

[0069] Alternatively, the nucleic acids of interest can be amplified from nucleic acid samples using amplification techniques. For instance, the disclosed nucleic acids may be used to define a pair of primers that can be used with the polymerase chain reaction (Mullis, et al., *Cold Spring Harbor Symp. Quant.* 51:263-273 (1986); Erlich et al., EP 50,424; EP 84,796, EP 258,017, EP 237,362; Mullis, EP 201,184; Mullis et al., U.S. Pat. No. 4,683,202; Erlich, U.S. Pat. No. 4,582,788; and Saiki, R. et al., U.S. Pat. No. 4,683,194) to amplify and obtain any desired nucleic acid or fragment directly from mRNA, from cDNA, from genomic libraries or cDNA libraries. PCR and other in vitro amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes.

[0070] In addition, two short segments of the nucleic acids of the present invention may be used in polymerase chain reaction protocols to amplify longer nucleic acids encoding *D. v. virgifera* protein homologues from DNA or RNA. For example, the skilled artisan can follow the RACE protocol (Frohman et al., Proc. Natl. Acad. Sci. USA 85:8998 (1988)) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Primers oriented in the 3' and 5' directions can be designed from the nucleic acids of the present invention. Using commercially available 3'RACE or 5'RACE systems (Gibco BRL, Life Technologies, Gaithersburg, Md. U.S.A.), specific 3' or 5' cDNA fragments can be isolated (Ohara et al., Proc. Natl. Acad. Sci. USA 86:5673 (1989); Loh et al., Science 243:217 (1989)). Products generated by the 3' and 5' RACE procedures can be combined to generate full-length cDNAs (Frohman and Martin, Techniques 1: 165 (1989)).

[0071] Nucleic acids of interest may also be synthesized, either completely or in part, especially where it is desirable to provide plant-preferred sequences, by well-known techniques as described in the technical literature. See, e.g., Caruthers et al., Cold Spring Harbor Symp. Quant. Biol. 47:411-418 (1982), and Adams et al., J. Am. Chem. Soc. 105:661 (1983). Thus, all or a portion of the nucleic acids of the present invention may be synthesized using codons preferred by a selected host. Species-preferred codons may be determined, for example, from the codons used most frequently in the proteins expressed in a particular host species. Other modifications of the nucleotide sequences may result in mutants having slightly altered activity.

[0072] Availability of the nucleotide sequences encoding *D. v. virgifera* proteins or fragments thereof facilitates immunological screening of cDNA expression libraries. Synthetic polypeptides representing portions of the amino acid sequences of *D. v. virgifera* proteins or fragments thereof may be synthesized. These polypeptides can be used to immunize animals to produce polyclonal or monoclonal antibodies with specificity for polypeptides or proteins comprising the amino acid sequences. These antibodies can be then be used to screen cDNA expression libraries to isolate full-length cDNA clones of interest (Lerner, Adv. Immunol. 36: 1 (1984); Sambrook et al., Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, (1989)). It is understood that people skilled in the art are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (see, for example,

Harlow and Lane, In *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1988)).

[0073] Another aspect of the present invention relates to a method for obtaining a nucleic acid comprising a nucleotide sequence encoding a *D. v. virgifera* protein homologue. In a preferred embodiment, the method of the present invention for obtaining a nucleic acid encoding all or a substantial portion of the amino acid sequence of a *D. v. virgifera* protein comprising: (a) probing a cDNA or genomic library with a hybridization probe comprising all or a portion of a nucleotide sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:9112; (b) identifying a DNA clone that hybridizes with the hybridization probe; (c) isolating the DNA clone identified in step (b); and (d) sequencing the cDNA or genomic fragment that comprises the clone isolated in step (c) wherein the sequenced nucleic acid molecule encodes all or a substantial portion of the amino acid sequence of the *D. v. virgifera* protein homologue.

[0074] In another preferred embodiment, the method of the present invention for obtaining a nucleic acid fragment encoding a substantial portion of the amino acid sequence of a *D. v. virgifera* protein homologue comprising: (a) synthesizing a first and a second oligonucleotide primers corresponding to a portion of one of the sequences set forth in SEQ ID NO:1 through SEQ ID NO: 9112; and (b) amplifying a cDNA insert present in a cloning vector using the first and second oligonucleotide primers of step (a) wherein the amplified nucleic acid molecule encodes all or a substantial portion of the amino acid sequence of the *D. v. virgifera* protein homologue.

[0075] (b) Protein and Peptide Molecules

[0076] A class of agents comprises one or more of the protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO:9112 or one or more of the protein or fragment thereof or peptide molecules encoded by other nucleic acid agents of the present invention. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment the protein or fragment molecules of the present invention are derived from *D. v. virgifera*.

[0077] The term "polypeptide", "peptide", or "protein", as used herein, refers to a polymer composed of amino acids connected by peptide bonds. The term applies to any amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to any naturally occurring amino acid polymers. The essential nature of such analogues of naturally occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally occurring amino acids. It is well known in the art that proteins or polypeptides may undergo modification, including but not limited to, disulfide bond formation, gamma-carboxylation of glutamic acid residues, glycosylation, lipid attachment, phosphorylation, oligomerization, hydroxylation and ADP-ribosylation. Exemplary modifications are described in most basic texts, such as, for example, *Proteins—Structure and Molecular Properties*, 2nd ed., T. E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as, for example, those provided by Wold, F., Post-translational Protein Modifications. Perspectives and Prospects, pp. 1-12 in *Post-translational Covalent Modification of Proteins*, B. C. Johnson, Ed.,