specifically excludes primer dimers that may be formed in the DNA thermal amplification reaction.

[0087] In certain embodiments, useful primer pairs will include one primer that overlaps with the junction point between the insert DNA and the flanking 5' or 3' genomic DNA. Such primers may be designed around the junction point between the 5' flanking DNA and the insert DNA (i.e., the junction between positions 1311 and 1312 of SEQ ID NO:1) as well as around the junction point between the insert DNA and the 3' flanking DNA (i.e., the junction between positions 6069 and 6070 of SEQ ID NO:1). Such primers may be designed to hybridize with about 10 nucleotides from either the flanking region or the insert DNA and with at least 1 nucleotide across the junction point in the insert DNA or the flanking region. Thus, for example, primers may comprise nucleotide sequences designed to hybridize with the nucleotides represented by at least the following positions of SEQ ID NO:1: 1311-1321, 1302-1312, 6060-6070, and/or 6069-6079.

[0088] In other embodiments, useful primer pairs will include one primer that overlaps with the junction point between the 5' end of the duplicated portion of the *csr1-2* coding sequence of the insert DNA (at position 5694 of SEQ ID NO:1) and the adjacent insert DNA (i.e., at position 5693 of SEQ ID NO:1). Such primers may be designed to hybridize with about 10 nucleotides from either the duplicated region or the adjacent insert DNA and with at least 1 nucleotide across the junction point (e.g., at least 5693-~~5603~~5703, or at least 5684-5694 of SEQ ID NO:1).

[0089] Methods for preparing and using probes and primers for use in the present invention are known in the art. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as the PCR primer analysis tool in Vector NTI version 6 (Informax Inc., Bethesda Md.); PrimerSelect (DNASTAR Inc., Madison, Wis.); and Primer (Version 0.5©, 1991, Whitehead Institute for Biomedical Research, Cambridge, Mass.). Additionally, the sequence can be visually scanned and primers manually identified using guidelines known to one of skill in the art.

[00125] As described above, in certain embodiments, useful primer pairs will include one primer that overlaps with the junction point between the insert DNA and the flanking 5' or 3' genomic DNA. Such primers may be designed around the junction point between the 5' flanking DNA and the insert DNA (i.e., the junction between positions 1311 and 1312 of SEQ ID NO:1) as well as around the junction point between the insert DNA and the 3' flanking DNA (i.e., the junction between positions 6069 and 6070 of SEQ ID NO:1). Such primers may be designed to hybridize with about 10 nucleotides from either the flanking region or the insert DNA and with at least 1 nucleotide across the junction point in the insert DNA or the flanking region. Thus, for example, primers may comprise nucleotide sequences designed to hybridize with the nucleotides represented by at least the following positions of SEQ ID NO:1: 1311-1321, 1302-1312, 6060-6070, and/or 6069-6079.

[00126] In other embodiments, useful primer pairs will include one primer that overlaps with the junction point between the 5' end of the duplicated portion of the *csr1-2* coding sequence of the insert DNA (at position 5694 of SEQ ID NO:1) and the 3' end of the adjacent insert DNA portion (i.e., at position 5693 of SEQ ID NO:1). Such primers may be designed to hybridize with about 10 nucleotides from either the duplicated region or the adjacent insert DNA and with at least 1 nucleotide across the junction point (e.g., at least 5693-~~5603~~5703, or at least 5684-5694 of SEQ ID NO:1).

[00127] As discussed elsewhere herein, any method to PCR amplify the event 127 nucleic acid molecule can be employed, including for example, real time PCR.

[00128] Thus, in some embodiments, a method of detecting the presence of event 127 nucleic acid molecules in a biological sample is provided. The method comprises (a) extracting a DNA sample from the biological sample; (b) providing a pair of DNA primer molecules (e.g., any combination of SEQ ID NOs:35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 67, 68, 69, and 70, where the combination amplifies a soybean event 127 region), including, but not limited to, i) the sequences of SEQ ID NO:35 and SEQ ID NO:36, ii) SEQ ID NO:37 and SEQ ID NO:38, iii) SEQ ID NO:39 and SEQ ID NO:40, iv) SEQ ID NO:41 and SEQ ID NO:42, v) SEQ ID

CLAIMS

What is claimed is:

1. A method for selective control of~~controlling~~ weeds in a cultivated area, comprising: applying an effective amount of an herbicidal composition comprising an AHAS-inhibiting imidazolinone herbicide to the cultivated soybean area having a soybean plant comprising a nucleic acid molecule that comprises a nucleic acid sequence of positions 1312-6069 of SEQ ID NO:1, wherein said nucleic acid sequence allows said soybean plant to be discriminately identified, and wherein the effective amount would inhibit the growth of weeds in the cultivated soybean area and of wild-type soybean plants.

2. The method of claim 1, wherein the nucleic acid molecule comprises a nucleic acid sequence of positions 1302-6079 of SEQ ID NO:1.

3. The method of claim 1, wherein the ~~event 127~~ nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO:1.

4. The method of claim 1, wherein the herbicidal composition further comprises one or more of other imidazolinone herbicides, other AHAS-inhibiting herbicides, EPSPS-inhibiting herbicides, GS-inhibiting herbicides, PPO-inhibiting herbicides, auxinic herbicides, and combinations thereof.~~the AHAS-inhibiting herbicide comprises an imidizolinone herbicide~~.

5. The method of claim 4, wherein the AHAS-inhibiting imidizolinone herbicide is selected from imazapyr, imazapic, or ~~any of the~~a combination~~s~~ thereof.

6. The method of claim 1 further comprising applying, to the cultivated soybean area, an effective amount of one or more of other imidazolinone ~~an~~ herbicides, other AHAS-ihibiting herbicides, ~~selected from the group consisting of~~ EPSPS-inhibiting herbicides, GS-inhibiting herbicides, PPO-inhibiting herbicides, auxinic herbicides, and combinations thereof.

7. The method of any one of claims 4 or 6, wherein the EPSPS-inhibiting herbicide comprises glyphosate and the PPO-inhibiting herbicide comprises saflufenacil.

~~7~~8. The method of claim 1, wherein the weeds are resistant to glyphosate.

9. The method of claim 1, wherein the method further comprises applying a strobilurin to the cultivated soybean area.

10. The method of claim 9, wherein strobilurin comprises pyraclostrobin.

11. The method of claim 1, wherein the herbicidal composition comprises

imazapyr;

imazapic;

or any one of the following:

a combination of imazapyr and imazapic;

a combination of imazapyr, imazapic, and bentazon;

a combination of imazapyr, imazapic, and pyraclostrobin;

a combination of imazapyr, imazapic, and saflufenacil;

a combination of imazapyr, imazapic, saflufenacil, and glyphosate;

a combination of imazapyr and bentazon;

a combination of imazapyr and pyraclostrobin;

a combination of imazapyr and saflufenacil;

a combination of imazapyr, saflufenacil, and glyphosate;

a combination of imazapyr and glyphosate;

a combination of imazapic and glyphosate; and

a combination of imazapic, saflufenacil, and glyphosate.

128. A method for selective controlling of glyphosate tolerant weeds in a soybean crop field, comprising:

applying an effective amount of an herbicidal composition comprising an AHAS-inhibiting imidazolinone herbicide to the soybean crop field having a soybean plant comprising a nucleic acid molecule that comprises a nucleic acid sequence of positions 1312-6069 of SEQ ID NO:1, and glyphosate tolerant weeds, wherein said nucleic acid sequence allows said soybean plant to be discriminately identified, and wherein the effective amount would inhibit the growth of glyphosate tolerant weeds in the soybean crop filed and of wild-type soybean plants.

139. The method of claim 128, wherein the soybean plant comprises a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO:1.

14~~0~~. The method of claim 12~~8~~, wherein the nucleic acid molecule comprises a nucleic acid sequence of positions 1302-6079 of SEQ ID NO:1.

15~~1~~. The method of claim 12~~8~~, wherein the AHAS-inhibiting imidazolinone herbicide is selected from imazapyr, ~~or~~ imazapic, or a combination thereof.

16. The method of claim 12, wherein the method further comprises applying a strobilurin to the soybean crop field.

17~~2~~. An isolated or recombinant nucleic acid molecule encoding a modified form of AHASL protein, comprising a serine to asparagine substitution at a position 653 (S653N) and comprising the nucleic acid sequence of positions 1312 to 6069 of SEQ ID NO:1, wherein the nucleic acid sequence allows the nucleic acid molecule to be discriminately identified.

18~~3~~. The isolated or recombinant nucleic acid molecule of claim 17~~2~~, wherein the nucleic acid molecule is in a recombinant nucleic acid construct.

19~~4~~. A transgenic soybean plant comprising the isolated or recombinant nucleic acid molecule of claim 17~~2~~.

20~~15~~. A transgenic soybean plant comprising a heterologous nucleic acid molecule comprising the nucleic acid sequence of nucleotides 1302 to 6079 of SEQ ID NO:1, wherein the nucleic acid sequence allows the nucleic acid molecule to be discriminately identified.

21~~16~~. The transgenic soybean plant of claim 20~~13~~, wherein the soybean plant is resistant to an AHAS-inhibiting herbicide.

22~~17~~. An isolated pair of nucleic acid primers for use in the amplification of a target nucleic acid molecule comprising:

a first and a second isolated nucleic acid molecule, wherein the first isolated nucleic acid molecule comprises a nucleic acid sequence selected from SEQ ID NOs:37, 39, 41, 43, and 67 and the second isolated nucleic acid molecule comprises a nucleic acid sequence selected from SEQ ID NOs:38, 40, 42, 44, and 68.

2318. The isolated pair of nucleic acid primers of claim 2217, wherein the first isolated nucleic acid molecule comprises the sequence of SEQ ID NO:41, and the second isolated nucleic acid molecule comprises the sequence of SEQ ID NO:42.

2419. A method for identifyingdetecting the presence of a soybean plant comprising a nucleic acid molecule comprising the nucleic acid sequence of positions 1312 to 6069 of SEQ ID NO:1 in a biological sample, comprising:

(a) forming a mixture comprising a biological sample containing soybean DNA and a first and second nucleic acid primer, wherein the first nucleic acid primer comprises a nucleic acid sequence selected from SEQ ID NOs:37, 39, 41, 43, and 67 and the second nucleic acid primer comprises a nucleic acid sequence selected from SEQ ID NOs:38, 40, 42, 44, and 68;

(b) reacting the mixture under conditions that allow the first and second nucleic acid primers to amplify a nucleic acid molecule; and

(c) detecting the presence or absence of the amplified nucleic acid molecule, wherein the presence of the amplified nucleic acid molecule allows the nucleic acid molecule to be discriminately identified and indicates that the biological sample comprises the soybean plant comprisinges a nucleic acid molecule comprising the nucleic acid sequence of positions 1312 to 6069 of SEQ ID NO:1.

~~20. A method for increasing yield in a soybean plant, the method comprising:~~

~~applying an effective amount of an AHAS-inhibiting herbicide to one or more soybean plants comprising a nucleic acid molecule that comprises a nucleic acid sequence from positions 1312-6069 of SEQ ID NO:1 and the surrounding area, wherein the AHAS-inhibiting herbicide reduces weed growth in the surrounding area; and~~

~~harvesting seed from the one or more soybean plants.~~

25~~1~~. A method for breeding an AHAS-inhibiting-imidazolinone-herbicide-resistant soybean plant, comprising:

(a) crossing a soybean plant comprising a nucleic acid molecule that comprises a nucleic acid sequence from positions 1312-6069 of SEQ ID NO:1 with a second soybean plant;

(b) obtaining seed from the cross of step (a);

(c) obtaining a DNA sample from the seed; and

(d) detecting the presence of a nucleic acid molecule that comprises a nucleic acid sequence from positions 1312-6069 of SEQ ID NO:1 in the sample, where the presence of the nucleic acid molecule that comprises a nucleic acid sequence from positions 1312-6069 of SEQ ID NO:1indicates that the seed is capable of producing an AHAS-inhibiting-imidazolinone-herbicide-resistant soybean plant, and wherein said nucleic acid sequence allows said soybean plant to be discriminately identified.

26~~2~~. A seed of a transgenic soybean plant comprising a nucleic acid molecule encoding a modified form of an AHASL protein, comprising a serine to asparagine substitution at a position 653 (S653N) and comprising ~~that~~ and comprisinges a nucleic acid sequence of~~from~~ positions 1312-6069 of SEQ ID NO:1, wherein said nucleic acid sequence allows said soybean plant to be discriminately identified~~-~~.

27~~3~~. The seed of claim 26~~2~~, wherein the nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO:1.

28~~4~~. The seed of claim 26~~3~~, wherein the seed is of a plant of, or is of a plant that is a progeny of, line 'BPS-CV127-9', a representative sample of said seed of said line ~~was~~ having been deposited under NCIMB Accession No. 41603.

29. The seed of claim 26, wherein the seed is treated with an herbicidal composition comprising one or more of an AHAS-inhibiting herbicide or a combination of AHAS-inhibiting herbicides.

30. A method for selective control of weeds in a cultivated soybean area, comprising:

planting the seed of claim 29 in the cultivated soybean area.

31~~25~~. A transgenic soybean plant~~, or part thereof,~~ produced by growing the seed of claim 26~~2~~.