg mL^{-1}), 0.24 µL Dream *Taq* polymerase (5 U µL^{-1}, Fermentas, St. Leon-Rot, Germany), and 3.6 µL DNA (10 ng µL^{-1}). The PCR was performed with 5 min initial denaturation at 94°C followed by 35 repetitions of 45 s denaturation at 94°C, 45 s annealing at 52–59°C, 45 s elongation at 72°C, and a 10 min final elongation at 72°C. For the amplification test, four samples were randomly chosen for each gene from a set of 80 different silver fir trees that were sampled in May 2011 in Mont Ventoux (44°10′44.35″N, 5°14′32.29″E, France). Amplification was evaluated by electrophoresis in 1% agarose gels. When amplification was too weak, the volume of $MgCl_2$ was increased to 1.8 µL. When faint ancillary bands appeared, no additional magnesium was added to the mastermix. If PCR products occurred as a single band, one sample was chosen for sequence analysis in each case to ensure that the region of interest was amplified (LGC Genomics GmbH, Berlin, Germany). Gene sequences were aligned to the corresponding contigs using the CodonCode Aligner software (default large gap settings) to reveal the location of the introns. The gene sequences were searched against the nr nucleotide database of NCBI (default discontiguous megaBLAST settings, web application).

In the specific approach, tBLASTn and subsequent sorting led to 321 contigs. For primer development, 185 contigs were picked. In the standard approach, the initial number of contigs was decreased to one third after the BLASTx step. Approximately half of the hits could be further annotated with Gene Ontologies. After filtering, 126 contigs were successfully assigned to enzyme-IDs and used for primer design (Fig. 1). In combination, 283 different contigs were annotated and only 28 were annotated with both approaches. Primer testing and sequencing resulted in 88 gene sequences (Table 2). Fifty-seven genes were annotated using the specific approach, and 42 using the standard approach. Eleven were annotated by both approaches. The assembly of the gene sequences and the corresponding cDNA contigs revealed 43 introns in 26 genes. The length of the gene sequences ranged from 262 to 1486 nt. All gene sequences aligned to sequences from the nr nucleotide database (NCBI) where the highest *E*-value was 5.00e^{-32}. Twelve gene sequences hit organelle DNA (10 chloroplast, one mitochondrial, and one ribosomal). The remaining 76 are involved in the biosynthesis of different compounds (21), regulation (20), primary metabolism (14), growth (11), stress response (8), and water transport (2). In the biosynthesis group, enzymes from the auxin pathways, the phenylpropanoid pathways, and the tetrapyrrol pathways were dominant. With the exception of the primary metabolism group, all groups included candidates for the analysis of adaptation at gene level that had been investigated in previous studies of conifers (e.g., González-Martínez et al., 2006).

CONCLUSIONS

The two approaches of the workflow are complementary, each contributing approximately half of the annotations in the final set of sequences. The standard approach can be run rapidly, but targets only well-known genes. The specific approach based on a review of the relevant literature is novel and provided a substantial amount of nonredundant annotations. As an advantage, it can be easily adjusted and extended freely to the researcher's interest. The quality-tested primers can be used for assessing the degree of gene polymorphism in ecological genetics studies.

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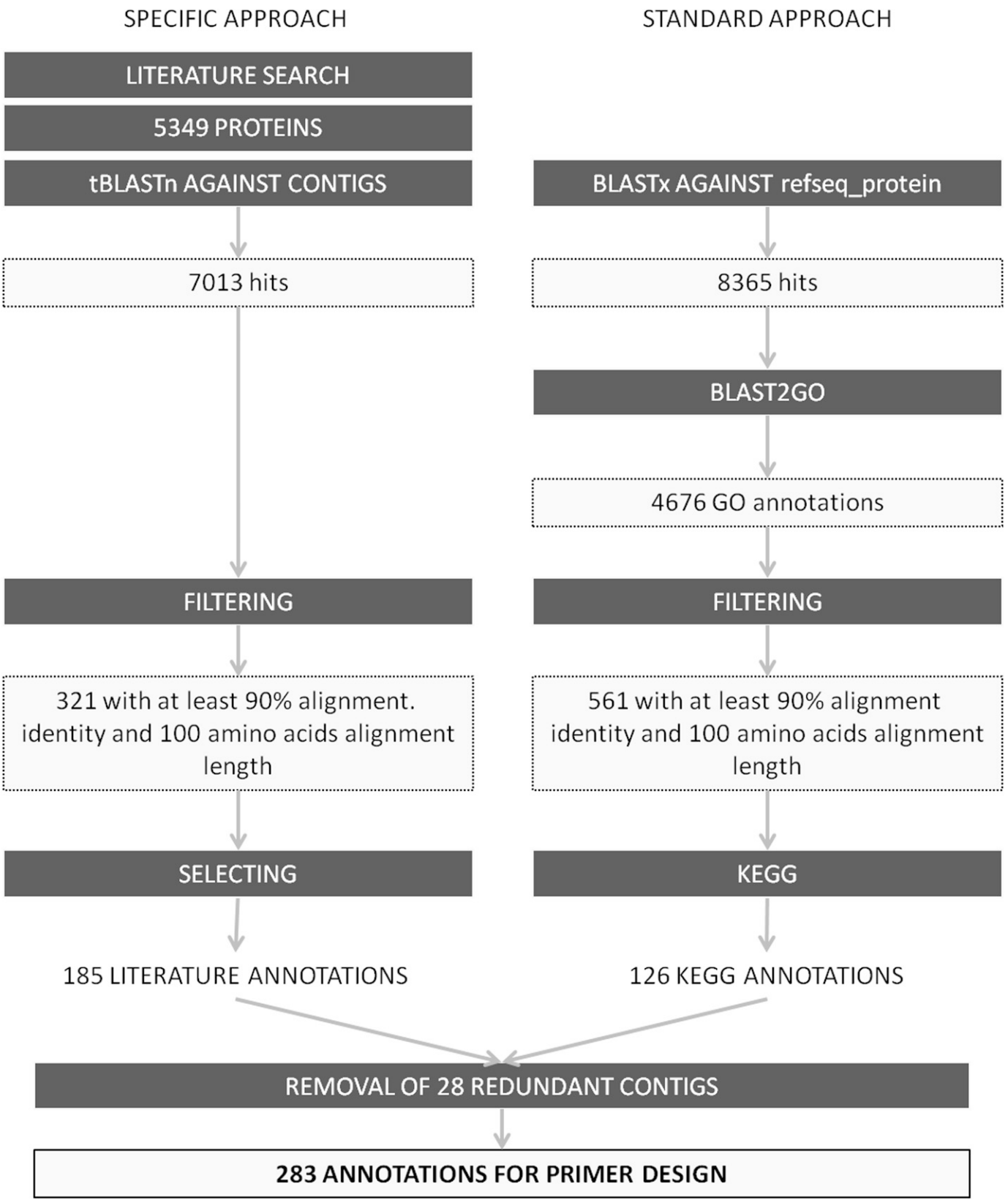

Fig. 1. Workflow of the annotation protocol. Numbers of the output after each step are given. The standard approach starts with 25 149 contigs. The specific approach uses them as the reference database for the tBLASTn step.

TABLE 2. Primers for resequencing of annotated gene fragments in *Abies alba*.[a]

Gene Locus ID	Primer sequences (5′–3′)	T_a (°C)	No. of introns	Intron length (nt)	Total length (nt)	Annotation approach	BLASTn of gene sequences against nr nucleotide database (*E*-value)	GO-ID biological process
95	F: ACAGAAACTAAAGCTAGTGTCG R: CCTTAATTTCACCCGTCTCAG	57	0	—	696	1	*Keteleeria davidiana* chloroplast DNA, complete sequence (0)	reductive pentose-phosphate cycle, photorespiration, oxidation reduction
215	F: CCAAGGACTCTGATCGAATCC R: GAAGCCAGCATTCAAAGACTC	56	2	411	1486	2	*Abies firma* clone 1 4-coumarate:CoA ligase (4CL) gene, partial cds (0)	response to UV, response to wounding, phenylpropanoid metabolic process, response to fungus
241	F: AACGTCCGTTAATACTTCGG R: AGTAAGTGTAGCCCTTCACG	56	3	256	1370	2	*Arabidopsis thaliana* fructose-bisphosphate aldolase, class I (FBA1) mRNA, complete cds (1E-125)	glycolysis
323	F: AAGCAAGCTTCTGAAATTCC R: TGGTAGAGTCTACCAAATGAG	53	2	278	804	1	*A. thaliana* plasma membrane H+-ATPase gene, complete cds (1E-90)	auxin biosynthetic process, ATP biosynthetic process, proton transport
1362	F: GAAGAGGTAGCTGCATTGGT R: GGGCTTATACCGTAAATATACCCA	59	0	—	871	1	*Ricinus communis* processing-splicing factor, putative, mRNA (0.0)	response to hypoxia, sucrose biosynthetic process, nuclear mRNA splicing, via spliceosome
1704	F: CAACTACTTCAGAGACAGAC R: AAAGATTCCCTCCAAATCAG	52	2	327	858	2	*Pinus taeda* mitogen-activated protein kinase 13 (MAPK13) mRNA, complete cds (2E-84)	
2387	F: TAAATGGCTCAATTCCTCCTACTG R: GTTCCAAGCTTCCACAATACTC	61	1	128	624	1	*Medicago truncatula* Alpha-1,4-galacturonosyltransferase (MTR_7g075840) mRNA, complete cds (8E-99)	
2565	F: GTGTCTGGAAGGGAATACAAGG R: CCTTGACTCCTTCATGGATCAG	58	0	—	432	1	PREDICTED: *Vitis vinifera* adenosylhomocysteinase-like, transcript variant 1 (LOC100253872), mRNA (1E-109)	embryonic development ending in seed dormancy, one-carbon metabolic process, posttranscriptional gene silencing, methylation-dependent chromatin silencing
2774	F: GTTACAGGAAGCCTTTCTGG R: GCGGGATGAATTATCTTGTC	55	0	—	502	2	*Citrus sinensis* pectinesterase mRNA, complete cds (5E-32)	cell wall modification
2937	F: TGAGCTGATTGCTAATGCGG R: GGACATGGTGGTCATTGAGG	58	0	—	622	2	*Solanum tuberosum* clone 154D06 fructose-bisphosphate aldolase-like mRNA, complete cds (5E-120)	glycolysis
2986	F: CTGTCTGTGACGGATCTAGC R: TGAGGATGGCTTACAACACG	57	0	—	355	1	*Populus trichocarpa* arogenate/prephenate dehydratase (PDT1), mRNA (1E-52)	L-phenylalanine biosynthetic process
3421	F: CTCATCTCTGCCAGAAAGAC R: GTAGAGCTTCATCTACGAGG	55	0	—	324	2	*Picea sitchensis* isolate CR201 phenylalanine ammonia lyase-like protein mRNA, partial cds (0.0)	phenylpropanoid metabolic process, biosynthetic process, L-phenylalanine catabolic process
3593	F: AGGACCTGAAATACCTTGCT R: TCCGTGTTTATCTCACAGGT	56	0	—	337	2	*Abies firma* chloroplast, partial genome (6E-170)	transport, respiratory electron transport chain, photosynthesis
3689	F: CGATTGCATCTCTGTACGCC R: GCTCTTGAGCCTCTTGACAC	58	0	—	619	2	*Pseudotsuga menziesii* var. *menziesii* haplotype Pm-TBE_412m2 thiazole biosynthetic enzyme (TBE) gene, complete cds (0.0)	thiamin biosynthetic process
3918	F: TTCCAAGGTCTTCTCAAGGT R: TGAAGAGTAGGAGTTTCGGT	55	0	—	400	2	*Pinus taeda* cellulose synthase catalytic subunit (CesA1) mRNA, complete cds (0.0)	cellulose biosynthetic process, cellular cell wall organization, secondary cell wall biogenesis, rhamnogalacturonan I side chain metabolic process
3942	F: GTATGATACCGATGTGACGA R: TTTGTAATGGATGCACTCGG	55	0	—	273	2	*Ricinus communis* proteasome subunit alpha type, putative, mRNA (8E-48)	ubiquitin-dependent protein catabolic process
3981	F: GGAGAAGTCTACAGTTCCAG R: ATAGTCCAGTGTCTTGAACTC	54	0	—	918	1	*Pinus radiata* UDP-glucose dehydrogenase gene, partial sequence (0.0)	oxidation reduction
4103	F: ATGGCCACCTTACTAAGAAGC R: CCACTTAAGGACCTTTACAGTCTC	57	0	—	841	1	*Pinus pinaster* mRNA for *S*-adenosylmethionine synthase 1 (sams1 gene) (0.0)	auxin biosynthetic process, one-carbon metabolic process
4492	F: TGGGTGCAACTGAAGATAGAG R: TTTCTACAACTAGCAAGCCTGAG	57	0	—	698	1	*Medicago truncatula* magnesium-chelatase subunit chlI (MTR_2g015390) mRNA, complete cds (4E-160)	auxin biosynthetic process, chlorophyll biosynthetic process, photosynthesis

TABLE 2. Continued.

Gene Locus ID	Primer sequences (5′–3′)	T_a (°C)	No. of introns	Intron length (nt)	Total length (nt)	Annotation approach	BLASTn of gene sequences against nr nucleotide database (*E*-value)	GO-ID biological process
4921	F: GAAGGTCGGCTATATCAGGT R: AGCTTAGACAGAGACTCAGG	56	0	—	664	2	PREDICTED: *Glycine max* proteasome subunit alpha type-4-like, transcript variant 1 (LOC100786457), mRNA (2E-147)	response to cadmium ion, ubiquitin-dependent protein catabolic process
5004	F: CAGATGTGAGCCATTACTTTGAC R: CAACCTCTGAATATAGCTGCCT	57	0	—	461	1	*Picea sitchensis* isolate VD401 magnesium chelatase H-like protein mRNA, partial cds (0)	chlorophyll biosynthetic process
5823	F: TGCTTGATATACGTCCTGGG R: CTAGACAGTGTTGCTCCACG	57	0	—	293	2	*Picea sitchensis* isolate VD401 phytochrome A-like protein mRNA, partial cds (0)	regulation of transcription, photomorphogenesis, tryptophan biosynthetic process
5945	F: CTGTCACTCAGATCTTCAGC R: AGATGATCAGCGAGATTCTC	55	0	—	339	2	*P. abies* (L.) Karst. Lhcb1*2-2 mRNA for light-harvesting chlorophyll a/b-binding protein (0.0)	photosynthesis, light harvesting, protein-chromophore linkage
6119	F: AGAGGATGTTGGGCATTATGG R: CATCACATGGTATCTCATCCGA	57	0	—	567	1	*Picea mariana* pyruvate dehydrogenase E1 beta subunit (Sb68) mRNA, partial cds (0.0)	pollen tube development, oxidation reduction
6594	F: TGGCTTTATCTTGGAGACTTCAC R: GAATAAGGTCATAGCCTGCCG	58	1	348	712	1	*Ricinus communis* phosphatidylinositol 4-kinase, putative, mRNA (5E-51)	phosphoinositide biosynthetic process, phosphoinositide phosphorylation, signal transduction, phosphoinositide-mediated signaling
6757	F: TATCATGCCCTGAAAGCGTC R: ACTTCCACAAGCAAGACACTC	58	5	177	939	1	*Arabidopsis thaliana* ribonucleoside-diphosphate reductase subunit M1 (RNR1) mRNA, complete cds (1E-39)	
7098	F: CTTTACTGTTGGAGGTAGATCAG R: GTTTGTTTGTCTTTGTACTCCC	55	0	—	782	1	*Arabidopsis thaliana* UDP-glucuronic acid decarboxylase (AUD1) mRNA, complete cds (1E-153)	dTDP-rhamnose biosynthetic process, D-xylose metabolic process
7208	F: GTTACATTCGTAAGTAGCTTGG R: AAATGGTCGAGAAGTCTACTG	54	0	—	326	1	*Pinus thunbergii* NADH dehydrogenase subunit 5 (nad5) gene, partial cds; mitochondrial (0)	transport, ATP synthesis coupled electron transport
7324	F: ATTGGAGATGGAGCCATGAC R: TCTCTGCATATGGGTAACCC	57	0	—	471	1	*Picea abies* 1-deoxy-D-xylulose 5-phosphate synthase type I (DXS1) mRNA, complete cds (0)	terpenoid biosynthetic process, thiamin biosynthetic process
8248	F: CAAGTATTCCGAAAGGCAGC R: ACAAAGGTGCCCACAATCTC	57	1	601	1128	2	*P. abies* mRNA for porin Mip1 (3E-154)	response to water deprivation, water transport, transmembrane transport, response to salt stress
8583	F: TCTCCTACATTGACGATCCC R: CCATCCAAGCACTTGAAGAG	56	0	—	393	2	*Picea sitchensis* isolate VA301 phenylalanine ammonia lyase-like protein mRNA, partial cds (5E-162)	phenylpropanoid metabolic process, biosynthetic process, L-phenylalanine catabolic process
8855	F: TATTTGCTGGTCGGGATTCG R: CTGCACTAGGTTCTCGAACG	58	2	275	926	2	*P. sylvestris* Lhca4*1-2 mRNA encoding Lhca4 protein (type 4 protein of light-harvesting complex of photosystem I) (partial) (7E-179)	photosynthesis, light harvesting
9366	F: AGTGAAAGCAACAACTTAGG R: TCTGGCTTCATTGATTTGTC	53	0	—	598	1	*Tamarix hispida* peroxiredoxin 2 (Prx2) mRNA, complete cds (5E-139)	cell redox homeostasis, oxidation reduction
9512	F: GTACTGGAGTAGCTGCACGA R: TACAAAGTGCTGCACAGCAG	59	1	99	415	2	*Cycas revoluta* class III HD-Zip protein HDZ32 gene, partial cds (4E-52)	regulation of transcription, DNA-dependent
9652	F: TGCAAAGAAAGTCAAGGCGA R: CCCATACGGTGTTAATGGCT	58	2	418	913	2	*Pinus pinaster* COBRA-like protein gene, partial cds (0)	
11301	F: GATGTTGTTCGTGCAAAGAC R: GCGAACTTAATTCCCTTCTC	54	0	—	490	2	*Pinus pinaster* mRNA for malate dehydrogenase (MDH gene) (0.0)	malate metabolic process, oxidation reduction, tricarboxylic acid cycle, glycolysis
13329	F: GATATGTGCCCAAGAACATTCTG R: CCTTGCATGCTTCAAGAAGG	57	0	—	350	1	PREDICTED: *Glycine max* probable rhamnose biosynthetic enzyme 1-like (LOC100789909), mRNA (7E-87)	
13536	F: CTGCTGATTCTGATCAGTCC R: TCCACAATGCAAACATAGGC	56	0	—	368	2	*Pinus thunbergii* PtANTL1 mRNA for AINTEGUMENTA-like protein, complete cds (0.0)	regulation of transcription, DNA-dependent

TABLE 2. Continued.

Gene Locus ID	Primer sequences (5′–3′)	T_a (°C)	No. of introns	Intron length (nt)	Total length (nt)	Annotation approach	BLASTn of gene sequences against nr nucleotide database (*E*-value)	GO-ID biological process
14455	F: GAACAAGATCGACTACTGCC R: TTTGATGGCCTTGAAAGCAG	56	0	—	834	2	*Pinus taeda* mRNA for alpha-1, 6-xylosyltransferase (x34.1 gene) (0.0)	root hair elongation, xyloglucan biosynthetic process
14479	F: CCACTCCCAAGTACTCAAAGG R: CAAGTGTGGCAATCCAACAC	57	0	—	588	1	*Picea abies* mRNA for translation elongation factor-1 alpha, partial (0.0)	translational elongation
14514	F: GGGTTCTGATTCTCCAAAGG R: CTGCATACTTGGCCAAAGTG	56	0	—	322	2	*Metasequoia glyptostroboides* fructose-1,6-diphosphate aldolase mRNA, complete cds (2E-74)	pentose-phosphate shunt, response to salt stress, glycolysis, response to cadmium ion
14585	F: TCTTGAATTCTTCCTATGTCCCAG R: AATTGCACATCTGCACAAACTC	57	1	193	915	1	PREDICTED: *Vitis vinifera* galacturonosyltransferase 8-like (LOC100258818), mRNA (6E-119)	homogalacturonan biosynthetic process
14887	F: GGTTAGACCAGTTCATAACC R: GTCTTCAAACTCTGACAAGG	53	0	—	1156	2	PREDICTED: *Glycine max* elongation factor 2-like (LOC100788357), mRNA (0.0)	
15135	F: TTGCAGGACTTCTTTAATGG R: TCTTCTTGTCAGATGGATCC	53	0	—	657	2	*Ricinus communis* heat shock protein, putative, mRNA (0.0)	oxidation reduction, response to stress, auxin biosynthetic process
15337	F: TTTATTGTATTCCTCCTAGGCCAG R: CACAATCTAAGCCACATTCTTCC	57	1	232	1086	1	*Picea glauca* isolate D8411049-162 cellulose synthase family protein gene, partial sequence (0.0)	cellulose biosynthetic process, cellular cell wall organization
15484	F: TTCGACGCCAACGTTATCTG R: GGCCCAGAGAATTGACATCC	58	0	—	663	2	*Pinus pinaster* phenylalanine ammonia-lyase (pal2) mRNA, complete cds (0.0)	phenylpropanoid metabolic process, biosynthetic process, L-phenylalanine catabolic process
15727	F: CACTGAAGGTTGTGGACGAG R: GTTCAGAAGGGCTGTGTAGG	58	0	—	325	2	*Pinus pinaster* mRNA for cytosolic serine hydroxymethyltransferase (cshmt gene) (2E-138)	L-serine metabolic process, one-carbon metabolic process, glycine metabolic process
15811	F: TTCGAGATCATCTGGACTGC R: CGACTGTTTCGACAGTGAGG	57	0	—	438	2	*Abies alba* genotype Lamacce 1 chalcone synthase (CHS) gene, CHS-A8 allele, complete cds (0)	biosynthetic process
15969	F: GGAAACCTTCTTGTTCACATCTG R: CTTGTCTGGAATCCTCCCTG	57	0	—	990	1	*Pinus contorta S*-adenosylmethionine synthetase (sams2) mRNA, complete cds (0.0)	auxin biosynthetic process, one-carbon metabolic process
16727	F: GGTGACTGTGAAGGCAATGG R: TCCCACATTTCTTTCCAGCT	58	0	—	331	2	*Populus* EST from severe drought-stressed opposite wood (0.000000003)	lipid transport
16816	F: CATCTTGGCTTCGTGATTGTC R: TGCAATTTGGCGTAATCGAC	57	3	132	562	2	*Pseudotsuga menziesii* class III homeodomain-leucine zipper (C3HDZ1) gene, complete cds (0)	
16883	F: CTCACAGAGGTCAGAAAGAATGG R: CTGCTTCAAAGGTTTGACAATCTC	58	0	—	710	1	*Pinus contorta S*-adenosylmethionine synthetase (sams2) mRNA, complete cds (0.0)	auxin biosynthetic process, one-carbon metabolic process
16979	F: CCTGGATAGTGAAATTGGAGG R: ATCCTTCTCTGAATGAGTTTCG	55	0	—	535	1	*Keteleeria davidiana* chloroplast DNA, complete sequence (0)	auxin biosynthetic process
17340	F: CTTGGTTAATTTCCGTCCTG R: CAGCTCCTACATTTAAACCC	54	0	—	281	2	*Abies firma* chloroplast, partial genome (0)	transport, photosynthesis, electron transport chain
17637	F: TGCTGAGAAAGTTGATTCTTCC R: GTATTCGAGGTGTAGATTGCTG	56	0	—	424	1	*Ricinus communis* transferase, transferring glycosyl groups, putative, mRNA (2E-69)	
17975	F: CAAACATTGCTGCAAAGCTC R: CCTATTCCAGCAACCAATATGTC	56	2	94	547	1	*Ricinus communis* cysteine synthase, putative, mRNA (1E-65)	cysteine biosynthetic process from serine
18135	F: GAGACTTTGGATTCGATCCC R: AGAAGGCCGCAAATATAGTG	55	1	132	683	2	*Picea abies* mRNA for putative chlorophyll A-B binding protein, (pPA0001 gene) (0)	photosynthesis, light harvesting in photosystem I
18444	F: ATTAATCTTTGCAGGGAAGC R: AGACGAGATGAAGTGTAGAC	54	0	—	313	2	*P. sylvestris* mRNA for polyubiquitin (3E-116)	
18599	F: GGAATGCATGATCCATTTCTG R: TACCTGAATTGTTCTTGCGA	55	0	—	678	1	*S. tuberosum* mRNA for NADH dehydrogenase, NADH-binding subunit (complex I) (0.0)	oxidation reduction
18680	F: CTGCGATGGATAAACTACCT R: GCTAGTGTTGCTATTGTGGG	55	1	214	465	2	*Picea glauca* isolate D761009-28 myb family protein gene, partial sequence (1E-140)	regulation of transcription

TABLE 2. Continued.

Gene Locus ID	Primer sequences (5′–3′)	T_a (°C)	No. of introns	Intron length (nt)	Total length (nt)	Annotation approach	BLASTn of gene sequences against nr nucleotide database (*E*-value)	GO-ID biological process
19005	F: GGAGATTGAGCAACGAAGAG R: TTTGAATCCCTGAAATCCTGG	56	0	—	368	1	*Abies firma* chloroplast, partial genome (0)	auxin biosynthetic process
19173	F: AGAACCAATCCCTGTTACAC R: GATCAGTTCCAATCACACCT	55	0	—	343	2	*Ricinus communis* proteasome subunit alpha type, putative, mRNA (2E-84)	defense response to bacterium, ubiquitin-dependent protein catabolic process, response to zinc ion
19540	F: ACCAATTCTCTTGTTCTCGG R: CGAACCATGTAAAGATCATTCC	55	0	—	634	1	*Cedrus deodara* chloroplast DNA, complete sequence (0)	plasma membrane ATP synthesis coupled proton transport, auxin biosynthetic process
20156	F: ATGGATCCCTGGAATTTATGC R: ATACTCTACCTACTACAGAATCCC	55	0	—	386	1	*Picea sitchensis* isolate VD401 magnesium chelatase H-like protein mRNA, partial cds (3E-110)	RNA processing, chlorophyll biosynthetic process
20318	F: ACAGCTCCCATTAATCTGAC R: CCAGAATTGTTCATTTCTCCAC	55	0	—	356	1	PREDICTED: *Glycine max* cellulose synthase-like protein D3-like (LOC100785985), mRNA (6E-69)	root hair elongation, cellulose biosynthetic process, response to cold, cellular cell wall organization, plant-type cell wall biogenesis
20694	F: GTCGAACAATGAAGACGAGG R: TGTGAGCGAAGAAACAAACC	56	0	—	346	1	PREDICTED: *Vitis vinifera* zinc finger CCCH domain-containing protein 49-like (LOC100259323), mRNA (6E-43)	cell wall modification, regulation of transcription
21136	F: AGACTGGTGTTACATTTGCGT R: CCAACAAGCTTCTCACTAATTTCC	57	1	229	535	1	*P. taeda* gene for protochlorophyllide reductase (3E-168)	oxidation reduction, chlorophyll biosynthetic process, photosynthesis
21165	F: ATGCACGATGTTCTTGATGC R: GGTGTCATGTTTATATGACAGTGG	57	2	204	644	1	PREDICTED: *Glycine max* premRNA-processing-splicing factor 8-like (LOC100804026), mRNA (4E-46)	response to hypoxia, sucrose biosynthetic process
21173	F: ACATTGTTGCTAACGATCCG R: AGACGAGGTAGAGATTGAGC	56	0	—	333	2	*Picea sitchensis* isolate VA100 basic endochitinase-like protein mRNA, partial cds (1E-138)	cell wall macromolecule catabolic process, chitin catabolic process
21890	F: GAAAGCTTACAGGGAAGCAG R: ACGATATCCAAGCATCATCC	55	1	358	607	2	*Picea sitchensis* isolate VD401 SWAP domain-containing protein-like protein mRNA, partial cds (2E-116)	RNA processing
21957	F: AACAACTTCACAGTTTCTCC R: GGAATCGGTAAATCAACGAC	54	0	—	292	2	*Abies firma* chloroplast, partial genome (2E-157)	auxin biosynthetic process, chlorophyll biosynthetic process, oxidation reduction, photosynthesis, dark reaction
22174	F: GATGATCCGGTTCGAATACC R: AAACGTAAGATACAAGTGGGTG	55	0	—	334	1	*Abies firma* chloroplast, partial genome (6E-157)	regulation of apoptosis, transcription, DNA-dependent
23660	F: AGGAAGATGTTAGGCTCGGG R: GAAGCCCTTCACAACTCCAG	58	1	781	1232	2	*P. abies* mRNA for porin Mip1 (6E-157)	response to water deprivation, water transport, transmembrane transport
23809	F: ATGCGCTCTATGTTAGAACG R: AATCTCAAGACGTTTACCGA	55	0	—	1058	2	*Abies firma* chloroplast, partial genome (9E-168)	oxidation reduction, chlorophyll biosynthetic process, photosynthesis, dark reaction
23850	F: GAAGATTTATTCGGCAACTG R: ATCTGATCCTCTGTTAAGGT	52	1	449	695	2	*Pinus taeda* mitogen-activated protein kinase 6 (MAPK6) mRNA, complete cds (4E-65)	auxin biosynthetic process, protein amino acid phosphorylation, conjugation, mitosis, cell division
23982	F: TGAGACTTGCTTGGGAAGAG R: AGCCCATTGTAAACGAAGGA	57	2	586	921	1	*Pisum sativum* nonphosphorylating glyceraldehyde-3-phosphate dehydrogenase (gapN) gene, complete cds (4E-33)	metabolic process
24523	F: TTCAGACTCGAACGTTTGCA R: AAGCTTTCATTCCCAGACGG	58	0	—	449	2	*Ginkgo biloba* catalase mRNA, complete cds (3E-98)	hydrogen peroxide catabolic process, oxidation reduction
24699	F: AAGATAAGCAGTTTGCTGCA R: AACATTCTTCTCGCCAACAG	56	0	—	262	2	*Ageratina adenophora* heat shock protein 70.58 mRNA, complete cds (2E-81)	auxin biosynthetic process, response to stress
24902	F: CCCTCTCAATCTTGAGGATGC R: CAGATGGACCTGTAATTTGAACCT	58	1	240	662	1	*Arabidopsis thaliana* ferredoxin–NADP+ reductase (RFNR2) mRNA, complete cds (3E-54)	electron transport chain
25060	F: CTGCAAGATACTTCAAAGATGCAC R: ATTTGGTGTAGAGAACATCTTCCC	58	2	163	624	1	PREDICTED: *Glycine max* ATP-citrate synthase beta chain protein 1-like (LOC100800904), mRNA (2E-74)	acetyl-CoA biosynthetic process, cellular carbohydrate metabolic process
26089	F: GATTATTGATTCTACCACCGGA R: TTTCTCAACAGCCTTGATGAC	55	1	281	1233	1	*Rosa multiflora* elongation factor 1-alpha mRNA, complete cds (0.0)	translational elongation

TABLE 2. Continued.

Gene Locus ID	Primer sequences (5′–3′)	T_a (°C)	No. of introns	Intron length (nt)	Total length (nt)	Annotation approach	BLASTn of gene sequences against nr nucleotide database (*E*-value)	GO-ID biological process
26764	F: GGGAATTGGCTCGTATCTGG R: GTTCTGCTTAGCAATCTTTGTCC	58	0	—	359	1	*Cucumis sativus* 6-phosphogluconate dehydrogenase (6PGDH) mRNA, complete cds (7E-55)	response to glucose stimulus, response to sucrose stimulus, response to fructose stimulus, response to salt stress, pentose-phosphate shunt, oxidation reduction, response to cadmium ion
27033	F: TTTACTCCACCATTACGAGG R: TTCGCAATGATAGGATTGCA	55	0	—	948	2	*Medicago truncatula* heat shock protein (MTR_7g024390) mRNA, complete cds (0)	response to virus, auxin biosynthetic process, protein folding, response to heat, response to bacterium, response to cadmium ion, response to high light intensity, response to hydrogen peroxide, protein amino acid phosphorylation
27963	F: TAGGCCCATAGCTAACAAACC R: TCGAATTGTTTCATCCTCCCA	57	0	—	318	1	*Keteleeria davidiana* chloroplast DNA, complete sequence (0)	transcription, DNA-dependent
28203	F: TGTGGACGAGGAGATATTCG R: TTCAGAAAGGGCTGTGTAGG	56	0	—	315	2	*Pinus pinaster* mRNA for cytosolic serine hydroxymethyltransferase (cshmt gene) (1E-128)	L-serine metabolic process, one-carbon metabolic process, glycine metabolic process
28456	F: GATTTCGAGAGCTGGTATCCC R: AGCTGTCGGTTGATGTTCTG	58	0	—	853	1	*Ricinus communis* oligosaccharyl transferase, putative, mRNA (7E-169)	protein amino acid glycosylation
28639	F: GTAGAATAAGTGGGAGCCGT R: ATAGGAAGAGCCGACATCGA	57	0	—	438	2	*Abies fabri* 26S ribosomal RNA gene, partial sequence (0)	
29437	F: CTTCAGGTGCTCGATATCGT R: TCAACTGGAAACGTTAGCTC	56	0	—	403	2	*Populus trichocarpa* argonaute protein group (AGO911), mRNA (2E-99)	

Note: — = not available; T_a = annealing temperature.

[a]Values are based on the sequence of one sample randomly chosen from a sample set of 80 trees from a population at Mont Ventoux (France).