

TABLE 1-continued

SEQ ID No.	Clone ID	NCBI gi	BLAST Method	Score	E value	% Ident	NCBI gi Description
3041	LIB3602-009-Q6-K1-F6	2828267	BLASTX	262	3.00E-23	75	(Y14044) geranylgeranyl reductase [<i>Arabidopsis thaliana</i>]
3042	LIB3602-102-Q1-K1-A1	7019693	BLASTX	304	7.00E-28	64	(AL138647) putative protein [<i>Arabidopsis thaliana</i>]
3043	LIB3602-016-Q6-K1-H4	6862921	BLASTX	170	9.00E-12	54	(AC018907) hypothetical protein [<i>Arabidopsis thaliana</i>]

Table 1 Legend

SEQ ID No.: Refers to the sequence identification number of nucleic acids listed in the Sequence Listing.

Clone ID: Refers to an assigned cDNA clone ID number.

NCBI gi: Refers to National Center for Biotechnology Information GenBank Identifier number which is the best match for a given nucleotide sequence.

Method: Refers to the method used in the sequence comparison of the designated nucleotide sequence with the designated GenBank sequence.

BLAST Score: Refers to the BLAST score that is generated by sequence comparison of the designated nucleotide sequence with the designated GenBank sequence using the method referenced in the "Method" column.

E value: The expected number of distinct segment pairs between two sequences with a score above the bit score for BLAST match.

% ident: Refers to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented.

NCBI gi Description: A description of the database entry referenced in the "NCBI gi" column.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20100005550A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1.-10. (canceled)

11. A transformed plant comprising a nucleic acid molecule which comprises:

- (a) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule; which is linked to;
- (b) a structural nucleic acid molecule, wherein said structural nucleic acid molecule comprises a nucleic acid sequence, wherein said nucleic acid sequence shares between 100% and 90% sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395, or the complement of SEQ ID NO: 1 through SEQ ID NO: 9395,

which is operably linked to

- (c) a 3' non-translated sequence that functions in said plant cell to cause the termination of transcription and the addition of polyadenylated ribonucleotides to said 3' end of said mRNA molecule.

12. The transformed plant according to claim **11**, wherein said nucleic acid sequence is the complement of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395.

13. The transformed plant according to claim **11**, wherein said nucleic acid sequence is in the antisense orientation of a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395.

14. The transformed plant according to claim **11**, wherein said nucleic acid sequence shares between 100% and 95% sequence identity with a nucleic acid sequence selected from

the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395 or the complement of SEQ ID NO: 1 through SEQ ID NO: 9395.

15. The transformed plant according to claim **14**, wherein said nucleic acid sequence shares between 100% and 98% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395 or the complement of SEQ ID NO: 1 through SEQ ID NO: 9395.

16. The transformed plant according to claim **15**, wherein said nucleic acid sequence shares between 100% and 99% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395 or the complement of SEQ ID NO: 1 through SEQ ID NO: 9395.

17. The transformed plant according to claim **16**, wherein said nucleic acid sequence shares 100% sequence identity with a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395 and the complement of SEQ ID NO: 1 through SEQ ID NO: 9395.

18. A transformed seed comprising a transformed plant cell comprising a nucleic acid molecule which comprises:

- (a) an exogenous promoter region which functions in said plant cell to cause the production of an mRNA molecule; which is linked to;
- (b) a structural nucleic acid molecule, wherein said structural nucleic acid molecule comprises a nucleic acid sequence, wherein said nucleic acid sequence shares between 100% and 90% sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 9395, or the complement of SEQ ID NO: 1 through SEQ ID NO: 9395,